
nipype Documentation

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Neuroimaging in Python team

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Michael Notter's Nipype guide

Be sure to read [Michael's excellent tutorials](#).

Interfaces, Workflows and Examples

- [Workflows](#)

1.1 `get_flirt_schedule()`

[Link to code](#)

2.1 workflows.dmri.camino.connectivity_mapping

2.1.1 create_connectivity_pipeline()

[Link to code](#)

Creates a pipeline that does the same connectivity processing as in the *dmri: Connectivity - Camino, CMTK, FreeSurfer* example script. Given a subject id (and completed Freesurfer reconstruction) diffusion-weighted image, b-values, and b-vectors, the workflow will return the subject's connectome as a Connectome File Format (CFF) file for use in Connectome Viewer (<http://www.cmtk.org>).

Example

```
>>> from nipy.workflow.dmri.camino.connectivity_mapping import create_
    ↪connectivity_pipeline
>>> conmapper = create_connectivity_pipeline("nipy_conmap")
>>> conmapper.inputs.inputnode.subjects_dir = '.'
>>> conmapper.inputs.inputnode.subject_id = 'subj1'
>>> conmapper.inputs.inputnode.dwi = 'data.nii.gz'
>>> conmapper.inputs.inputnode.bvecs = 'bvecs'
>>> conmapper.inputs.inputnode.bvals = 'bvals'
>>> conmapper.run() # doctest: +SKIP
```

Inputs:

```
inputnode.subject_id
inputnode.subjects_dir
inputnode.dwi
inputnode.bvecs
inputnode.bvals
inputnode.resolution_network_file
```

Outputs:

```
outputnode.connectome
outputnode.cmatrix
outputnode.gpickled_network
```

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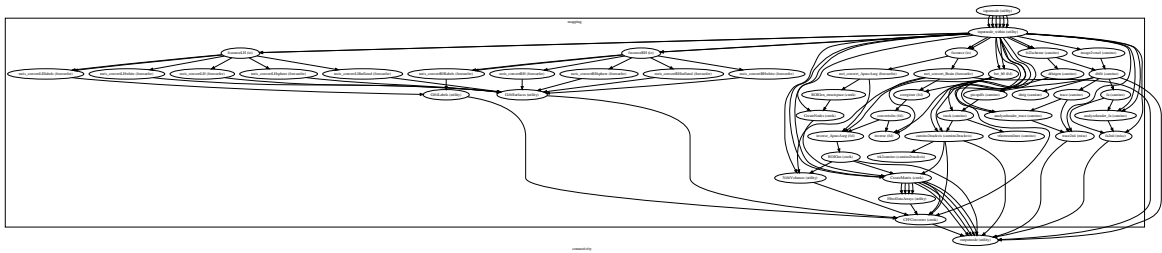
(continued from previous page)

```

outputnode.fa
outputnode.struct
outputnode.trace
outputnode.tracts
outputnode.tensors

```

Graph



2.2 workflows.dmri.camino.diffusion

2.2.1 create_camino_dti_pipeline()

[Link to code](#)

Creates a pipeline that does the same diffusion processing as in the `../users/examples/dmri_camino_dti` example script. Given a diffusion-weighted image, b-values, and b-vectors, the workflow will return the tractography computed from diffusion tensors and from PICO probabilistic tractography.

Example

```

>>> import os
>>> nipyype_camino_dti = create_camino_dti_pipeline("nipyype_camino_dti")
>>> nipyype_camino_dti.inputs.inputnode.dwi = os.path.abspath('dwi.nii')
>>> nipyype_camino_dti.inputs.inputnode.bvecs = os.path.abspath('bvecs')
>>> nipyype_camino_dti.inputs.inputnode.bvals = os.path.abspath('bvals')
>>> nipyype_camino_dti.run() # doctest: +SKIP

```

Inputs:

```

inputnode.dwi
inputnode.bvecs
inputnode.bvals

```

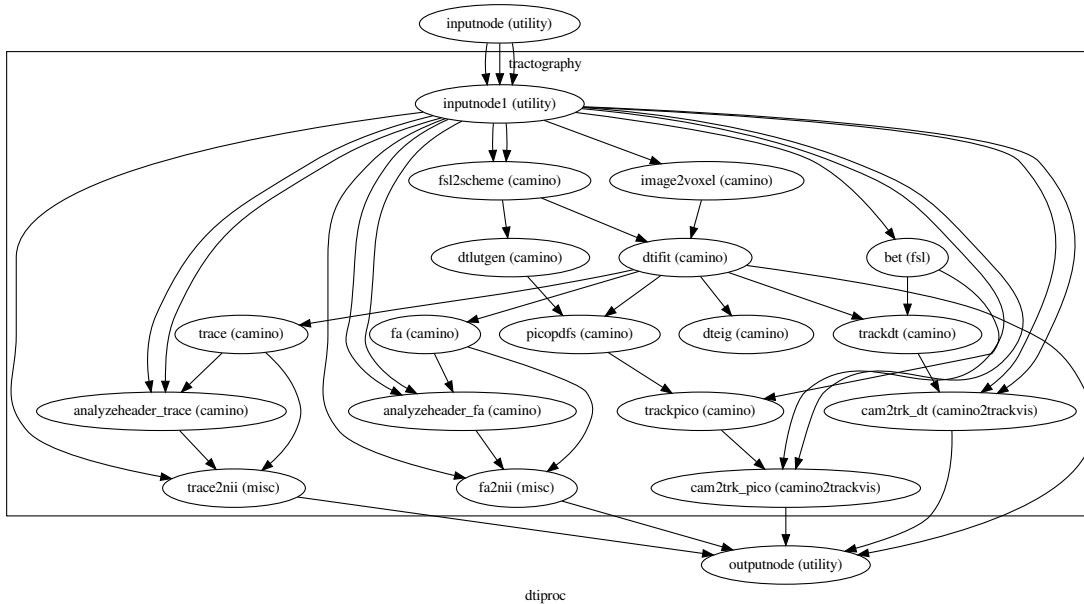
Outputs:

```

outputnode.fa
outputnode.trace
outputnode.tracts_pico
outputnode.tracts_dt
outputnode.tensors

```

Graph



2.3 workflows.dmri.camino.group_connectivity

2.3.1 create_group_connectivity_pipeline()

[Link to code](#)

Creates a pipeline that performs basic Camino structural connectivity processing on groups of subjects. Given a diffusion-weighted image, and text files containing the associated b-values and b-vectors, the workflow will return each subjects' connectomes in a Connectome File Format (CFF) file, for use in Connectome Viewer (<http://www.cmtk.org>).

Example

```
>>> import nipype.interfaces.freesurfer as fs
>>> import nipype.workflows.dmri.camino.group_connectivity as groupwork
>>> subjects_dir = '.'
>>> data_dir = '.'
>>> output_dir = '.'
>>> fs.FSCommand.set_default_subjects_dir(subjects_dir)
>>> group_list = {}
>>> group_list['group1'] = ['subj1', 'subj2']
>>> group_list['group2'] = ['subj3', 'subj4']
>>> template_args = dict(dwi=[['subject_id', 'dwi']], bvecs=[['subject_id', 'bvecs
↪']], bvals=[['subject_id', 'bvals']])
>>> group_id = 'group1'
>>> l1pipeline = groupwork.create_group_connectivity_pipeline(group_list, group_
↪id, data_dir, subjects_dir, output_dir, template_args)
>>> l1pipeline.run() # doctest: +SKIP
```

Inputs:

```
group_list: Dictionary of subject lists, keyed by group name
group_id: String containing the group name
data_dir: Path to the data directory
subjects_dir: Path to the Freesurfer 'subjects' directory
output_dir: Path for the output files
template_args_dict: Dictionary of template arguments for the connectivity_
↳ pipeline datasource
e.g.      info = dict(dwi=[['subject_id', 'dwi']],
                      bvecs=[['subject_id', 'bvecs']],
                      bvals=[['subject_id', 'bvals']])
```

2.4 workflows.dmri.connectivity.group_connectivity

2.4.1 concatcsv()

[Link to code](#)

This function will concatenate two “comma-separated value” text files, but remove the first row (usually column headers) from all but the first file.

2.4.2 create_average_networks_by_group_workflow()

[Link to code](#)

Creates a fourth-level pipeline to average the networks for two groups and merge them into a single CFF file. This pipeline will also output the average networks in .gexf format, for visualization in other graph viewers, such as Gephi.

Example

```
>>> import nipyne.workflows.dmri.connectivity.group_connectivity as groupwork
>>> from nipyne.testing import example_data
>>> subjects_dir = '.'
>>> data_dir = '.'
>>> output_dir = '.'
>>> group_list = {}
>>> group_list['group1'] = ['subj1', 'subj2']
>>> group_list['group2'] = ['subj3', 'subj4']
>>> l4pipeline = groupwork.create_average_networks_by_group_workflow(group_list,
↳ data_dir, subjects_dir, output_dir)
>>> l4pipeline.run() # doctest: +SKIP
```

Inputs:

```
group_list: Dictionary of subject lists, keyed by group name
data_dir: Path to the data directory
subjects_dir: Path to the Freesurfer 'subjects' directory
output_dir: Path for the output files
title: String to use as a title for the output merged CFF file (default 'group')
```

2.4.3 create_merge_group_network_results_workflow()

[Link to code](#)

Creates a third-level pipeline to merge the Connectome File Format (CFF) outputs from each group and combines them into a single CFF file for each group. This version of the third-level pipeline also concatenates the comma-separated value files for the NetworkX metrics and the connectivity matrices into single files.

Example

```
>>> import nipype.workflows.dmri.connectivity.group_connectivity as groupwork
>>> from nipype.testing import example_data
>>> subjects_dir = '.'
>>> data_dir = '.'
>>> output_dir = '.'
>>> group_list = {}
>>> group_list['group1'] = ['subj1', 'subj2']
>>> group_list['group2'] = ['subj3', 'subj4']
>>> l3pipeline = groupwork.create_merge_group_network_results_workflow(group_list,
↳ data_dir, subjects_dir, output_dir)
>>> l3pipeline.run()                                # doctest: +SKIP
```

Inputs:

```
group_list: Dictionary of subject lists, keyed by group name
data_dir: Path to the data directory
subjects_dir: Path to the Freesurfer 'subjects' directory
output_dir: Path for the output files
title: String to use as a title for the output merged CFF file (default 'group')
```

2.4.4 create_merge_group_networks_workflow()

[Link to code](#)

Creates a third-level pipeline to merge the Connectome File Format (CFF) outputs from each group and combines them into a single CFF file for each group.

Example

```
>>> import nipype.workflows.dmri.connectivity.group_connectivity as groupwork
>>> from nipype.testing import example_data
>>> subjects_dir = '.'
>>> data_dir = '.'
>>> output_dir = '.'
>>> group_list = {}
>>> group_list['group1'] = ['subj1', 'subj2']
>>> group_list['group2'] = ['subj3', 'subj4']
>>> l3pipeline = groupwork.create_merge_group_networks_workflow(group_list, data_
↳ dir, subjects_dir, output_dir)
>>> l3pipeline.run()                                # doctest: +SKIP
```

Inputs:

```
group_list: Dictionary of subject lists, keyed by group name
data_dir: Path to the data directory
subjects_dir: Path to the Freesurfer 'subjects' directory
output_dir: Path for the output files
title: String to use as a title for the output merged CFF file (default 'group')
```

2.4.5 create_merge_network_results_by_group_workflow()

[Link to code](#)

Creates a second-level pipeline to merge the Connectome File Format (CFF) outputs from the group-level MR-trix structural connectivity processing pipeline into a single CFF file for each group.

Example

```
>>> import nipype.workflows.dmri.connectivity.group_connectivity as groupwork
>>> from nipype.testing import example_data
>>> subjects_dir = '.'
>>> data_dir = '.'
>>> output_dir = '.'
>>> group_list = {}
>>> group_list['group1'] = ['subj1', 'subj2']
>>> group_list['group2'] = ['subj3', 'subj4']
>>> group_id = 'group1'
>>> l2pipeline = groupwork.create_merge_network_results_by_group_workflow(group_
↳ list, group_id, data_dir, subjects_dir, output_dir)
>>> l2pipeline.run()                                # doctest: +SKIP
```

Inputs:

```
group_list: Dictionary of subject lists, keyed by group name
group_id: String containing the group name
data_dir: Path to the data directory
subjects_dir: Path to the Freesurfer 'subjects' directory
output_dir: Path for the output files
```

2.4.6 create_merge_networks_by_group_workflow()

[Link to code](#)

Creates a second-level pipeline to merge the Connectome File Format (CFF) outputs from the group-level MR-trix structural connectivity processing pipeline into a single CFF file for each group.

Example

```
>>> import nipype.workflows.dmri.connectivity.group_connectivity as groupwork
>>> from nipype.testing import example_data
>>> subjects_dir = '.'
>>> data_dir = '.'
>>> output_dir = '.'
>>> group_list = {}
>>> group_list['group1'] = ['subj1', 'subj2']
>>> group_list['group2'] = ['subj3', 'subj4']
>>> group_id = 'group1'
>>> l2pipeline = groupwork.create_merge_networks_by_group_workflow(group_list,
↳ group_id, data_dir, subjects_dir, output_dir)
>>> l2pipeline.run()                                # doctest: +SKIP
```

Inputs:

```
group_list: Dictionary of subject lists, keyed by group name
group_id: String containing the group name
data_dir: Path to the data directory
subjects_dir: Path to the Freesurfer 'subjects' directory
output_dir: Path for the output files
```

2.4.7 pullnodeIDs ()

[Link to code](#)

This function will return the values contained, for each node in a network, given an input key. By default it will return the node names

2.5 workflows.dmri.connectivity.nx

2.5.1 create_cmats_to_csv_pipeline()

[Link to code](#)

Creates a workflow to convert the outputs from CreateMatrix into a single comma-separated value text file. An extra column / field is also added to the text file. Typically, the user would connect the subject name to this field.

Example

```
>>> from nipyype.workflows.dmri.connectivity.nx import create_cmats_to_csv_pipeline
>>> csv = create_cmats_to_csv_pipeline("cmats_to_csv", "subject_id")
>>> csv.inputs.inputnode.extra_field = 'subj1'
>>> csv.inputs.inputnode.matlab_matrix_files = ['subj1_cmatrix.mat', 'subj1_mean_
↪ fiber_length.mat', 'subj1_median_fiber_length.mat', 'subj1_fiber_length_std.mat
↪']
>>> csv.run() # doctest: +SKIP
```

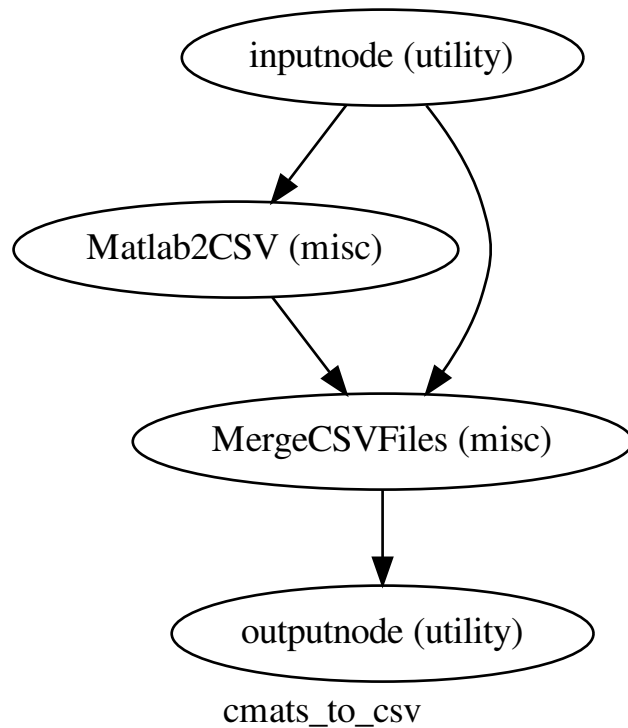
Inputs:

```
inputnode.extra_field
inputnode.matlab_matrix_files
```

Outputs:

```
outputnode.csv_file
```

Graph



2.5.2 create_networkx_pipeline()

[Link to code](#)

Creates a workflow to calculate various graph measures (via NetworkX) on an input network. The output measures are then converted to comma-separated value text files, and an extra column / field is also added. Typically, the user would connect the subject name to this field.

Example

```

>>> from nipy.workflows.dmri.connectivity.nx import create_networkx_pipeline
>>> nx = create_networkx_pipeline("networkx", "subject_id")
>>> nx.inputs.inputnode.extra_field = 'subj1'
>>> nx.inputs.inputnode.network_file = 'subj1.pck'
>>> nx.run()                                # doctest: +SKIP

```

Inputs:

```

inputnode.extra_field
inputnode.network_file

```

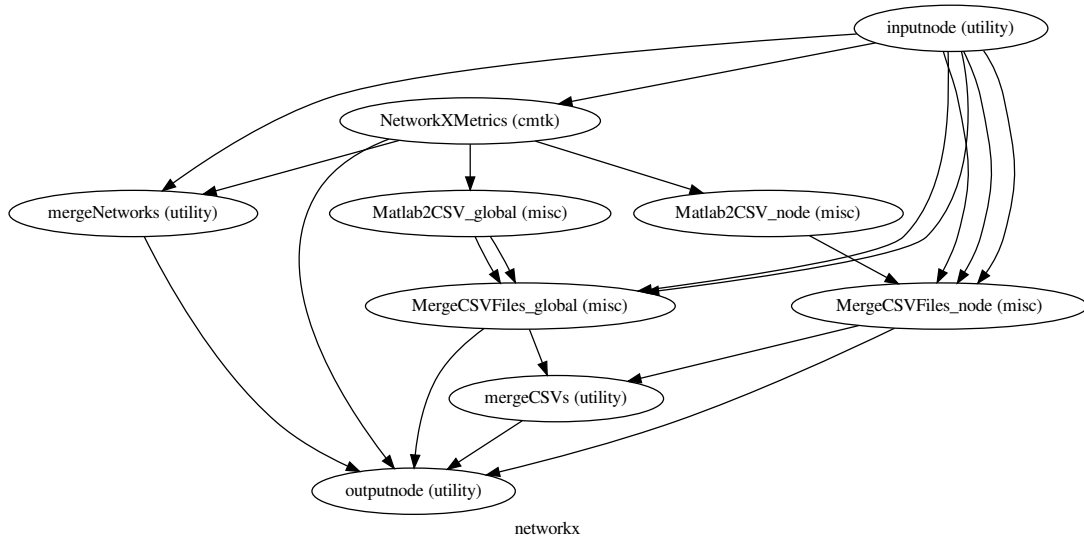
Outputs:

```

outputnode.network_files
outputnode.csv_files
outputnode.matlab_files

```

Graph



2.5.3 add_global_to_filename()

[Link to code](#)

2.5.4 add_nodal_to_filename()

[Link to code](#)

2.6 workflows.dmri.dipy.denoise

2.6.1 nlmeans_pipeline()

[Link to code](#)

Workflow that performs nlmeans denoising

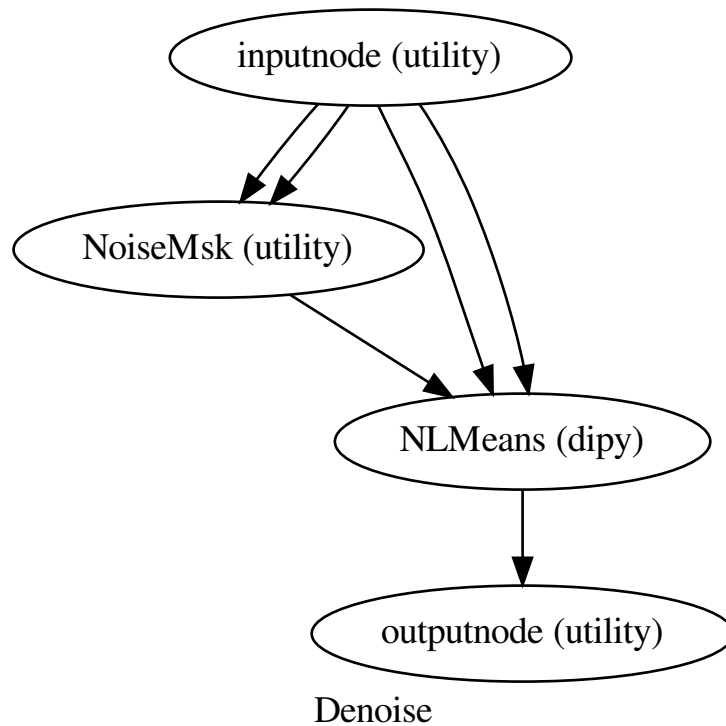
Example

```

>>> from nipy.workflows.dmri.dipy.denoise import nlmeans_pipeline
>>> denoise = nlmeans_pipeline()
>>> denoise.inputs.inputnode.in_file = 'diffusion.nii'
>>> denoise.inputs.inputnode.in_mask = 'mask.nii'
>>> denoise.run() # doctest: +SKIP

```

Graph



2.6.2 `bg_mask()`

[Link to code](#)

Rough mask of background from brain masks

2.6.3 `csf_mask()`

[Link to code](#)

Artesanal mask of csf in T2w-like images

2.7 `workflows.dmri.dtitk.tensor_registration`

2.7.1 `affine_tensor_pipeline()`

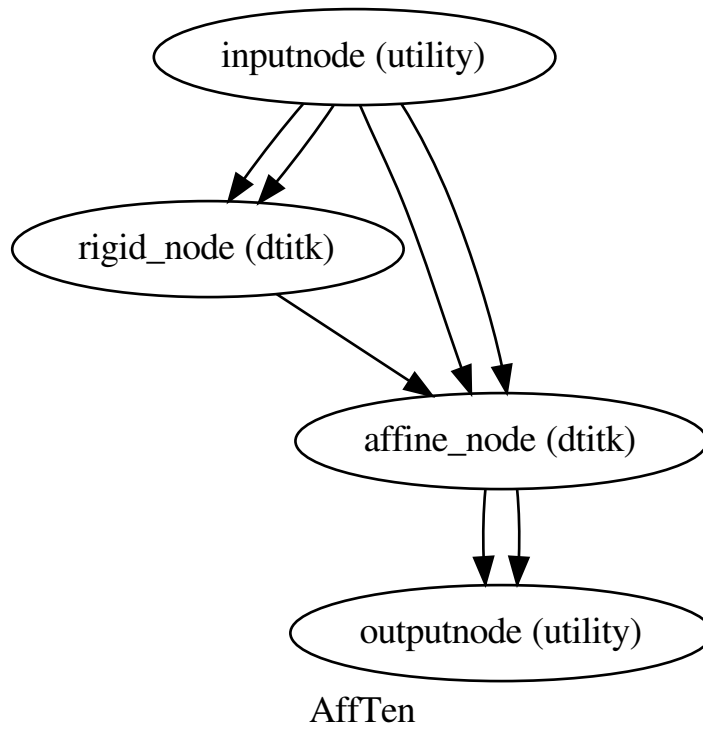
[Link to code](#)

Workflow that performs a linear registration (Rigid followed by Affine)

Example

```
>>> from nipy.workflows.dmri.dtitk.tensor_registration import affine_tensor_
    ↳ pipeline
>>> affine = affine_tensor_pipeline()
>>> affine.inputs.inputnode.fixed_file = 'im1.nii'
>>> affine.inputs.inputnode.moving_file = 'im2.nii'
>>> affine.run() # doctest: +SKIP
```

Graph



2.7.2 diffeomorphic_tensor_pipeline()

[Link to code](#)

Workflow that performs a diffeomorphic registration (Rigid and Affine followed by Diffeomorphic) Note: the requirements for a diffeomorphic registration specify that the dimension 0 is a power of 2 so images are resliced prior to registration. Remember to move origin and reslice prior to applying xfm to another file!

Example

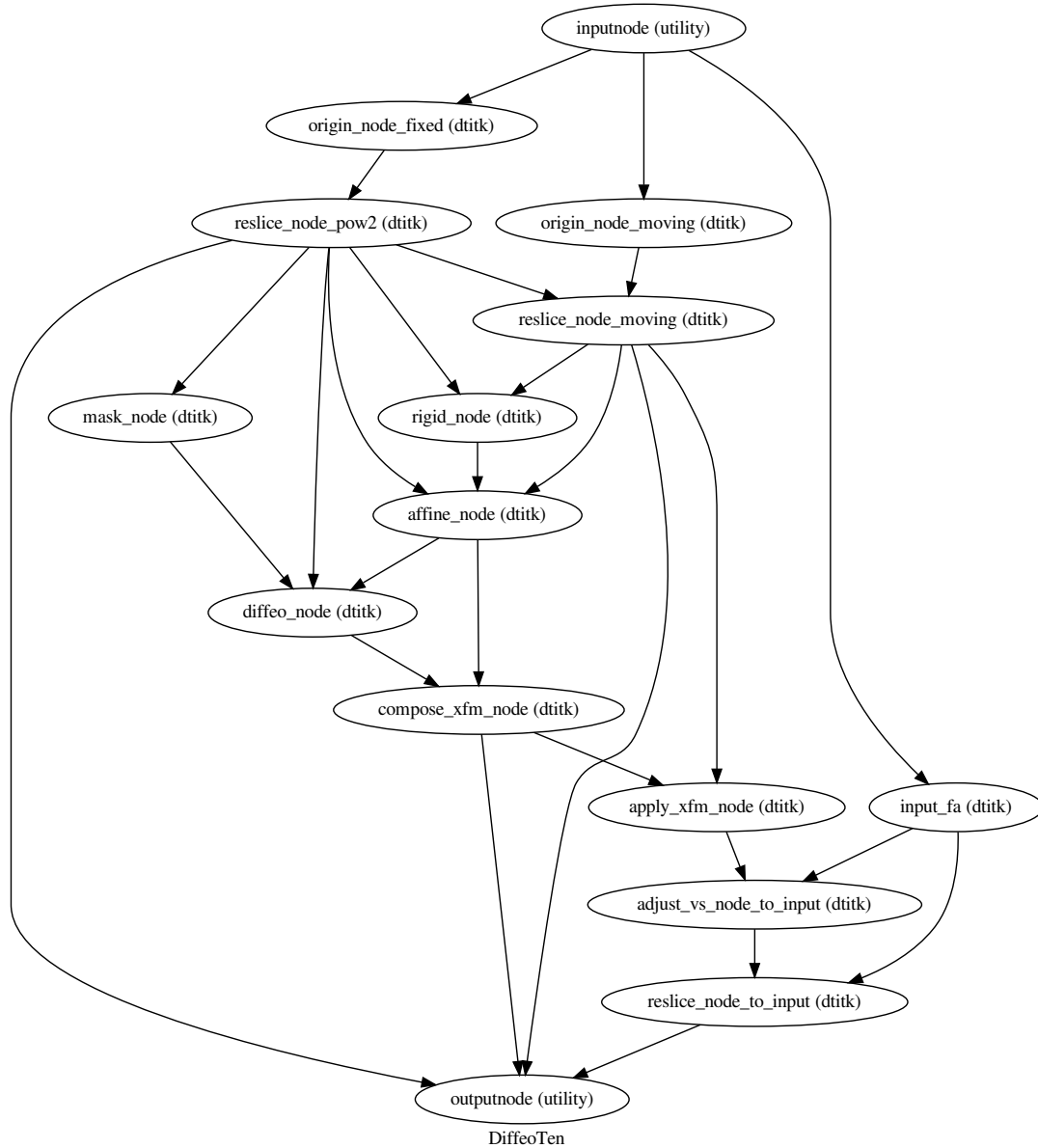
```
>>> from nipy.workflows.dmri.dtitk.tensor_registration import diffeomorphic_
    ↳ tensor_pipeline
>>> diffeo = diffeomorphic_tensor_pipeline()
>>> diffeo.inputs.inputnode.fixed_file = 'im1.nii'
```

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```
>>> diffeo.inputs.inputnode.moving_file = 'im2.nii'
>>> diffeo.run() # doctest: +SKIP
```

Graph



2.8 workflows.dmri.fsl.artifacts

2.8.1 all_fmb_pipeline()

[Link to code](#)

Builds a pipeline including three artifact corrections: head-motion correction (HMC), susceptibility-derived distortion correction (SDC), and Eddy currents-derived distortion correction (ECC).

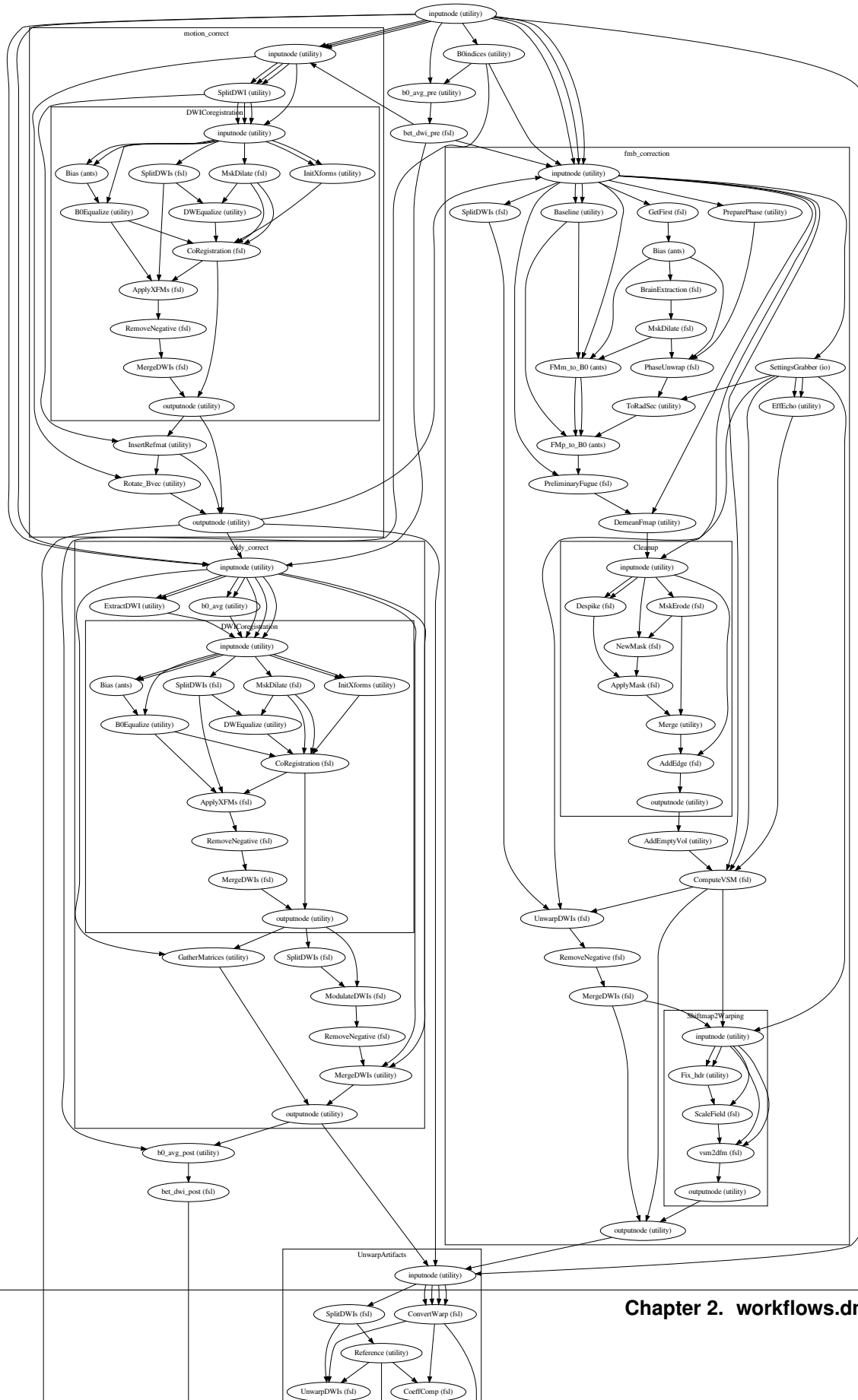
The displacement fields from each kind of distortions are combined. Thus, only one interpolation occurs between input data and result.

Warning: this workflow rotates the gradients table (*b*-vectors) [Leemans09].

Examples

```
>>> from nipyne.workflows.dmri.fsl.artifacts import all_fmb_pipeline
>>> allcorr = all_fmb_pipeline()
>>> allcorr.inputs.inputnode.in_file = 'epi.nii'
>>> allcorr.inputs.inputnode.in_bval = 'diffusion.bval'
>>> allcorr.inputs.inputnode.in_bvec = 'diffusion.bvec'
>>> allcorr.inputs.inputnode.bmap_mag = 'magnitude.nii'
>>> allcorr.inputs.inputnode.bmap pha = 'phase.nii'
>>> allcorr.inputs.inputnode.epi_param = 'epi_param.txt'
>>> allcorr.run() # doctest: +SKIP
```

Graph



2.8.2 all_fsl_pipeline()

[Link to code](#)

Workflow that integrates FSL `topup` and `eddy`.

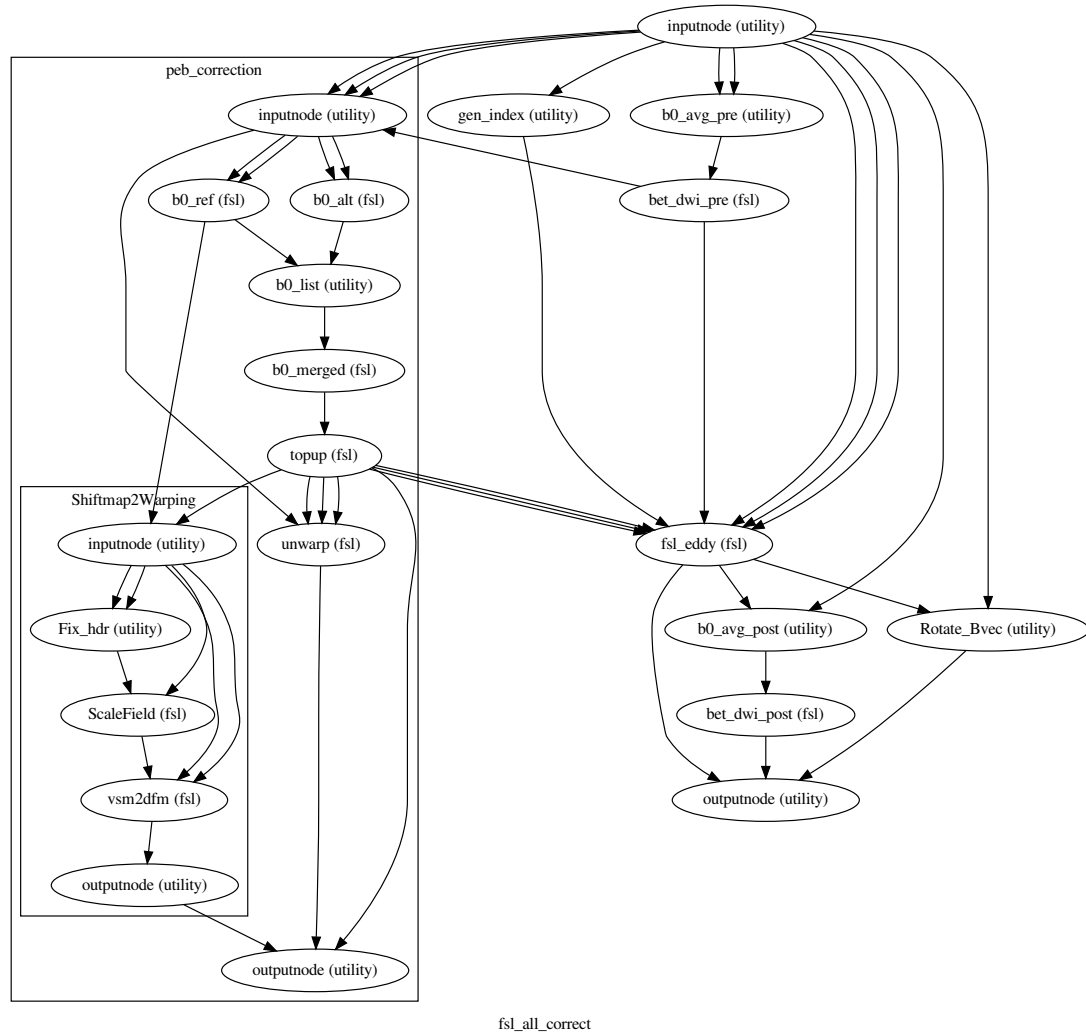
Warning: this workflow rotates the gradients table (*b*-vectors) [[Leemans09](#)].

Warning: this workflow does not perform jacobian modulation of each *DWI* [[Jones10](#)].

Examples

```
>>> from nipyype.workflows.dmri.fsl.artifacts import all_fsl_pipeline
>>> allcorr = all_fsl_pipeline()
>>> allcorr.inputs.inputnode.in_file = 'epi.nii'
>>> allcorr.inputs.inputnode.alt_file = 'epi_rev.nii'
>>> allcorr.inputs.inputnode.in_bval = 'diffusion.bval'
>>> allcorr.inputs.inputnode.in_bvec = 'diffusion.bvec'
>>> allcorr.run() # doctest: +SKIP
```

Graph



2.8.3 all_peb_pipeline()

[Link to code](#)

Builds a pipeline including three artifact corrections: head-motion correction (HMC), susceptibility-derived distortion correction (SDC), and Eddy currents-derived distortion correction (ECC).

Warning: this workflow rotates the gradients table (*b*-vectors) [Leemans09].

Examples

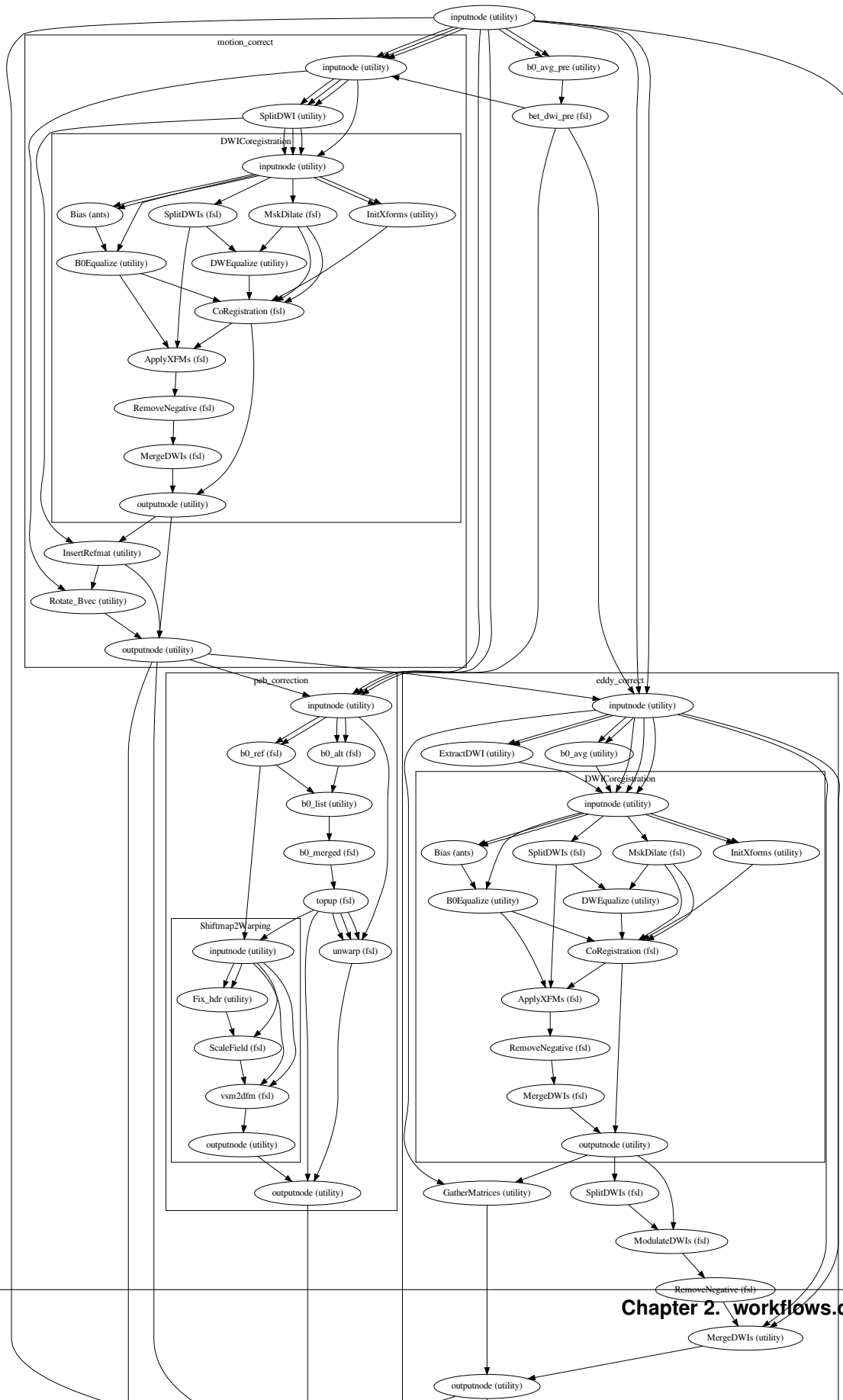
```
>>> from nipy.workflows.dmri.fsl.artifacts import all_peb_pipeline
>>> allcorr = all_peb_pipeline()
>>> allcorr.inputs.inputnode.in_file = 'epi.nii'
>>> allcorr.inputs.inputnode.alt_file = 'epi_rev.nii'
```

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```
>>> allcorr.inputs.inputnode.in_bval = 'diffusion.bval'
>>> allcorr.inputs.inputnode.in_bvec = 'diffusion.bvec'
>>> allcorr.run() # doctest: +SKIP
```

Graph



2.8.4 ecc_pipeline()

[Link to code](#)

ECC stands for Eddy currents correction.

Creates a pipeline that corrects for artifacts induced by Eddy currents in dMRI sequences. It takes a series of diffusion weighted images and linearly co-registers them to one reference image (the average of all b0s in the dataset).

DWIs are also modulated by the determinant of the Jacobian as indicated by [Jones10] and [Rohde04].

A list of rigid transformation matrices can be provided, sourcing from a `hmc_pipeline()` workflow, to initialize registrations in a *motion free* framework.

A list of affine transformation matrices is available as output, so that transforms can be chained ([discussion here](#)).

References

Example

```
>>> from nipy.workflows.dmri.fsl.artifacts import ecc_pipeline
>>> ecc = ecc_pipeline()
>>> ecc.inputs.inputnode.in_file = 'diffusion.nii'
>>> ecc.inputs.inputnode.in_bval = 'diffusion.bval'
>>> ecc.inputs.inputnode.in_mask = 'mask.nii'
>>> ecc.run() # doctest: +SKIP
```

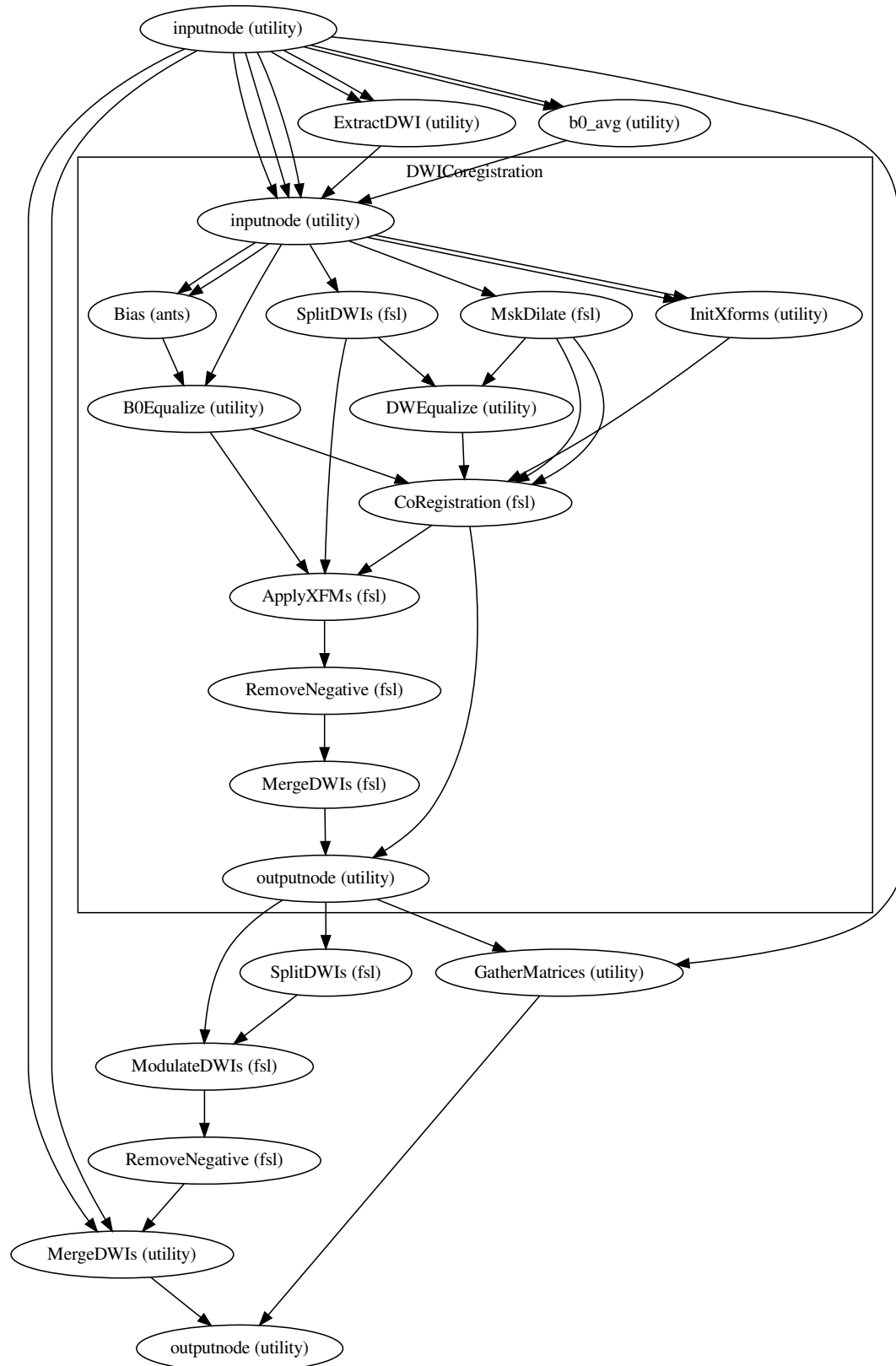
Inputs:

```
inputnode.in_file - input dwi file
inputnode.in_mask - weights mask of reference image (a file with data range sin_
↳ [0.0, 1.0], indicating the weight of each voxel when computing the metric.
inputnode.in_bval - b-values table
inputnode.in_xfms - list of matrices to initialize registration (from head-motion_
↳ correction)
```

Outputs:

```
outputnode.out_file - corrected dwi file
outputnode.out_xfms - list of transformation matrices
```

Graph



eddy_correct

2.8.5 hmc_pipeline()

[Link to code](#)

HMC stands for head-motion correction.

Creates a pipeline that corrects for head motion artifacts in dMRI sequences. It takes a series of diffusion weighted images and rigidly co-registers them to one reference image. Finally, the *b*-matrix is rotated accordingly [Leemans09] making use of the rotation matrix obtained by FLIRT.

Search angles have been limited to 4 degrees, based on results in [Yendiki13].

A list of rigid transformation matrices is provided, so that transforms can be chained. This is useful to correct for artifacts with only one interpolation process (as previously discussed [here](#)), and also to compute nuisance regressors as proposed by [Yendiki13].

Warning: This workflow rotates the *b*-vectors, so please be advised that not all the dicom converters ensure the consistency between the resulting nifti orientation and the gradients table (e.g. dcm2nii checks it).

References

Example

```
>>> from nipy.workflows.dmri.fsl.artifacts import hmc_pipeline
>>> hmc = hmc_pipeline()
>>> hmc.inputs.inputnode.in_file = 'diffusion.nii'
>>> hmc.inputs.inputnode.in_bvec = 'diffusion.bvec'
>>> hmc.inputs.inputnode.in_bval = 'diffusion.bval'
>>> hmc.inputs.inputnode.in_mask = 'mask.nii'
>>> hmc.run() # doctest: +SKIP
```

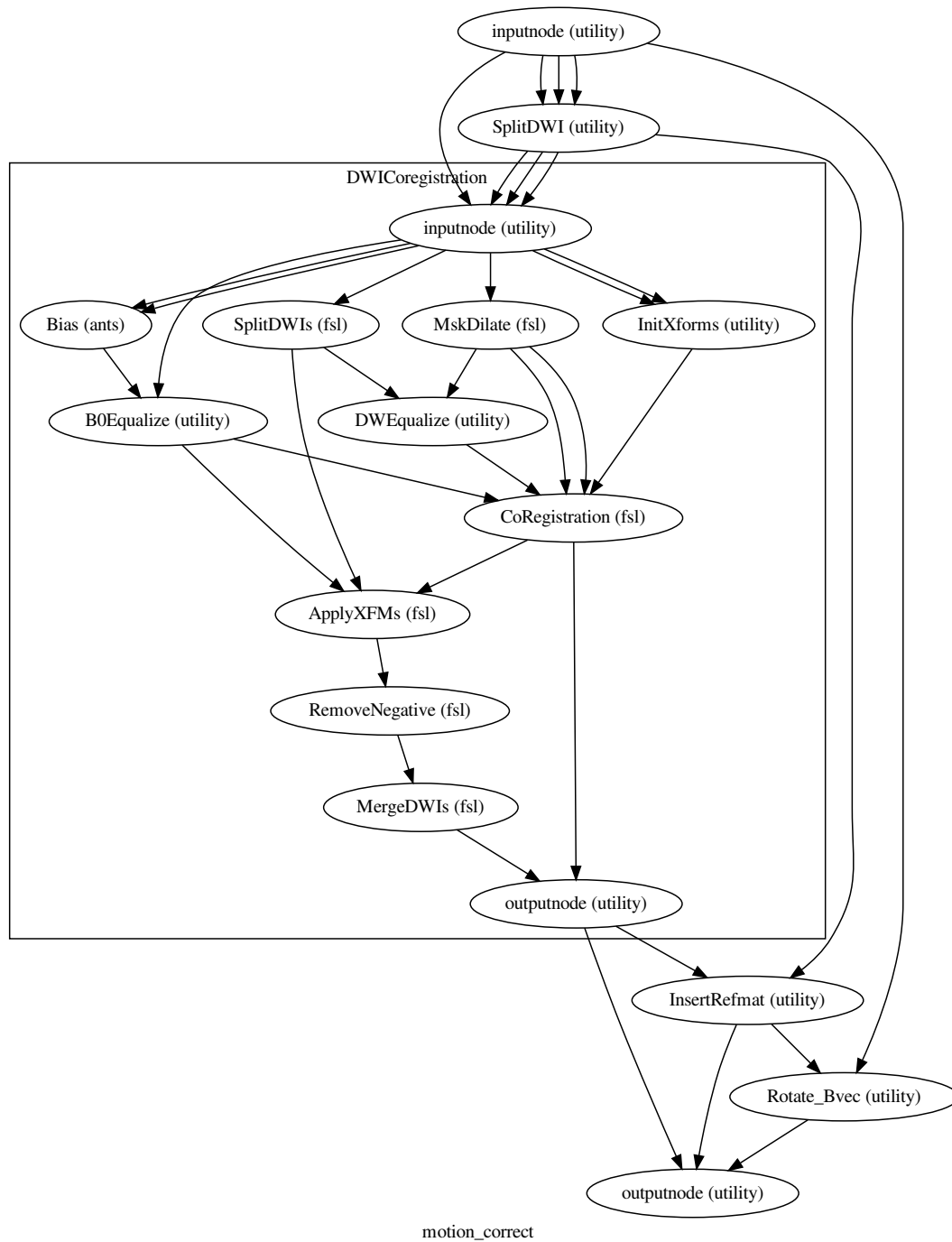
Inputs:

```
inputnode.in_file - input dwi file
inputnode.in_mask - weights mask of reference image (a file with data range in [0.
→0, 1.0], indicating the weight of each voxel when computing the metric.
inputnode.in_bval - b-values file
inputnode.in_bvec - gradients file (b-vectors)
inputnode.ref_num (optional, default=0) index of the b0 volume that should be
→taken as reference
```

Outputs:

```
outputnode.out_file - corrected dwi file
outputnode.out_bvec - rotated gradient vectors table
outputnode.out_xfms - list of transformation matrices
```

Graph

2.8.6 `remove_bias()`

[Link to code](#)

This workflow estimates a single multiplicative bias field from the averaged *b0* image, as suggested in

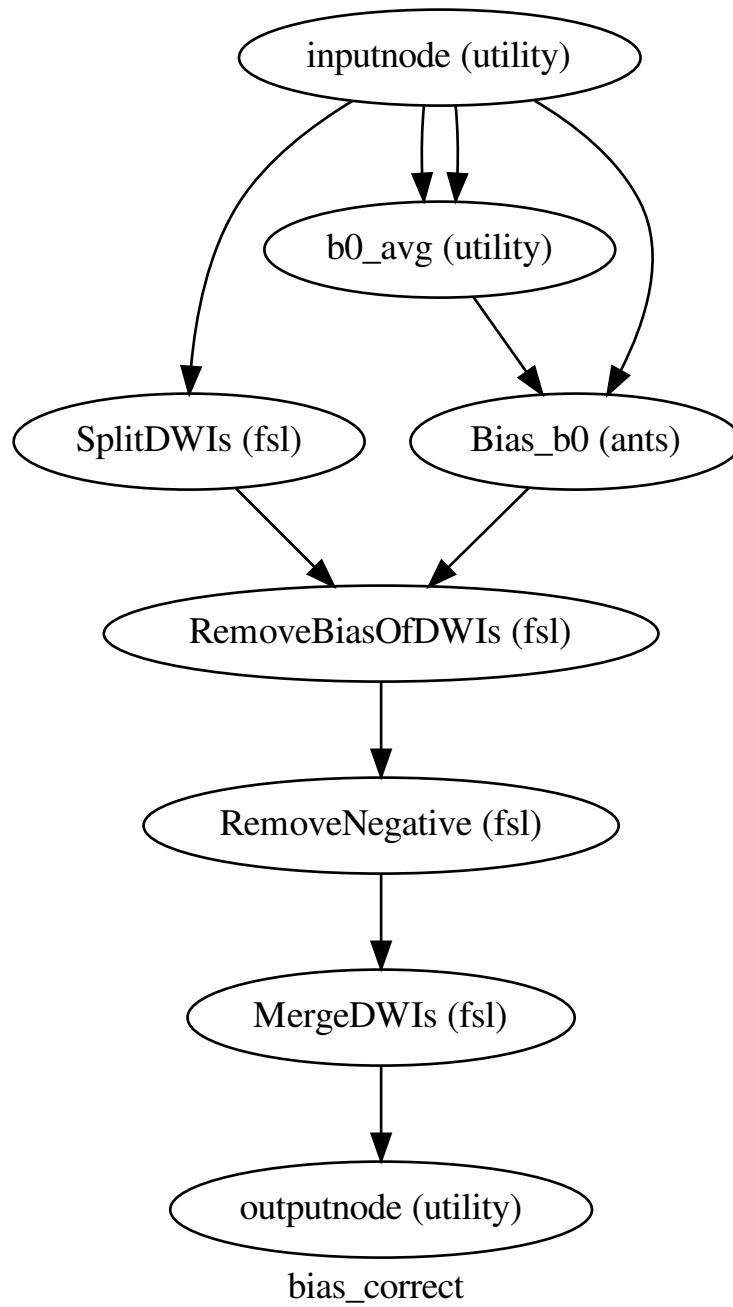
[Jeurissen2014].

References

Example

```
>>> from nipyype.workflows.dmri.fsl.artifacts import remove_bias
>>> bias = remove_bias()
>>> bias.inputs.inputnode.in_file = 'epi.nii'
>>> bias.inputs.inputnode.in_bval = 'diffusion.bval'
>>> bias.inputs.inputnode.in_mask = 'mask.nii'
>>> bias.run() # doctest: +SKIP
```

Graph



2.8.7 sdc_fmb()

[Link to code](#)

SDC stands for susceptibility distortion correction. FMB stands for fieldmap-based.

The fieldmap based (FMB) method implements SDC by using a mapping of the B0 field as proposed by [Jezzard95]. This workflow uses the implementation of FSL (FUGUE). Phase unwrapping is performed using PRELUDE [Jenkinson03]. Preparation of the fieldmap is performed reproducing the script in FSL `fsl_prepare_fieldmap`.

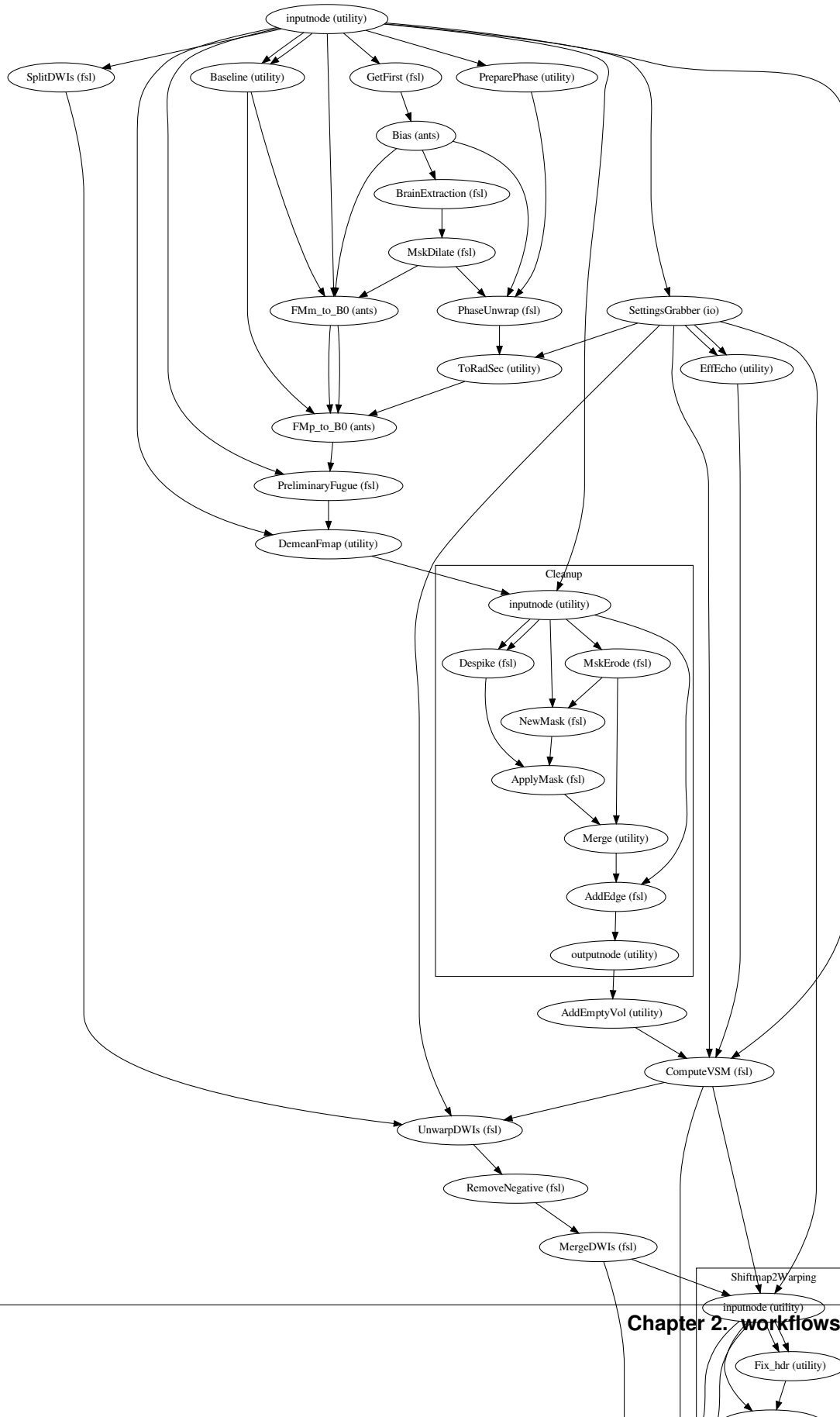
Example

```
>>> from nipy.workflows.dmri.fsl.artifacts import sdc_fmb
>>> fmb = sdc_fmb()
>>> fmb.inputs.inputnode.in_file = 'diffusion.nii'
>>> fmb.inputs.inputnode.in_ref = list(range(0, 30, 6))
>>> fmb.inputs.inputnode.in_mask = 'mask.nii'
>>> fmb.inputs.inputnode.bmap_mag = 'magnitude.nii'
>>> fmb.inputs.inputnode.bmap pha = 'phase.nii'
>>> fmb.inputs.inputnode.settings = 'epi_param.txt'
>>> fmb.run() # doctest: +SKIP
```

Warning: Only SIEMENS format fieldmaps are supported.

References

Graph



2.8.8 `sdc_peb()`

[Link to code](#)

SDC stands for susceptibility distortion correction. PEB stands for phase-encoding-based.

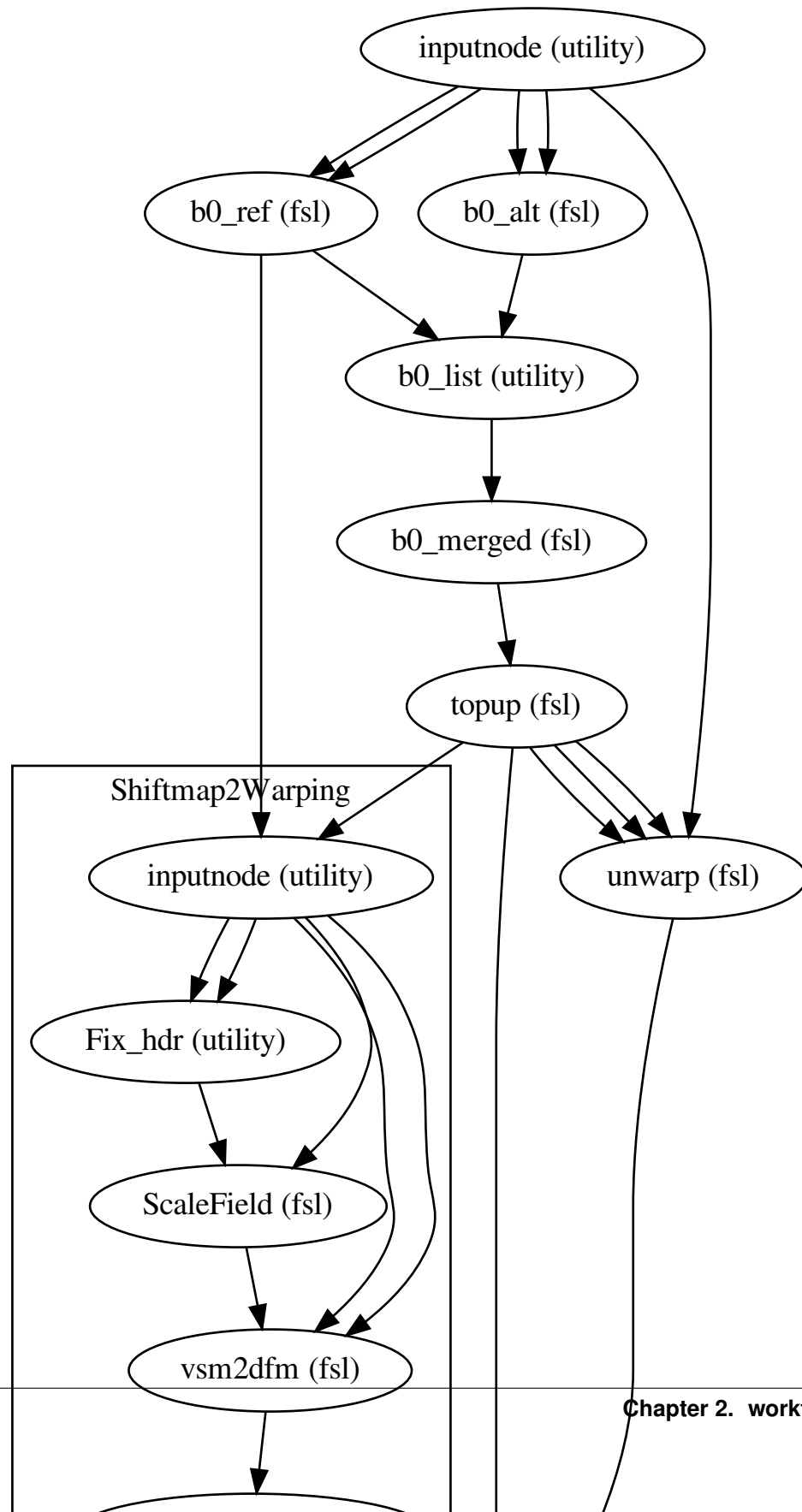
The phase-encoding-based (PEB) method implements SDC by acquiring diffusion images with two different encoding directions [Andersson2003]. The most typical case is acquiring with opposed phase-gradient blips (e.g. $A \ggg P$ and $P \ggg A$, or equivalently, $-y$ and y) as in [Chiou2000], but it is also possible to use orthogonal configurations [Cordes2000] (e.g. $A \ggg P$ and $L \ggg R$, or equivalently $-y$ and x). This workflow uses the implementation of FSL (TOPUP).

Example

```
>>> from nipy.workflows.dmri.fsl.artifacts import sdc_peb
>>> peb = sdc_peb()
>>> peb.inputs.inputnode.in_file = 'epi.nii'
>>> peb.inputs.inputnode.alt_file = 'epi_rev.nii'
>>> peb.inputs.inputnode.in_bval = 'diffusion.bval'
>>> peb.inputs.inputnode.in_mask = 'mask.nii'
>>> peb.run() # doctest: +SKIP
```

References

Graph



2.9 workflows.dmri.fsl.dti

2.9.1 bedpostx_parallel()

[Link to code](#)

Does the same as `create_bedpostx_pipeline()` by splitting the input dMRI in small ROIs that are better suited for parallel processing).

Example

```
>>> from nipyype.workflows.dmri.fsl.dti import bedpostx_parallel
>>> params = dict(n_fibres = 2, fudge = 1, burn_in = 1000,
...               n_jumps = 1250, sample_every = 25)
>>> bpwf = bedpostx_parallel('nipyype_bedpostx_parallel', params=params)
>>> bpwf.inputs.inputnode.dwi = 'diffusion.nii'
>>> bpwf.inputs.inputnode.mask = 'mask.nii'
>>> bpwf.inputs.inputnode.bvecs = 'bvecs'
>>> bpwf.inputs.inputnode.bvals = 'bvals'
>>> bpwf.run(plugin='CondorDAGMan') # doctest: +SKIP
```

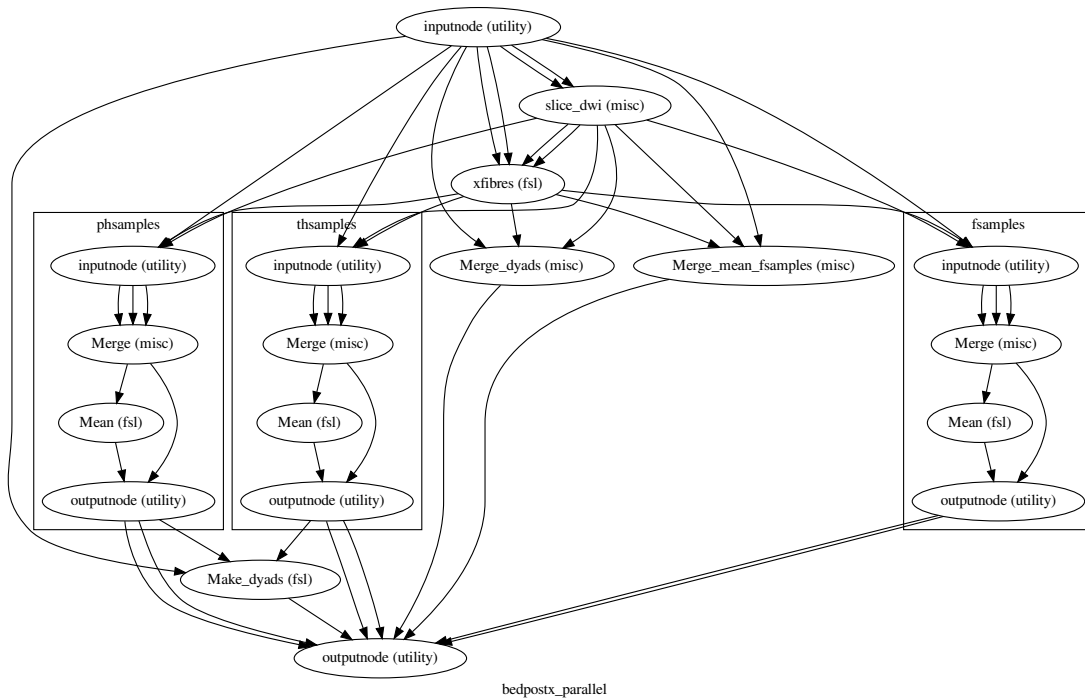
Inputs:

```
inputnode.dwi
inputnode.mask
inputnode.bvecs
inputnode.bvals
```

Outputs:

```
outputnode wraps all XFibres outputs
```

Graph



2.9.2 create_bedpostx_pipeline()

[Link to code](#)

Creates a pipeline that does the same as bedpostx script from FSL - calculates diffusion model parameters (distributions not MLE) voxelwise for the whole volume (by splitting it slicewise).

Example

```
>>> from nipy.workflows.dmri.fsl.dti import create_bedpostx_pipeline
>>> params = dict(n_fibres = 2, fudge = 1, burn_in = 1000,
...               n_jumps = 1250, sample_every = 25)
>>> bpwf = create_bedpostx_pipeline('nipy_bedpostx', params)
>>> bpwf.inputs.inputnode.dwi = 'diffusion.nii'
>>> bpwf.inputs.inputnode.mask = 'mask.nii'
>>> bpwf.inputs.inputnode.bvecs = 'bvecs'
>>> bpwf.inputs.inputnode.bvals = 'bvals'
>>> bpwf.run() # doctest: +SKIP
```

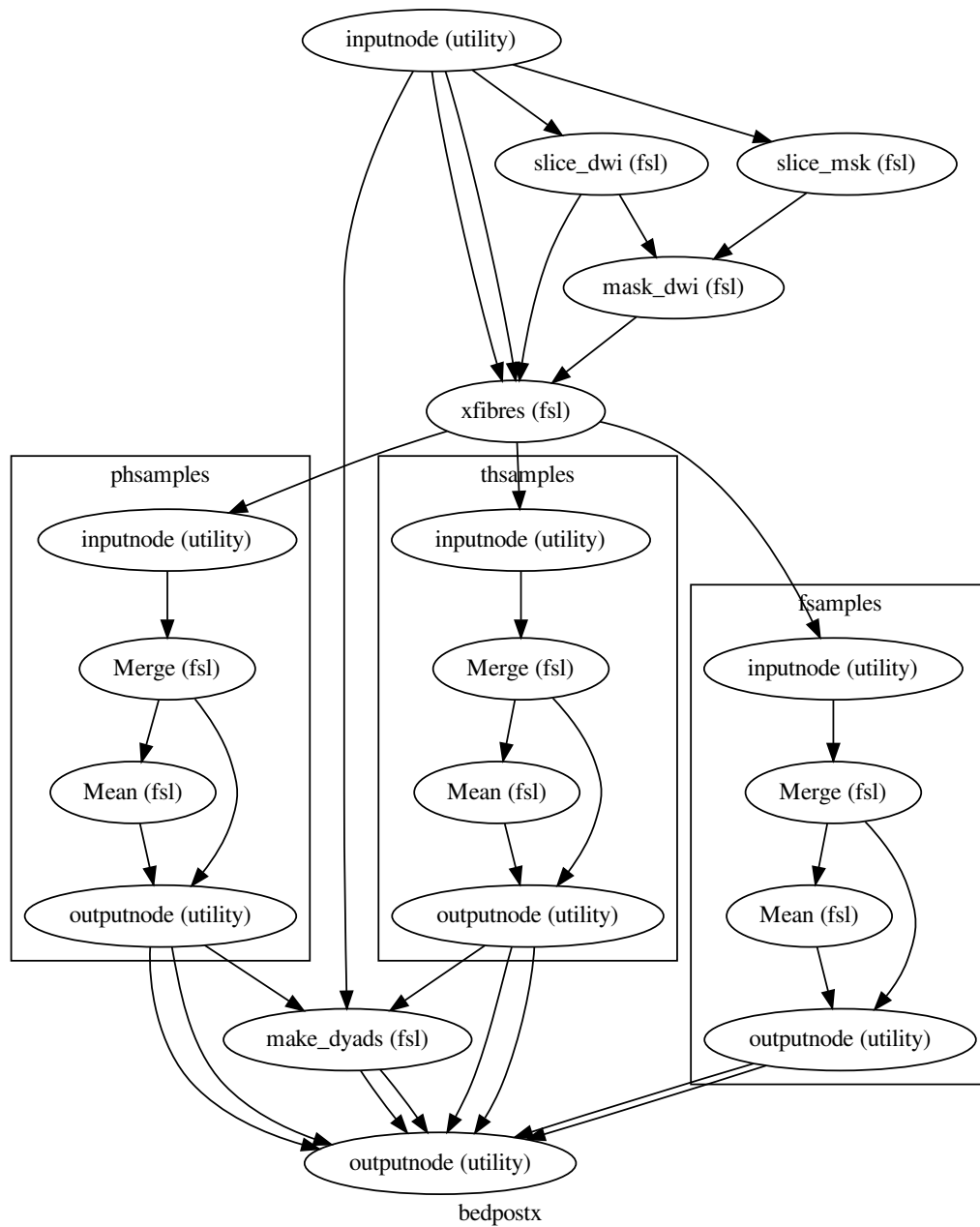
Inputs:

```
inputnode.dwi
inputnode.mask
inputnode.bvecs
inputnode.bvals
```

Outputs:

```
outputnode wraps all XFibres outputs
```

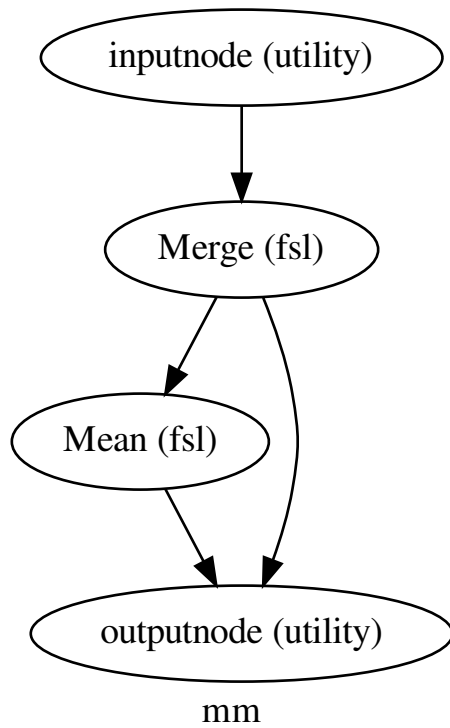

Graph



2.9.3 merge_and_mean()

[Link to code](#)

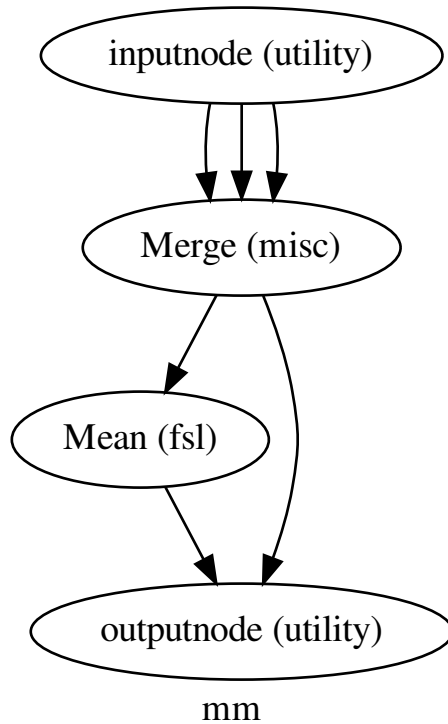
Graph



2.9.4 merge_and_mean_parallel()

[Link to code](#)

Graph



2.9.5 transpose()

[Link to code](#)

2.10 workflows.dmri.fsl.epi

2.10.1 create_dmri_preprocessing()

[Link to code](#)

Creates a workflow that chains the necessary pipelines to correct for motion, eddy currents, and, if selected, susceptibility artifacts in EPI dMRI sequences.

Deprecated since version 0.9.3: Use `nipyne.workflows.dmri.preprocess.epi.all_fmb_pipeline()` or `nipyne.workflows.dmri.preprocess.epi.all_peb_pipeline()` instead.

Warning: This workflow rotates the b-vectors, so please be advised that not all the dicom converters ensure the consistency between the resulting nifti orientation and the b matrix table (e.g. `dcm2nii` checks it).

Example

```
>>> nipyre_dmri_preprocess = create_dmri_preprocessing('nipyre_dmri_prep')
>>> nipyre_dmri_preprocess.inputs.inputnode.in_file = 'diffusion.nii'
>>> nipyre_dmri_preprocess.inputs.inputnode.in_bvec = 'diffusion.bvec'
>>> nipyre_dmri_preprocess.inputs.inputnode.ref_num = 0
>>> nipyre_dmri_preprocess.inputs.inputnode.fieldmap_mag = 'magnitude.nii'
>>> nipyre_dmri_preprocess.inputs.inputnode.fieldmap pha = 'phase.nii'
>>> nipyre_dmri_preprocess.inputs.inputnode.te_diff = 2.46
>>> nipyre_dmri_preprocess.inputs.inputnode.epi_echospacing = 0.77
>>> nipyre_dmri_preprocess.inputs.inputnode.epi_rev_encoding = False
>>> nipyre_dmri_preprocess.inputs.inputnode.pi_accel_factor = True
>>> nipyre_dmri_preprocess.run() # doctest: +SKIP
```

Inputs:

```
inputnode.in_file - The diffusion data
inputnode.in_bvec - The b-matrix file, in FSL format and consistent with the in_
↳file orientation
inputnode.ref_num - The reference volume (a b=0 volume in dMRI)
inputnode.fieldmap_mag - The magnitude of the fieldmap
inputnode.fieldmap pha - The phase difference of the fieldmap
inputnode.te_diff - TE increment used (in msec.) on the fieldmap acquisition_
↳(generally 2.46ms for 3T scanners)
inputnode.epi_echospacing - The EPI EchoSpacing parameter (in msec.)
inputnode.epi_rev_encoding - True if reverse encoding was used (generally False)
inputnode.pi_accel_factor - Parallel imaging factor (aka GRAPPA acceleration_
↳factor)
inputnode.vsm_sigma - Sigma (in mm.) of the gaussian kernel used for in-slice_
↳smoothing of the deformation field (voxel shift map, vsm)
```

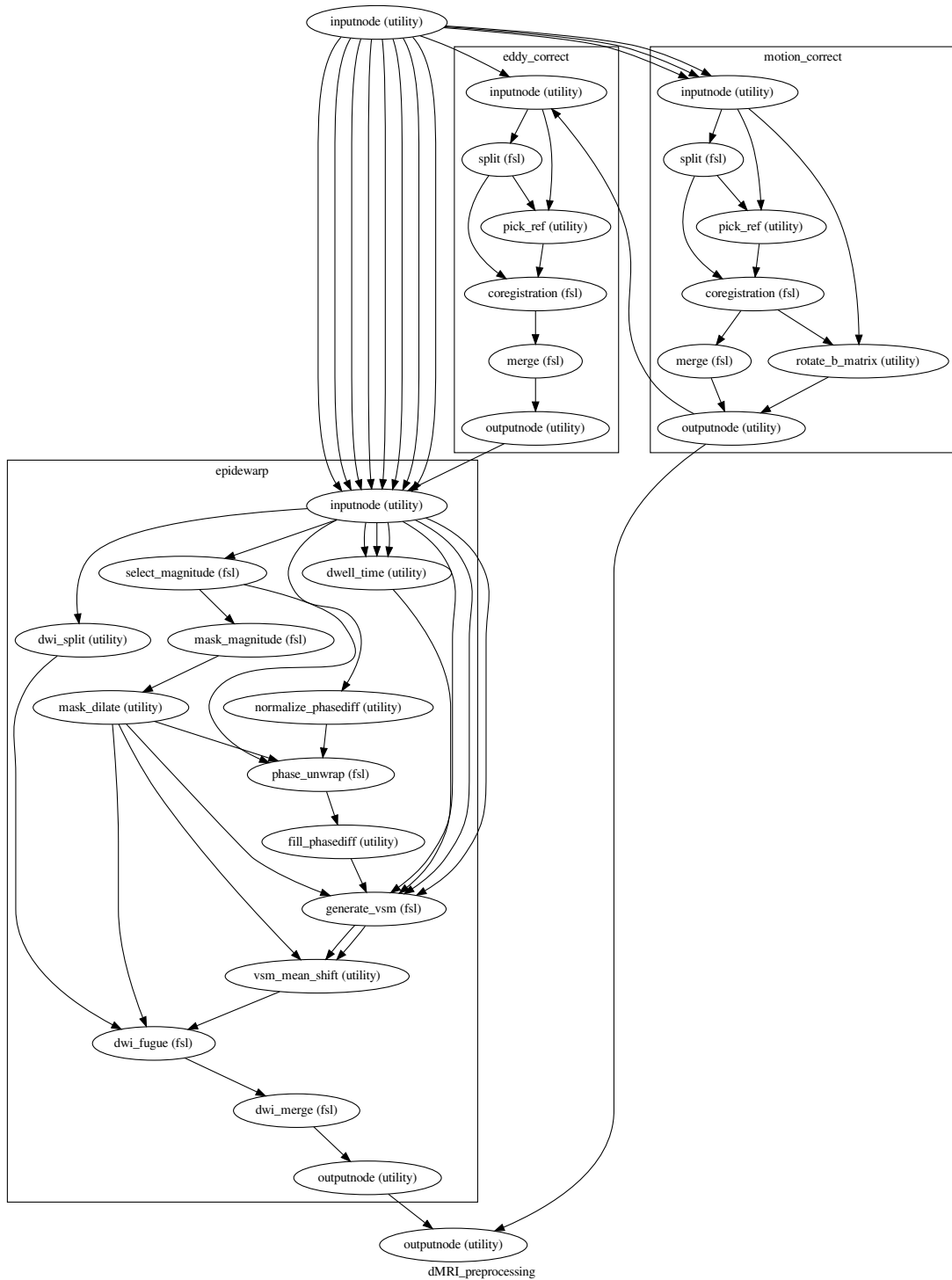
Outputs:

```
outputnode.dmri_corrected
outputnode.bvec_rotated
```

Optional arguments:

```
use_fieldmap - True if there are fieldmap files that should be used (default True)
fieldmap_registration - True if registration to fieldmap should be performed_
↳(default False)
```

Graph



2.10.2 create_eddy_correct_pipeline()

[Link to code](#)

Deprecated since version 0.9.3: Use `nipype.workflows.dmri.preprocess.epi.ecc_pipeline()` instead.

Creates a pipeline that replaces `eddy_correct` script in FSL. It takes a series of diffusion weighted images and linearly co-registers them to one reference image. No rotation of the B-matrix is performed, so this pipeline should be executed after the motion correction pipeline.

Example

```
>>> nipype_eddycorrect = create_eddy_correct_pipeline('nipype_eddycorrect')
>>> nipype_eddycorrect.inputs.inputnode.in_file = 'diffusion.nii'
>>> nipype_eddycorrect.inputs.inputnode.ref_num = 0
>>> nipype_eddycorrect.run() # doctest: +SKIP
```

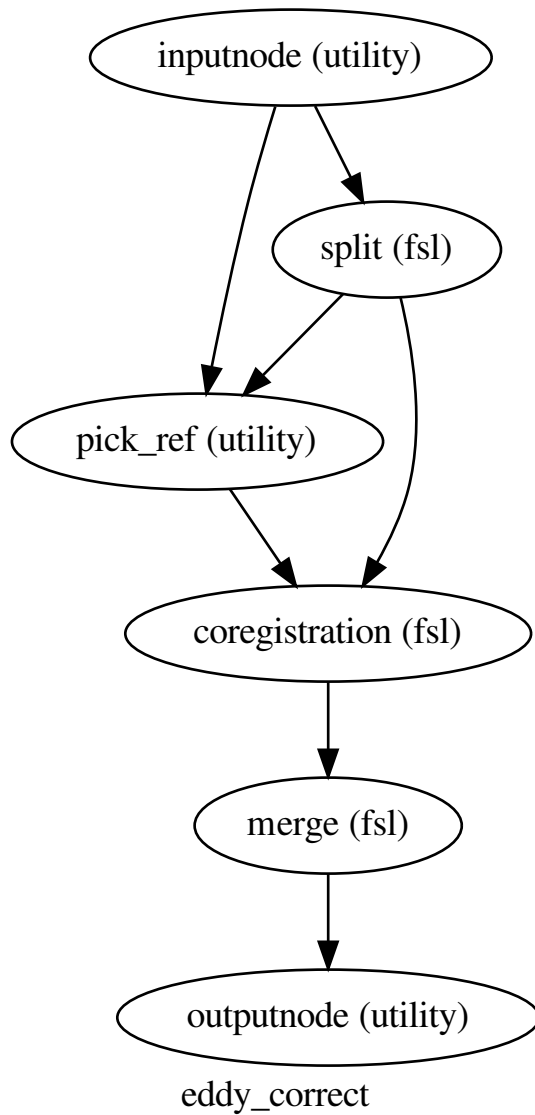
Inputs:

```
inputnode.in_file
inputnode.ref_num
```

Outputs:

```
outputnode.eddy_corrected
```

Graph



2.10.3 create_epidewarp_pipeline()

[Link to code](#)

Replaces the epidewarp.fsl script (<http://www.nmr.mgh.harvard.edu/~greve/fbirn/b0/epidewarp.fsl>) for susceptibility distortion correction of dMRI & fMRI acquired with EPI sequences and the fieldmap information (Jezzard et al., 1995) using FSL's FUGUE. The registration to the (warped) fieldmap (strictly following the original script) is available using `fieldmap_registration=True`.

Warning: This workflow makes use of `epidewarp.fsl` a script of FSL deprecated long time ago. The use of this workflow is not recommended, use `nipytype.workflows.dmri.preprocess.epi.sdc_fmb()` instead.

Example

```
>>> nipytype_epicorrect = create_epidewarp_pipeline('nipytype_epidewarp', fieldmap_
↳registration=False)
>>> nipytype_epicorrect.inputs.inputnode.in_file = 'diffusion.nii'
>>> nipytype_epicorrect.inputs.inputnode.fieldmap_mag = 'magnitude.nii'
>>> nipytype_epicorrect.inputs.inputnode.fieldmap pha = 'phase.nii'
>>> nipytype_epicorrect.inputs.inputnode.te_diff = 2.46
>>> nipytype_epicorrect.inputs.inputnode.epi_echospacing = 0.77
>>> nipytype_epicorrect.inputs.inputnode.epi_rev_encoding = False
>>> nipytype_epicorrect.inputs.inputnode.ref_num = 0
>>> nipytype_epicorrect.inputs.inputnode.pi_accel_factor = 1.0
>>> nipytype_epicorrect.run() # doctest: +SKIP
```

Inputs:

inputnode.in_file - The volume acquired **with** EPI sequence
inputnode.fieldmap_mag - The magnitude of the fieldmap
inputnode.fieldmap pha - The phase difference of the fieldmap
inputnode.te_diff - Time difference between TE **in** ms.
inputnode.epi_echospacing - The echo spacing (aka dwell time) **in** the EPI sequence
inputnode.epi_ph_encoding_dir - The phase encoding direction **in** EPI acquisition,
↳ (default y)
inputnode.epi_rev_encoding - **True if** it **is** acquired **with** reverse encoding
inputnode.pi_accel_factor - Acceleration factor used **for** EPI parallel imaging,
↳ (GRAPPA)
inputnode.vsm_sigma - Sigma value of the gaussian smoothing **filter** applied to the,
↳ vsm (voxel shift **map**)
inputnode.ref_num - The reference volume (B=0 **in** dMRI **or** a central frame **in** fMRI)

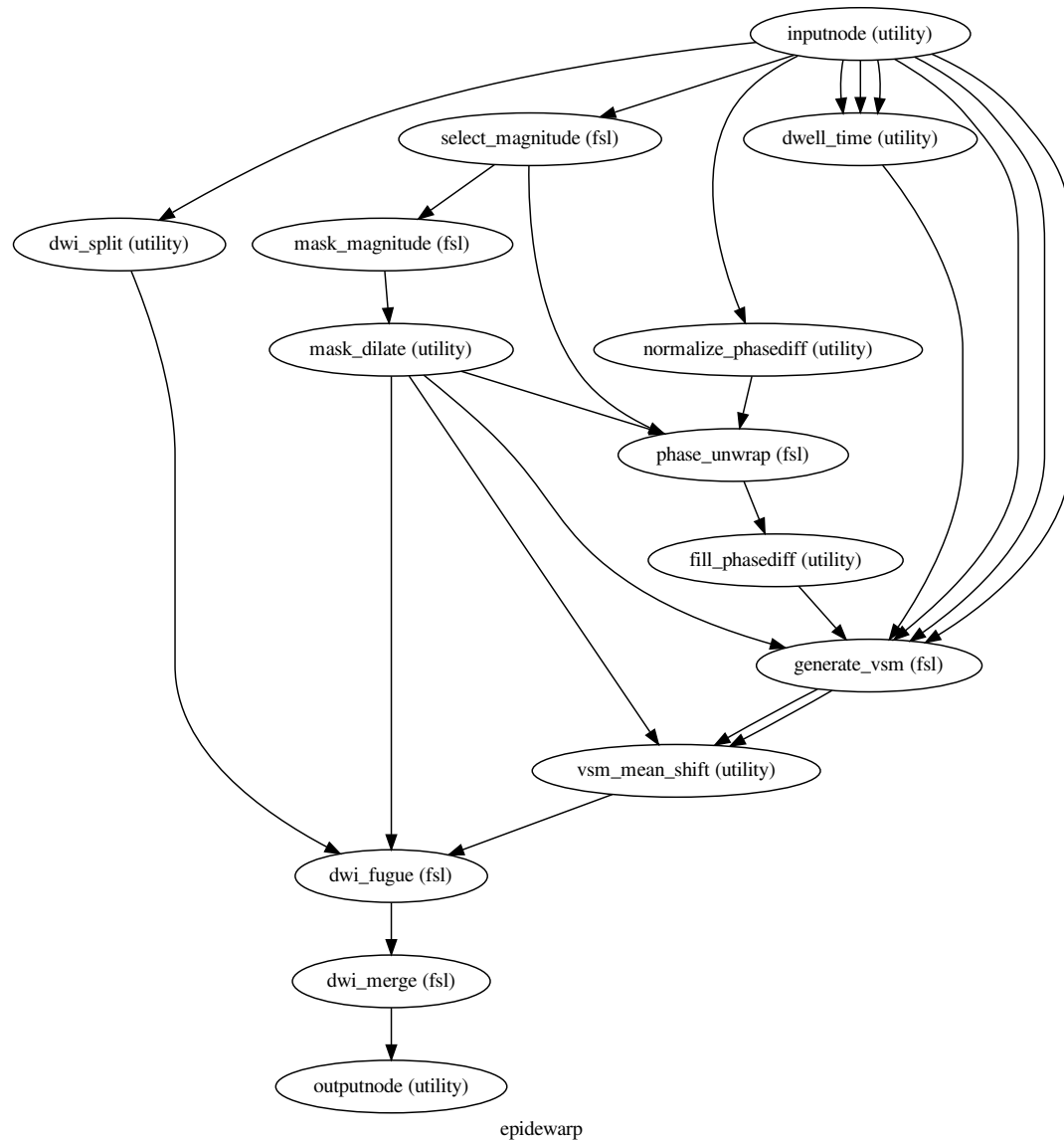
Outputs:

```
outputnode.epi_corrected
```

Optional arguments:

fieldmap_registration - **True if** registration to fieldmap should be done (default,
↳ **False**)

Graph



2.10.4 create_motion_correct_pipeline()

[Link to code](#)

Creates a pipeline that corrects for motion artifact in dMRI sequences. It takes a series of diffusion weighted images and rigidly co-registers them to one reference image. Finally, the b-matrix is rotated accordingly (Lee-mans et al. 2009 - <http://www.ncbi.nlm.nih.gov/pubmed/19319973>), making use of the rotation matrix obtained by FLIRT.

Deprecated since version 0.9.3: Use `nipy.workflows.dmri.preprocess.epi.hmc_pipeline()` instead.

Warning: This workflow rotates the b-vectors, so please be advised that not all the dicom converters ensure the consistency between the resulting nifti orientation and the b matrix table (e.g. dcm2nii checks it).

Example

```
>>> nipy_motioncorrect = create_motion_correct_pipeline('nipy_motioncorrect')
>>> nipy_motioncorrect.inputs.inputnode.in_file = 'diffusion.nii'
>>> nipy_motioncorrect.inputs.inputnode.in_bvec = 'diffusion.bvec'
>>> nipy_motioncorrect.inputs.inputnode.ref_num = 0
>>> nipy_motioncorrect.run() # doctest: +SKIP
```

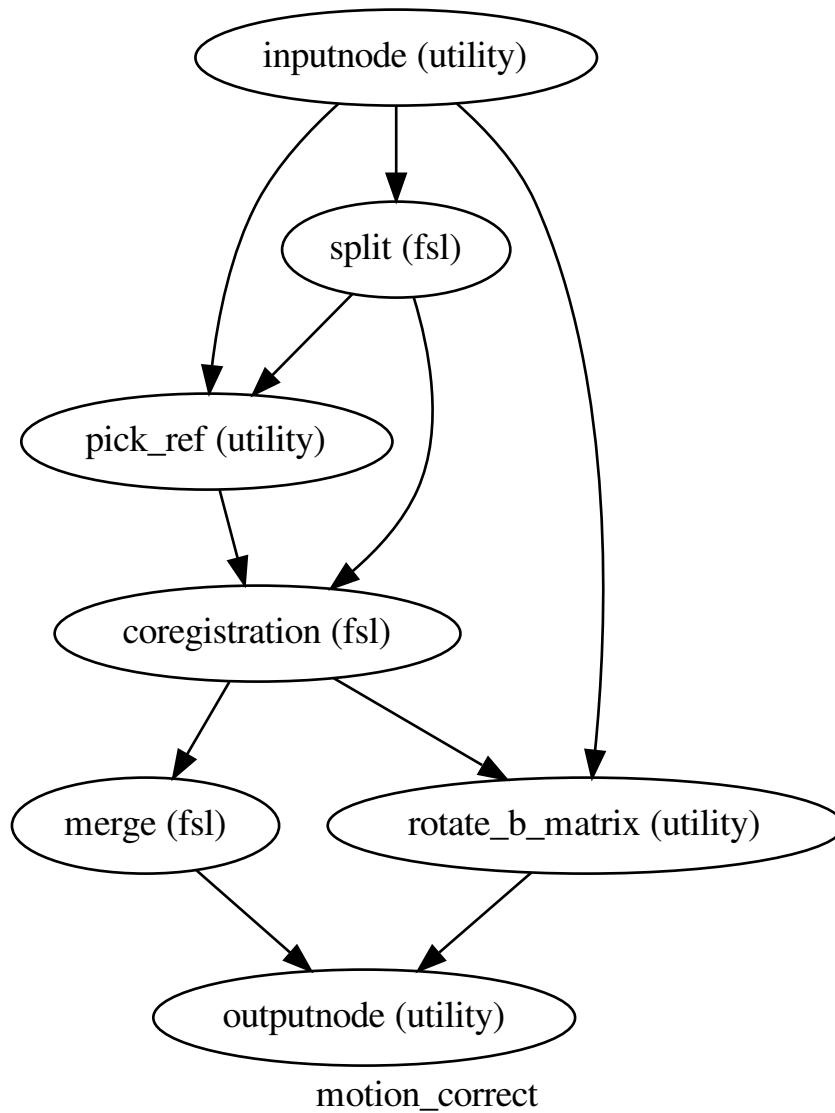
Inputs:

```
inputnode.in_file
inputnode.ref_num
inputnode.in_bvec
```

Outputs:

```
outputnode.motion_corrected
outputnode.out_bvec
```

Graph

**2.10.5 fieldmap_correction()**

[Link to code](#)

Deprecated since version 0.9.3: Use `nipyne.workflows.dmri.preprocess.epi.sdc_fmb()` instead.

Fieldmap-based retrospective correction of EPI images for the susceptibility distortion artifact (Jezzard et al., 1995). Fieldmap images are assumed to be already registered to EPI data, and a brain mask is required.

Replaces the former workflow, still available as `create_epidewarp_pipeline()`. The difference with respect the epidewarp pipeline is that now the workflow uses the new `fsl_prepare_fieldmap` available as of FSL 5.0.

Example

```
>>> nipy_epicorrect = fieldmap_correction('nipy_epidewarp')
>>> nipy_epicorrect.inputs.inputnode.in_file = 'diffusion.nii'
>>> nipy_epicorrect.inputs.inputnode.in_mask = 'brainmask.nii'
>>> nipy_epicorrect.inputs.inputnode.fieldmap pha = 'phase.nii'
>>> nipy_epicorrect.inputs.inputnode.fieldmap_mag = 'magnitude.nii'
>>> nipy_epicorrect.inputs.inputnode.te_diff = 2.46
>>> nipy_epicorrect.inputs.inputnode.epi_echospacing = 0.77
>>> nipy_epicorrect.inputs.inputnode.encoding_direction = 'y'
>>> nipy_epicorrect.run() # doctest: +SKIP
```

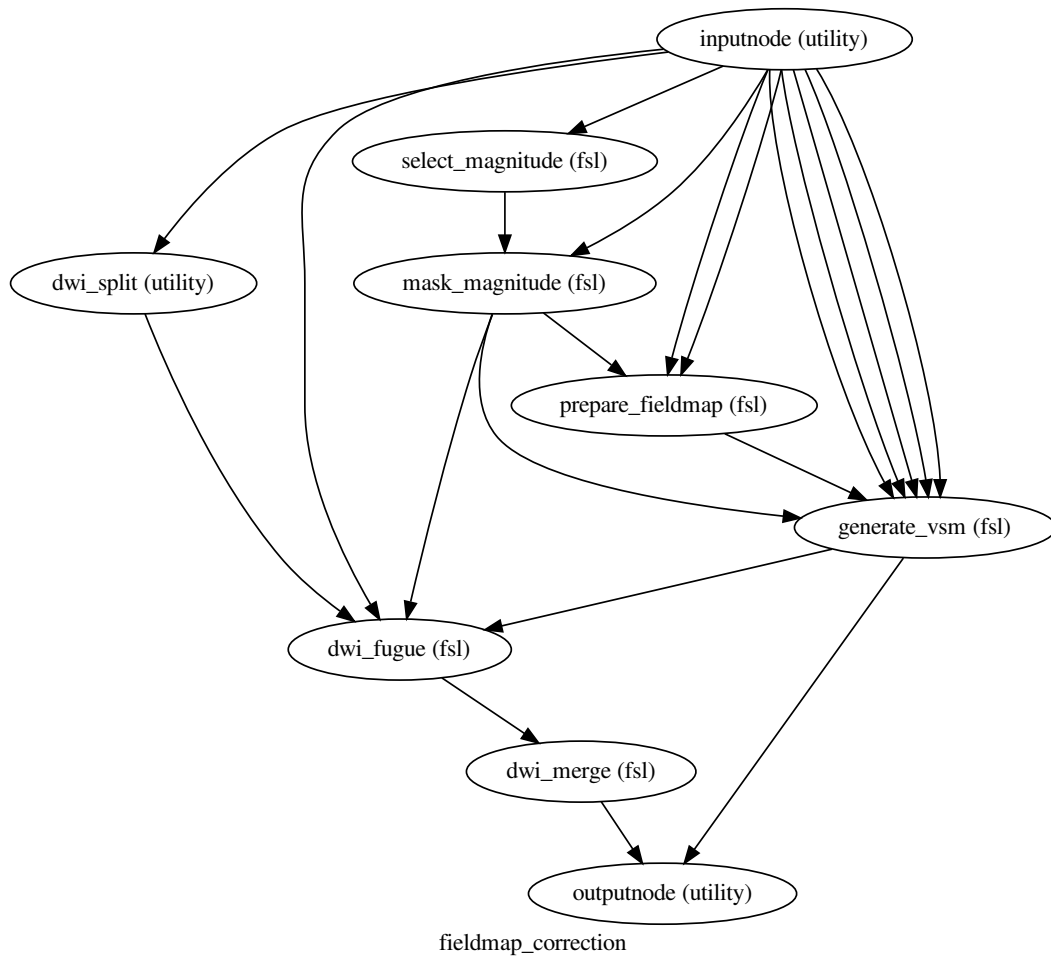
Inputs:

```
inputnode.in_file - The volume acquired with EPI sequence
inputnode.in_mask - A brain mask
inputnode.fieldmap pha - The phase difference map from the fieldmapping,
↳ registered to in_file
inputnode.fieldmap_mag - The magnitude maps (usually 4D, one magnitude per GRE
↳ scan)
                        from the fieldmapping, registered to in_file
inputnode.te_diff - Time difference in msec. between TE in ms of the fieldmapping
↳ (usually a GRE sequence).
inputnode.epi_echospacing - The effective echo spacing (aka dwell time) in msec.
↳ of the EPI sequence. If
                        EPI was acquired with parallel imaging, then the
↳ effective echo spacing is
                        eff_es = es / acc_factor.
inputnode.encoding_direction - The phase encoding direction in EPI acquisition
↳ (default y)
inputnode.vsm_sigma - Sigma value of the gaussian smoothing filter applied to the
↳ vsm (voxel shift map)
```

Outputs:

```
outputnode.epi_corrected
outputnode.out_vsm
```

Graph



2.10.6 topup_correction()

[Link to code](#)

Deprecated since version 0.9.3: Use `nipy.workflow.dmri.preprocess.epi.sdc_peb()` instead.

Corrects for susceptibility distortion of EPI images when one reverse encoding dataset has been acquired

Example

```

>>> nipy_epicorrect = topup_correction('nipy_topup')
>>> nipy_epicorrect.inputs.inputnode.in_file_dir = 'epi.nii'
>>> nipy_epicorrect.inputs.inputnode.in_file_rev = 'epi_rev.nii'
>>> nipy_epicorrect.inputs.inputnode.encoding_direction = ['y', 'y-']
>>> nipy_epicorrect.inputs.inputnode.ref_num = 0
>>> nipy_epicorrect.run() # doctest: +SKIP

```

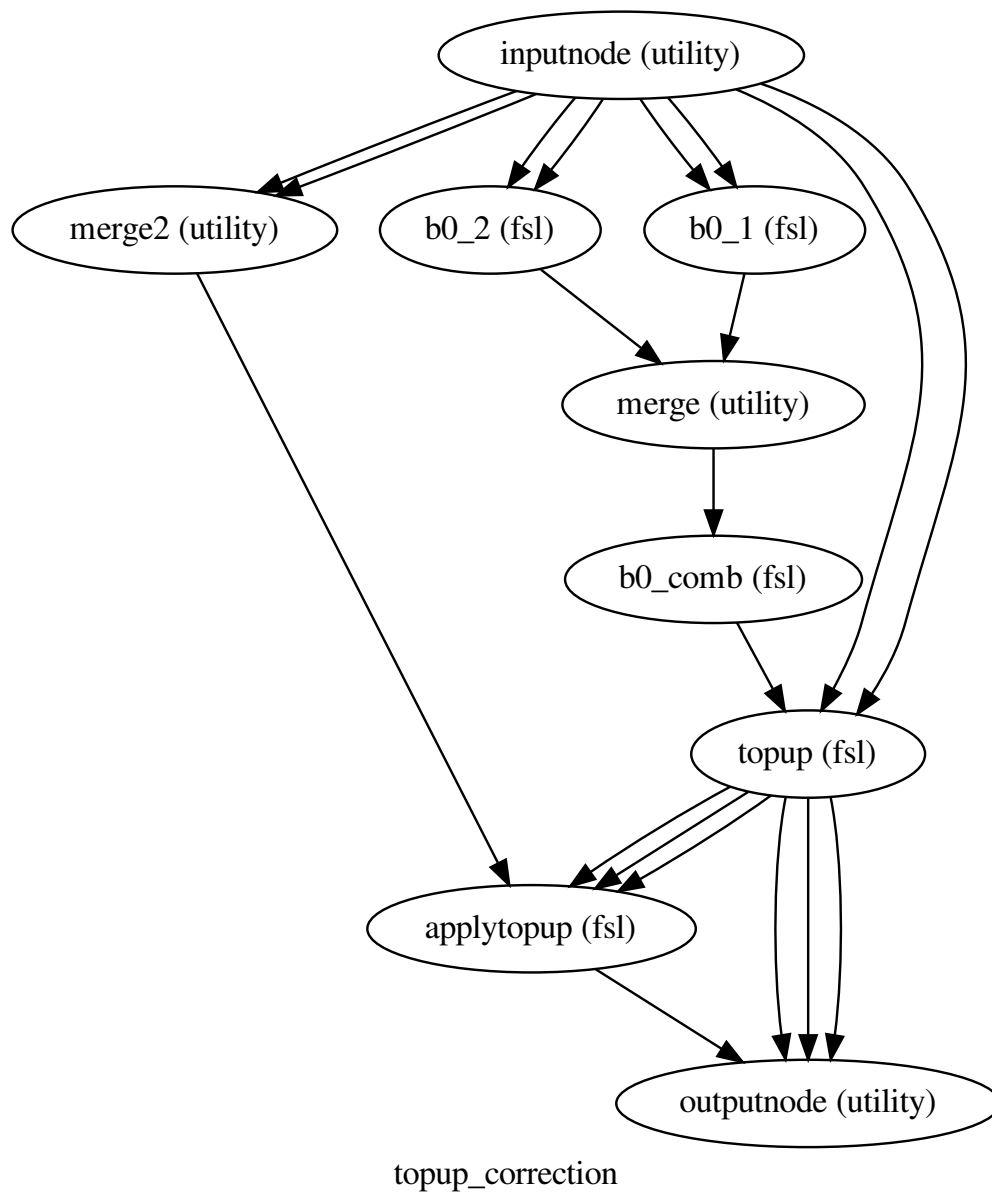
Inputs:

```
inputnode.in_file_dir - EPI volume acquired in 'forward' phase encoding
inputnode.in_file_rev - EPI volume acquired in 'reversed' phase encoding
inputnode.encoding_direction - Direction encoding of in_file_dir
inputnode.ref_num - Identifier of the reference volumes (usually B0 volume)
```

Outputs:

```
outputnode.epi_corrected
```

Graph



2.11 workflows.dmri.fsl.tbss

2.11.1 create_tbss_1_preproc()

[Link to code](#)

Preprocess FA data for TBSS: erodes a little and zero end slicers and creates masks(for use in FLIRT & FNIRT from FSL). A pipeline that does the same as tbss_1_preproc script in FSL

Example

```
>>> from nipy.workflows.dmri.fsl import tbss
>>> tbss1 = tbss.create_tbss_1_preproc()
>>> tbss1.inputs.inputnode.fa_list = ['s1_FA.nii', 's2_FA.nii', 's3_FA.nii']
```

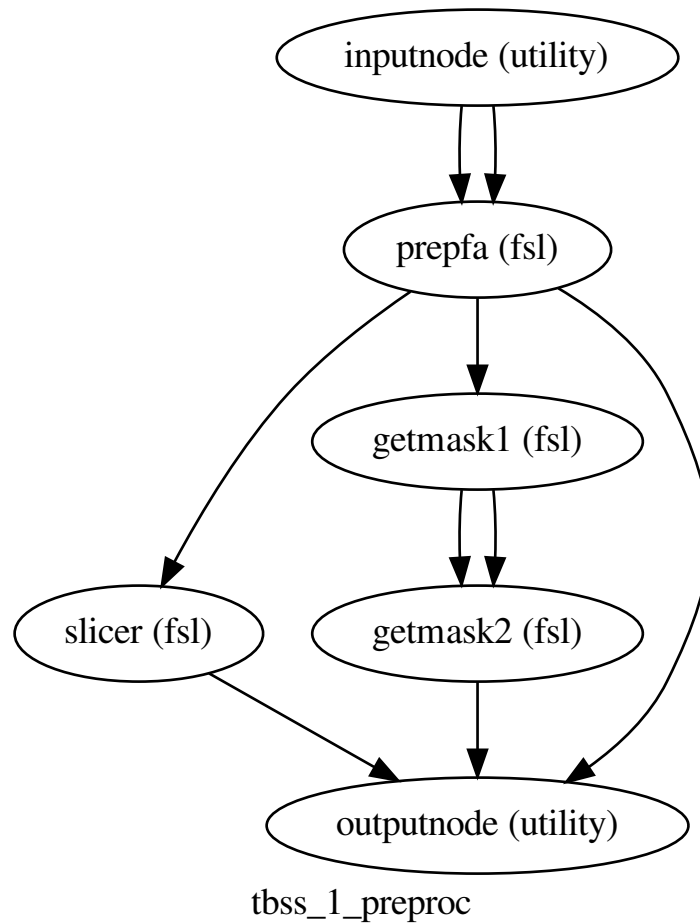
Inputs:

```
inputnode.fa_list
```

Outputs:

```
outputnode.fa_list
outputnode.mask_list
outputnode.slices
```

Graph



2.11.2 create_tbss_2_reg()

[Link to code](#)

TBSS nonlinear registration: A pipeline that does the same as 'tbss_2_reg -t' script in FSL. '-n' option is not supported at the moment.

Example

```

>>> from nipy.workflows.dmri.fsl import tbss
>>> tbss2 = create_tbss_2_reg(name="tbss2")
>>> tbss2.inputs.inputnode.target = fsl.Info.standard_image("FMRIB58_FA_1mm.nii.gz")
>>> tbss2.inputs.inputnode.fa_list = ['s1_FA.nii', 's2_FA.nii', 's3_FA.nii']
>>> tbss2.inputs.inputnode.mask_list = ['s1_mask.nii', 's2_mask.nii', 's3_mask.nii']

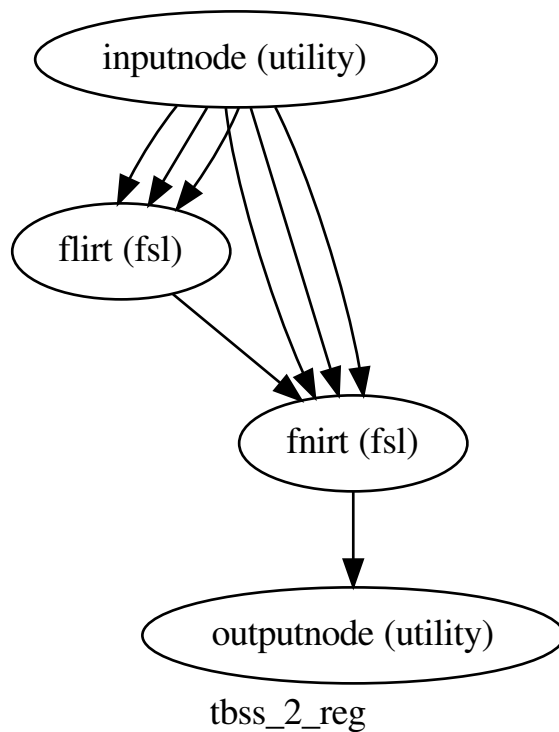
```


Inputs:

```
inputnode.fa_list  
inputnode.mask_list  
inputnode.target
```

Outputs:

```
outputnode.field_list
```

Graph**2.11.3 create_tbss_3_postreg()**[Link to code](#)

Post-registration processing: derive mean_FA and mean_FA_skeleton from mean of all subjects in study. Target is assumed to be FMRIB58_FA_1mm. A pipeline that does the same as 'tbss_3_postreg -S' script from FSL Setting 'estimate_skeleton to False will use precomputed FMRIB58_FA-skeleton_1mm skeleton (same as 'tbss_3_postreg -T').

Example

```
>>> from nipype.workflows.dmri.fsl import tbss
>>> tbss3 = tbss.create_tbss_3_postreg()
>>> tbss3.inputs.inputnode.fa_list = ['s1_wrapped_FA.nii', 's2_wrapped_FA.nii',
↪ 's3_wrapped_FA.nii']
```

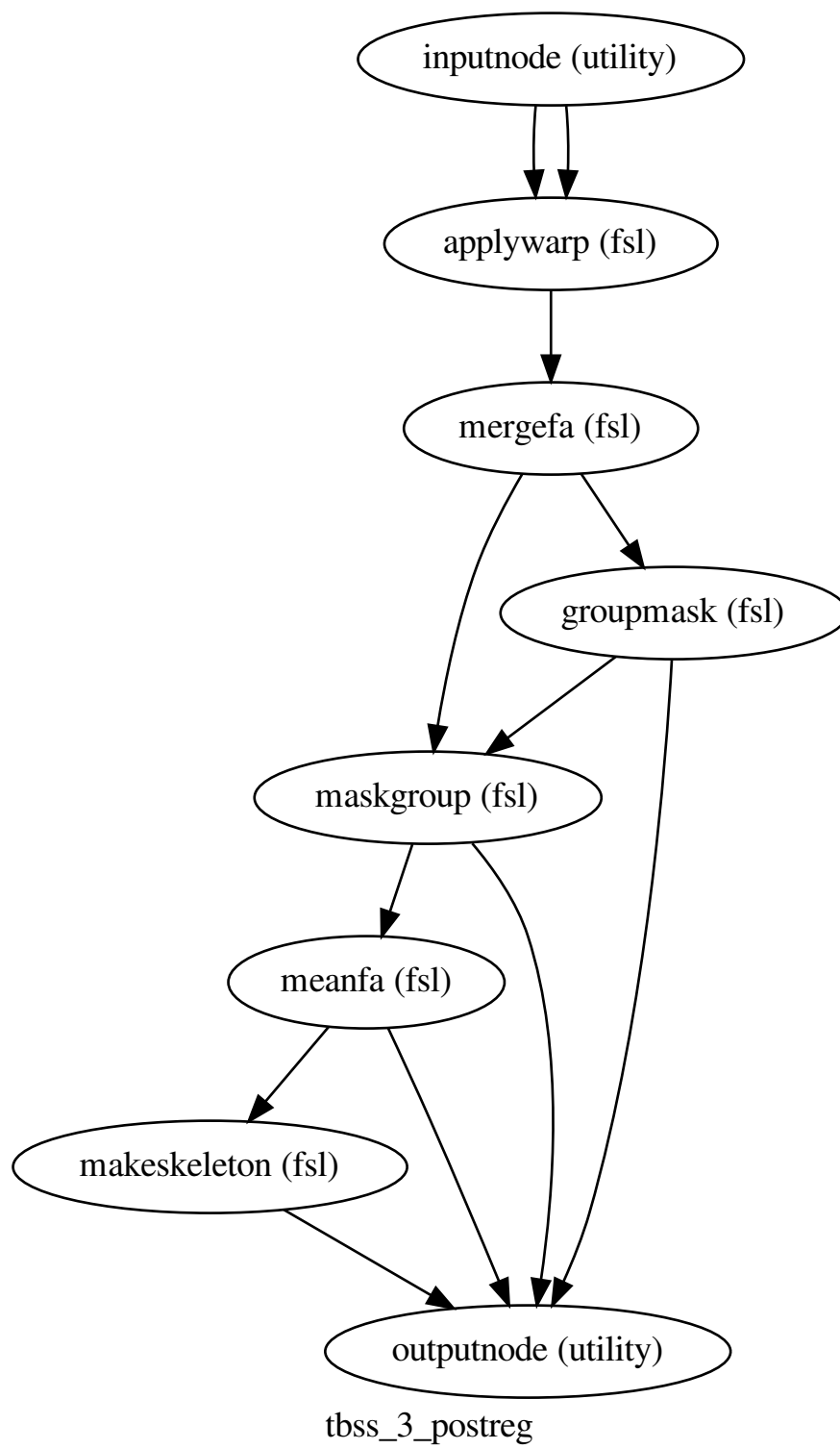
Inputs:

```
inputnode.field_list
inputnode.fa_list
```

Outputs:

```
outputnode.groupmask
outputnode.skeleton_file
outputnode.meanfa_file
outputnode.mergefa_file
```

Graph



2.11.4 `create_tbss_4_prestats()`

[Link to code](#)

Post-registration processing: Creating skeleton mask using a threshold projecting all FA data onto skeleton.

A pipeline that does the same as `tbss_4_prestats` script from FSL

Example

```
>>> from nipy.workflows.dmri.fsl import tbss
>>> tbss4 = tbss.create_tbss_4_prestats(name='tbss4')
>>> tbss4.inputs.inputnode.skeleton_thresh = 0.2
```

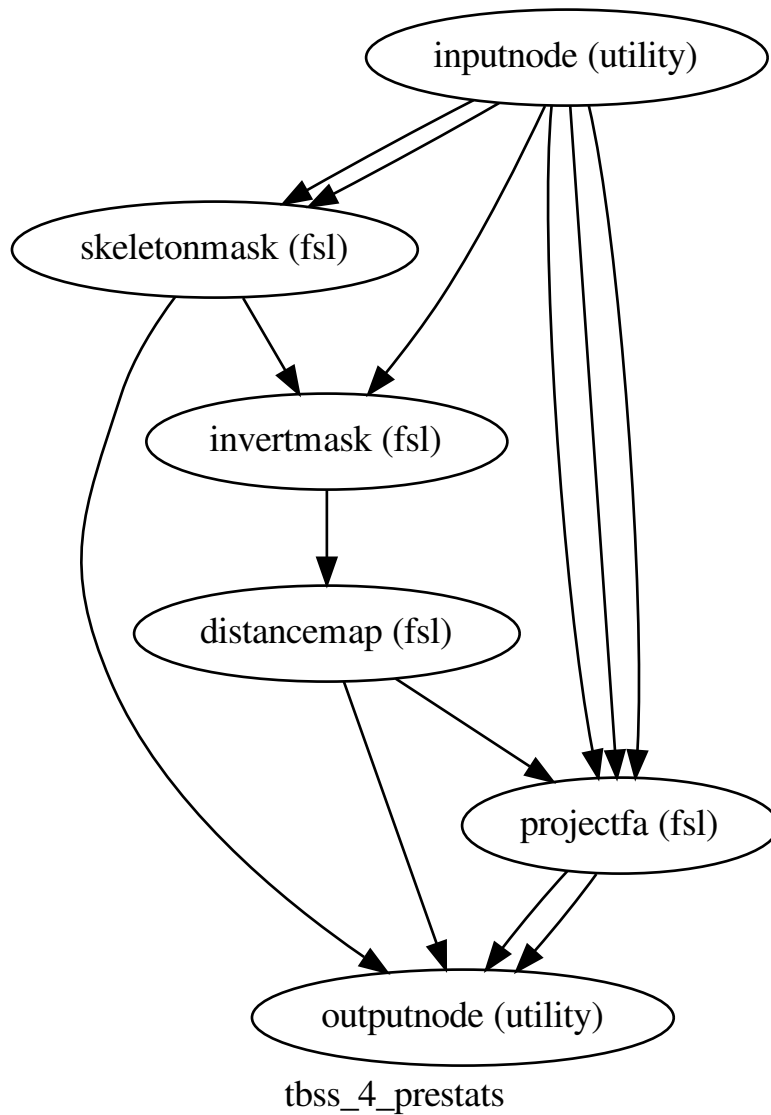
Inputs:

```
inputnode.skeleton_thresh
inputnode.groupmask
inputnode.skeleton_file
inputnode.meanfa_file
inputnode.mergefa_file
```

Outputs:

```
outputnode.all_FA_skeletonised
outputnode.mean_FA_skeleton_mask
outputnode.distance_map
outputnode.skeleton_file
```

Graph



2.11.5 create_tbss_all()

[Link to code](#)

Create a pipeline that combines create_tbss_* pipelines

Example

```
>>> from nipy.workflows.dmri.fsl import tbss
>>> tbss_wf = tbss.create_tbss_all('tbss', estimate_skeleton=True)
>>> tbss_wf.inputs.inputnode.skeleton_thresh = 0.2
>>> tbss_wf.inputs.inputnode.fa_list = ['s1_wrapped_FA.nii', 's2_wrapped_FA.nii',
↪ 's3_wrapped_FA.nii']
```

```
>>> tbss_wf = tbss.create_tbss_all('tbss', estimate_skeleton=False)
>>> tbss_wf.inputs.inputnode.skeleton_thresh = 0.2
>>> tbss_wf.inputs.inputnode.fa_list = ['s1_wrapped_FA.nii', 's2_wrapped_FA.nii',
↪ 's3_wrapped_FA.nii']
```

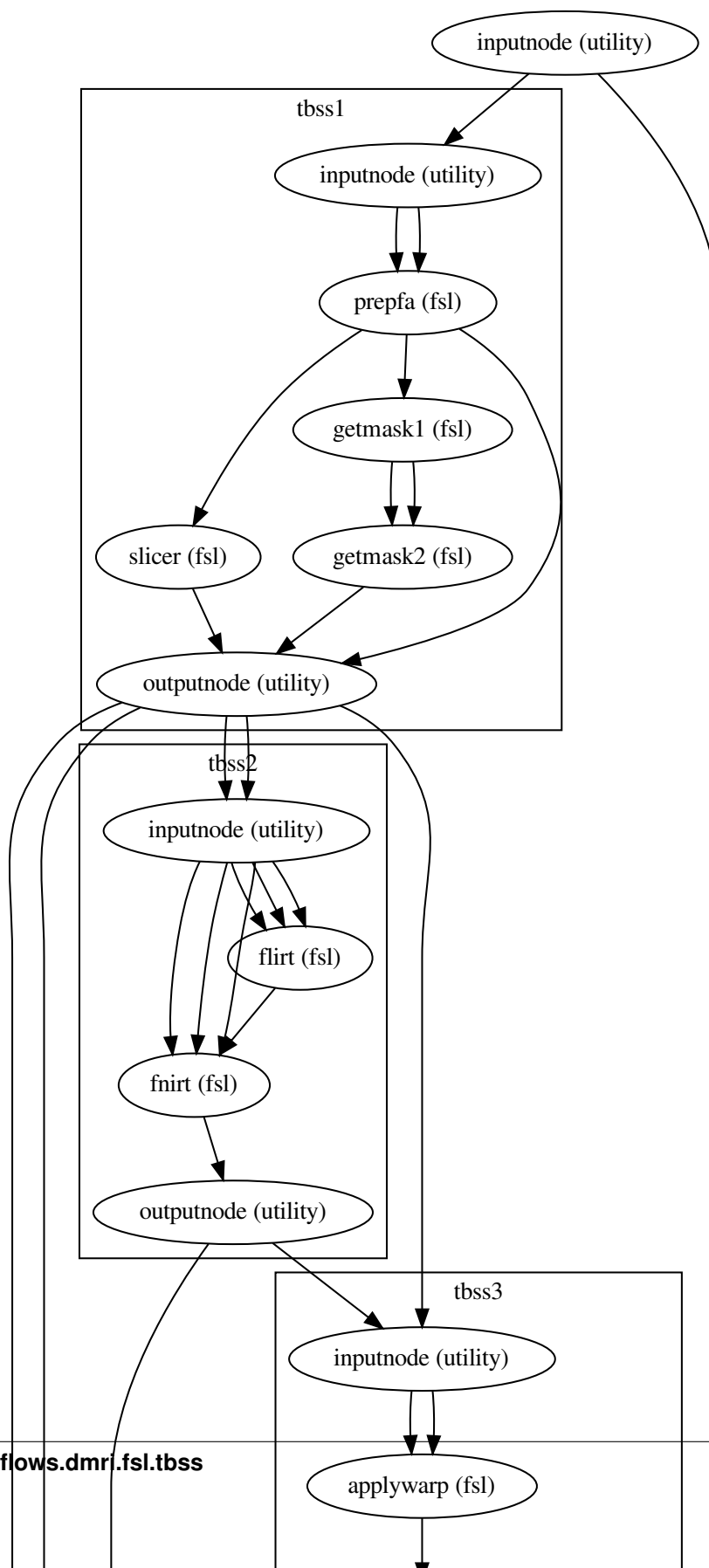
Inputs:

```
inputnode.fa_list
inputnode.skeleton_thresh
```

Outputs:

```
outputnode.meanfa_file
outputnode.projectedfa_file
outputnode.skeleton_file
outputnode.skeleton_mask
```

Graph



2.11.6 create_tbss_non_FA()

[Link to code](#)

A pipeline that implement tbss_non_FA in FSL

Example

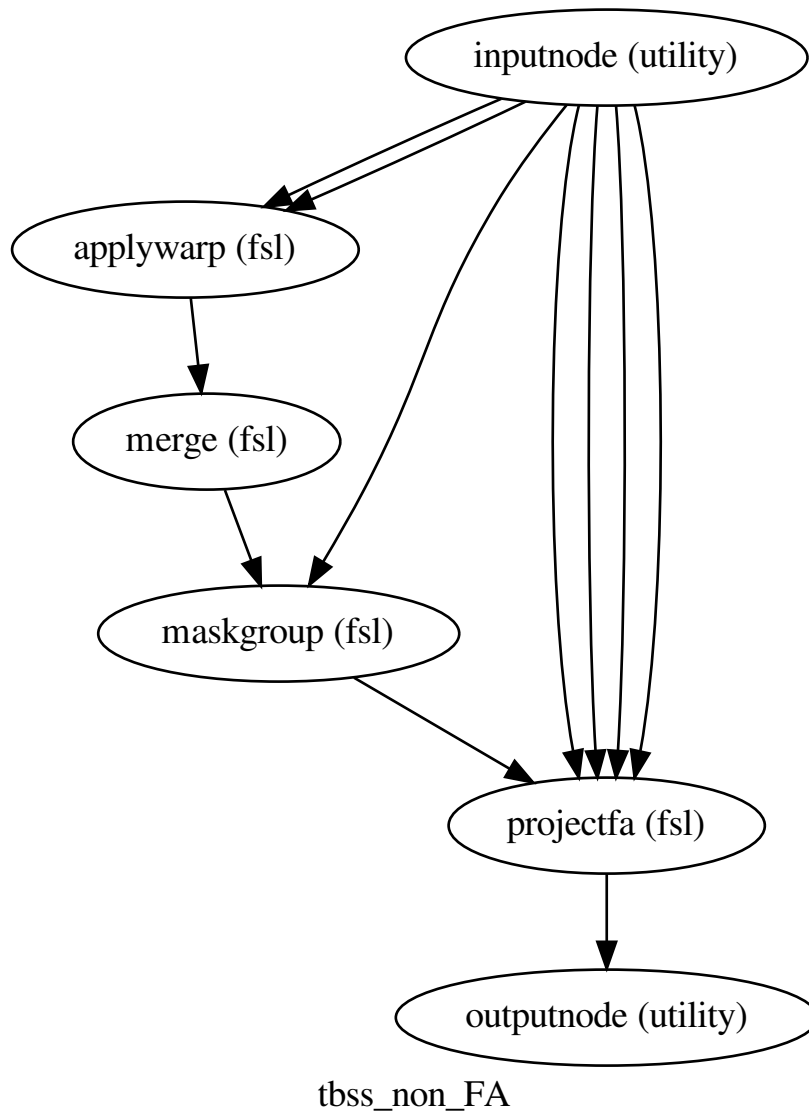
```
>>> from nipyre.workflows.dmri.fsl import tbss
>>> tbss_MD = tbss.create_tbss_non_FA()
>>> tbss_MD.inputs.inputnode.file_list = []
>>> tbss_MD.inputs.inputnode.field_list = []
>>> tbss_MD.inputs.inputnode.skeleton_thresh = 0.2
>>> tbss_MD.inputs.inputnode.groupmask = './xxx'
>>> tbss_MD.inputs.inputnode.meanfa_file = './xxx'
>>> tbss_MD.inputs.inputnode.distance_map = []
>>> tbss_MD.inputs.inputnode.all_FA_file = './xxx'
```

Inputs:

```
inputnode.file_list
inputnode.field_list
inputnode.skeleton_thresh
inputnode.groupmask
inputnode.meanfa_file
inputnode.distance_map
inputnode.all_FA_file
```

Outputs:

```
outputnode.projected_nonFA_file
```


Graph**2.11.7 tbss1_op_string()**[Link to code](#)**2.11.8 tbss4_op_string()**[Link to code](#)

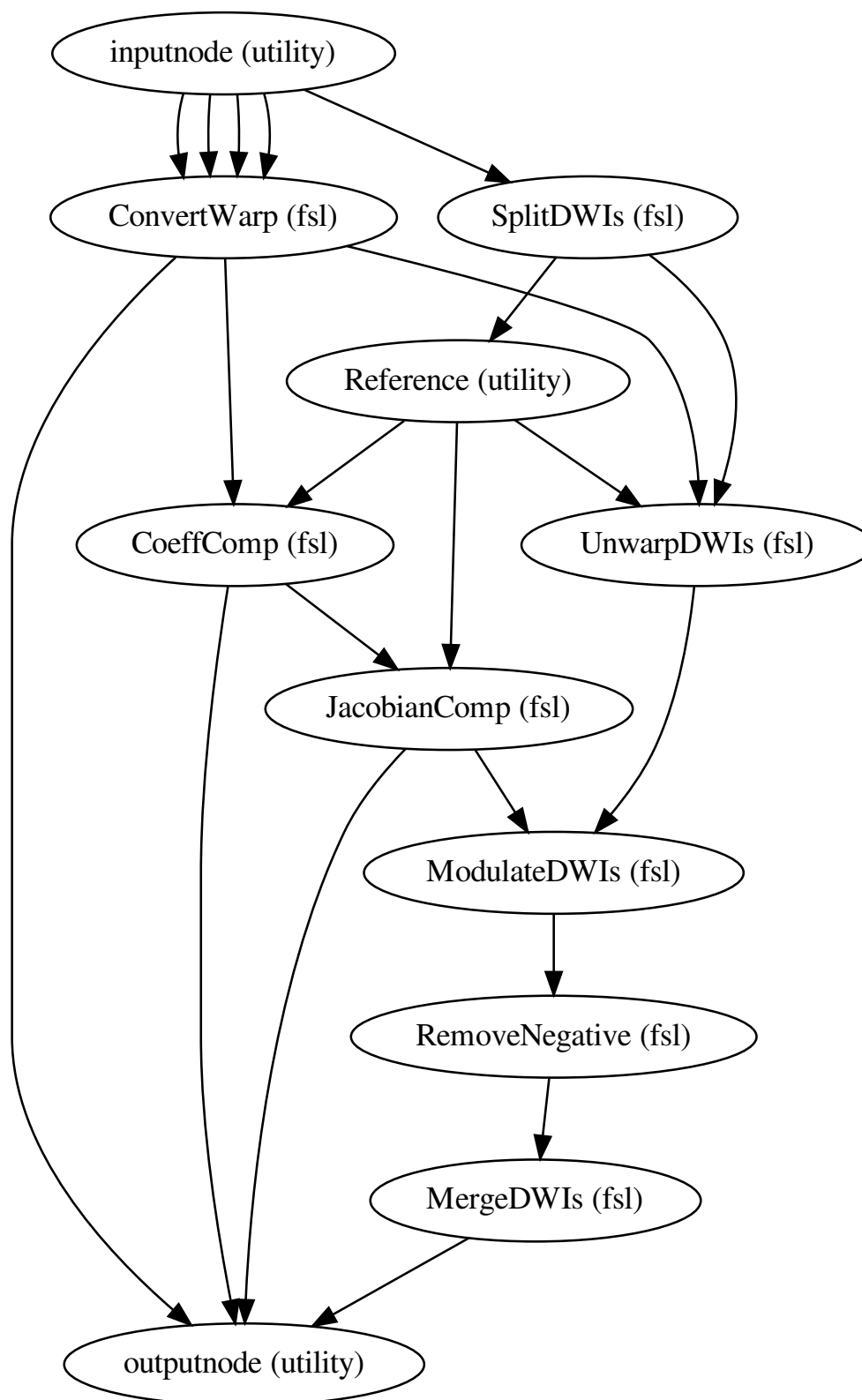
2.12 workflows.dmri.fsl.utils

2.12.1 `apply_all_corrections()`

[Link to code](#)

Combines two lists of linear transforms with the deformation field map obtained typically after the SDC process. Additionally, computes the corresponding bspline coefficients and the map of determinants of the jacobian.

Graph



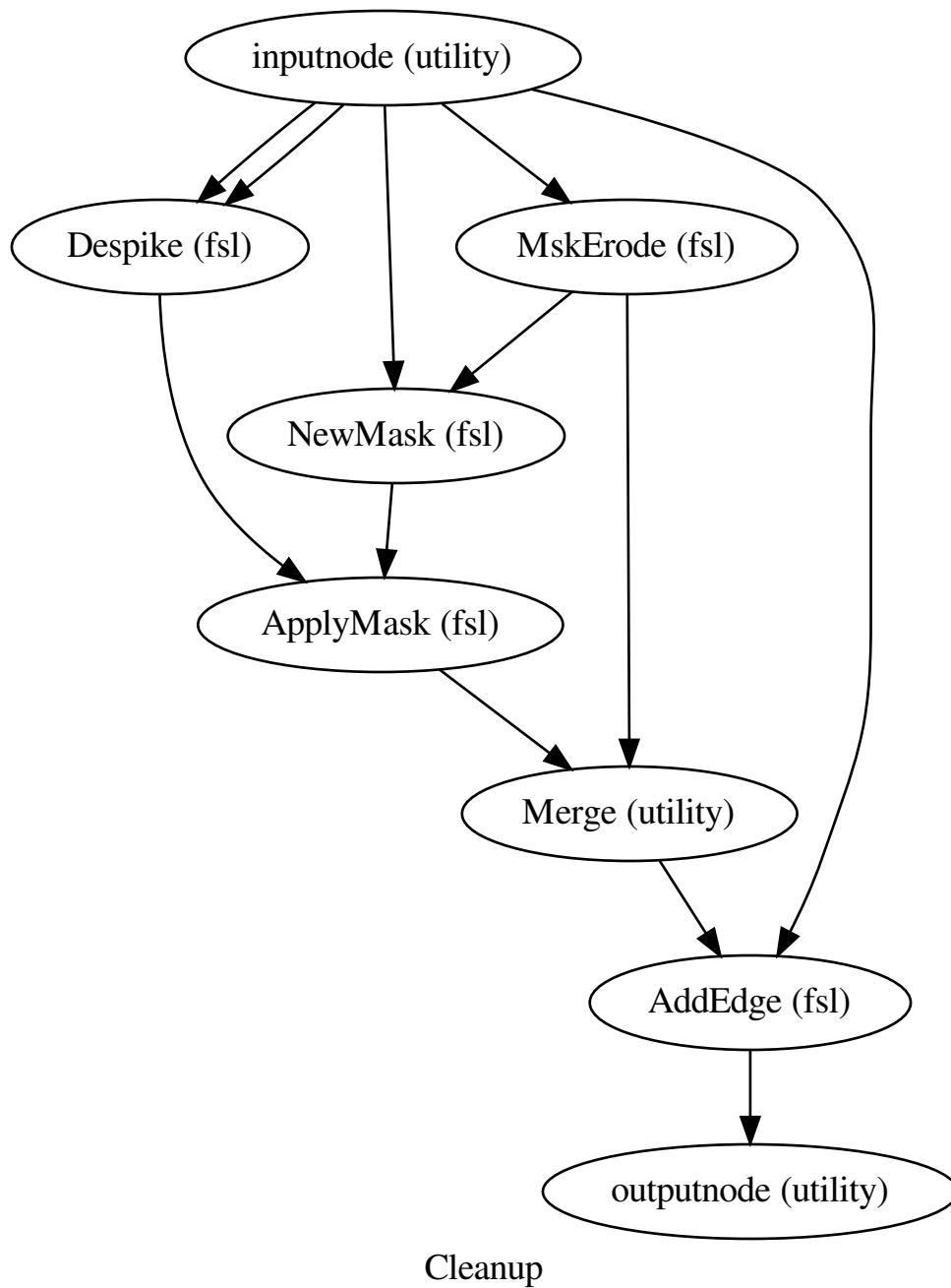
UnwarpArtifacts

2.12.2 cleanup_edge_pipeline()

[Link to code](#)

Perform some de-spiking filtering to clean up the edge of the fieldmap (copied from fsl_prepare_fieldmap)

Graph

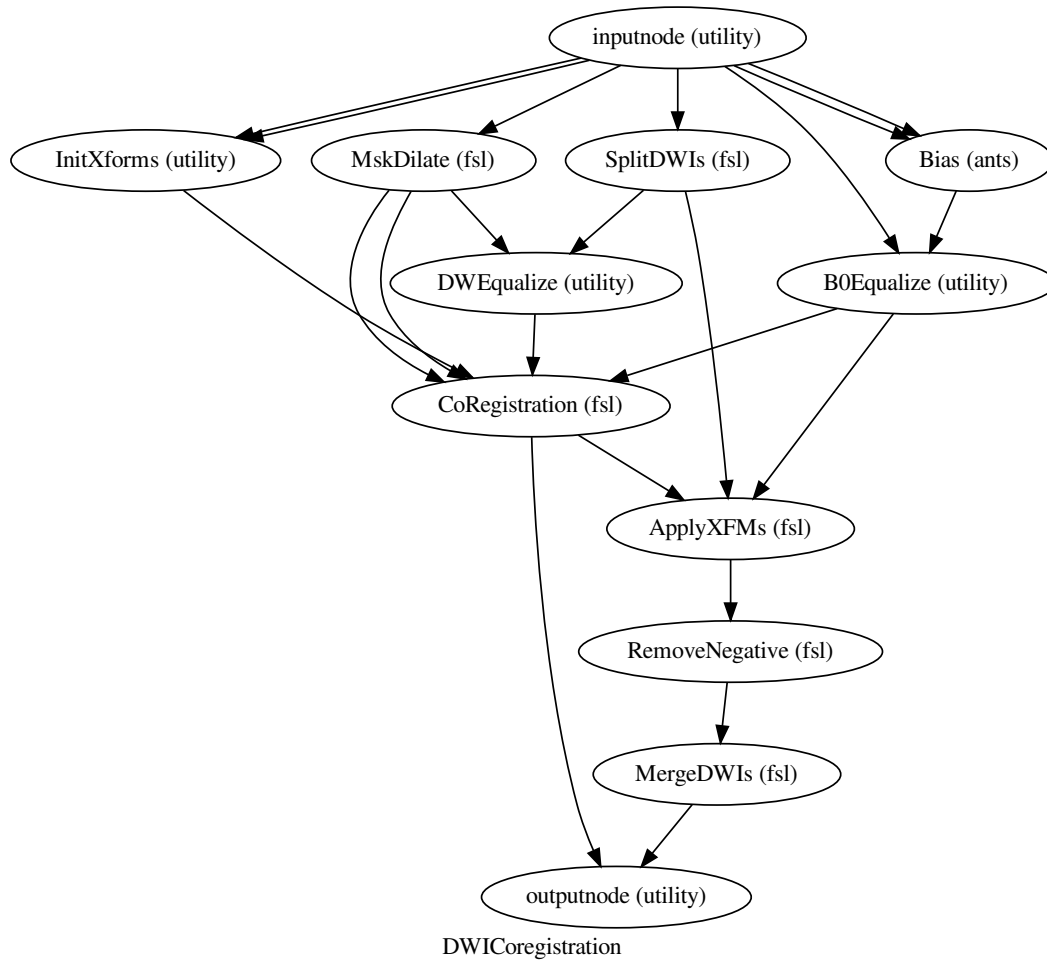


2.12.3 dwi_flirt()

[Link to code](#)

Generates a workflow for linear registration of dwi volumes

Graph

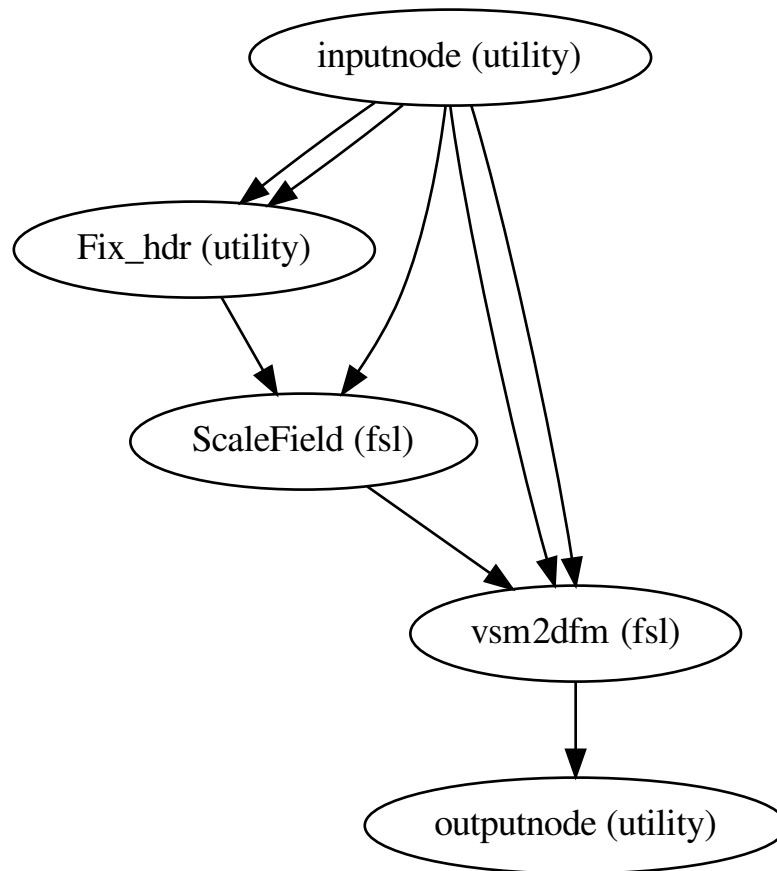


2.12.4 vsm2warp()

[Link to code](#)

Converts a voxel shift map (vsm) to a displacements field (warp).

Graph



Shiftmap2Warping

2.12.5 add_empty_vol()[Link to code](#)

Adds an empty vol to the phase difference image

2.12.6 b0_average()[Link to code](#)

A function that averages the *b0* volumes from a DWI dataset. As current dMRI data are being acquired with all b-values > 0.0, the *lowb* volumes are selected by specifying the parameter `max_b`.

Warning: *b0* should be already registered (head motion artifact should be corrected).

2.12.7 `b0_indices()`

[Link to code](#)

Extract the indices of slices in a b-values file with a low b value

2.12.8 `compute_readout()`

[Link to code](#)

Computes readout time from epi params (see [eddy documentation](#)).

Warning: `params['echospadding']` should be in *sec* units.

2.12.9 `copy_hdr()`

[Link to code](#)

2.12.10 `demean_image()`

[Link to code](#)

Demean image data inside mask

2.12.11 `eddy_rotate_bvecs()`

[Link to code](#)

Rotates the input bvec file accordingly with a list of parameters sourced from `eddy`, as explained [here](#).

2.12.12 `enhance()`

[Link to code](#)

2.12.13 `extract_bval()`

[Link to code](#)

Writes an image containing only the volumes with b-value specified at input

2.12.14 `hmc_split()`

[Link to code](#)

Selects the reference and moving volumes from a dwi dataset for the purpose of HMC.

2.12.15 `insert_mat()`

[Link to code](#)

2.12.16 `rads2radsec()`

[Link to code](#)

Converts input phase difference map to rads

2.12.17 `recompose_dwi()`

[Link to code](#)

Recompose back the dMRI data accordingly the b-values table after EC correction

2.12.18 `recompose_xfm()`

[Link to code](#)

Insert identity transformation matrices in b0 volumes to build up a list

2.12.19 `remove_comp()`

[Link to code](#)

Removes the volume `valid` from the 4D nifti file

2.12.20 `reorient_bvecs()`

[Link to code](#)

Checks reorientations of `in_dwi` w.r.t. `old_dwi` and reorients the `in_bvec` table accordingly.

2.12.21 `rotate_bvecs()`

[Link to code](#)

Rotates the input bvec file accordingly with a list of matrices.

Note: the input affine matrix transforms points in the destination image to their corresponding coordinates in the original image. Therefore, this matrix should be inverted first, as we want to know the target position of \vec{r} .

2.12.22 `siemens2rads()`

[Link to code](#)

Converts input phase difference map to rads

2.12.23 `time_avg()`

[Link to code](#)

Average the input time-series, selecting the indices given in index

Warning: time steps should be already registered (corrected for head motion artifacts).

2.13 `workflows.dmri.mrtrix.connectivity_mapping`

2.13.1 `create_connectivity_pipeline()`

[Link to code](#)

Creates a pipeline that does the same connectivity processing as in the *dmri: Connectivity - MRtrix, CMTK, FreeSurfer* example script. Given a subject id (and completed Freesurfer reconstruction) diffusion-weighted image, b-values, and b-vectors, the workflow will return the subject's connectome as a Connectome File Format (CFF) file for use in Connectome Viewer (<http://www.cmtk.org>).

Example

```
>>> from nipy.workflows.dmri.mrtrix.connectivity_mapping import create_
    connectivity_pipeline
>>> connmapper = create_connectivity_pipeline("nipy_conmap")
>>> connmapper.inputs.inputnode.subjects_dir = '.'
>>> connmapper.inputs.inputnode.subject_id = 'subj1'
```

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```

>>> conmapper.inputs.inputnode.dwi = 'data.nii.gz'
>>> conmapper.inputs.inputnode.bvecs = 'bvecs'
>>> conmapper.inputs.inputnode.bvals = 'bvals'
>>> conmapper.run()                                # doctest: +SKIP

```

Inputs:

```

inputnode.subject_id
inputnode.subjects_dir
inputnode.dwi
inputnode.bvecs
inputnode.bvals
inputnode.resolution_network_file

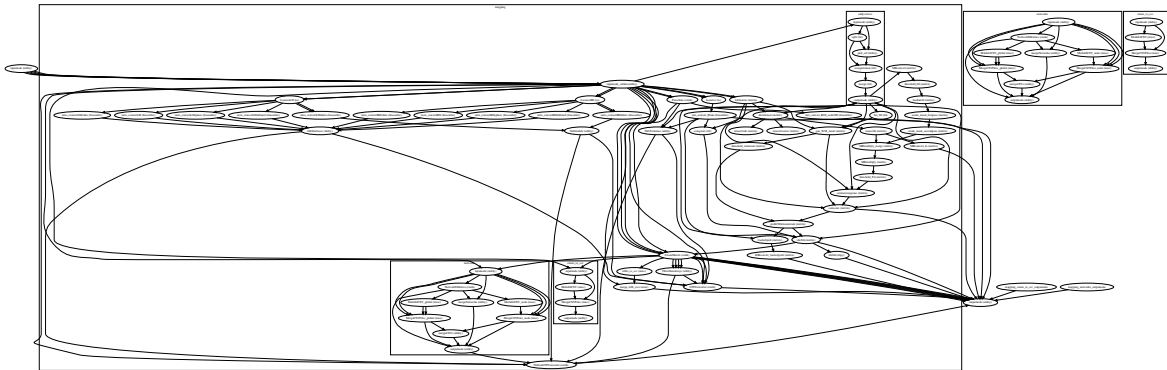
```

Outputs:

```

outputnode.connectome
outputnode.cmatrix
outputnode.networks
outputnode.fa
outputnode.struct
outputnode.tracts
outputnode.rois
outputnode.odfs
outputnode.filtered_tractography
outputnode.tdi
outputnode.nxstatscff
outputnode.nxcsv
outputnode.cmatrices_csv
outputnode.mean_fiber_length
outputnode.median_fiber_length
outputnode.fiber_length_std

```

Graph

2.14 workflows.dmri.mrtrix.diffusion

2.14.1 create_mrtrix_dti_pipeline()

[Link to code](#)

Creates a pipeline that does the same diffusion processing as in the `../users/examples/dmri_mrtrix_dti` example script. Given a diffusion-weighted image, b-values, and b-vectors, the workflow will return the tractography

computed from spherical deconvolution and probabilistic streamline tractography

Example

```
>>> dti = create_mrtrix_dti_pipeline("mrtrix_dti")
>>> dti.inputs.inputnode.dwi = 'data.nii'
>>> dti.inputs.inputnode.bvals = 'bvals'
>>> dti.inputs.inputnode.bvecs = 'bvecs'
>>> dti.run() # doctest: +SKIP
```

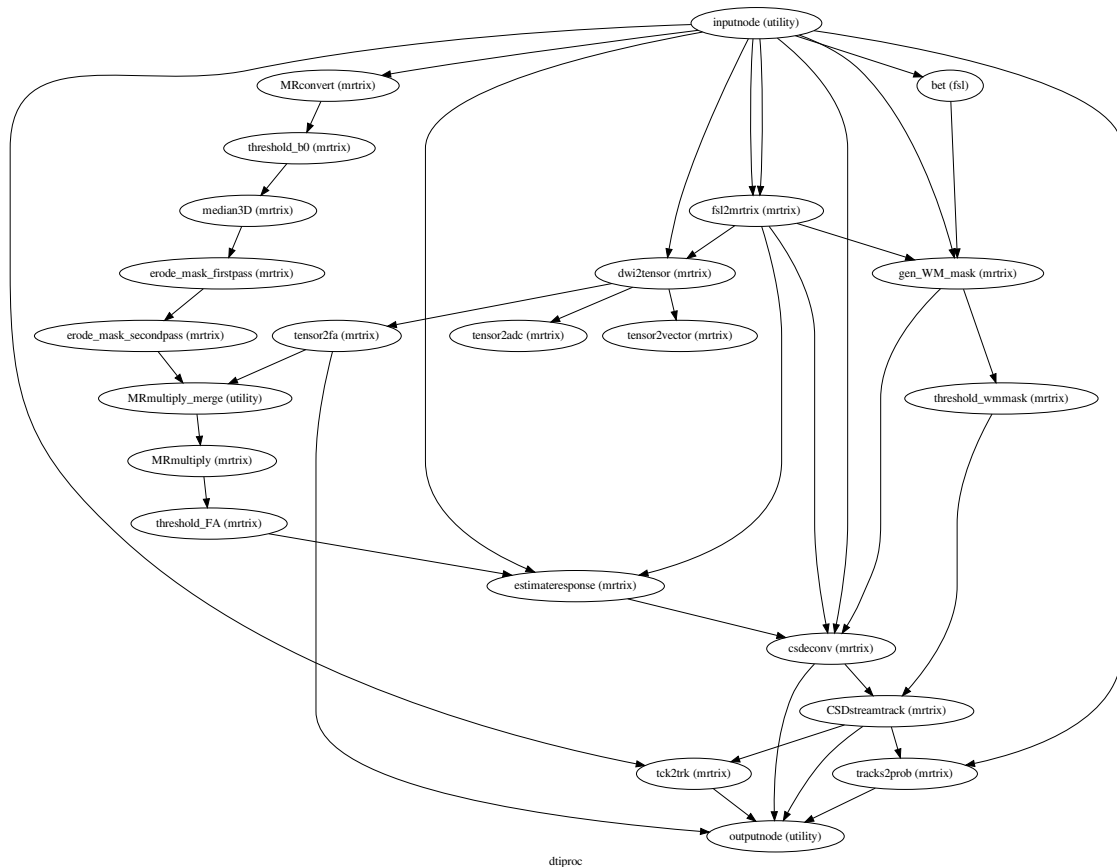
Inputs:

```
inputnode.dwi
inputnode.bvecs
inputnode.bvals
```

Outputs:

```
outputnode.fa
outputnode.tdi
outputnode.tracts_tck
outputnode.tracts_trk
outputnode.csdeconv
```

Graph



2.15 workflows.dmri.mrtrix.group_connectivity

2.15.1 create_group_connectivity_pipeline()

[Link to code](#)

Creates a pipeline that performs MRtrix structural connectivity processing on groups of subjects. Given a diffusion-weighted image, and text files containing the associated b-values and b-vectors, the workflow will return each subjects' connectomes in a Connectome File Format (CFF) file, for use in Connectome Viewer (<http://www.cmtk.org>).

Example

```
>>> import nipype.interfaces.freesurfer as fs
>>> import nipype.workflows.dmri.mrtrix.group_connectivity as groupwork
>>> import cmp # doctest: +SKIP
>>> from nipype.testing import example_data
>>> subjects_dir = '.'
>>> data_dir = '.'
>>> output_dir = '.'
>>> fs.FSCommand.set_default_subjects_dir(subjects_dir)
>>> group_list = {}
>>> group_list['group1'] = ['subj1', 'subj2']
>>> group_list['group2'] = ['subj3', 'subj4']
>>> template_args = dict(dwi=[['subject_id', 'dwi']], bvecs=[['subject_id', 'bvecs'
↪']], bvals=[['subject_id', 'bvals']])
>>> group_id = 'group1'
>>> llpipeline = groupwork.create_group_connectivity_pipeline(group_list, group_
↪id, data_dir, subjects_dir, output_dir, template_args)
>>> parcellation_name = 'scale500'
>>> llpipeline.inputs.connectivity.mapping.Parcellate.parcellation_name = _
↪parcellation_name
>>> cmp_config = cmp.configuration.PipelineConfiguration() # doctest: +SKIP
>>> cmp_config.parcellation_scheme = "Lausanne2008" # doctest: +SKIP
>>> llpipeline.inputs.connectivity.mapping.inputnode_within.resolution_network_
↪file = cmp_config._get_lausanne_parcellation('Lausanne2008')[parcellation_name][
↪'node_information_graphml'] # doctest: +SKIP
>>> llpipeline.run() # doctest: +SKIP
```

Inputs:

```
group_list: Dictionary of subject lists, keyed by group name
group_id: String containing the group name
data_dir: Path to the data directory
subjects_dir: Path to the Freesurfer 'subjects' directory
output_dir: Path for the output files
template_args_dict: Dictionary of template arguments for the connectivity_
↪pipeline datasources
                    e.g.    info = dict(dwi=[['subject_id', 'dwi']],
                                         bvecs=[['subject_id', 'bvecs']],
                                         bvals=[['subject_id', 'bvals']])
```


3.1 workflows.fmri.fsl.estimate

3.1.1 create_fixed_effects_flow()

[Link to code](#)

Create a fixed-effects workflow

This workflow is used to combine registered copes and varcopes across runs for an individual subject

Example

```
>>> fixedfx = create_fixed_effects_flow()
>>> fixedfx.base_dir = '.'
>>> fixedfx.inputs.inputs.spec.copes = [['cope1run1.nii.gz', 'cope1run2.nii.gz'], [
↪ 'cope2run1.nii.gz', 'cope2run2.nii.gz']] # per contrast
>>> fixedfx.inputs.inputs.spec.varcopes = [['varcope1run1.nii.gz', 'varcope1run2.
↪ nii.gz'], ['varcope2run1.nii.gz', 'varcope2run2.nii.gz']] # per contrast
>>> fixedfx.inputs.inputs.spec.dof_files = ['dofrun1', 'dofrun2'] # per run
>>> fixedfx.run() #doctest: +SKIP
```

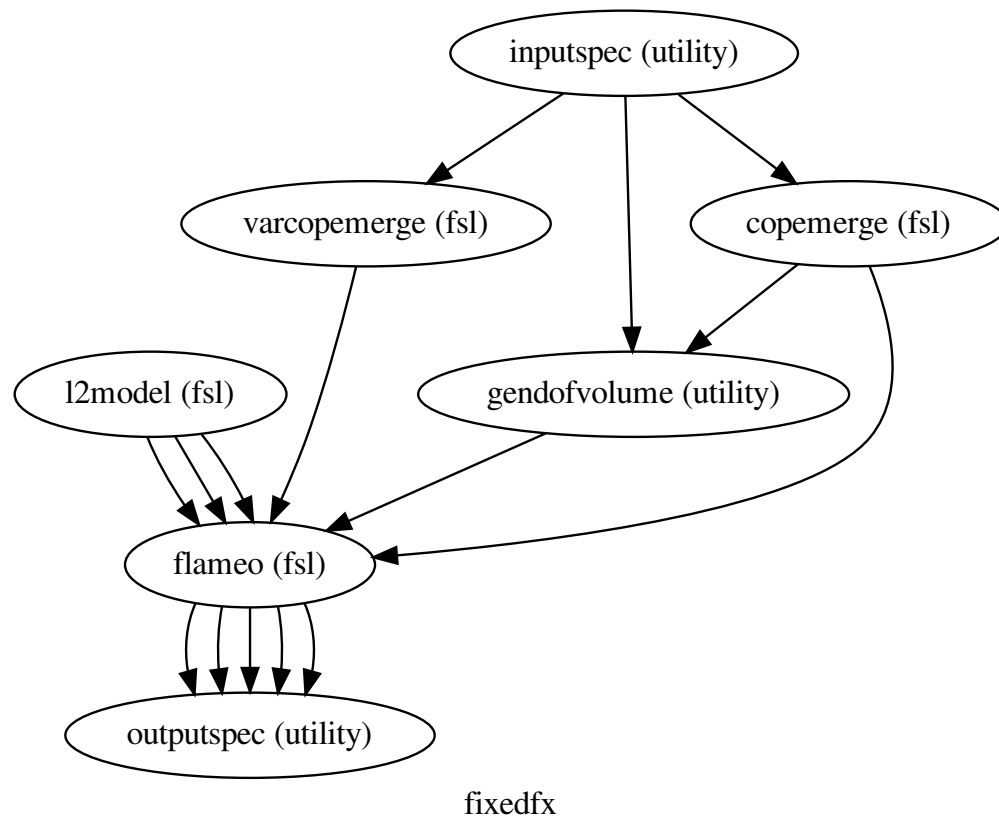
Inputs:

```
inputs.spec.copes : list of list of cope files (one list per contrast)
inputs.spec.varcopes : list of list of varcope files (one list per
                      contrast)
inputs.spec.dof_files : degrees of freedom files for each run
```

Outputs:

```
outputs.spec.res4d : 4d residual time series
outputs.spec.copes : contrast parameter estimates
outputs.spec.varcopes : variance of contrast parameter estimates
outputs.spec.zstats : z statistics of contrasts
outputs.spec.tstats : t statistics of contrasts
```

Graph



3.1.2 create_modelfit_workflow()

[Link to code](#)

Create an FSL individual modelfitting workflow

Example

```

>>> modelfit = create_modelfit_workflow()
>>> modelfit.base_dir = '.'
>>> info = dict()
>>> modelfit.inputs.inputspec.session_info = info
>>> modelfit.inputs.inputspec.interscan_interval = 3.
>>> modelfit.inputs.inputspec.film_threshold = 1000
>>> modelfit.run() #doctest: +SKIP

```

Inputs:

```

inputspec.session_info : info generated by modelgen.SpecifyModel
inputspec.interscan_interval : interscan interval
inputspec.contrasts : list of contrasts

```

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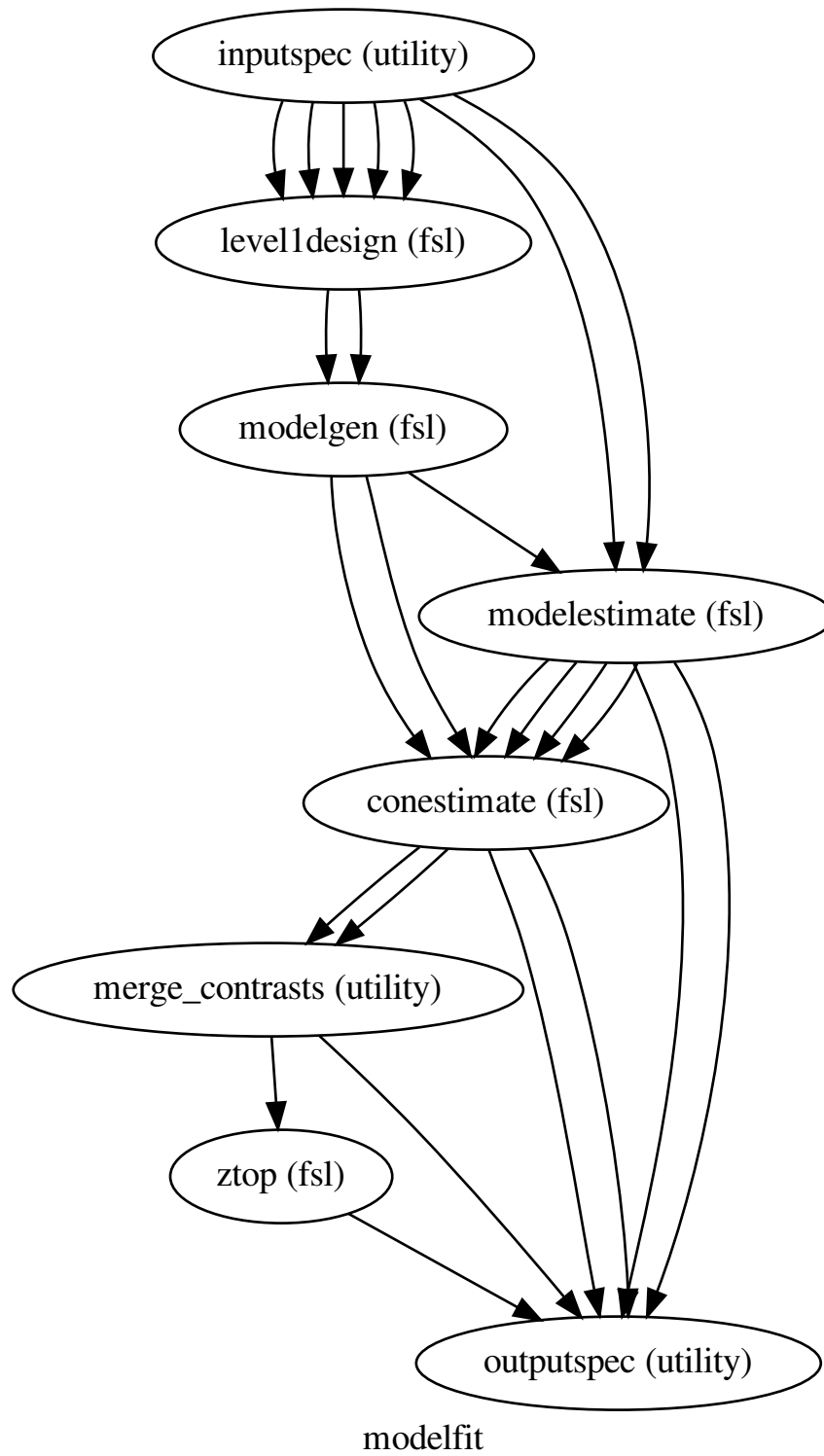
(continued from previous page)

```
inputspec.film_threshold : image threshold for FILM estimation
inputspec.model_serial_correlations
inputspec.bases
```

Outputs:

```
outputspec.copes
outputspec.varcopes
outputspec.dof_file
outputspec.pfiles
outputspec.zfiles
outputspec.parameter_estimates
```

Graph

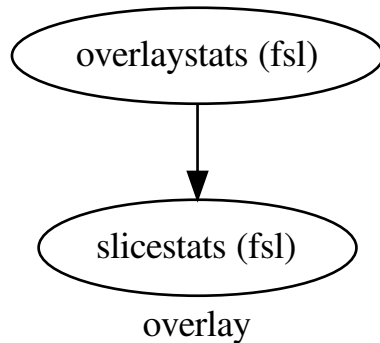


3.1.3 create_overlay_workflow()

[Link to code](#)

Setup overlay workflow

Graph



3.2 workflows.fmri.fsl.preprocess

3.2.1 create_featreg_preproc()

[Link to code](#)

Create a FEAT preprocessing workflow with registration to one volume of the first run

Parameters

```

name : name of workflow (default: featpreproc)
highpass : boolean (default: True)
whichvol : which volume of the first run to register to ('first', 'middle', 'last'
↔, 'mean')
whichrun : which run to draw reference volume from (integer index or 'first',
↔ 'middle', 'last')
  
```

Inputs:

```

inputspec.func : functional runs (filename or list of filenames)
inputspec.fwhm : fwhm for smoothing with SUSAN
inputspec.highpass : HWHM in TRs (if created with highpass=True)
  
```

Outputs:

```

outputspec.reference : volume to which runs are realigned
outputspec.motion_parameters : motion correction parameters
outputspec.realigned_files : motion corrected files
outputspec.motion_plots : plots of motion correction parameters
outputspec.mask : mask file used to mask the brain
outputspec.smoothed_files : smoothed functional data
  
```

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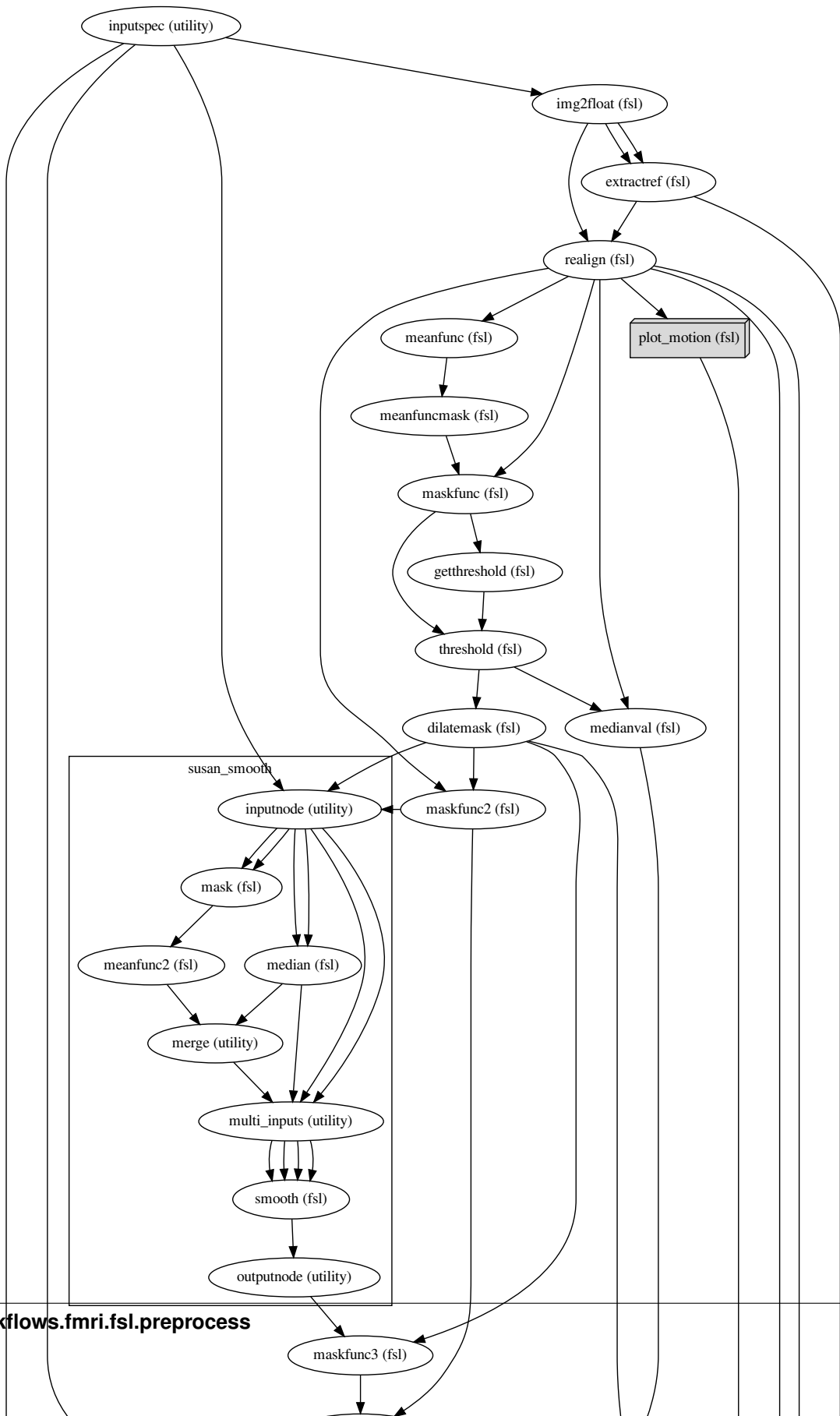
```
outputspec.highpassed_files : highpassed functional data (if highpass=True)
outputspec.mean : mean file
```

Example

```
>>> preproc = create_featreg_preproc()
>>> preproc.inputs.inputsfunc = ['f3.nii', 'f5.nii']
>>> preproc.inputs.inputsfunc.fwhm = 5
>>> preproc.inputs.inputsfunc.highpass = 128./(2*2.5)
>>> preproc.base_dir = '/tmp'
>>> preproc.run() # doctest: +SKIP
```

```
>>> preproc = create_featreg_preproc(highpass=False, whichvol='mean')
>>> preproc.inputs.inputsfunc = 'f3.nii'
>>> preproc.inputs.inputsfunc.fwhm = 5
>>> preproc.base_dir = '/tmp'
>>> preproc.run() # doctest: +SKIP
```

Graph



3.2.2 create_fsl_fs_preproc()

[Link to code](#)

Create a FEAT preprocessing workflow together with freesurfer

Parameters

```
name : name of workflow (default: preproc)
highpass : boolean (default: True)
whichvol : which volume of the first run to register to ('first', 'middle', 'mean
→')
```

Inputs:

```
inputspec.func : functional runs (filename or list of filenames)
inputspec.fwhm : fwhm for smoothing with SUSAN
inputspec.highpass : HWHM in TRs (if created with highpass=True)
inputspec.subject_id : freesurfer subject id
inputspec.subjects_dir : freesurfer subjects dir
```

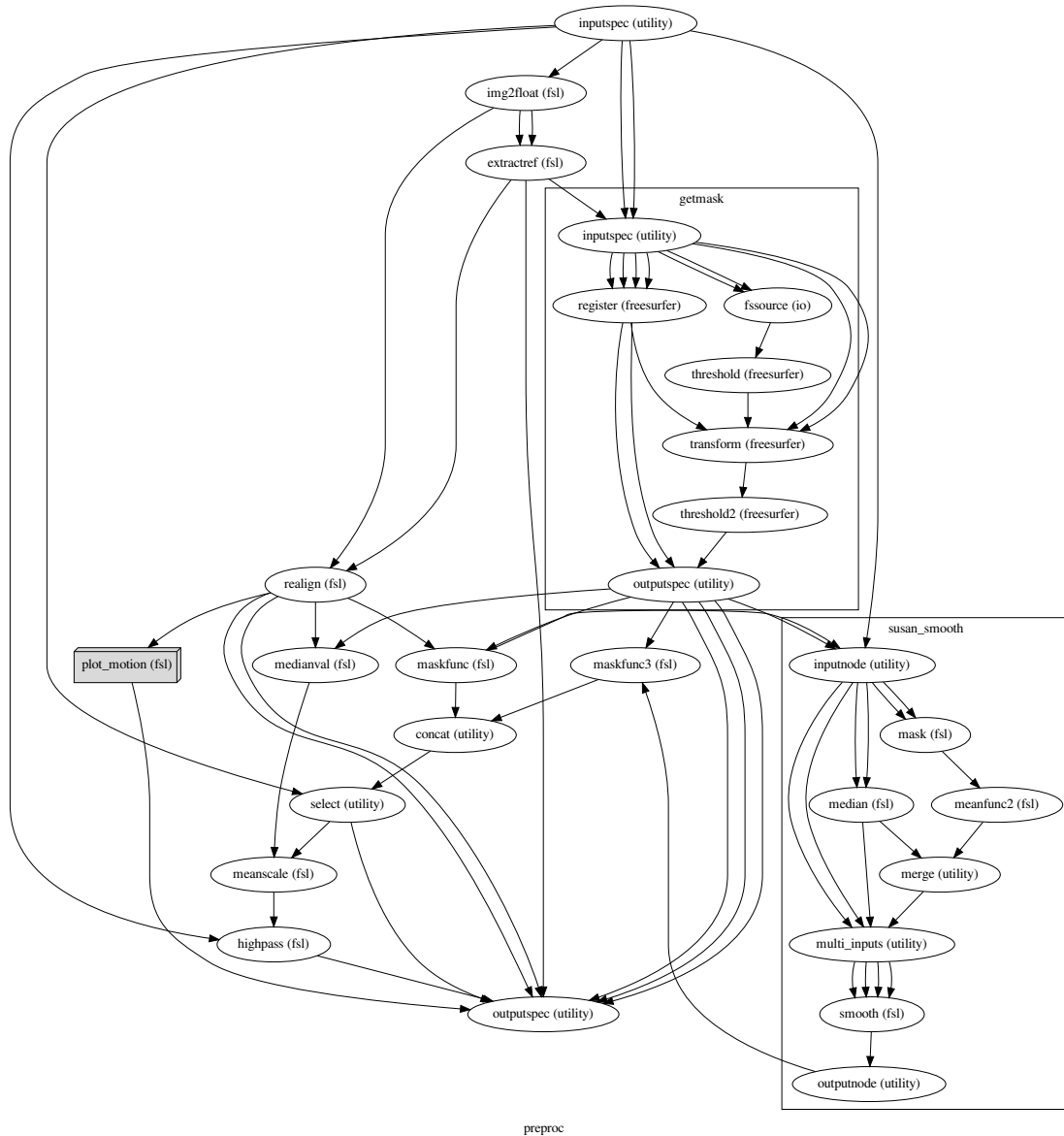
Outputs:

```
outputspec.reference : volume to which runs are realigned
outputspec.motion_parameters : motion correction parameters
outputspec.realigned_files : motion corrected files
outputspec.motion_plots : plots of motion correction parameters
outputspec.mask_file : mask file used to mask the brain
outputspec.smoothed_files : smoothed functional data
outputspec.highpassed_files : highpassed functional data (if highpass=True)
outputspec.reg_file : bregister registration files
outputspec.reg_cost : bregister registration cost files
```

Example

```
>>> preproc = create_fsl_fs_preproc(whichvol='first')
>>> preproc.inputs.inputspec.highpass = 128./(2*2.5)
>>> preproc.inputs.inputspec.func = ['f3.nii', 'f5.nii']
>>> preproc.inputs.inputspec.subjects_dir = '.'
>>> preproc.inputs.inputspec.subject_id = 's1'
>>> preproc.inputs.inputspec.fwhm = 6
>>> preproc.run() # doctest: +SKIP
```

Graph



3.2.3 create_parallelfat_preproc()

[Link to code](#)

Preprocess each run with FSL independently of the others

Parameters

name : name of workflow (default: featpreproc)
 highpass : boolean (default: **True**)

Inputs:

```
inputspec.func : functional runs (filename or list of filenames)
inputspec.fwhm : fwhm for smoothing with SUSAN
inputspec.highpass : HWHM in TRs (if created with highpass=True)
```

Outputs:

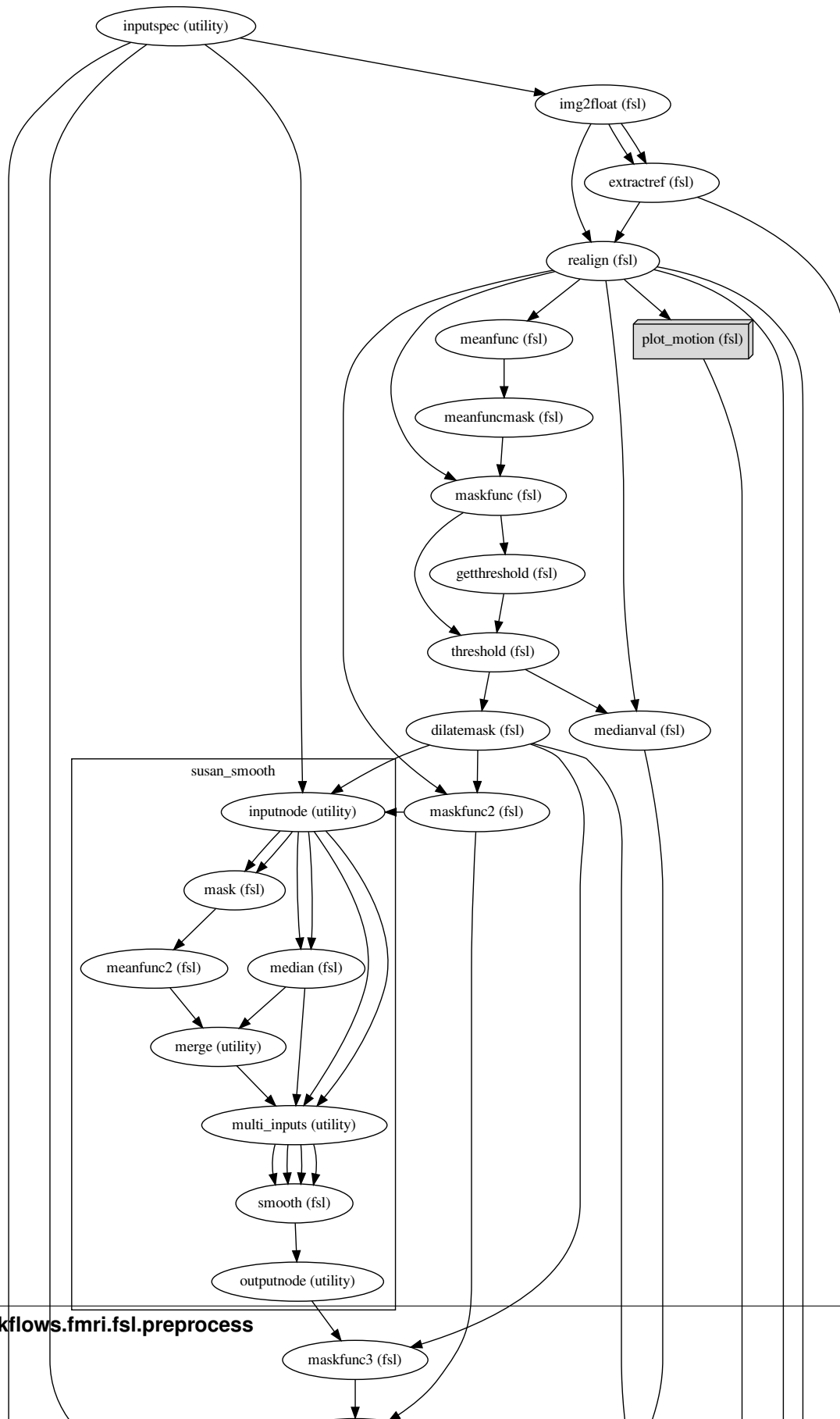
```
outputspec.reference : volume to which runs are realigned
outputspec.motion_parameters : motion correction parameters
outputspec.realigned_files : motion corrected files
outputspec.motion_plots : plots of motion correction parameters
outputspec.mask : mask file used to mask the brain
outputspec.smoothed_files : smoothed functional data
outputspec.highpassed_files : highpassed functional data (if highpass=True)
outputspec.mean : mean file
```

Example

```
>>> preproc = create_parallelfat_preproc()
>>> preproc.inputs.inputspec.func = ['f3.nii', 'f5.nii']
>>> preproc.inputs.inputspec.fwhm = 5
>>> preproc.inputs.inputspec.highpass = 128./(2*2.5)
>>> preproc.base_dir = '/tmp'
>>> preproc.run() # doctest: +SKIP
```

```
>>> preproc = create_parallelfat_preproc(highpass=False)
>>> preproc.inputs.inputspec.func = 'f3.nii'
>>> preproc.inputs.inputspec.fwhm = 5
>>> preproc.base_dir = '/tmp'
>>> preproc.run() # doctest: +SKIP
```

Graph



3.2.4 create_susan_smooth()

[Link to code](#)

Create a SUSAN smoothing workflow

Parameters

```
name : name of workflow (default: susan_smooth)
separate_masks : separate masks for each run
```

Inputs:

```
inputnode.in_files : functional runs (filename or list of filenames)
inputnode.fwhm : fwhm for smoothing with SUSAN (float or list of floats)
inputnode.mask_file : mask used for estimating SUSAN thresholds (but not for
↳smoothing)
```

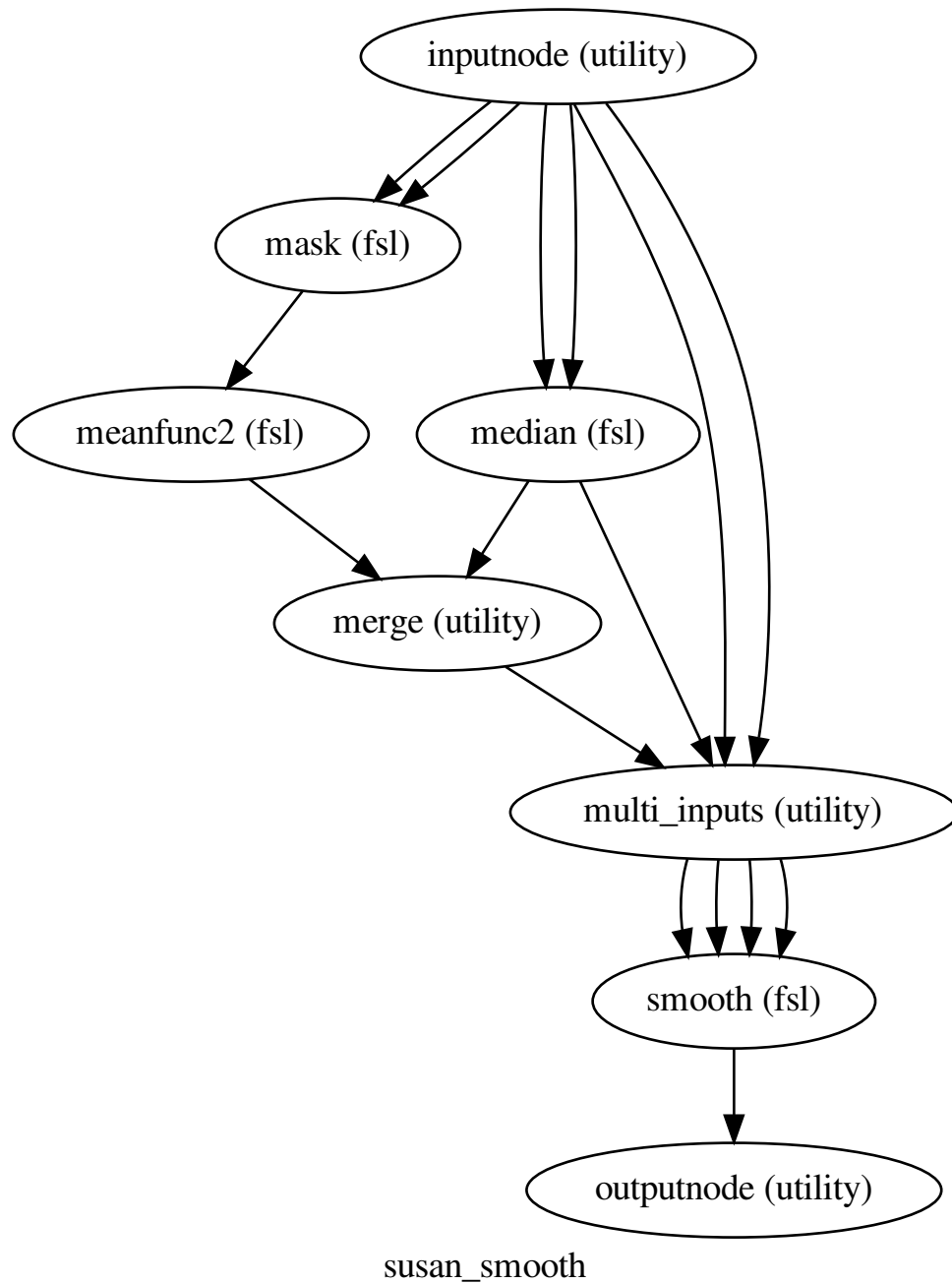
Outputs:

```
outputnode.smoothed_files : functional runs (filename or list of filenames)
```

Example

```
>>> smooth = create_susan_smooth()
>>> smooth.inputs.inputnode.in_files = 'f3.nii'
>>> smooth.inputs.inputnode.fwhm = 5
>>> smooth.inputs.inputnode.mask_file = 'mask.nii'
>>> smooth.run() # doctest: +SKIP
```


Graph

**3.2.5 chooseindex()**[Link to code](#)

3.2.6 create_reg_workflow()

[Link to code](#)

Create a FEAT preprocessing workflow

Parameters

```
name : name of workflow (default: 'registration')
```

Inputs:

```
inputspec.source_files : files (filename or list of filenames to register)
inputspec.mean_image : reference image to use
inputspec.anatomical_image : anatomical image to coregister to
inputspec.target_image : registration target
```

Outputs:

```
outputspec.func2anat_transform : FLIRT transform
outputspec.anat2target_transform : FLIRT+FNIRT transform
outputspec.transformed_files : transformed files in target space
outputspec.transformed_mean : mean image in target space
```

Example

3.2.7 getbtthresh()

[Link to code](#)

3.2.8 getmeanscale()

[Link to code](#)

3.2.9 getthresnop()

[Link to code](#)

3.2.10 getusans()

[Link to code](#)

3.2.11 pickfirst()

[Link to code](#)

3.2.12 pickmiddle()

[Link to code](#)

3.2.13 pickrun()

[Link to code](#)

pick file from list of files

3.2.14 pickvol()

[Link to code](#)

3.3 workflows.fmri.spm.preprocess

3.3.1 create_DARTEL_template()

[Link to code](#)

Create a vbm workflow that generates DARTEL-based template

Example

```
>>> preproc = create_DARTEL_template()
>>> preproc.inputs.inputs.spec.structural_files = [
...     os.path.abspath('s1.nii'), os.path.abspath('s3.nii')]
>>> preproc.inputs.inputs.spec.template_prefix = 'Template'
>>> preproc.run() # doctest: +SKIP
```

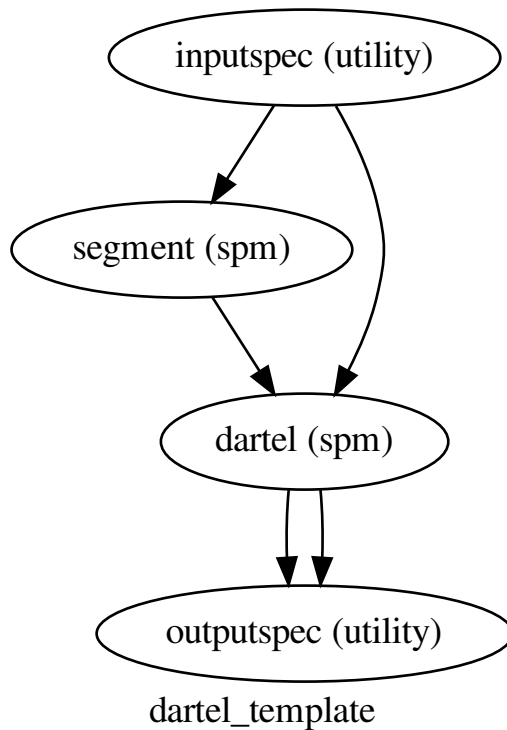
Inputs:

```
inputs.spec.structural_files : structural data to be used to create templates
inputs.spec.template_prefix : prefix for dartel template
```

Outputs:

```
outputs.spec.template_file : DARTEL template
outputs.spec.flow_fields : warps from input struct files to the template
```

Graph



3.3.2 create_spm_preproc()

[Link to code](#)

Create an spm preprocessing workflow with freesurfer registration and artifact detection.

The workflow realigns and smooths and registers the functional images with the subject's freesurfer space.

Example

```

>>> preproc = create_spm_preproc()
>>> preproc.base_dir = '.'
>>> preproc.inputs.inputspec.fwhm = 6
>>> preproc.inputs.inputspec.subject_id = 's1'
>>> preproc.inputs.inputspec.subjects_dir = '.'
>>> preproc.inputs.inputspec.functionals = ['f3.nii', 'f5.nii']
>>> preproc.inputs.inputspec.norm_threshold = 1
>>> preproc.inputs.inputspec.zintensity_threshold = 3

```

Inputs:

```

inputspec.functionals : functional runs use 4d nifti
inputspec.subject_id : freesurfer subject id
inputspec.subjects_dir : freesurfer subjects dir

```

(continues on next page)

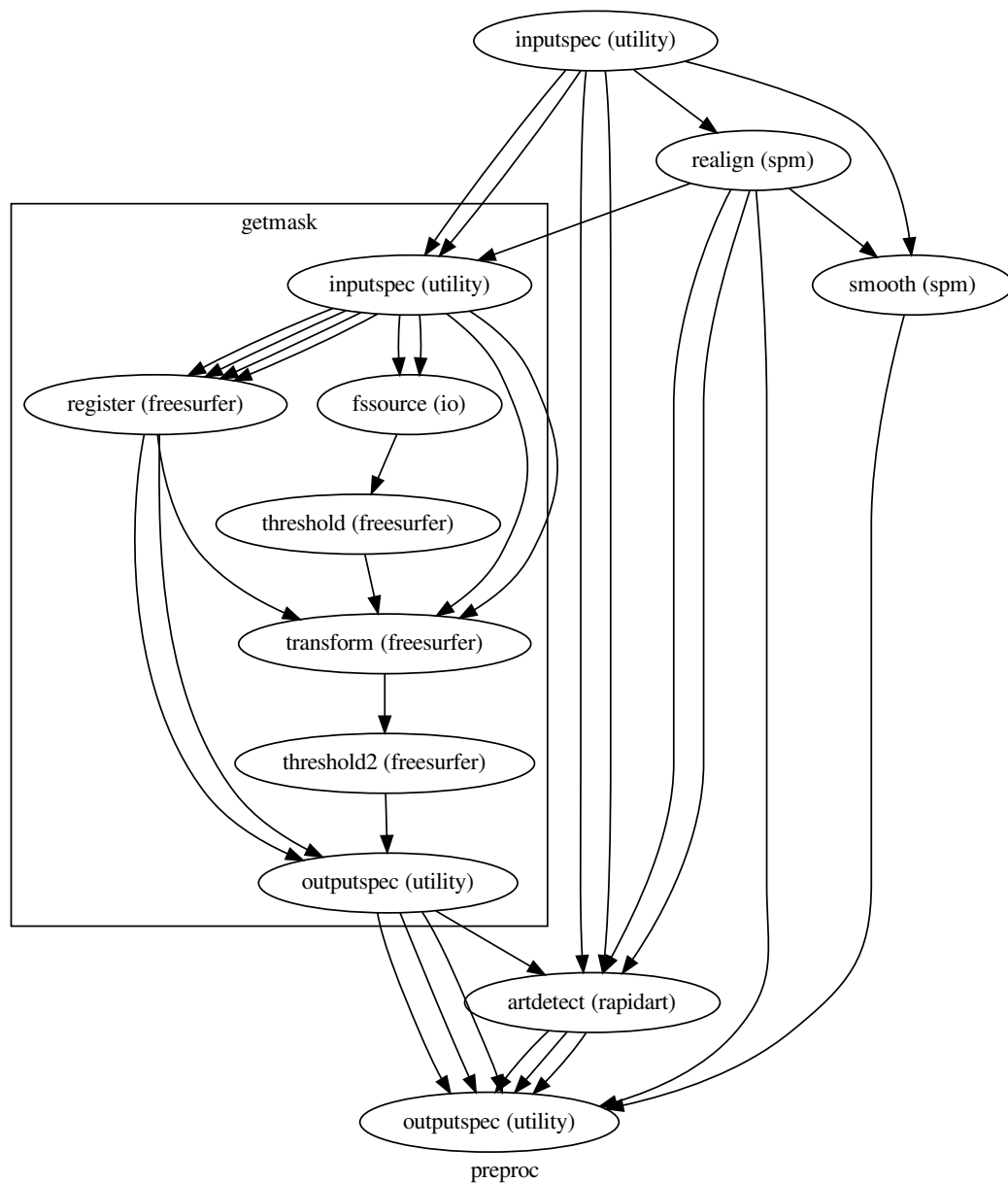
(continued from previous page)

```
inputspec.fwhm : smoothing fwhm
inputspec.norm_threshold : norm threshold for outliers
inputspec.zintensity_threshold : intensity threshold in z-score
```

Outputs:

```
outputspec.realignment_parameters : realignment parameter files
outputspec.smoothed_files : smoothed functional files
outputspec.outlier_files : list of outliers
outputspec.outlier_stats : statistics of outliers
outputspec.outlier_plots : images of outliers
outputspec.mask_file : binary mask file in reference image space
outputspec.reg_file : registration file that maps reference image to
                      freesurfer space
outputspec.reg_cost : cost of registration (useful for detecting misalignment)
```

Graph

3.3.3 `create_vbm_preproc()`

[Link to code](#)

Create a vbm workflow that generates DARTEL-based warps to MNI space

Based on: <http://www.fil.ion.ucl.ac.uk/~john/misc/VBMclass10.pdf>

Example

```
>>> preproc = create_vbm_preproc()
>>> preproc.inputs.inputs_spec.fwhm = 8
>>> preproc.inputs.inputs_spec.structural_files = [
...     os.path.abspath('s1.nii'), os.path.abspath('s3.nii')]
>>> preproc.inputs.inputs_spec.template_prefix = 'Template'
>>> preproc.run() # doctest: +SKIP
```

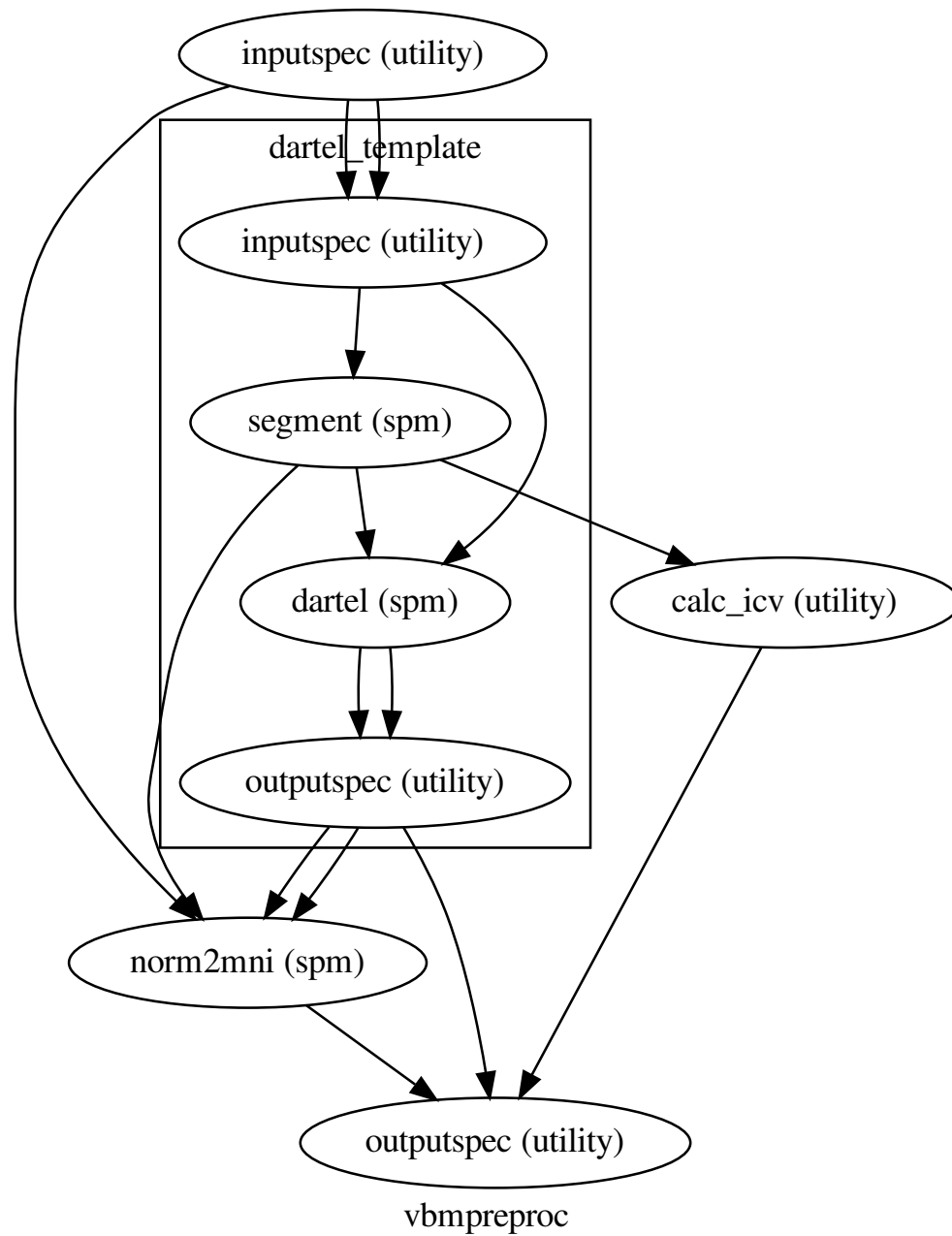
Inputs:

```
inputs_spec.structural_files : structural data to be used to create templates
inputs_spec.fwhm: single of triplet for smoothing when normalizing to MNI space
inputs_spec.template_prefix : prefix for dartel template
```

Outputs:

```
outputs_spec.normalized_files : normalized gray matter files
outputs_spec.template_file : DARTEL template
outputs_spec.icv : intracranial volume (cc - assuming dimensions in mm)
```

Graph



4.1 workflows.misc.utils

4.1.1 `get_affine()`

[Link to code](#)

4.1.2 `get_data_dims()`

[Link to code](#)

4.1.3 `get_vox_dims()`

[Link to code](#)

4.1.4 `id_list_from_lookup_table()`

[Link to code](#)

4.1.5 `region_list_from_volume()`

[Link to code](#)

4.1.6 `select_aparc()`

[Link to code](#)

4.1.7 `select_aparc_annot()`

[Link to code](#)

5.1 workflows.rsfmri.fsl.resting

5.1.1 create_realign_flow()

[Link to code](#)

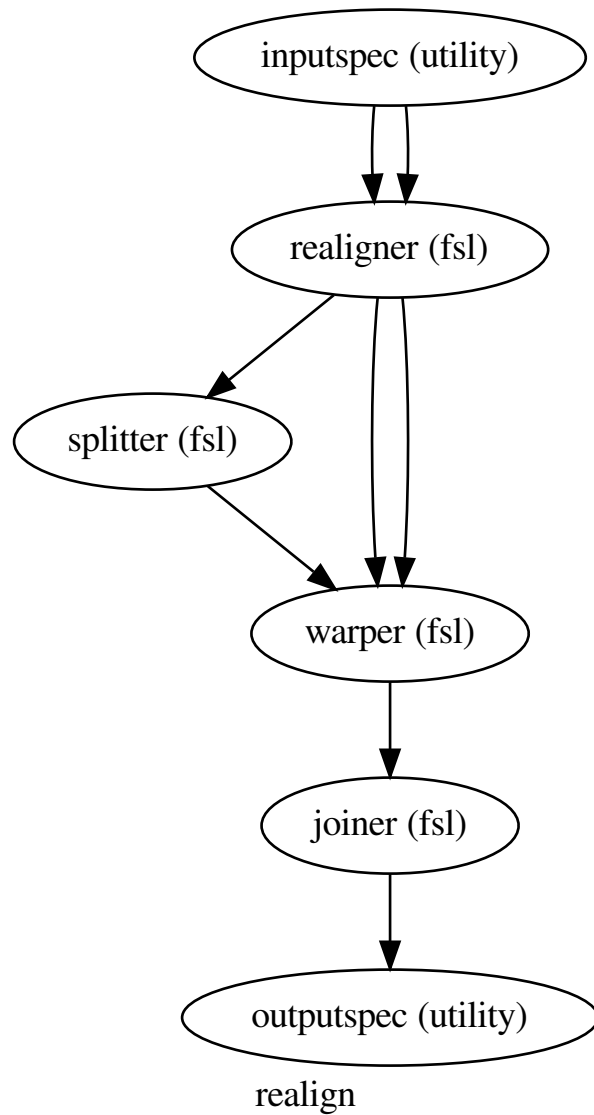
Realign a time series to the middle volume using spline interpolation

Uses MCFLIRT to realign the time series and ApplyWarp to apply the rigid body transformations using spline interpolation (unknown order).

Example

```
>>> wf = create_realign_flow()
>>> wf.inputs.inputs.spec.func = 'f3.nii'
>>> wf.run() # doctest: +SKIP
```

Graph



5.1.2 `create_resting_preproc()`

[Link to code](#)

Create a “resting” time series preprocessing workflow
The noise removal is based on Behzadi et al. (2007)

Parameters

name : name of workflow (default: restpreproc)

Inputs:

```
inputspec.func : functional run (filename or list of filenames)
```

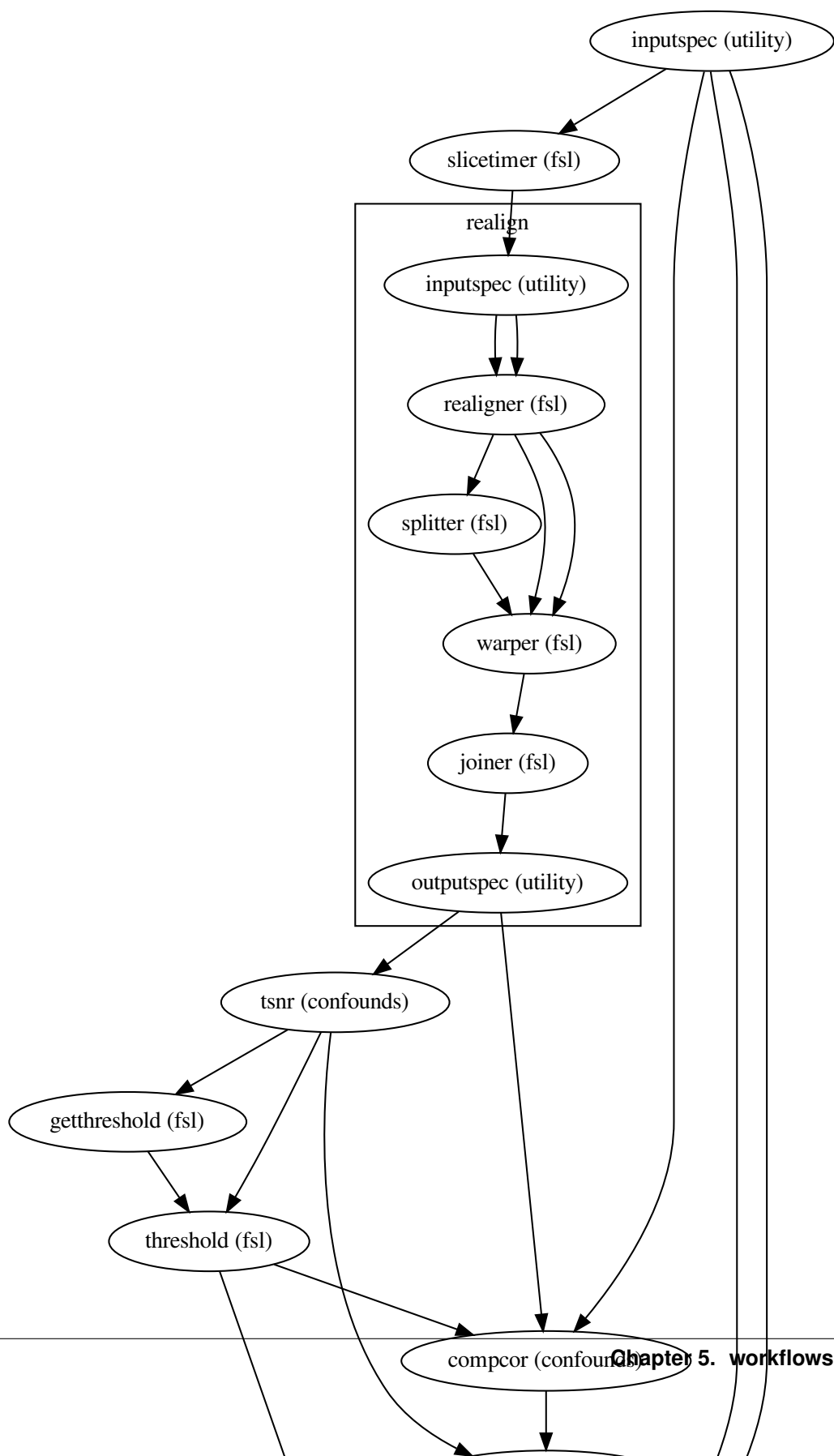
Outputs:

```
outputspec.noise_mask_file : voxels used for PCA to derive noise  
                           components  
outputspec.filtered_file : bandpass filtered and noise-reduced time  
                           series
```

Example

```
>>> TR = 3.0  
>>> wf = create_resting_preproc()  
>>> wf.inputs.inputspec.func = 'f3.nii'  
>>> wf.inputs.inputspec.num_noise_components = 6  
>>> wf.inputs.inputspec.highpass_sigma = 100/(2*TR)  
>>> wf.inputs.inputspec.lowpass_sigma = 12.5/(2*TR)  
>>> wf.run() # doctest: +SKIP
```

Graph



5.1.3 `select_volume()`

[Link to code](#)

Return the middle index of a file

6.1 workflows.smri.ants.ANTSBuildTemplate

6.1.1 ANTSTemplateBuildSingleIterationWF()

[Link to code](#)

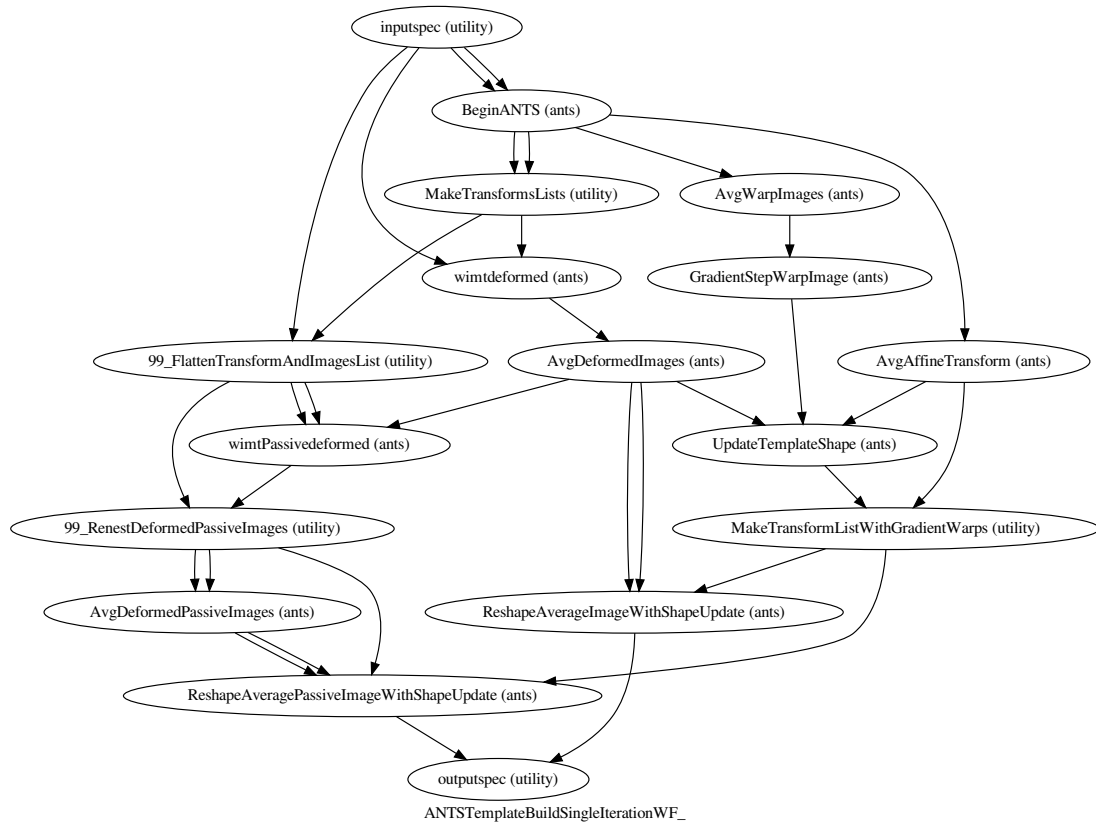
Inputs:

```
inputspec.images :  
inputspec.fixed_image :  
inputspec.ListOfPassiveImagesDictionaries :
```

Outputs:

```
outputspec.template :  
outputspec.transforms_list :  
outputspec.passive_deformed_templates :
```

Graph



6.1.2 FlattenTransformAndImagesList()

[Link to code](#)

6.1.3 GetFirstListElement()

Link to code

6.1.4 MakeListsOfTransformLists()

Link to code

6.1.5 MakeTransformListWithGradientWarps()

Link to code

6.1.6 RenestDeformedPassiveImages()

[Link to code](#)

6.2 workflows.smri.ants.antsRegistrationBuildTemplate

6.2.1 antsRegistrationTemplateBuildSingleIterationWF()

[Link to code](#)

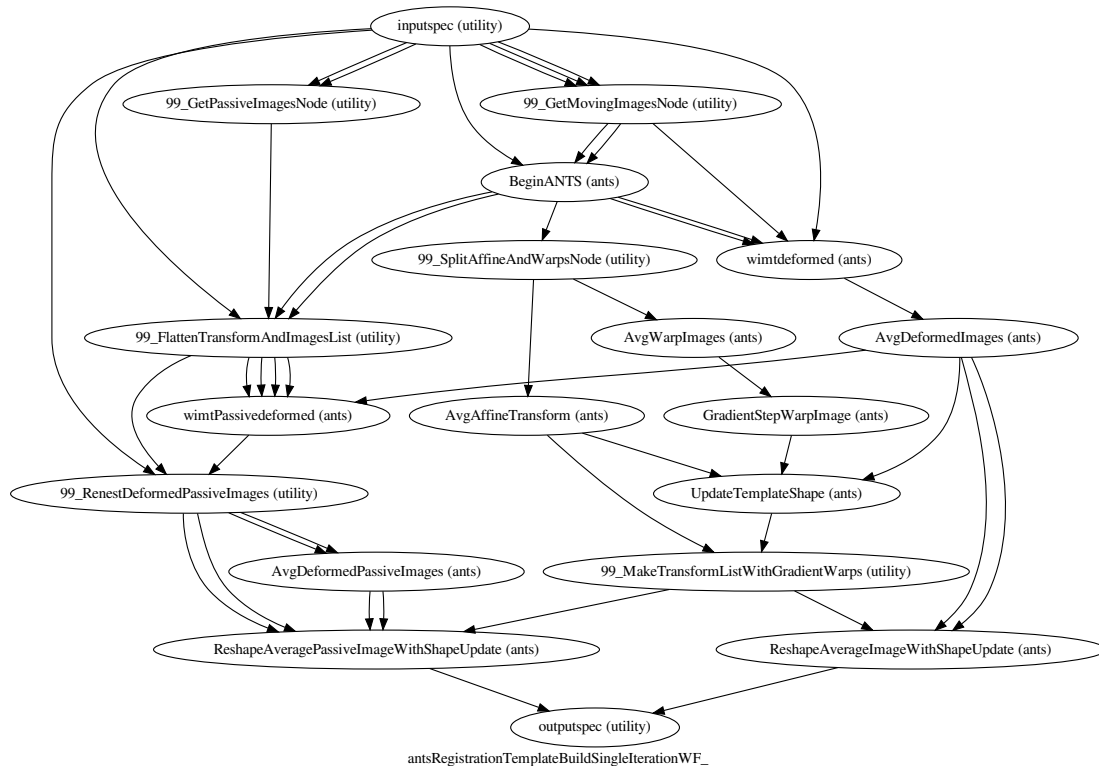
Inputs:

```
inputspec.images :
inputspec.fixed_image :
inputspec.ListOfPassiveImagesDictionaries :
inputspec.interpolationMapping :
```

Outputs:

```
outputspec.template :
outputspec.transforms_list :
outputspec.passive_deformed_templates :
```

Graph



6.2.2 FlattenTransformAndImagesList()

[Link to code](#)

6.2.3 GetFirstListElement()

[Link to code](#)

6.2.4 GetMovingImages ()

[Link to code](#)

This currently ONLY works when registrationImageTypes has length of exactly 1. When the new multi-variate registration is introduced, it will be expanded.

6.2.5 GetPassiveImages ()

[Link to code](#)

6.2.6 MakeTransformListWithGradientWarps ()

[Link to code](#)

6.2.7 RenestDeformedPassiveImages ()

[Link to code](#)

6.2.8 SplitAffineAndWarpComponents ()

[Link to code](#)

6.2.9 makeListOfOneElement ()

[Link to code](#)

6.3 workflows.smri.freesurfer.autorecon1

6.3.1 checkT1s ()

[Link to code](#)

Verifying size of inputs and setting workflow parameters

6.3.2 create_AutoRecon1 ()

[Link to code](#)

Creates the AutoRecon1 workflow in nipy.

Inputs:: inputspec.T1_files : T1 files (mandatory) inputspec.T2_file : T2 file (optional) inputspec.FLAIR_file : FLAIR file (optional) inputspec.cw256 : Conform inputs to 256 FOV (optional) inputspec.num_threads: Number of threads to use with EM Register (default=1)

Output:

6.4 workflows.smri.freesurfer.autorecon2

6.4.1 copy_ltas ()

[Link to code](#)

6.5 workflows.smri.freesurfer.bem

6.5.1 create_bem_flow ()

[Link to code](#)

Uses MNE's Watershed algorithm to create Boundary Element Meshes (BEM) for a subject's brain, inner/outer skull, and skin. The surfaces are returned in the desired (by default, stereolithic .stl) format.

Example

```
>>> from nipy.workflows.smri.freesurfer import create_bem_flow
>>> bemflow = create_bem_flow()
>>> bemflow.inputs.inputs.spec.subject_id = 'subj1'
>>> bemflow.inputs.inputs.spec.subjects_dir = '.'
>>> bemflow.run() # doctest: +SKIP
```

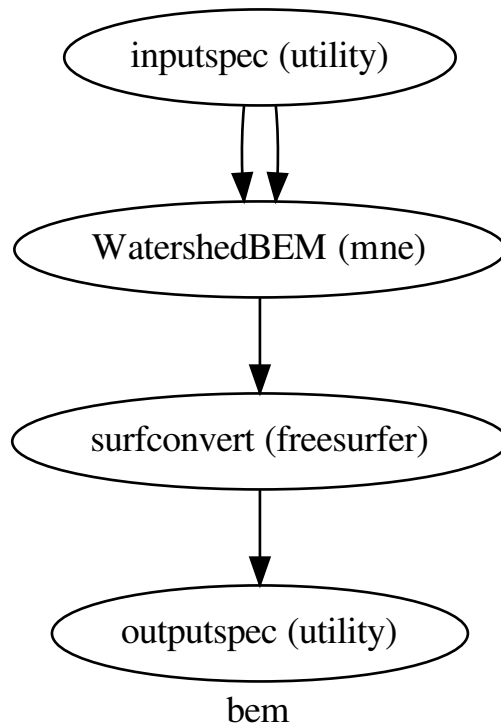
Inputs:

```
inputs.spec.subject_id : freesurfer subject id
inputs.spec.subjects_dir : freesurfer subjects directory
```

Outputs:

```
outputs.spec.meshes : output boundary element meshes in (by default)
                      stereolithographic (.stl) format
```

Graph



6.6 workflows.smri.freesurfer.recon

6.6.1 create_reconall_workflow()

[Link to code](#)

Creates the ReconAll workflow in Nipype. This workflow is designed to run the same commands as FreeSurfer's reconall script but with the added features that a Nipype workflow provides. Before running this workflow, it is necessary to have the FREESURFER_HOME environmental variable set to the directory containing the version of FreeSurfer to be used in this workflow.

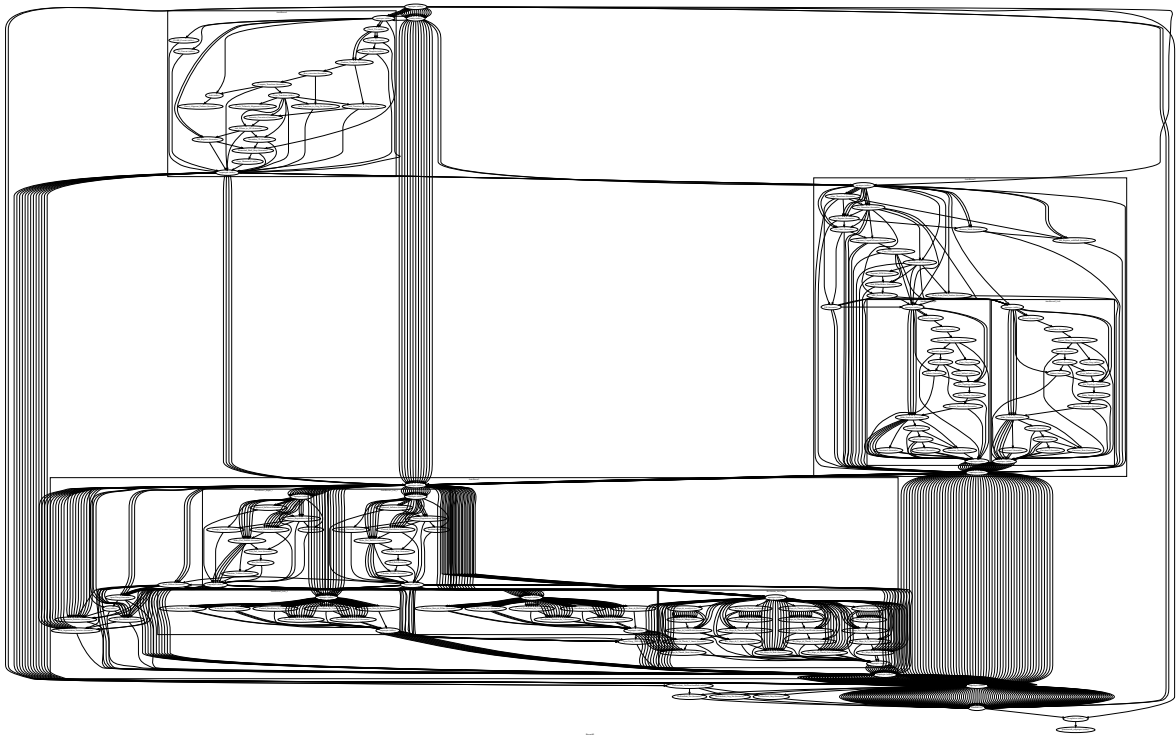
Example

```
>>> from nipype.workflows.smri.freesurfer import create_reconall_workflow
>>> recon_all = create_reconall_workflow()
>>> recon_all.inputs.inputs.spec.subject_id = 'subj1'
>>> recon_all.inputs.inputs.spec.subjects_dir = '.'
>>> recon_all.inputs.inputs.spec.T1_files = 'T1.nii.gz'
>>> recon_all.run() # doctest: +SKIP
```

Inputs:: inputs.spec.subjects_dir : subjects directory (mandatory) inputs.spec.subject_id : name of subject (mandatory) inputs.spec.T1_files : T1 files (mandatory) inputs.spec.T2_file : T2 file (optional) inputs.spec.FLAIR_file : FLAIR file (optional) inputs.spec.cw256 : Conform inputs to 256 FOV (optional) inputs.spec.num_threads: Number of threads on nodes that utilize OpenMP (default=1) plugin_args : Dictionary of plugin args to set to nodes that utilize OpenMP (optional)

Outputs:: postdatasink_outputs.spec.subject_id : name of the datasinked output folder in the subjects directory
Note: The input subject_id is not passed to the commands in the workflow. Commands that require subject_id are reading implicit inputs from {SUBJECTS_DIR}/{subject_id}. For those commands the subject_id is set to the default value and SUBJECTS_DIR is set to the node directory. The implicit inputs are then copied to the node directory in order to mimic a SUBJECTS_DIR structure. For example, if the command implicitly reads in brainmask.mgz, the interface would copy that input file to {node_dir}/{subject_id}/mri/brainmask.mgz and set SUBJECTS_DIR to node_dir. The workflow only uses the input subject_id to datasink the outputs to {subjects_dir}/{subject_id}.

Graph



6.6.2 create_skullstripped_recon_flow()

[Link to code](#)

Performs recon-all on volumes that are already skull stripped. FreeSurfer fails to perform skullstripping on some volumes (especially MP2RAGE). This can be avoided by doing skullstripping before running recon-all (using for example SPECTRE algorithm).

Example

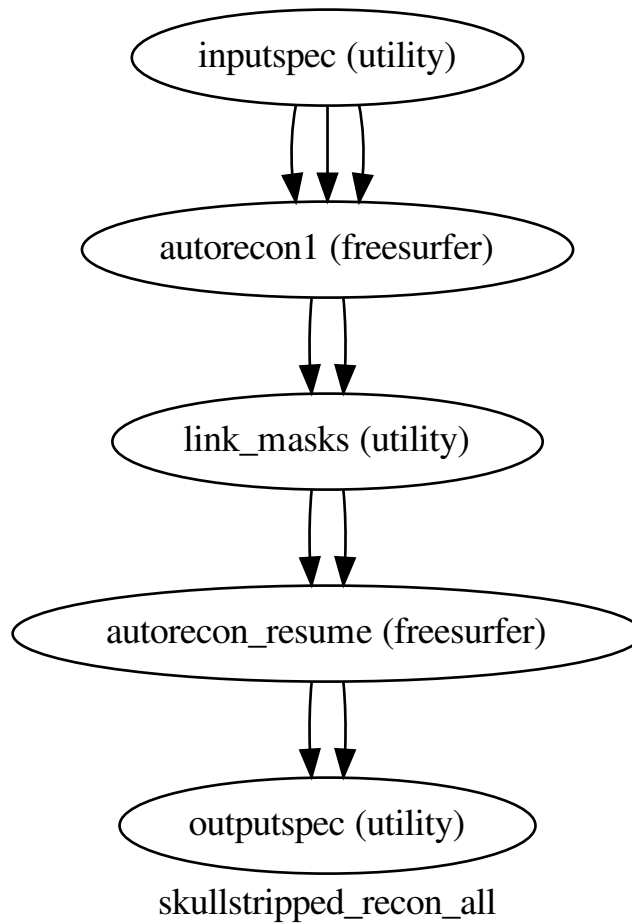
```
>>> from nipy.workflows.smri.freesurfer import create_skullstripped_recon_flow
>>> recon_flow = create_skullstripped_recon_flow()
>>> recon_flow.inputs.inputs.spec.subject_id = 'subj1'
>>> recon_flow.inputs.inputs.spec.T1_files = 'T1.nii.gz'
>>> recon_flow.run() # doctest: +SKIP
```

Inputs:: inputs.spec.T1_files : skullstripped T1_files (mandatory) inputs.spec.subject_id : freesurfer subject id (optional) inputs.spec.subjects_dir : freesurfer subjects directory (optional)

Outputs:

```
outputs.spec.subject_id : freesurfer subject id
outputs.spec.subjects_dir : freesurfer subjects directory
```

Graph



6.7 workflows.smri.freesurfer.utils

6.7.1 create_get_stats_flow()

[Link to code](#)

Retrieves stats from labels

Parameters

name [string] name of workflow

withreg [boolean] indicates whether to register source to label

Example

Inputs:


```

inputspec.source_file : reference image for mask generation
inputspec.label_file : label file from which to get ROIs

(optionally with registration)
inputspec.reg_file : bbreg file (assumes reg from source to label
inputspec.inverse : boolean whether to invert the registration
inputspec.subjects_dir : freesurfer subjects directory

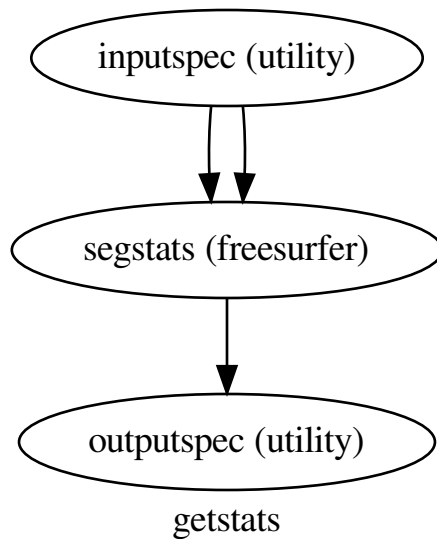
```

Outputs:

```

outputspec.stats_file : stats file

```

Graph**6.7.2 create_getmask_flow()**

[Link to code](#)

Registers a source file to freesurfer space and create a brain mask in source space
 Requires fsl tools for initializing registration

Parameters

name [string] name of workflow

dilate_mask [boolean] indicates whether to dilate mask or not

Example

```

>>> getmask = create_getmask_flow()
>>> getmask.inputs.inputspec.source_file = 'mean.nii'

```

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```
>>> getmask.inputs.inputs.spec.subject_id = 's1'
>>> getmask.inputs.inputs.spec.subjects_dir = '.'
>>> getmask.inputs.inputs.spec.contrast_type = 't2'
```

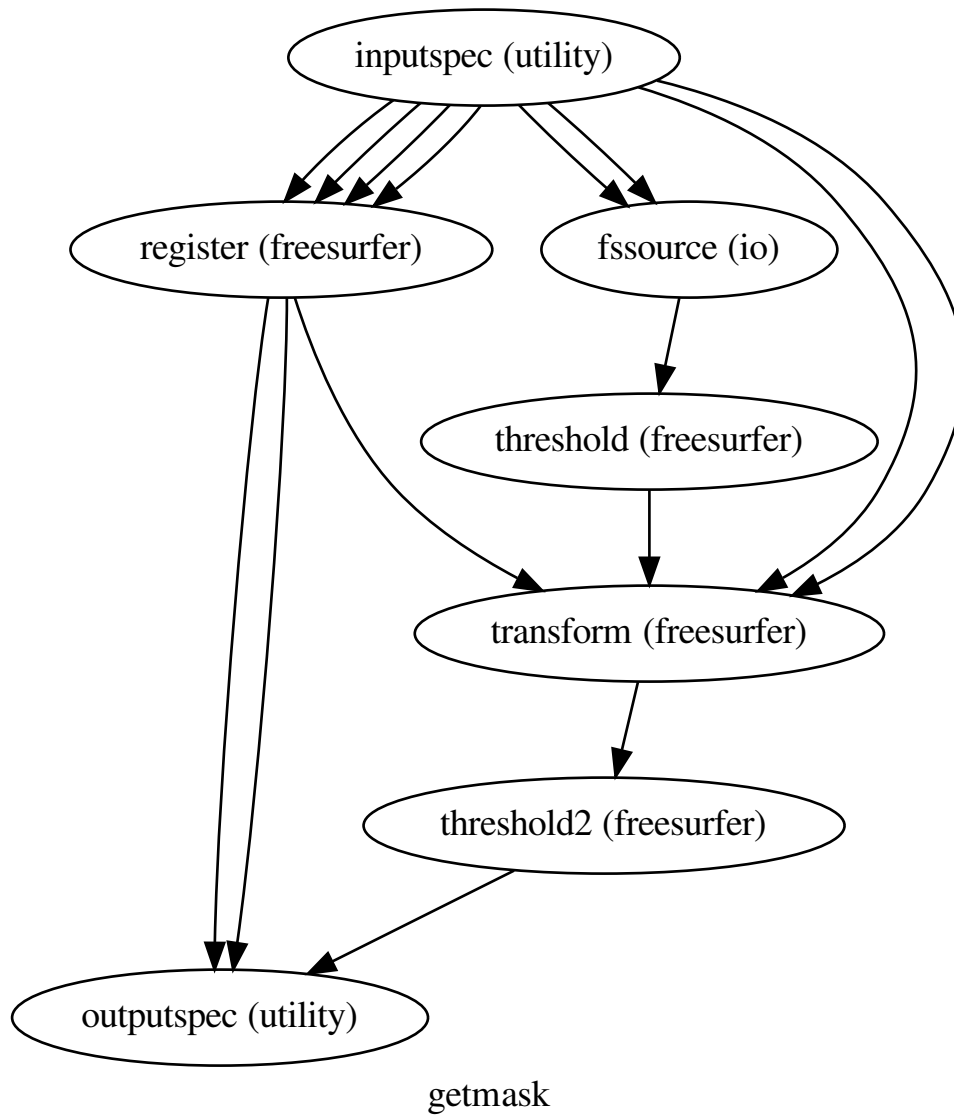
Inputs:

```
inputs.spec.source_file : reference image for mask generation
inputs.spec.subject_id : freesurfer subject id
inputs.spec.subjects_dir : freesurfer subjects directory
inputs.spec.contrast_type : MR contrast of reference image
```

Outputs:

```
outputs.spec.mask_file : binary mask file in reference image space
outputs.spec.reg_file : registration file that maps reference image to
                        freesurfer space
outputs.spec.reg_cost : cost of registration (useful for detecting misalignment)
```

Graph



6.7.3 create_tessellation_flow()

[Link to code](#)

Tessellates the input subject's aseg.mgz volume and returns the surfaces for each region in stereolithic (.stl) format

Example

```
>>> from nipy.workflows.smri.freesurfer import create_tessellation_flow
>>> tessflow = create_tessellation_flow()
>>> tessflow.inputs.inputs.spec.subject_id = 'subj1'
>>> tessflow.inputs.inputs.spec.subjects_dir = '.'
>>> tessflow.inputs.inputs.spec.lookup_file = 'FreeSurferColorLUT.txt' # doctest:
↳+SKIP
>>> tessflow.run() # doctest: +SKIP
```

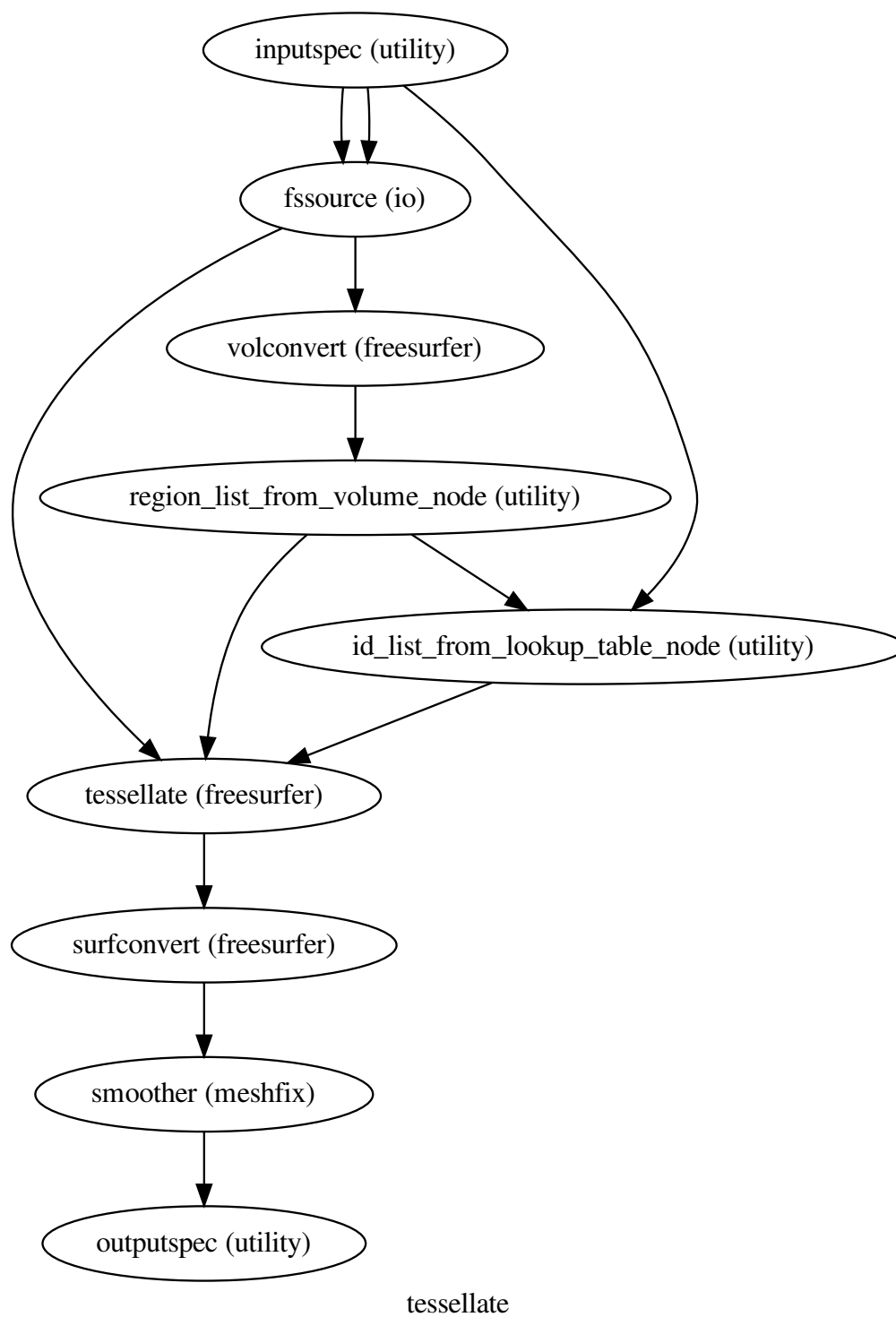
Inputs:

```
inputs.spec.subject_id : freesurfer subject id
inputs.spec.subjects_dir : freesurfer subjects directory
inputs.spec.lookup_file : lookup file from freesurfer directory
```

Outputs:

```
outputs.spec.meshes : output region meshes in (by default) stereolithographic (
↳stl) format
```

Graph



6.7.4 `copy_file()`

[Link to code](#)

Create a function to copy a file that can be modified by a following node without changing the original file.

6.7.5 `copy_files()`

[Link to code](#)

Create a function to copy a file that can be modified by a following node without changing the original file

6.7.6 `get_aparc_aseg()`

[Link to code](#)

Return the aparc+aseg.mgz file

6.7.7 `getdefaultconfig()`

[Link to code](#)

6.7.8 `mkdir_p()`

[Link to code](#)

6.8 `workflows.smri.niftyreg.groupwise`

6.8.1 `create_groupwise_average()`

[Link to code](#)

Create the overall workflow that embeds all the rigid, affine and non-linear components.

Inputs:

```
inputspec.in_files - The input files to be registered
inputspec.ref_file - The initial reference image that the input files
                    are registered to
inputspec.rmask_file - Mask of the reference image
inputspec.in_trans_files - Initial transformation files (affine or
                    cpps)
```

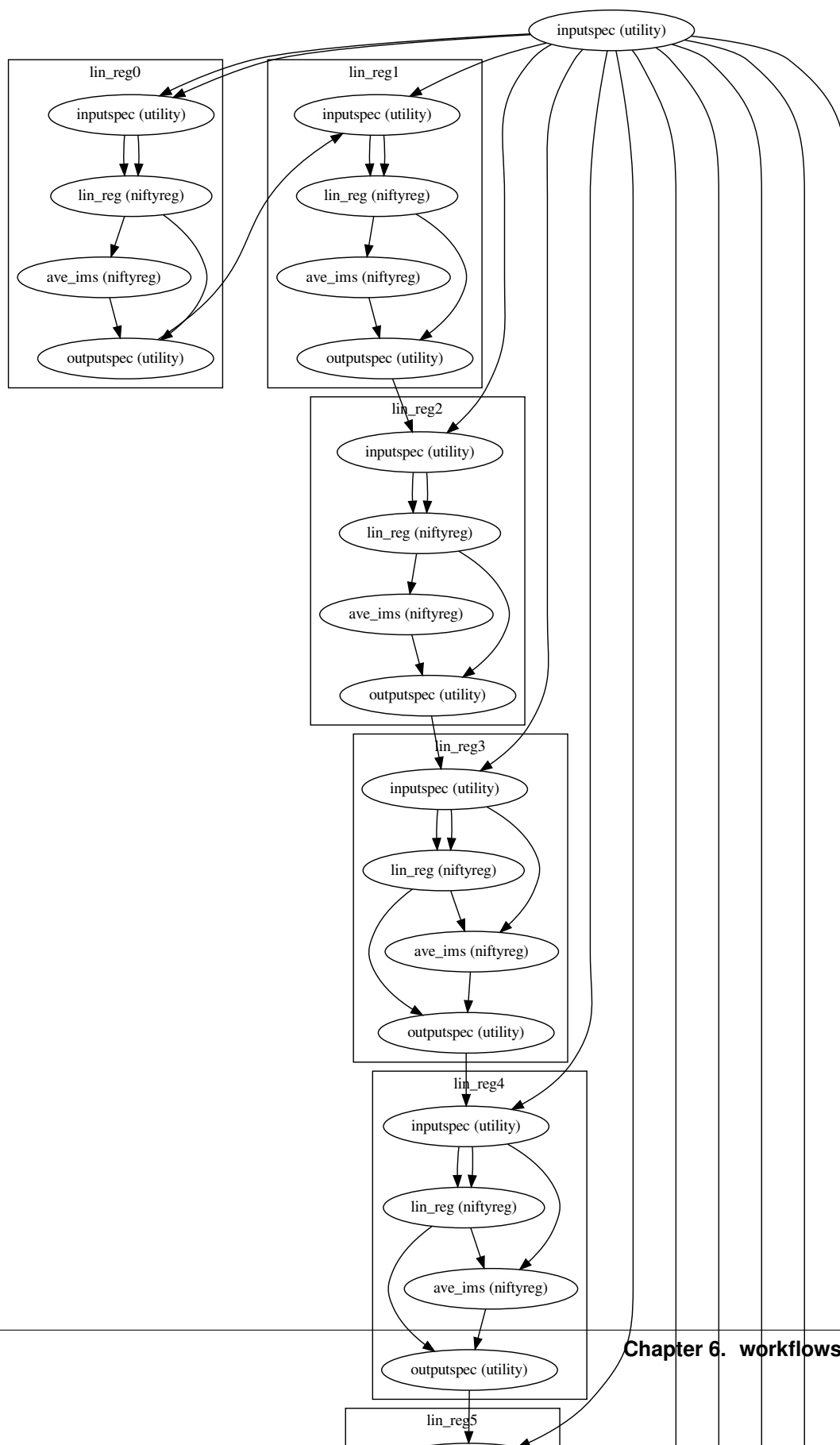
Outputs:

```
outputspec.average_image - The average image
outputspec.cpp_files - The bspline transformation files
```

Example

```
>>> from nipy.workflows.smri.niftyreg import create_groupwise_average
>>> node = create_groupwise_average('groupwise_av') # doctest: +SKIP
>>> node.inputs.inputspec.in_files = [
...     'file1.nii.gz', 'file2.nii.gz'] # doctest: +SKIP
>>> node.inputs.inputspec.ref_file = ['ref.nii.gz'] # doctest: +SKIP
>>> node.inputs.inputspec.rmask_file = ['mask.nii.gz'] # doctest: +SKIP
>>> node.run() # doctest: +SKIP
```


Graph



6.8.2 create_linear_gw_step()

[Link to code](#)

Creates a workflow that performs linear co-registration of a set of images using RegAladin, producing an average image and a set of affine transformation matrices linking each of the floating images to the average.

Inputs:

```
inputspec.in_files - The input files to be registered
inputspec.ref_file - The initial reference image that the input files
                    are registered to
inputspec.rmask_file - Mask of the reference image
inputspec.in_aff_files - Initial affine transformation files
```

Outputs:

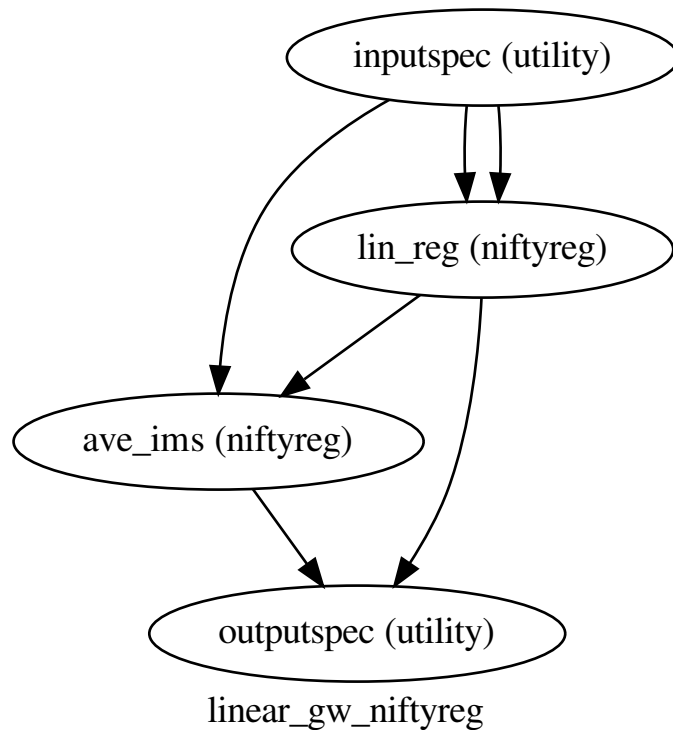
```
outputspec.average_image - The average image
outputspec.aff_files - The affine transformation files
```

Optional arguments:

```
linear_options_hash - An options dictionary containing a list of
                     parameters for RegAladin that take
                     the same form as given in the interface (default None)
demean - Selects whether to demean the transformation matrices when
         performing the averaging (default True)
initial_affines - Selects whether to iterate over initial affine
                 images, which we generally won't have (default False)
```

Example

```
>>> from nipy.workflows.smri.niftyreg import create_linear_gw_step
>>> lgw = create_linear_gw_step('my_linear_coreg') # doctest: +SKIP
>>> lgw.inputs.inputspec.in_files = [
...     'file1.nii.gz', 'file2.nii.gz'] # doctest: +SKIP
>>> lgw.inputs.inputspec.ref_file = ['ref.nii.gz'] # doctest: +SKIP
>>> lgw.run() # doctest: +SKIP
```

Graph**6.8.3 create_nonlinear_gw_step()**[Link to code](#)

Creates a workflow that perform non-linear co-registrations of a set of images using RegF3d, producing an non-linear average image and a set of cpp transformation linking each of the floating images to the average.

Inputs:

```

inputspec.in_files - The input files to be registered
inputspec.ref_file - The initial reference image that the input files
                    are registered to
inputspec.rmask_file - Mask of the reference image
inputspec.in_trans_files - Initial transformation files (affine or
                        cpps)
  
```

Outputs:

```

outputspec.average_image - The average image
outputspec.cpp_files - The bspline transformation files
  
```

Optional arguments:

```

nonlinear_options_hash - An options dictionary containing a list of
                        parameters for RegAladin that take the
  
```

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```

same form as given in the interface (default None)
initial_affines - Selects whether to iterate over initial affine
                  images, which we generally won't have (default False)

```

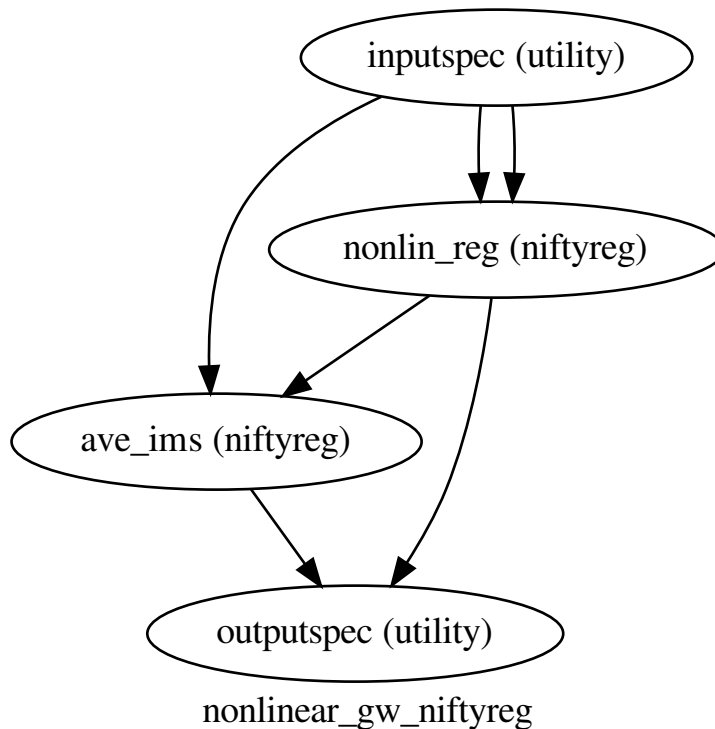
Example

```

>>> from nipy.workflows.smri.niftyreg import create_nonlinear_gw_step
>>> nlc = create_nonlinear_gw_step('nonlinear_coreg') # doctest: +SKIP
>>> nlc.inputs.inputs.spec.in_files = [
...     'file1.nii.gz', 'file2.nii.gz'] # doctest: +SKIP
>>> nlc.inputs.inputs.spec.ref_file = ['ref.nii.gz'] # doctest: +SKIP
>>> nlc.run() # doctest: +SKIP

```

Graph



- Examples

7.1 Introduction

This script, `camino_dti_tutorial.py`, demonstrates the ability to perform basic diffusion analysis in a Nipype pipeline:

```
python dmri_camino_dti.py
```

We perform this analysis using the FSL course data, which can be acquired from here: http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz

Import necessary modules from nipype.

```
import os # system functions
import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.utility as util # utility
import nipype.pipeline.engine as pe # pypeline engine
import nipype.interfaces.camino as camino
import nipype.interfaces.fsl as fsl
import nipype.interfaces.camino2trackvis as cam2trk
import nipype.algorithms.misc as misc
```

We use the following functions to scrape the voxel and data dimensions of the input images. This allows the pipeline to be flexible enough to accept and process images of varying size. The SPM Face tutorial (`fmri_spm_face.py`) also implements this inferral of voxel size from the data.

```
def get_vox_dims(volume):
    import nibabel as nb
    from nipype.utils import NUMPY_MMAP
    if isinstance(volume, list):
        volume = volume[0]
    nii = nb.load(volume, mmap=NUMPY_MMAP)
    hdr = nii.header
    voxdims = hdr.get_zooms()
    return [float(voxdims[0]), float(voxdims[1]), float(voxdims[2])]

def get_data_dims(volume):
    import nibabel as nb
```

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```

from nipy.utils import NUMPY_MMAP
if isinstance(volume, list):
    volume = volume[0]
nii = nb.load(volume, mmap=NUMPY_MMAP)
hdr = nii.header
datadims = hdr.get_data_shape()
return [int(datadims[0]), int(datadims[1]), int(datadims[2])]

def get_affine(volume):
    import nibabel as nb
    from nipy.utils import NUMPY_MMAP
    nii = nb.load(volume, mmap=NUMPY_MMAP)
    return nii.affine

subject_list = ['subj1']
fsl.FSLCommand.set_default_output_type('NIFTI')

```

Map field names to individual subject runs

```

info = dict(
    dwi=[['subject_id', 'data']],
    bvecs=[['subject_id', 'bvecs']],
    bvals=[['subject_id', 'bvals']])

infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")

```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

Now we create a `nipy.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipy.pipeline.engine.Node` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```

datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=list(info.keys())),
    name='datasource')

datasource.inputs.template = "%s/%s"

# This needs to point to the fdt folder you can find after extracting
# http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz
datasource.inputs.base_directory = os.path.abspath('fsl_course_data/fdt/')

datasource.inputs.field_template = dict(dwi='%s/%s.nii.gz')
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True

```

An `inputnode` is used to pass the data obtained by the data grabber to the actual processing functions

```
inputnode = pe.Node(
```

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```
interface=util.IdentityInterface(fields=["dwi", "bvecs", "bvals"]),
name="inputnode")
```

7.1.1 Setup for Diffusion Tensor Computation

In this section we create the nodes necessary for diffusion analysis. First, the diffusion image is converted to voxel order.

```
image2voxel = pe.Node(interface=camino.Image2Voxel(), name="image2voxel")
fsl2scheme = pe.Node(interface=camino.FSL2Scheme(), name="fsl2scheme")
fsl2scheme.inputs.usegradmod = True
```

Second, diffusion tensors are fit to the voxel-order data.

```
dtifit = pe.Node(interface=camino.DTIFit(), name='dtifit')
```

Next, a lookup table is generated from the schemefile and the signal-to-noise ratio (SNR) of the unweighted (q=0) data.

```
dtlutgen = pe.Node(interface=camino.DTLUTGen(), name="dtlutgen")
dtlutgen.inputs.snr = 16.0
dtlutgen.inputs.inversion = 1
```

In this tutorial we implement probabilistic tractography using the PICO algorithm. PICO tractography requires an estimate of the fibre direction and a model of its uncertainty in each voxel; this is produced using the following node.

```
picopdfs = pe.Node(interface=camino.PicoPDFs(), name="picopdfs")
picopdfs.inputs.inputmodel = 'dt'
```

An FSL BET node creates a brain mask is generated from the diffusion image for seeding the PICO tractography.

```
bet = pe.Node(interface=fsl.BET(), name="bet")
bet.inputs.mask = True
```

Finally, tractography is performed. First DT streamline tractography.

```
trackdt = pe.Node(interface=camino.TrackDT(), name="trackdt")
```

Now camino's Probabilistic Index of connectivity algorithm. In this tutorial, we will use only 1 iteration for time-saving purposes.

```
trackpico = pe.Node(interface=camino.TrackPICO(), name="trackpico")
trackpico.inputs.iterations = 1
```

Currently, the best program for visualizing tracts is TrackVis. For this reason, a node is included to convert the raw tract data to .trk format. Solely for testing purposes, another node is added to perform the reverse.

```
cam2trk_dt = pe.Node(interface=cam2trk.Camino2Trackvis(), name="cam2trk_dt")
cam2trk_dt.inputs.min_length = 30
cam2trk_dt.inputs.voxel_order = 'LAS'

cam2trk_pico = pe.Node(
    interface=cam2trk.Camino2Trackvis(), name="cam2trk_pico")
cam2trk_pico.inputs.min_length = 30
cam2trk_pico.inputs.voxel_order = 'LAS'

trk2camino = pe.Node(interface=cam2trk.Trackvis2Camino(), name="trk2camino")
```

Tracts can also be converted to VTK and OOG formats, for use in programs such as GeomView and Paraview, using the following two nodes. For VTK use VtkStreamlines.

```

procstreamlines = pe.Node(
    interface=camino.ProcStreamlines(), name="procstreamlines")
procstreamlines.inputs.outputtracts = 'oogl'

```

We can also produce a variety of scalar values from our fitted tensors. The following nodes generate the fractional anisotropy and diffusivity trace maps and their associated headers.

```

fa = pe.Node(interface=camino.ComputeFractionalAnisotropy(), name='fa')
trace = pe.Node(interface=camino.ComputeTensorTrace(), name='trace')
dteig = pe.Node(interface=camino.ComputeEigensystem(), name='dteig')

analyzeheader_fa = pe.Node(
    interface=camino.AnalyzeHeader(), name="analyzeheader_fa")
analyzeheader_fa.inputs.datatype = "double"
analyzeheader_trace = analyzeheader_fa.clone('analyzeheader_trace')

fa2nii = pe.Node(interface=misc.CreateNifti(), name='fa2nii')
trace2nii = fa2nii.clone("trace2nii")

```

Since we have now created all our nodes, we can now define our workflow and start making connections.

```

tractography = pe.Workflow(name='tractography')

tractography.connect([(inputnode, bet, [("dwi", "in_file")])])

```

File format conversion

```

tractography.connect([(inputnode, image2voxel, [("dwi", "in_file")]),
                      (inputnode, fsl2scheme, [("bvecs", "bvec_file"),
                                                ("bvals", "bval_file")])])

```

Tensor fitting

```

tractography.connect([(image2voxel, dtifit, [['voxel_order', 'in_file']]),
                      (fsl2scheme, dtifit, [['scheme', 'scheme_file']])])

```

Workflow for applying DT streamline tractogpahy

```

tractography.connect([(bet, trackdt, [("mask_file", "seed_file")])])
tractography.connect([(dtifit, trackdt, [("tensor_fitted", "in_file")])])

```

Workflow for applying PICO

```

tractography.connect([(bet, trackpico, [("mask_file", "seed_file")])])
tractography.connect([(fsl2scheme, dtlutgen, [("scheme", "scheme_file")])])
tractography.connect([(dtlutgen, picopdfs, [("dtLUT", "luts")])])
tractography.connect([(dtifit, picopdfs, [("tensor_fitted", "in_file")])])
tractography.connect([(picopdfs, trackpico, [("pdfs", "in_file")])])

# ProcStreamlines might throw memory errors - comment this line out in such case
tractography.connect([(trackdt, procstreamlines, [("tracked", "in_file")])])

```

Connecting the Fractional Anisotropy and Trace nodes is simple, as they obtain their input from the This is also where our voxel- and data-grabbing functions come in. We pass these functions, along with the original DWI image from the input node, to the header-generating nodes. This ensures that the files

```

tractography.connect([(dtifit, fa, [("tensor_fitted", "in_file")])])
tractography.connect([(fa, analyzeheader_fa, [("fa", "in_file")])])
tractography.connect([(inputnode, analyzeheader_fa,
                      [(['dwi', get_vox_dims), 'voxel_dims'],
                       [(['dwi', get_data_dims), 'data_dims']])])])

```

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```

tractography.connect([(fa, fa2nii, [('fa', 'data_file')])])
tractography.connect([(inputnode, fa2nii, [('dwi', get_affine), 'affine'])])
tractography.connect([(analyzeheader_fa, fa2nii, [('header', 'header_file')])])

tractography.connect([(dtifit, trace, [("tensor_fitted", "in_file")])])
tractography.connect([(trace, analyzeheader_trace, [("trace", "in_file")])])
tractography.connect([(inputnode, analyzeheader_trace,
                        [([('dwi', get_vox_dims), 'voxel_dims'],
                          [([('dwi', get_data_dims), 'data_dims'])])])])
tractography.connect([(trace, trace2nii, [('trace', 'data_file')])])
tractography.connect([(inputnode, trace2nii, [([('dwi', get_affine),
                                                'affine'])])])
tractography.connect([(analyzeheader_trace, trace2nii, [('header',
                                                         'header_file')])])

tractography.connect([(dtifit, dteig, [("tensor_fitted", "in_file")])])

tractography.connect([(trackpico, cam2trk_pico, [('tracked', 'in_file')])])
tractography.connect([(trackdt, cam2trk_dt, [('tracked', 'in_file')])])
tractography.connect([(inputnode, cam2trk_pico,
                        [([('dwi', get_vox_dims), 'voxel_dims'],
                          [([('dwi', get_data_dims), 'data_dims'])])])])

tractography.connect([(inputnode, cam2trk_dt,
                        [([('dwi', get_vox_dims), 'voxel_dims'],
                          [([('dwi', get_data_dims), 'data_dims'])])])])

```

Finally, we create another higher-level workflow to connect our tractography workflow with the info and data-grabbing nodes declared at the beginning. Our tutorial can is now extensible to any arbitrary number of subjects by simply adding their names to the subject list and their data to the proper folders.

```

workflow = pe.Workflow(name="workflow")
workflow.base_dir = os.path.abspath('camino_dti_tutorial')
workflow.connect([(infosource, datasource, [('subject_id', 'subject_id')]),
                  (datasource, tractography,
                   [([('dwi', 'inputnode.dwi'), ('bvals', 'inputnode.bvals'),
                     ('bvecs', 'inputnode.bvecs')])])])

```

The following functions run the whole workflow and produce a .dot and .png graph of the processing pipeline.

```

if __name__ == '__main__':
    workflow.run()
    workflow.write_graph()

```

You can choose the format of the exported graph with the `format` option. For example `workflow.write_graph(format='eps')`

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

dMRI: Connectivity - Camino, CMTK, FreeSurfer

8.1 Introduction

This script, `connectivity_tutorial.py`, demonstrates the ability to perform connectivity mapping using Nipype for pipelining, Freesurfer for Reconstruction / Parcellation, Camino for tensor-fitting and tractography, and the Connectome Mapping Toolkit (CMTK) for connectivity analysis:

```
python connectivity_tutorial.py
```

We perform this analysis using the FSL course data, which can be acquired from here:

- http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz

This pipeline also requires the Freesurfer directory for 'subj1' from the FSL course data. To save time, this data can be downloaded from here:

- <http://dl.dropbox.com/u/315714/subj1.zip?dl=1>

A data package containing the outputs of this pipeline can be obtained from here:

- <http://db.tt/1vx4vLeP>

Along with Camino, Camino-Trackvis, FSL, and Freesurfer, you must also have the Connectome File Format library installed as well as the Connectome Mapper.

These are written by Stephan Gerhard and can be obtained from:

<http://www.cmtk.org/>

Or on github at:

CFFlib: <https://github.com/LTS5/cfflib> CMP: <https://github.com/LTS5/cmp>

Output data can be visualized in the ConnectomeViewer

ConnectomeViewer: <https://github.com/LTS5/connectomeviewer>

First, we import the necessary modules from nipype.

```
import inspect

import os.path as op # system functions
import cmp # connectome mapper
import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.utility as util # utility
import nipype.pipeline.engine as pe # pypeline engine
import nipype.interfaces.camino as camino
import nipype.interfaces.fsl as fsl
import nipype.interfaces.camino2trackvis as cam2trk
```

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```
import nipy.interfaces.freesurfer as fs # freesurfer
import nipy.interfaces.cmtk as cmtk
import nipy.algorithms.misc as misc
```

We define the following functions to scrape the voxel and data dimensions of the input images. This allows the pipeline to be flexible enough to accept and process images of varying size. The SPM Face tutorial (fmri_spm_face.py) also implements this inferral of voxel size from the data. We also define functions to select the proper parcellation/segregation file from Freesurfer's output for each subject. For the mapping in this tutorial, we use the aparc+seg.mgz file. While it is possible to change this to use the regions defined in aparc.a2009s+aseg.mgz, one would also have to write/obtain a network resolution map defining the nodes based on those

```
def get_vox_dims(volume):
    import nibabel as nb
    from nipy.utils import NUMPY_MMAP
    if isinstance(volume, list):
        volume = volume[0]
    nii = nb.load(volume, mmap=NUMPY_MMAP)
    hdr = nii.header
    voxdims = hdr.get_zooms()
    return [float(voxdims[0]), float(voxdims[1]), float(voxdims[2])]

def get_data_dims(volume):
    import nibabel as nb
    from nipy.utils import NUMPY_MMAP
    if isinstance(volume, list):
        volume = volume[0]
    nii = nb.load(volume, mmap=NUMPY_MMAP)
    hdr = nii.header
    datadims = hdr.get_data_shape()
    return [int(datadims[0]), int(datadims[1]), int(datadims[2])]

def get_affine(volume):
    import nibabel as nb
    from nipy.utils import NUMPY_MMAP
    nii = nb.load(volume, mmap=NUMPY_MMAP)
    return nii.affine

def select_aparc(list_of_files):
    for in_file in list_of_files:
        if 'aparc+aseg.mgz' in in_file:
            idx = list_of_files.index(in_file)
    return list_of_files[idx]

def select_aparc_annot(list_of_files):
    for in_file in list_of_files:
        if '.aparc.annot' in in_file:
            idx = list_of_files.index(in_file)
    return list_of_files[idx]
```

These need to point to the main Freesurfer directory as well as the freesurfer subjects directory. No assumptions are made about where the directory of subjects is placed. Recon-all must have been run on subj1 from the FSL course data.

```
fs_dir = op.abspath('/usr/local/freesurfer')
subjects_dir = op.abspath(op.join(op.curdir, './subjects'))
fsl.FSLCommand.set_default_output_type('NIFTI')
```

This needs to point to the fdt folder you can find after extracting http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz

```
data_dir = op.abspath('fsl_course_data/fdt/')
fs.FSLCommand.set_default_subjects_dir(subjects_dir)
subject_list = ['subj1']
```

An infsource node is used to loop through the subject list and define the input files. For our purposes, these are the diffusion-weighted MR image, b vectors, and b values. The info dictionary is used to provide a template of the naming of these files. For instance, the 4D nifti diffusion image is stored in the FSL course data as data.nii.gz.

```
infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")
infosource.iterables = ('subject_id', subject_list)

info = dict(
    dwi=[['subject_id', 'data']],
    bvecs=[['subject_id', 'bvecs']],
    bvals=[['subject_id', 'bvals']])
```

A datasource node is used to perform the actual data grabbing. Templates for the associated images are used to obtain the correct images. The data are assumed to lie in data_dir/subject_id/.

```
datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=list(info.keys())),
    name='datasource')

datasource.inputs.template = "%s/%s"
datasource.inputs.base_directory = data_dir
datasource.inputs.field_template = dict(dwi='%s/%s.nii.gz')
datasource.inputs.template_args = info
datasource.inputs.base_directory = data_dir
datasource.inputs.sort_filelist = True
```

FreeSurferSource nodes are used to retrieve a number of image files that were automatically generated by the recon-all process. Here we use three of these nodes, two of which are defined to return files for solely the left and right hemispheres.

```
FreeSurferSource = pe.Node(interface=nio.FreeSurferSource(), name='fssource')
FreeSurferSource.inputs.subjects_dir = subjects_dir

FreeSurferSourceLH = pe.Node(
    interface=nio.FreeSurferSource(), name='fssourceLH')
FreeSurferSourceLH.inputs.subjects_dir = subjects_dir
FreeSurferSourceLH.inputs.hemi = 'lh'

FreeSurferSourceRH = pe.Node(
    interface=nio.FreeSurferSource(), name='fssourceRH')
FreeSurferSourceRH.inputs.subjects_dir = subjects_dir
FreeSurferSourceRH.inputs.hemi = 'rh'
```

Since the b values and b vectors come from the FSL course, we must convert it to a scheme file for use in Camino.

```
fsl2scheme = pe.Node(interface=camino.FSL2Scheme(), name="fsl2scheme")
fsl2scheme.inputs.usegradmod = True
```

FSL's Brain Extraction tool is used to create a mask from the b0 image

```
b0Strip = pe.Node(interface=fsl.BET(mask=True), name='bet_b0')
```

FSL's FLIRT function is used to coregister the b0 mask and the structural image. A convert_xfm node is then used to obtain the inverse of the transformation matrix. FLIRT is used once again to apply the inverse transformation to the parcellated brain image.

```
coregister = pe.Node(interface=fsl.FLIRT(dof=6), name='coregister')
coregister.inputs.cost = ('corratio')

convertxfm = pe.Node(interface=fsl.ConvertXFM(), name='convertxfm')
convertxfm.inputs.invert_xfm = True

inverse = pe.Node(interface=fsl.FLIRT(), name='inverse')
inverse.inputs.interp = ('nearestneighbour')

inverse_AparcAseg = pe.Node(interface=fsl.FLIRT(), name='inverse_AparcAseg')
inverse_AparcAseg.inputs.interp = ('nearestneighbour')
```

A number of conversion operations are required to obtain NIFTI files from the FreesurferSource for each subject. Nodes are used to convert the following:

- Original structural image to NIFTI
- Parcellated white matter image to NIFTI
- Parcellated whole-brain image to NIFTI
- **Pial, white, inflated, and spherical surfaces for both the left and right hemispheres** are converted to GIFTI for visualization in ConnectomeViewer
- Parcellated annotation files for the left and right hemispheres are also converted to GIFTI

```
mri_convert_Brain = pe.Node(
    interface=fs.MRIConvert(), name='mri_convert_Brain')
mri_convert_Brain.inputs.out_type = 'nii'

mri_convert_WMParc = mri_convert_Brain.clone('mri_convert_WMParc')
mri_convert_AparcAseg = mri_convert_Brain.clone('mri_convert_AparcAseg')

mris_convertLH = pe.Node(interface=fs.MRIsConvert(), name='mris_convertLH')
mris_convertLH.inputs.out_datatype = 'gii'
mris_convertRH = mris_convertLH.clone('mris_convertRH')
mris_convertRHwhite = mris_convertLH.clone('mris_convertRHwhite')
mris_convertLHwhite = mris_convertLH.clone('mris_convertLHwhite')
mris_convertRHinflated = mris_convertLH.clone('mris_convertRHinflated')
mris_convertLHinflated = mris_convertLH.clone('mris_convertLHinflated')
mris_convertRHsphere = mris_convertLH.clone('mris_convertRHsphere')
mris_convertLHsphere = mris_convertLH.clone('mris_convertLHsphere')
mris_convertLHlabels = mris_convertLH.clone('mris_convertLHlabels')
mris_convertRHlabels = mris_convertLH.clone('mris_convertRHlabels')
```

An inputnode is used to pass the data obtained by the data grabber to the actual processing functions

```
inputnode = pe.Node(
    interface=util.IdentityInterface(
        fields=["dwi", "bvecs", "bvals", "subject_id"]),
    name="inputnode")
```

In this section we create the nodes necessary for diffusion analysis. First, the diffusion image is converted to voxel order, since this is the format in which Camino does its processing.

```
image2voxel = pe.Node(interface=camino.Image2Voxel(), name="image2voxel")
```

Second, diffusion tensors are fit to the voxel-order data. If desired, these tensors can be converted to a Nifti tensor image using the DT2Nifti interface.

```
dtifit = pe.Node(interface=camino.DTIFit(), name='dtifit')
```

Next, a lookup table is generated from the schemefile and the signal-to-noise ratio (SNR) of the unweighted (q=0) data.

```
dtlutgen = pe.Node(interface=camino.DTLUTGen(), name="dtlutgen")
dtlutgen.inputs.snr = 16.0
dtlutgen.inputs.inversion = 1
```

In this tutorial we implement probabilistic tractography using the PICO algorithm. PICO tractography requires an estimate of the fibre direction and a model of its uncertainty in each voxel; this probability distribution map is produced using the following node.

```
picopdfs = pe.Node(interface=camino.PicoPDFs(), name="picopdfs")
picopdfs.inputs.inputmodel = 'dt'
```

Finally, tractography is performed. In this tutorial, we will use only one iteration for time-saving purposes. It is important to note that we use the TrackPICO interface here. This interface now expects the files required for PICO tracking (i.e. the output from picopdfs). Similar interfaces exist for alternative types of tracking, such as Bayesian tracking with Dirac priors (TrackBayesDirac).

```
track = pe.Node(interface=camino.TrackPICO(), name="track")
track.inputs.iterations = 1
```

Currently, the best program for visualizing tracts is TrackVis. For this reason, a node is included to convert the raw tract data to .trk format. Solely for testing purposes, another node is added to perform the reverse.

```
camino2trackvis = pe.Node(
    interface=camino2trk.Camino2Trackvis(), name="camino2trk")
camino2trackvis.inputs.min_length = 30
camino2trackvis.inputs.voxel_order = 'LAS'
trk2camino = pe.Node(interface=camino2trk.Trackvis2Camino(), name="trk2camino")
```

Tracts can also be converted to VTK and OOGL formats, for use in programs such as GeomView and Paraview, using the following two nodes.

```
vtkstreamlines = pe.Node(
    interface=camino.VtkStreamlines(), name="vtkstreamlines")
procstreamlines = pe.Node(
    interface=camino.ProcStreamlines(), name="procstreamlines")
procstreamlines.inputs.outputtracts = 'oogl'
```

We can easily produce a variety of scalar values from our fitted tensors. The following nodes generate the fractional anisotropy and diffusivity trace maps and their associated headers, and then merge them back into a single .nii file.

```
fa = pe.Node(interface=camino.ComputeFractionalAnisotropy(), name='fa')
trace = pe.Node(interface=camino.ComputeTensorTrace(), name='trace')
dteig = pe.Node(interface=camino.ComputeEigensystem(), name='dteig')

analyzeheader_fa = pe.Node(
    interface=camino.AnalyzeHeader(), name='analyzeheader_fa')
analyzeheader_fa.inputs.datatype = 'double'
analyzeheader_trace = pe.Node(
    interface=camino.AnalyzeHeader(), name='analyzeheader_trace')
```

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```
analyzeheader_trace.inputs.datatype = 'double'

fa2nii = pe.Node(interface=misc.CreateNifti(), name='fa2nii')
trace2nii = fa2nii.clone("trace2nii")
```

This section adds the Connectome Mapping Toolkit (CMTK) nodes. These interfaces are fairly experimental and may not function properly. In order to perform connectivity mapping using CMTK, the parcellated structural data is rewritten using the indices and parcellation scheme from the connectome mapper (CMP). This process has been written into the ROIgen interface, which will output a remapped aparc+aseg image as well as a dictionary of label information (i.e. name, display colours) pertaining to the original and remapped regions. These label values are input from a user-input lookup table, if specified, and otherwise the default Freesurfer LUT (/freesurfer/FreeSurferColorLUT.txt).

```
roigen = pe.Node(interface=cmtk.ROIgen(), name="ROIgen")
cmp_config = cmp.configuration.PipelineConfiguration(
    parcellation_scheme="NativeFreesurfer")
cmp_config.parcellation_scheme = "NativeFreesurfer"
roigen.inputs.LUT_file = cmp_config.get_freeview_lut("NativeFreesurfer") [
    'freesurferaparc']
roigen_structspace = roigen.clone('ROIgen_structspace')
```

The CreateMatrix interface takes in the remapped aparc+aseg image as well as the label dictionary and fiber tracts and outputs a number of different files. The most important of which is the connectivity network itself, which is stored as a ‘gpickle’ and can be loaded using Python’s NetworkX package (see CreateMatrix docstring). Also outputted are various NumPy arrays containing detailed tract information, such as the start and endpoint regions, and statistics on the mean and standard deviation for the fiber length of each connection. These matrices can be used in the ConnectomeViewer to plot the specific tracts that connect between user-selected regions.

```
creatematrix = pe.Node(interface=cmtk.CreateMatrix(), name="CreateMatrix")
creatematrix.inputs.count_region_intersections = True
createnodes = pe.Node(interface=cmtk.CreateNodes(), name="CreateNodes")
createnodes.inputs.resolution_network_file = cmp_config.parcellation [
    'freesurferaparc'] ['node_information_graphml']
```

Here we define the endpoint of this tutorial, which is the CFFConverter node, as well as a few nodes which use the Nipyype Merge utility. These are useful for passing lists of the files we want packaged in our CFF file.

```
CFFConverter = pe.Node(interface=cmtk.CFFConverter(), name="CFFConverter")

giftiSurfaces = pe.Node(interface=util.Merge(8), name="GiftiSurfaces")
giftiLabels = pe.Node(interface=util.Merge(2), name="GiftiLabels")
niftiVolumes = pe.Node(interface=util.Merge(3), name="NiftiVolumes")
fiberDataArrays = pe.Node(interface=util.Merge(4), name="FiberDataArrays")
gpickledNetworks = pe.Node(interface=util.Merge(1), name="NetworkFiles")
```

Since we have now created all our nodes, we can define our workflow and start making connections.

```
mapping = pe.Workflow(name='mapping')
```

First, we connect the input node to the early conversion functions. FreeSurfer input nodes:

```
mapping.connect([(inputnode, FreeSurferSource, [ ("subject_id",
                                                  "subject_id") ])])
mapping.connect([(inputnode, FreeSurferSourceLH, [ ("subject_id",
                                                    "subject_id") ])])
mapping.connect([(inputnode, FreeSurferSourceRH, [ ("subject_id",
                                                    "subject_id") ])])
```

Required conversions for processing in Camino:


```
mapping.connect([(inputnode, image2voxel, [("dwi", "in_file")]),
                 (inputnode, fsl2scheme,
                  [("bvecs", "bvec_file"),
                   ("bvals", "bval_file")]), (image2voxel, dtifit,
                  [(['voxel_order', 'in_file'])),
                 (fsl2scheme, dtifit, [(['scheme', 'scheme_file'])))])])
```

Nifti conversions for the parcellated white matter image (used in Camino's conmap), and the subject's stripped brain image from Freesurfer:

```
mapping.connect([(FreeSurferSource, mri_convert_WMParc, [('wmparc',
                                                         'in_file')])])
mapping.connect([(FreeSurferSource, mri_convert_Brain, [('brain',
                                                         'in_file')])])
```

Surface conversions to GIFTI (pial, white, inflated, and sphere for both hemispheres)

```
mapping.connect([(FreeSurferSourceLH, mris_convertLH, [('pial', 'in_file')])])
mapping.connect([(FreeSurferSourceRH, mris_convertRH, [('pial', 'in_file')])])
mapping.connect([(FreeSurferSourceLH, mris_convertLHwhite, [('white',
                                                            'in_file')])])
mapping.connect([(FreeSurferSourceRH, mris_convertRHwhite, [('white',
                                                            'in_file')])])
mapping.connect([(FreeSurferSourceLH, mris_convertLHinflated, [('inflated',
                                                                'in_file')])])
mapping.connect([(FreeSurferSourceRH, mris_convertRHinflated, [('inflated',
                                                                'in_file')])])
mapping.connect([(FreeSurferSourceLH, mris_convertLHsphere, [('sphere',
                                                             'in_file')])])
mapping.connect([(FreeSurferSourceRH, mris_convertRHsphere, [('sphere',
                                                             'in_file')])])
```

The annotation files are converted using the pial surface as a map via the MRIsConvert interface. One of the functions defined earlier is used to select the lh.aparc.annot and rh.aparc.annot files specifically (rather than i.e. rh.aparc.a2009s.annot) from the output list given by the FreeSurferSource.

```
mapping.connect([(FreeSurferSourceLH, mris_convertLHlabels, [('pial',
                                                            'in_file')])])
mapping.connect([(FreeSurferSourceRH, mris_convertRHlabels, [('pial',
                                                            'in_file')])])
mapping.connect([(FreeSurferSourceLH, mris_convertLHlabels,
                 [(['annot', select_aparc_annot), 'annot_file']])])
mapping.connect([(FreeSurferSourceRH, mris_convertRHlabels,
                 [(['annot', select_aparc_annot), 'annot_file']])])
```

This section coregisters the diffusion-weighted and parcellated white-matter / whole brain images. At present the conmap node connection is left commented, as there have been recent changes in Camino code that have presented some users with errors.

```
mapping.connect([(inputnode, b0Strip, [('dwi', 'in_file')])])
mapping.connect([(b0Strip, coregister, [('out_file', 'in_file')])])
mapping.connect([(mri_convert_Brain, coregister, [('out_file', 'reference')])])
mapping.connect([(coregister, convertxfm, [('out_matrix_file', 'in_file')])])
mapping.connect([(b0Strip, inverse, [('out_file', 'reference')])])
mapping.connect([(convertxfm, inverse, [('out_file', 'in_matrix_file')])])
mapping.connect([(mri_convert_WMParc, inverse, [('out_file', 'in_file')])])
```

The tractography pipeline consists of the following nodes. Further information about the tractography can be found in `nipy/examples/dmri_camino_dti.py`.

```
mapping.connect([(b0Strip, track, [("mask_file", "seed_file")])])
mapping.connect([(fsl2scheme, dtlutgen, [("scheme", "scheme_file")])])
mapping.connect([(dtlutgen, picopdfs, [("dtLUT", "luts")])])
mapping.connect([(dtifit, picopdfs, [("tensor_fitted", "in_file")])])
mapping.connect([(picopdfs, track, [("pdfs", "in_file")])])
```

Connecting the Fractional Anisotropy and Trace nodes is simple, as they obtain their input from the tensor fitting. This is also where our voxel- and data-grabbing functions come in. We pass these functions, along with the original DWI image from the input node, to the header-generating nodes. This ensures that the files will be correct and readable.

```
mapping.connect([(dtifit, fa, [("tensor_fitted", "in_file")])])
mapping.connect([(fa, analyzeheader_fa, [("fa", "in_file")])])
mapping.connect([(inputnode, analyzeheader_fa,
                  [(['dwi', get_vox_dims), 'voxel_dims'],
                   [(['dwi', get_data_dims), 'data_dims'])])])
mapping.connect([(fa, fa2nii, [('fa', 'data_file')])])
mapping.connect([(inputnode, fa2nii, [(['dwi', get_affine), 'affine'])])])
mapping.connect([(analyzeheader_fa, fa2nii, [('header', 'header_file')])])

mapping.connect([(dtifit, trace, [("tensor_fitted", "in_file")])])
mapping.connect([(trace, analyzeheader_trace, [("trace", "in_file")])])
mapping.connect([(inputnode, analyzeheader_trace,
                  [(['dwi', get_vox_dims), 'voxel_dims'],
                   [(['dwi', get_data_dims), 'data_dims'])])])
mapping.connect([(trace, trace2nii, [('trace', 'data_file')])])
mapping.connect([(inputnode, trace2nii, [(['dwi', get_affine), 'affine'])])])
mapping.connect([(analyzeheader_trace, trace2nii, [('header',
                                                    'header_file')])])

mapping.connect([(dtifit, dteig, [("tensor_fitted", "in_file")])])
```

The output tracts are converted to Trackvis format (and back). Here we also use the voxel- and data-grabbing functions defined at the beginning of the pipeline.

```
mapping.connect([(track, camino2trackvis, [('tracked', 'in_file')]),
                  (track, vtkstreamlines, [('tracked', 'in_file')]),
                  (camino2trackvis, trk2camino, [('trackvis', 'in_file')])])
mapping.connect([(inputnode, camino2trackvis,
                  [(['dwi', get_vox_dims), 'voxel_dims'],
                   [(['dwi', get_data_dims), 'data_dims'])])])
```

Here the CMTK connectivity mapping nodes are connected. The original aparc+aseg image is converted to NIFTI, then registered to the diffusion image and delivered to the ROIgen node. The remapped parcellation, original tracts, and label file are then given to CreateMatrix.

```
mapping.connect(createnodes, 'node_network', creatematrix,
                'resolution_network_file')
mapping.connect([(FreeSurferSource, mri_convert_AparcAseg,
                  [(['aparc_aseg', select_aparc), 'in_file'])])])

mapping.connect([(b0Strip, inverse_AparcAseg, [('out_file', 'reference')])])
mapping.connect([(convertxfm, inverse_AparcAseg, [('out_file',
                                                    'in_matrix_file')])])
mapping.connect([(mri_convert_AparcAseg, inverse_AparcAseg, [('out_file',
                                                            'in_file')])])
mapping.connect([(mri_convert_AparcAseg, roigen_structspace,
                  [('out_file', 'aparc_aseg_file')])])
```

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```

mapping.connect([(roigen_structspace, createnodes, [{"roi_file",
                                                    "roi_file"}])])

mapping.connect([(inverse_AparcAseg, roigen, [{"out_file",
                                                "aparc_aseg_file"}])])

mapping.connect([(roigen, creatematrix, [{"roi_file", "roi_file"}])])
mapping.connect([(camino2trackvis, creatematrix, [{"trackvis",
                                                  "tract_file"}])])

mapping.connect([(inputnode, creatematrix, [{"subject_id",
                                              "out_matrix_file"}])])
mapping.connect([(inputnode, creatematrix, [{"subject_id",
                                              "out_matrix_mat_file"}])])

```

The merge nodes defined earlier are used here to create lists of the files which are destined for the CFFConverter.

```

mapping.connect([(creatematrix, gpickledNetworks, [{"matrix_files", "in1"}])])

mapping.connect([(mris_convertLH, giftiSurfaces, [{"converted", "in1"}])])
mapping.connect([(mris_convertRH, giftiSurfaces, [{"converted", "in2"}])])
mapping.connect([(mris_convertLHwhite, giftiSurfaces, [{"converted", "in3"}])])
mapping.connect([(mris_convertRHwhite, giftiSurfaces, [{"converted", "in4"}])])
mapping.connect([(mris_convertLHinflated, giftiSurfaces, [{"converted",
                                                         "in5"}])])
mapping.connect([(mris_convertRHinflated, giftiSurfaces, [{"converted",
                                                         "in6"}])])
mapping.connect([(mris_convertLHsphere, giftiSurfaces, [{"converted",
                                                         "in7"}])])
mapping.connect([(mris_convertRHSphere, giftiSurfaces, [{"converted",
                                                         "in8"}])])

mapping.connect([(mris_convertLHlabels, giftiLabels, [{"converted", "in1"}])])
mapping.connect([(mris_convertRHlabels, giftiLabels, [{"converted", "in2"}])])

mapping.connect([(roigen, niftiVolumes, [{"roi_file", "in1"}])])
mapping.connect([(inputnode, niftiVolumes, [{"dwi", "in2"}])])
mapping.connect([(mri_convert_Brain, niftiVolumes, [{"out_file", "in3"}])])

mapping.connect([(creatematrix, fiberDataArrays, [{"endpoint_file", "in1"}])])
mapping.connect([(creatematrix, fiberDataArrays, [{"endpoint_file_mm",
                                                    "in2"}])])
mapping.connect([(creatematrix, fiberDataArrays, [{"fiber_length_file",
                                                    "in3"}])])
mapping.connect([(creatematrix, fiberDataArrays, [{"fiber_label_file",
                                                    "in4"}])])

```

This block actually connects the merged lists to the CFF converter. We pass the surfaces and volumes that are to be included, as well as the tracts and the network itself. The currently running pipeline (dmri_connectivity.py) is also scraped and included in the CFF file. This makes it easy for the user to examine the entire processing pathway used to generate the end product.

```

CFFConverter.inputs.script_files = op.abspath(
    inspect.getfile(inspect.currentframe()))
mapping.connect([(giftiSurfaces, CFFConverter, [{"out", "gifti_surfaces"}])])
mapping.connect([(giftiLabels, CFFConverter, [{"out", "gifti_labels"}])])
mapping.connect([(gpickledNetworks, CFFConverter, [{"out",
                                                    "gpickled_networks"}])])
mapping.connect([(niftiVolumes, CFFConverter, [{"out", "nifti_volumes"}])])

```

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```
mapping.connect([(fiberDataArrays, CFFConverter, [("out", "data_files")])])
mapping.connect([(creatematrix, CFFConverter, [("filtered_tractographies",
                                              "tract_files")])])
mapping.connect([(inputnode, CFFConverter, [("subject_id", "title")])])
```

Finally, we create another higher-level workflow to connect our mapping workflow with the info and datagrabbing nodes declared at the beginning. Our tutorial can is now extensible to any arbitrary number of subjects by simply adding their names to the subject list and their data to the proper folders.

```
connectivity = pe.Workflow(name="connectivity")
connectivity.base_dir = op.abspath('dmri_connectivity')
connectivity.connect([(infosource, datasource, [('subject_id', 'subject_id')]),
                      (datasource, mapping,
                       [('dwi', 'inputnode.dwi'), ('bvals', 'inputnode.bvals'),
                       ('bvecs', 'inputnode.bvecs')]),
                      (infosource, mapping, [('subject_id',
                                              'inputnode.subject_id')])])
```

The following functions run the whole workflow and produce graphs describing the processing pipeline. By default, `write_graph` outputs a `.dot` file and a `.png` image, but here we set it to output the image as a vector graphic, by passing the `format='eps'` argument.

```
if __name__ == '__main__':
    connectivity.run()
    connectivity.write_graph(format='eps')
```

The output CFF file of this pipeline can be loaded in the [Connectome Viewer](#). After loading the network into memory it can be examined in 3D or as a connectivity matrix using the default scripts produced by the Code Oracle. To compare networks, one must use the MergeCNetworks interface to merge two networks into a single CFF file. Statistics can then be run using the Network Brain Statistics (NBS) plugin Surfaces can also be loaded along with their labels from the `aparc+aseg` file. The tractography is included in the file so that region-to-region fibers can be individually plotted using the Code Oracle.

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

dMRI: Connectivity - MRtrix, CMTK, FreeSurfer

9.1 Introduction

This script, `connectivity_tutorial_advanced.py`, demonstrates the ability to perform connectivity mapping using Nipype for pipelining, Freesurfer for Reconstruction / Segmentation, MRtrix for spherical deconvolution and tractography, and the Connectome Mapping Toolkit (CMTK) for further parcellation and connectivity analysis:

```
python connectivity_tutorial_advanced.py
```

We perform this analysis using the FSL course data, which can be acquired from here:

- http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz

This pipeline also requires the Freesurfer directory for 'subj1' from the FSL course data. To save time, this data can be downloaded from here:

- <http://dl.dropbox.com/u/315714/subj1.zip?dl=1>

The result of this processing will be the connectome for subj1 as a Connectome File Format (CFF) File, using the Lausanne2008 parcellation scheme. A data package containing the outputs of this pipeline can be obtained from here:

- <http://db.tt/909Q3AC1>

See also:

connectivity_tutorial.py Original tutorial using Camino and the NativeFreesurfer Parcellation Scheme

www.cmtk.org For more info about the parcellation scheme

Warning: The ConnectomeMapper (<https://github.com/LTS5/cmp> or www.cmtk.org) must be installed for this tutorial to function!

9.2 Packages and Data Setup

Import necessary modules from nipype.

```
import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.utility as util # utility
import nipype.pipeline.engine as pe # pipeline engine
import nipype.interfaces.fsl as fsl
import nipype.interfaces.freesurfer as fs # freesurfer
import nipype.interfaces.mrtrix as mrtrix
```

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```

import nipyype.algorithms.misc as misc
import nipyype.interfaces.cmtk as cmtk
import nipyype.interfaces.dipy as dipy
import inspect
import os
import os.path as op # system functions
from nipyype.workflows.dmri.fsl.dti import create_eddy_correct_pipeline
from nipyype.workflows.dmri.camino.connectivity_mapping import select_aparc_annot
from nipyype.utils.misc import package_check
import warnings
from nipyype.workflows.dmri.connectivity.nx import create_networkx_pipeline,
↳ create_cmats_to_csv_pipeline
from nipyype.workflows.smri.freesurfer import create_tessellation_flow

try:
    package_check('cmp')
except Exception as e:
    warnings.warn('cmp not installed')
else:
    import cmp

```

This needs to point to the freesurfer subjects directory (Recon-all must have been run on subj1 from the FSL course data) Alternatively, the reconstructed subject data can be downloaded from:

- <http://dl.dropbox.com/u/315714/subj1.zip>

```

subjects_dir = op.abspath(op.join(op.curdir, './subjects'))
fs.FSLCommand.set_default_subjects_dir(subjects_dir)
fsl.FSLCommand.set_default_output_type('NIFTI')

fs_dir = os.environ['FREESURFER_HOME']
lookup_file = op.join(fs_dir, 'FreeSurferColorLUT.txt')

```

This needs to point to the fdt folder you can find after extracting

- http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz

```

data_dir = op.abspath(op.join(op.curdir, 'exdata/'))
subject_list = ['subj1']

```

Use infosource node to loop through the subject list and define the input files. For our purposes, these are the diffusion-weighted MR image, b vectors, and b values.

```

infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")
infosource.iterables = ('subject_id', subject_list)

info = dict(
    dwi=[['subject_id', 'data']],
    bvecs=[['subject_id', 'bvecs']],
    bvals=[['subject_id', 'bvals']])

```

Use datasource node to perform the actual data grabbing. Templates for the associated images are used to obtain the correct images.

```

datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=list(info.keys())),
    name='datasource')

```

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```

datasource.inputs.template = "%s/%s"
datasource.inputs.base_directory = data_dir
datasource.inputs.field_template = dict(dwi='%s/%s.nii.gz')
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True

```

The input node and Freesurfer sources declared here will be the main conduits for the raw data to the rest of the processing pipeline.

```

inputnode = pe.Node(
    interface=util.IdentityInterface(
        fields=["subject_id", "dwi", "bvecs", "bvals", "subjects_dir"]),
    name="inputnode")
inputnode.inputs.subjects_dir = subjects_dir

FreeSurferSource = pe.Node(interface=nio.FreeSurferSource(), name='fssource')
FreeSurferSourceLH = FreeSurferSource.clone('fssourceLH')
FreeSurferSourceLH.inputs.hemi = 'lh'
FreeSurferSourceRH = FreeSurferSource.clone('fssourceRH')
FreeSurferSourceRH.inputs.hemi = 'rh'

```

9.3 Creating the workflow's nodes

9.3.1 Conversion nodes

A number of conversion operations are required to obtain NIFTI files from the FreesurferSource for each subject. Nodes are used to convert the following:

- Original structural image to NIFTI
- Pial, white, inflated, and spherical surfaces for both the left and right hemispheres are converted to GIFTI for visualization in ConnectomeViewer
- Parcellated annotation files for the left and right hemispheres are also converted to GIFTI

```

mri_convert_Brain = pe.Node(
    interface=fs.MRConvert(), name='mri_convert_Brain')
mri_convert_Brain.inputs.out_type = 'nii'
mri_convert_ROI_scale500 = mri_convert_Brain.clone('mri_convert_ROI_scale500')

mris_convertLH = pe.Node(interface=fs.MRIsConvert(), name='mris_convertLH')
mris_convertLH.inputs.out_datatype = 'gii'
mris_convertRH = mris_convertLH.clone('mris_convertRH')
mris_convertRHwhite = mris_convertLH.clone('mris_convertRHwhite')
mris_convertLHwhite = mris_convertLH.clone('mris_convertLHwhite')
mris_convertRHinflated = mris_convertLH.clone('mris_convertRHinflated')
mris_convertLHinflated = mris_convertLH.clone('mris_convertLHinflated')
mris_convertRHsphere = mris_convertLH.clone('mris_convertRHsphere')
mris_convertLHsphere = mris_convertLH.clone('mris_convertLHsphere')
mris_convertLHlabels = mris_convertLH.clone('mris_convertLHlabels')
mris_convertRHlabels = mris_convertLH.clone('mris_convertRHlabels')

```

9.3.2 Diffusion processing nodes

See also:

dmri_mrtrix_dti.py Tutorial that focuses solely on the MRtrix diffusion processing

<http://www.brain.org.au/software/mrtrix/index.html> MRtrix's online documentation

b-values and b-vectors stored in FSL's format are converted into a single encoding file for MRTrix.

```
fsl2mrtrix = pe.Node(interface=mrtrix.FSL2MRTrix(), name='fsl2mrtrix')
```

Distortions induced by eddy currents are corrected prior to fitting the tensors. The first image is used as a reference for which to warp the others.

```
eddycorrect = create_eddy_correct_pipeline(name='eddycorrect')
eddycorrect.inputs.inputnode.ref_num = 1
```

Tensors are fitted to each voxel in the diffusion-weighted image and from these three maps are created:

- Major eigenvector in each voxel
- Apparent diffusion coefficient
- Fractional anisotropy

```
dwi2tensor = pe.Node(interface=mrtrix.DWI2Tensor(), name='dwi2tensor')
tensor2vector = pe.Node(interface=mrtrix.Tensor2Vector(), name='tensor2vector')
tensor2adc = pe.Node(
    interface=mrtrix.Tensor2ApparentDiffusion(), name='tensor2adc')
tensor2fa = pe.Node(
    interface=mrtrix.Tensor2FractionalAnisotropy(), name='tensor2fa')
MRconvert_fa = pe.Node(interface=mrtrix.MRConvert(), name='MRconvert_fa')
MRconvert_fa.inputs.extension = 'nii'
```

These nodes are used to create a rough brain mask from the b0 image. The b0 image is extracted from the original diffusion-weighted image, put through a simple thresholding routine, and smoothed using a 3x3 median filter.

```
MRconvert = pe.Node(interface=mrtrix.MRConvert(), name='MRconvert')
MRconvert.inputs.extract_at_axis = 3
MRconvert.inputs.extract_at_coordinate = [0]
threshold_b0 = pe.Node(interface=mrtrix.Threshold(), name='threshold_b0')
median3d = pe.Node(interface=mrtrix.MedianFilter3D(), name='median3d')
```

The brain mask is also used to help identify single-fiber voxels. This is done by passing the brain mask through two erosion steps, multiplying the remaining mask with the fractional anisotropy map, and thresholding the result to obtain some highly anisotropic within-brain voxels.

```
erode_mask_firstpass = pe.Node(
    interface=mrtrix.Erode(), name='erode_mask_firstpass')
erode_mask_secondpass = pe.Node(
    interface=mrtrix.Erode(), name='erode_mask_secondpass')
MRmultiply = pe.Node(interface=mrtrix.MRMultiply(), name='MRmultiply')
MRmult_merge = pe.Node(interface=util.Merge(2), name='MRmultiply_merge')
threshold_FA = pe.Node(interface=mrtrix.Threshold(), name='threshold_FA')
threshold_FA.inputs.absolute_threshold_value = 0.7
```

For whole-brain tracking we also require a broad white-matter seed mask. This is created by generating a white matter mask, given a brainmask, and thresholding it at a reasonably high level.

```
bet = pe.Node(interface=fsl.BET(mask=True), name='bet_b0')
gen_WM_mask = pe.Node(
    interface=mrtrix.GenerateWhiteMatterMask(), name='gen_WM_mask')
threshold_wmmask = pe.Node(
    interface=mrtrix.Threshold(), name='threshold_wmmask')
threshold_wmmask.inputs.absolute_threshold_value = 0.4
```

The spherical deconvolution step depends on the estimate of the response function in the highly anisotropic voxels we obtained above.

Warning: For damaged or pathological brains one should take care to lower the maximum harmonic order of these steps.

```
estimatereponse = pe.Node(
    interface=mrtrix.EstimateResponseForSH(), name='estimatereponse')
estimatereponse.inputs.maximum_harmonic_order = 6
csdeconv = pe.Node(
    interface=mrtrix.ConstrainedSphericalDeconvolution(), name='csdeconv')
csdeconv.inputs.maximum_harmonic_order = 6
```

Finally, we track probabilistically using the orientation distribution functions obtained earlier. The tracts are then used to generate a tract-density image, and they are also converted to TrackVis format.

```
probCSDstreamtrack = pe.Node(
    interface=mrtrix.ProbabilisticSphericallyDeconvolutedStreamlineTrack(),
    name='probCSDstreamtrack')
probCSDstreamtrack.inputs.inputmodel = 'SD_PROB'
probCSDstreamtrack.inputs.desired_number_of_tracks = 150000
tracks2prob = pe.Node(interface=mrtrix.Tracks2Prob(), name='tracks2prob')
tracks2prob.inputs.colour = True
MRconvert_tracks2prob = MRconvert_fa.clone(name='MRconvert_tracks2prob')
tck2trk = pe.Node(interface=mrtrix.MRTrkx2TrackVis(), name='tck2trk')
trk2tdi = pe.Node(interface=dipy.TrackDensityMap(), name='trk2tdi')
```

9.3.3 Structural segmentation nodes

The following node identifies the transformation between the diffusion-weighted image and the structural image. This transformation is then applied to the tracts so that they are in the same space as the regions of interest.

```
coregister = pe.Node(interface=fsl.FLIRT(dof=6), name='coregister')
coregister.inputs.cost = ('normmi')
```

Parcellation is performed given the aparc+aseg image from Freesurfer. The CMTK Parcellation step subdivides these regions to return a higher-resolution parcellation scheme. The parcellation used here is entitled “scale500” and returns 1015 regions.

```
parcellation_name = 'scale500'
parcellate = pe.Node(interface=cmtk.Parcellate(), name="Parcellate")
parcellate.inputs.parcellation_name = parcellation_name
```

The CreateMatrix interface takes in the remapped aparc+aseg image as well as the label dictionary and fiber tracts and outputs a number of different files. The most important of which is the connectivity network itself, which is stored as a ‘gpickle’ and can be loaded using Python’s NetworkX package (see CreateMatrix docstring). Also outputted are various NumPy arrays containing detailed tract information, such as the start and endpoint regions, and statistics on the mean and standard deviation for the fiber length of each connection. These matrices can be used in the ConnectomeViewer to plot the specific tracts that connect between user-selected regions. Here we choose the Lausanne2008 parcellation scheme, since we are incorporating the CMTK parcellation step.

```
parcellation_name = 'scale500'
cmp_config = cmp.configuration.PipelineConfiguration()
cmp_config.parcellation_scheme = "Lausanne2008"
createnodes = pe.Node(interface=cmtk.CreateNodes(), name="CreateNodes")
createnodes.inputs.resolution_network_file = cmp_config._get_lausanne_
    ↳parcellation(
        'Lausanne2008')[parcellation_name]['node_information_graphml']
```

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```
creatematrix = pe.Node(interface=cmtk.CreateMatrix(), name="CreateMatrix")
creatematrix.inputs.count_region_intersections = True
```

Next we define the endpoint of this tutorial, which is the CFFConverter node, as well as a few nodes which use the Nipype Merge utility. These are useful for passing lists of the files we want packaged in our CFF file. The inspect.getfile command is used to package this script into the resulting CFF file, so that it is easy to look back at the processing parameters that were used.

```
CFFConverter = pe.Node(interface=cmtk.CFFConverter(), name="CFFConverter")
CFFConverter.inputs.script_files = op.abspath(
    inspect.getfile(inspect.currentframe()))
giftiSurfaces = pe.Node(interface=util.Merge(9), name="GiftiSurfaces")
giftiLabels = pe.Node(interface=util.Merge(2), name="GiftiLabels")
niftiVolumes = pe.Node(interface=util.Merge(3), name="NiftiVolumes")
fiberDataArrays = pe.Node(interface=util.Merge(4), name="FiberDataArrays")
gpickledNetworks = pe.Node(interface=util.Merge(2), name="NetworkFiles")
```

We also create a workflow to calculate several network metrics on our resulting file, and another CFF converter which will be used to package these networks into a single file.

```
networkx = create_networkx_pipeline(name='networkx')
cmats_to_csv = create_cmats_to_csv_pipeline(name='cmats_to_csv')
NxStatsCFFConverter = pe.Node(
    interface=cmtk.CFFConverter(), name="NxStatsCFFConverter")
NxStatsCFFConverter.inputs.script_files = op.abspath(
    inspect.getfile(inspect.currentframe()))

tessflow = create_tessellation_flow(name='tessflow', out_format='gii')
tessflow.inputs.inputs.spec.lookup_file = lookup_file
```

9.4 Connecting the workflow

Here we connect our processing pipeline.

9.4.1 Connecting the inputs, FreeSurfer nodes, and conversions

```
mapping = pe.Workflow(name='mapping')
```

First, we connect the input node to the FreeSurfer input nodes.

```
mapping.connect([(inputnode, FreeSurferSource, [ ("subjects_dir",
                                                  "subjects_dir") ])])
mapping.connect([(inputnode, FreeSurferSource, [ ("subject_id",
                                                  "subject_id") ])])

mapping.connect([(inputnode, FreeSurferSourceLH, [ ("subjects_dir",
                                                    "subjects_dir") ])])
mapping.connect([(inputnode, FreeSurferSourceLH, [ ("subject_id",
                                                    "subject_id") ])])

mapping.connect([(inputnode, FreeSurferSourceRH, [ ("subjects_dir",
                                                    "subjects_dir") ])])
mapping.connect([(inputnode, FreeSurferSourceRH, [ ("subject_id",
                                                    "subject_id") ])])
```

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```
mapping.connect([(inputnode, tessflow, [("subjects_dir",
                                         "inputspec.subjects_dir")])])
mapping.connect([(inputnode, tessflow, [("subject_id",
                                         "inputspec.subject_id")])])

mapping.connect([(inputnode, parcellate, [("subjects_dir", "subjects_dir")])])
mapping.connect([(inputnode, parcellate, [("subject_id", "subject_id")])])
mapping.connect([(parcellate, mri_convert_ROI_scale500, [('roi_file',
                                                         'in_file')])])
```

Nifti conversion for subject's stripped brain image from Freesurfer:

```
mapping.connect([(FreeSurferSource, mri_convert_Brain, [('brain',
                                                         'in_file')])])
```

Surface conversions to GIFTI (pial, white, inflated, and sphere for both hemispheres)

```
mapping.connect([(FreeSurferSourceLH, mris_convertLH, [('pial', 'in_file')])])
mapping.connect([(FreeSurferSourceRH, mris_convertRH, [('pial', 'in_file')])])
mapping.connect([(FreeSurferSourceLH, mris_convertLHwhite, [('white',
                                                            'in_file')])])
mapping.connect([(FreeSurferSourceRH, mris_convertRHwhite, [('white',
                                                            'in_file')])])
mapping.connect([(FreeSurferSourceLH, mris_convertLHinflated, [('inflated',
                                                                'in_file')])])
mapping.connect([(FreeSurferSourceRH, mris_convertRHinflated, [('inflated',
                                                                'in_file')])])
mapping.connect([(FreeSurferSourceLH, mris_convertLHsphere, [('sphere',
                                                             'in_file')])])
mapping.connect([(FreeSurferSourceRH, mris_convertRHSphere, [('sphere',
                                                             'in_file')])])
```

The annotation files are converted using the pial surface as a map via the MRIsConvert interface. One of the functions defined earlier is used to select the lh.aparc.annot and rh.aparc.annot files specifically (rather than e.g. rh.aparc.a2009s.annot) from the output list given by the FreeSurferSource.

```
mapping.connect([(FreeSurferSourceLH, mris_convertLHlabels, [('pial',
                                                            'in_file')])])
mapping.connect([(FreeSurferSourceRH, mris_convertRHlabels, [('pial',
                                                            'in_file')])])

mapping.connect([(FreeSurferSourceLH, mris_convertLHlabels,
                 [(['annot', select_aparc_annot), 'annot_file']])])
mapping.connect([(FreeSurferSourceRH, mris_convertRHlabels,
                 [(['annot', select_aparc_annot), 'annot_file']])])
```

9.4.2 Diffusion Processing

Now we connect the tensor computations:

```
mapping.connect([(inputnode, fsl2mrtrix, [("bvecs", "bvec_file"),
                                           ("bvals", "bval_file")])])
mapping.connect([(inputnode, eddycorrect, [("dwi", "inputnode.in_file")])])
mapping.connect([(eddycorrect, dwi2tensor, [("outputnode.eddy_corrected",
                                           "in_file")])])
mapping.connect([(fsl2mrtrix, dwi2tensor, [("encoding_file",
                                           "encoding_file")])])
```

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```
mapping.connect([
    (dwi2tensor, tensor2vector, [['tensor', 'in_file']]),
    (dwi2tensor, tensor2adc, [['tensor', 'in_file']]),
    (dwi2tensor, tensor2fa, [['tensor', 'in_file']]),
])
mapping.connect([(tensor2fa, MRmult_merge, [("FA", "in1")])])
mapping.connect([(tensor2fa, MRconvert_fa, [("FA", "in_file")])])
```

This block creates the rough brain mask to be multiplied, multiplies it with the fractional anisotropy image, and thresholds it to get the single-fiber voxels.

```
mapping.connect([(eddycorrect, MRconvert, [("outputnode.eddy_corrected",
                                          "in_file")])])
mapping.connect([(MRconvert, threshold_b0, [("converted", "in_file")])])
mapping.connect([(threshold_b0, median3d, [("out_file", "in_file")])])
mapping.connect([(median3d, erode_mask_firstpass, [("out_file", "in_file")])])
mapping.connect([(erode_mask_firstpass, erode_mask_secondpass, [("out_file",
                                                                "in_file")])])
mapping.connect([(erode_mask_secondpass, MRmult_merge, [("out_file", "in2")])])
mapping.connect([(MRmult_merge, MRmultiply, [("out", "in_files")])])
mapping.connect([(MRmultiply, threshold_FA, [("out_file", "in_file")])])
```

Here the thresholded white matter mask is created for seeding the tractography.

```
mapping.connect([(eddycorrect, bet, [("outputnode.eddy_corrected",
                                     "in_file")])])
mapping.connect([(eddycorrect, gen_WM_mask, [("outputnode.eddy_corrected",
                                              "in_file")])])
mapping.connect([(bet, gen_WM_mask, [("mask_file", "binary_mask")])])
mapping.connect([(fsl2mrtrix, gen_WM_mask, [("encoding_file",
                                              "encoding_file")])])
mapping.connect([(gen_WM_mask, threshold_wmmask, [("WMprobabilitymap",
                                                  "in_file")])])
```

Next we estimate the fiber response distribution.

```
mapping.connect([(eddycorrect, estimatorresponse, [("outputnode.eddy_corrected",
                                                    "in_file")])])
mapping.connect([(fsl2mrtrix, estimatorresponse, [("encoding_file",
                                                    "encoding_file")])])
mapping.connect([(threshold_FA, estimatorresponse, [("out_file",
                                                    "mask_image")])])
```

Run constrained spherical deconvolution.

```
mapping.connect([(eddycorrect, csdeconv, [("outputnode.eddy_corrected",
                                          "in_file")])])
mapping.connect([(gen_WM_mask, csdeconv, [("WMprobabilitymap",
                                          "mask_image")])])
mapping.connect([(estimatorresponse, csdeconv, [("response",
                                                  "response_file")])])
mapping.connect([(fsl2mrtrix, csdeconv, [("encoding_file", "encoding_file")])])
```

Connect the tractography and compute the tract density image.

```
mapping.connect([(threshold_wmmask, probCSDstreamtrack, [("out_file",
                                                         "seed_file")])])
mapping.connect([(csdeconv, probCSDstreamtrack, [("spherical_harmonics_image",
                                                  "in_file")])])
```

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```
mapping.connect([(probCSDstreamtrack, tracks2prob, [("tracked", "in_file")])])
mapping.connect([(eddycorrect, tracks2prob, [("outputnode.eddy_corrected",
                                             "template_file")])])
mapping.connect([(tracks2prob, MRconvert_tracks2prob, [("tract_image",
                                                         "in_file")])])
```

9.4.3 Structural Processing

First, we coregister the diffusion image to the structural image

```
mapping.connect([(eddycorrect, coregister, [("outputnode.eddy_corrected",
                                             "in_file")])])
mapping.connect([(mri_convert_Brain, coregister, [('out_file', 'reference')])])
```

The MRtrix-tracked fibers are converted to TrackVis format (with voxel and data dimensions grabbed from the DWI). The connectivity matrix is created with the transformed .trk fibers and the parcellation file.

```
mapping.connect([(eddycorrect, tck2trk, [("outputnode.eddy_corrected",
                                           "image_file")])])
mapping.connect([(mri_convert_Brain, tck2trk, [("out_file",
                                                "registration_image_file")])])
mapping.connect([(coregister, tck2trk, [("out_matrix_file", "matrix_file")])])
mapping.connect([(probCSDstreamtrack, tck2trk, [("tracked", "in_file")])])
mapping.connect([(tck2trk, creatematrix, [("out_file", "tract_file")])])
mapping.connect([(tck2trk, trk2tdi, [("out_file", "in_file")])])
mapping.connect([(inputnode, creatematrix, [("subject_id",
                                             "out_matrix_file")])])
mapping.connect([(inputnode, creatematrix, [("subject_id",
                                             "out_matrix_mat_file")])])
mapping.connect([(parcellate, creatematrix, [("roi_file", "roi_file")])])
mapping.connect([(parcellate, createnodes, [("roi_file", "roi_file")])])
mapping.connect([(createnodes, creatematrix, [("node_network",
                                                "resolution_network_file")])])
```

The merge nodes defined earlier are used here to create lists of the files which are destined for the CFFConverter.

```
mapping.connect([(mris_convertLH, giftiSurfaces, [("converted", "in1")])])
mapping.connect([(mris_convertRH, giftiSurfaces, [("converted", "in2")])])
mapping.connect([(mris_convertLHwhite, giftiSurfaces, [("converted", "in3")])])
mapping.connect([(mris_convertRHwhite, giftiSurfaces, [("converted", "in4")])])
mapping.connect([(mris_convertLHinflated, giftiSurfaces, [("converted",
                                                           "in5")])])
mapping.connect([(mris_convertRHinflated, giftiSurfaces, [("converted",
                                                           "in6")])])
mapping.connect([(mris_convertLHsphere, giftiSurfaces, [("converted",
                                                         "in7")])])
mapping.connect([(mris_convertRHsphere, giftiSurfaces, [("converted",
                                                         "in8")])])
mapping.connect([(tessflow, giftiSurfaces, [("outputspec.meshes", "in9")])])

mapping.connect([(mris_convertLHlabels, giftiLabels, [("converted", "in1")])])
mapping.connect([(mris_convertRHlabels, giftiLabels, [("converted", "in2")])])

mapping.connect([(parcellate, niftiVolumes, [("roi_file", "in1")])])
mapping.connect([(eddycorrect, niftiVolumes, [("outputnode.eddy_corrected",
                                                "in2")])])
mapping.connect([(mri_convert_Brain, niftiVolumes, [("out_file", "in3")])])
```

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```

mapping.connect([(creatematrix, fiberDataArrays, [("endpoint_file", "in1")])])
mapping.connect([(creatematrix, fiberDataArrays, [("endpoint_file_mm",
                                                    "in2")])])
mapping.connect([(creatematrix, fiberDataArrays, [("fiber_length_file",
                                                    "in3")])])
mapping.connect([(creatematrix, fiberDataArrays, [("fiber_label_file",
                                                    "in4")])])

```

This block actually connects the merged lists to the CFF converter. We pass the surfaces and volumes that are to be included, as well as the tracts and the network itself. The currently running pipeline (`dmri_connectivity_advanced.py`) is also scraped and included in the CFF file. This makes it easy for the user to examine the entire processing pathway used to generate the end product.

```

mapping.connect([(giftiSurfaces, CFFConverter, [("out", "gifti_surfaces")])])
mapping.connect([(giftiLabels, CFFConverter, [("out", "gifti_labels")])])
mapping.connect([(creatematrix, CFFConverter, [("matrix_files",
                                                "gpickled_networks")])])
mapping.connect([(niftiVolumes, CFFConverter, [("out", "nifti_volumes")])])
mapping.connect([(fiberDataArrays, CFFConverter, [("out", "data_files")])])
mapping.connect([(creatematrix, CFFConverter, [("filtered_tractographies",
                                                "tract_files")])])
mapping.connect([(inputnode, CFFConverter, [("subject_id", "title")])])

```

The graph theoretical metrics are computed using the networkx workflow and placed in another CFF file

```

mapping.connect([(inputnode, networkx, [("subject_id",
                                         "inputnode.extra_field")])])
mapping.connect([(creatematrix, networkx, [("intersection_matrix_file",
                                         "inputnode.network_file")])])

mapping.connect([(networkx, NxStatsCFFConverter, [("outputnode.network_files",
                                                  "gpickled_networks")])])
mapping.connect([(giftiSurfaces, NxStatsCFFConverter, [("out",
                                                         "gifti_surfaces")])])
mapping.connect([(giftiLabels, NxStatsCFFConverter, [("out",
                                                         "gifti_labels")])])
mapping.connect([(niftiVolumes, NxStatsCFFConverter, [("out",
                                                         "nifti_volumes")])])
mapping.connect([(fiberDataArrays, NxStatsCFFConverter, [("out",
                                                         "data_files")])])
mapping.connect([(inputnode, NxStatsCFFConverter, [("subject_id", "title")])])

mapping.connect([(inputnode, cmats_to_csv, [("subject_id",
                                              "inputnode.extra_field")])])
mapping.connect([(creatematrix, cmats_to_csv,
                  [("matlab_matrix_files", "inputnode.matlab_matrix_files")])])

```

9.4.4 Create a higher-level workflow

Finally, we create another higher-level workflow to connect our mapping workflow with the info and datagrabbing nodes declared at the beginning. Our tutorial is now extensible to any arbitrary number of subjects by simply adding their names to the subject list and their data to the proper folders.

```

connectivity = pe.Workflow(name="connectivity")

connectivity.base_dir = op.abspath('dmri_connectivity_advanced')

```

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```
connectivity.connect([(infosource, datasource, [('subject_id', 'subject_id')]),
                      (datasource, mapping,
                       [('dwi', 'inputnode.dwi'), ('bvals', 'inputnode.bvals'),
                        ('bvecs', 'inputnode.bvecs')]),
                      (infosource, mapping, [('subject_id',
                                                'inputnode.subject_id')])])])
```

The following functions run the whole workflow and produce a .dot and .png graph of the processing pipeline.

```
if __name__ == '__main__':
    connectivity.run()
    connectivity.write_graph()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

dMRI: DTI - Diffusion Toolkit, FSL

A pipeline example that uses several interfaces to perform analysis on diffusion weighted images using Diffusion Toolkit tools.

This tutorial is based on the 2010 FSL course and uses data freely available at the FSL website at: http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz

More details can be found at <http://www.fmrib.ox.ac.uk/fslcourse/lectures/practicals/fdt/index.htm>

In order to run this tutorial you need to have Diffusion Toolkit and FSL tools installed and accessible from matlab/command line. Check by calling `fsinfo` and `dtk` from the command line.

Tell python where to find the appropriate functions.

```
import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.fsl as fsl # fsl
import nipype.interfaces.diffusion_toolkit as dtk
import nipype.interfaces.utility as util # utility
import nipype.pipeline.engine as pe # pipeline engine
import os # system functions
from nipype.workflows.dmri.fsl.dti import create_eddy_correct_pipeline
```

Confirm package dependencies are installed. (This is only for the tutorial, rarely would you put this in your own code.)

```
from nipype.utils.misc import package_check

package_check('numpy', '1.3', 'tutorial1')
package_check('scipy', '0.7', 'tutorial1')
package_check('IPython', '0.10', 'tutorial1')
```

10.1 Setting up workflows

This is a generic workflow for DTI data analysis using the FSL

10.2 Data specific components

The nipype tutorial contains data for two subjects. Subject data is in two subdirectories, `dwis1` and `dwis2`. Each subject directory contains each of the following files: `bvec`, `bval`, diffusion weighted data, a set of target masks, a seed file, and a transformation matrix.

Below we set some variables to inform the `datasource` about the layout of our data. We specify the location of the data, the subject sub-directories and a dictionary that maps each run to a mnemonic (or field) for the run type (dwi or bvals). These fields become the output fields of the `datasource` node in the pipeline. Specify the subject directories

```
subject_list = ['subj1']
```

Map field names to individual subject runs

```
info = dict(
    dwi=[['subject_id', 'dwi']],
    bvecs=[['subject_id', 'bvecs']],
    bvals=[['subject_id', 'bvals']])

infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")
```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

Now we create a `nipy.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipy.pipeline.engine.Node` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```
datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=list(info.keys())),
    name='datasource')

datasource.inputs.template = "%s/%s"

# This needs to point to the fdt folder you can find after extracting
# http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz
datasource.inputs.base_directory = os.path.abspath('fsl_course_data/fdt/')

datasource.inputs.field_template = dict(dwi='%s/%s.nii.gz')
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True
```

10.3 Setup for Diffusion Tensor Computation

Here we will create a generic workflow for DTI computation

```
computeTensor = pe.Workflow(name='computeTensor')
```

extract the volume with b=0 (nodif_brain)

```
fslroi = pe.Node(interface=fsl.ExtractROI(), name='fslroi')
fslroi.inputs.t_min = 0
fslroi.inputs.t_size = 1
```

create a brain mask from the `nodif_brain`

```
bet = pe.Node(interface=fsl.BET(), name='bet')
bet.inputs.mask = True
bet.inputs.frac = 0.34
```

correct the diffusion weighted images for eddy_currents

```
eddycorrect = create_eddy_correct_pipeline('eddycorrect')
eddycorrect.inputs.inputnode.ref_num = 0
```

compute the diffusion tensor in each voxel

```
dtifit = pe.Node(interface=dtk.DTIRecon(), name='dtifit')
```

connect all the nodes for this workflow

```
computeTensor.connect([(fslroi, bet, [('roi_file', 'in_file')]),
                        (eddycorrect, dtifit, [('outputnode.eddy_corrected',
                                                'DWI']))])
```

10.4 Setup for Tracktography

Here we will create a workflow to enable deterministic tracktography

```
tractography = pe.Workflow(name='tractography')

dtk_tracker = pe.Node(interface=dtk.DTITracker(), name="dtk_tracker")
dtk_tracker.inputs.invert_x = True

smooth_trk = pe.Node(interface=dtk.SplineFilter(), name="smooth_trk")
smooth_trk.inputs.step_length = 0.5
```

connect all the nodes for this workflow

```
tractography.connect([(dtk_tracker, smooth_trk, [('track_file',
                                                  'track_file']))])
```

Setup data storage area

```
datasink = pe.Node(interface=nio.DataSink(), name='datasink')
datasink.inputs.base_directory = os.path.abspath('dtireresults')
```

```
def getstripdir(subject_id):
    return os.path.join(
        os.path.abspath('data/workingdir/dwiproc'),
        '_subject_id_%s' % subject_id)
```

10.5 Setup the pipeline that combines the 2 workflows: tractography & computeTensor

```
dwiproc = pe.Workflow(name="dwiproc")
dwiproc.base_dir = os.path.abspath('dtk_dti_tutorial')
dwiproc.connect([(infosource, datasource, [('subject_id', 'subject_id')]),
                 (datasource, computeTensor,
                  [('dwi', 'fslroi.in_file'), ('bvals', 'dtifit.bvals'),
```

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```
        ('bvecs', 'dtifit.bvecs'),
        ('dwi', 'eddycorrect.inputnode.in_file'))),
    (computeTensor, tractography,
     [('bet.mask_file', 'dtk_tracker.mask1_file'),
      ('dtifit.tensor', 'dtk_tracker.tensor_file')]))

if __name__ == '__main__':
    dwiproc.run()
    dwiproc.write_graph()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

dMRI: HARDI - Diffusion Toolkit, FSL

A pipeline example that uses several interfaces to perform analysis on diffusion weighted images using Diffusion Toolkit tools.

This tutorial is based on the 2010 FSL course and uses data freely available at the FSL website at: http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz

More details can be found at <http://www.fmrib.ox.ac.uk/fslcourse/lectures/practicals/fdt/index.htm>

In order to run this tutorial you need to have Diffusion Toolkit and FSL tools installed and accessible from matlab/command line. Check by calling `fsinfo` and `dtk` from the command line.

Tell python where to find the appropriate functions.

```
import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.fsl as fsl # fsl
import nipype.interfaces.diffusion_toolkit as dtk
import nipype.interfaces.utility as util # utility
import nipype.pipeline.engine as pe # pipeline engine
import os # system functions
from nipype.workflows.dmri.fsl.dti import create_eddy_correct_pipeline
```

Confirm package dependencies are installed. (This is only for the tutorial, rarely would you put this in your own code.)

```
from nipype.utils.misc import package_check

package_check('numpy', '1.3', 'tutorial11')
package_check('scipy', '0.7', 'tutorial11')
package_check('IPython', '0.10', 'tutorial11')
```

11.1 Setting up workflows

This is a generic workflow for DTI data analysis using the FSL

11.2 Data specific components

The nipype tutorial contains data for two subjects. Subject data is in two subdirectories, `dwis1` and `dwis2`. Each subject directory contains each of the following files: `bvec`, `bval`, diffusion weighted data, a set of target masks, a seed file, and a transformation matrix.

Below we set some variables to inform the `datasource` about the layout of our data. We specify the location of the data, the subject sub-directories and a dictionary that maps each run to a mnemonic (or field) for the run type (`dwi` or `bvals`). These fields become the output fields of the `datasource` node in the pipeline. Specify the subject directories

```
subject_list = ['siemens_hardi_test']
```

Map field names to individual subject runs

```
info = dict(
    dwi=[['subject_id', 'siemens_hardi_test_data']],
    bvecs=[['subject_id', 'siemens_hardi_test_data.bvec']],
    bvals=[['subject_id', 'siemens_hardi_test_data.bval']])

infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")
```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

Now we create a `nipy.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipy.pipeline.engine.Node` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```
datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=list(info.keys())),
    name='datasource')

datasource.inputs.template = "%s/%s"

# This needs to point to the fdt folder you can find after extracting
# http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz
datasource.inputs.base_directory = os.path.abspath('data')

datasource.inputs.field_template = dict(dwi='%s/%s.nii')
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True
```

11.3 Setup for ODF Computation

Here we will create a generic workflow for ODF computation

```
compute_ODF = pe.Workflow(name='compute_ODF')
```

extract the volume with `b=0` (`nodif_brain`)

```
fslroi = pe.Node(interface=fsl.ExtractROI(), name='fslroi')
fslroi.inputs.t_min = 0
fslroi.inputs.t_size = 1
```

create a brain mask from the `nodif_brain`

```
bet = pe.Node(interface=fsl.BET(), name='bet')
bet.inputs.mask = True
bet.inputs.frac = 0.34
```

correct the diffusion weighted images for eddy_currents

```
eddycorrect = create_eddy_correct_pipeline('eddycorrect')
eddycorrect.inputs.inputnode.ref_num = 0

hardi_mat = pe.Node(interface=dtk.HARDIMat(), name='hardi_mat')

odf_recon = pe.Node(interface=dtk.ODFRecon(), name='odf_recon')
```

connect all the nodes for this workflow

```
compute_ODF.connect(
    [(fslroi, bet, [ ('roi_file', 'in_file') ]),
     (eddycorrect, odf_recon, [ ('outputnode.eddy_corrected', 'DWI') ]),
     (eddycorrect, hardi_mat,
      [ ('outputnode.eddy_corrected',
        'reference_file') ]), (hardi_mat, odf_recon, [ ('out_file', 'matrix') ])]
```

11.4 Setup for Tracktography

Here we will create a workflow to enable deterministic tracktography

```
tractography = pe.Workflow(name='tractography')

odf_tracker = pe.Node(interface=dtk.ODFTracker(), name="odf_tracker")

smooth_trk = pe.Node(interface=dtk.SplineFilter(), name="smooth_trk")
smooth_trk.inputs.step_length = 1
```

connect all the nodes for this workflow

```
tractography.connect([(odf_tracker, smooth_trk, [ ('track_file',
                                                    'track_file') ])]])
```

11.5 Setup the pipeline that combines the 2 workflows: tractography and compute_ODF

```
dwiproc = pe.Workflow(name="dwiproc")
dwiproc.base_dir = os.path.abspath('dtk_odf_tutorial')
dwiproc.connect([(infosource, datasource, [ ('subject_id', 'subject_id') ]),
                 (datasource, compute_ODF,
                  [ ('dwi', 'fslroi.in_file'), ('bvals', 'hardi_mat.bvals'),
                    ('bvecs', 'hardi_mat.bvecs'),
                    ('dwi', 'eddycorrect.inputnode.in_file') ]),
                 (compute_ODF, tractography,
                  [ ('bet.mask_file', 'odf_tracker.mask1_file'),
                    ('odf_recon.ODF', 'odf_tracker.ODF'),
                    ('odf_recon.max', 'odf_tracker.max') ])]])

dwiproc.inputs.compute_ODF.hardi_mat.oblique_correction = True
```

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```
dwiproc.inputs.compute_ODF.odf_recon.n_directions = 31
dwiproc.inputs.compute_ODF.odf_recon.n_b0 = 5
dwiproc.inputs.compute_ODF.odf_recon.n_output_directions = 181

if __name__ == '__main__':
    dwiproc.run()
    dwiproc.write_graph()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

CHAPTER 12

dMRI: DTI, FSL

A pipeline example that uses several interfaces to perform analysis on diffusion weighted images using FSL FDT tools.

This tutorial is based on the 2010 FSL course and uses data freely available at the FSL website at: http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz

More details can be found at <http://www.fmrib.ox.ac.uk/fslcourse/lectures/practicals/fdt/index.htm>

In order to run this tutorial you need to have fsl tools installed and accessible from matlab/command line. Check by calling fslinfo from the command line.

Tell python where to find the appropriate functions.

```
import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.fsl as fsl # fsl
import nipype.interfaces.utility as util # utility
import nipype.pipeline.engine as pe # pipeline engine
import os # system functions
from nipype.workflows.dmri.fsl.dti import create_eddy_correct_pipeline, \
    create_bedpostx_pipeline
```

Confirm package dependencies are installed. (This is only for the tutorial, rarely would you put this in your own code.)

```
from nipype.utils.misc import package_check

package_check('numpy', '1.3', 'tutorial1')
package_check('scipy', '0.7', 'tutorial1')
package_check('IPython', '0.10', 'tutorial1')
```

12.1 Setting up workflows

This is a generic workflow for DTI data analysis using the FSL

12.2 Data specific components

The nipype tutorial contains data for two subjects. Subject data is in two subdirectories, `dwis1` and `dwis2`. Each subject directory contains each of the following files: `bvec`, `bval`, diffusion weighted data, a set of target masks, a seed file, and a transformation matrix.

Below we set some variables to inform the `datasource` about the layout of our data. We specify the location of the data, the subject sub-directories and a dictionary that maps each run to a mnemonic (or field) for the run type (`dwi` or `bvals`). These fields become the output fields of the `datasource` node in the pipeline. Specify the subject directories

```
subject_list = ['subj1']
```

Map field names to individual subject runs

```
info = dict(
    dwi=[['subject_id', 'data']],
    bvecs=[['subject_id', 'bvecs']],
    bvals=[['subject_id', 'bvals']],
    seed_file=[['subject_id', 'MASK_average_thal_right']],
    target_masks=[
        'subject_id', [
            'MASK_average_M1_right', 'MASK_average_S1_right',
            'MASK_average_occipital_right', 'MASK_average_pfc_right',
            'MASK_average_pmc_right', 'MASK_average_ppc_right',
            'MASK_average_temporal_right'
        ]
    ]
)

infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")
```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

Now we create a `nipyne.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipyne.pipeline.engine.Node` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```
datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=list(info.keys())),
    name='datasource')

datasource.inputs.template = "%s/%s"

# This needs to point to the fdt folder you can find after extracting
# http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz
datasource.inputs.base_directory = os.path.abspath('fsl_course_data/fdt/')

datasource.inputs.field_template = dict(
    dwi='%s/%s.nii.gz',
    seed_file="%s.bedpostX/%s.nii.gz",
    target_masks="%s.bedpostX/%s.nii.gz")
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True
```

12.3 Setup for Diffusion Tensor Computation

Here we will create a generic workflow for DTI computation

```
computeTensor = pe.Workflow(name='computeTensor')
```

extract the volume with b=0 (nodif_brain)

```
fslroi = pe.Node(interface=fsl.ExtractROI(), name='fslroi')
fslroi.inputs.t_min = 0
fslroi.inputs.t_size = 1
```

create a brain mask from the nodif_brain

```
bet = pe.Node(interface=fsl.BET(), name='bet')
bet.inputs.mask = True
bet.inputs.frac = 0.34
```

correct the diffusion weighted images for eddy_currents

```
eddycorrect = create_eddy_correct_pipeline('eddycorrect')
eddycorrect.inputs.inputnode.ref_num = 0
```

compute the diffusion tensor in each voxel

```
dtifit = pe.Node(interface=fsl.DTIFit(), name='dtifit')
```

connect all the nodes for this workflow

```
computeTensor.connect(
    [(fslroi, bet, [('roi_file', 'in_file')]),
     (eddycorrect, dtifit, [('outputnode.eddy_corrected', 'dwi')]),
     (infosource, dtifit,
      [['subject_id', 'base_name']]), (bet, dtifit, [('mask_file', 'mask')])])
```

12.4 Setup for Tracktography

Here we will create a workflow to enable probabilistic tracktography and hard segmentation of the seed region

```
tractography = pe.Workflow(name='tractography')
tractography.base_dir = os.path.abspath('fsl_dti_tutorial')
```

estimate the diffusion parameters: phi, theta, and so on

```
bedpostx = create_bedpostx_pipeline()
bedpostx.get_node("xfibres").iterables = ("n_fibres", [1, 2])

flirt = pe.Node(interface=fsl.FLIRT(), name='flirt')
flirt.inputs.in_file = fsl.Info.standard_image('MNI152_T1_2mm_brain.nii.gz')
flirt.inputs.dof = 12
```

perform probabilistic tracktography

```
probtrackx = pe.Node(interface=fsl.ProbTrackX(), name='probtrackx')
probtrackx.inputs.mode = 'seedmask'
probtrackx.inputs.c_thresh = 0.2
probtrackx.inputs.n_steps = 2000
probtrackx.inputs.step_length = 0.5
probtrackx.inputs.n_samples = 5000
probtrackx.inputs.opd = True
probtrackx.inputs.os2t = True
probtrackx.inputs.loop_check = True
```

perform hard segmentation on the output of probtrackx

```
findthebiggest = pe.Node(interface=fsl.FindTheBiggest(), name='findthebiggest')
```

connect all the nodes for this workflow

```
tractography.add_nodes([bedpostx, flirt])
tractography.connect([(bedpostx, probtrackx,
                        [('outputnode.thsamples',
                          'thsamples'), ('outputnode.phsamples', 'phsamples'),
                          ('outputnode.fsamples', 'fsamples')]),
                      (probtrackx, findthebiggest, [('targets', 'in_files')]),
                      (flirt, probtrackx, [('out_matrix_file', 'xfm')])])
```

Setup data storage area

```
datasink = pe.Node(interface=nio.DataSink(), name='datasink')
datasink.inputs.base_directory = os.path.abspath('dtireresults')

def getstripdir(subject_id):
    import os
    return os.path.join(
        os.path.abspath('data/workingdir/dwiproc'),
        '_subject_id_%s' % subject_id)
```

12.5 Setup the pipeline that combines the 2 workflows: tractography & computeTensor

```
dwiproc = pe.Workflow(name="dwiproc")
dwiproc.base_dir = os.path.abspath('fsl_dti_tutorial')
dwiproc.connect(
    [(infosource, datasource, [('subject_id', 'subject_id')]),
     (datasource, computeTensor,
      [('dwi', 'fslroi.in_file'), ('bvals', 'dtifit.bvals'),
       ('bvecs', 'dtifit.bvecs'), ('dwi', 'eddycorrect.inputnode.in_file')]),
     (datasource, tractography,
      [('bvals', 'bedpostx.inputnode.bvals'),
       ('bvecs', 'bedpostx.inputnode.bvecs'), ('seed_file', 'probtrackx.seed'),
       ('target_masks', 'probtrackx.target_masks')]),
     (computeTensor, tractography,
      [('eddycorrect.outputnode.eddy_corrected', 'bedpostx.inputnode.dwi'),
       ('bet.mask_file', 'bedpostx.inputnode.mask'), ('bet.mask_file',
                                                       'probtrackx.mask'),
       ('fslroi.roi_file', 'flirt.reference')]), (infosource, datasink, [
        ('subject_id', 'container'), (('subject_id', getstripdir),
                                      'strip_dir')
    ]), (tractography, datasink, [('findthebiggest.out_file',
                                   'fbiggest.@biggestsegmentation')]))

if __name__ == '__main__':
    dwiproc.run()
    dwiproc.write_graph()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the examples directory.

dmRI: Group connectivity - Camino, FSL, FreeSurfer

13.1 Introduction

This script, `dmri_group_connectivity_camino.py`, runs group-based connectivity analysis using the `dmri.camino.connectivity_mapping` Nipype workflow. Further detail on the processing can be found in *dmRI: Connectivity - Camino, CMTK, FreeSurfer*. This tutorial can be run using:

```
python dmri_group_connectivity_camino.py
```

We perform this analysis using one healthy subject and two subjects who suffer from Parkinson's disease. The whole package (960 mb as `.tar.gz` / 1.3 gb uncompressed) including the Freesurfer directories for these subjects, can be acquired from here:

- <http://db.tt/b6F1t0QV>

A data package containing the outputs of this pipeline can be obtained from here:

- <http://db.tt/kNvAI751>

Along with Camino, Camino-Trackvis, FSL, and Freesurfer, you must also have the Connectome File Format library installed as well as the Connectome Mapper.

- Camino: <http://web4.cs.ucl.ac.uk/research/medic/camino/pmwiki/pmwiki.php?n=Main.HomePage>
- Camino-Trackvis: <http://www.nitrc.org/projects/camino-trackvis/>
- FSL: <http://www.fmrib.ox.ac.uk/fsl/>
- Freesurfer: <http://surfer.nmr.mgh.harvard.edu/>
- CMTK: <http://www.cmtk.org/>
- CFF: `sudo apt-get install python-cfflib`

Or on github at:

- CFFlib: <https://github.com/LTS5/cfflib>
- CMP: <https://github.com/LTS5/cmp>

Output data can be visualized in ConnectomeViewer, TrackVis, and anything that can view Nifti files.

- ConnectomeViewer: <https://github.com/LTS5/connectomeviewer>
- TrackVis: <http://trackvis.org/>

The fiber data is available in Numpy arrays, and the connectivity matrix is also produced as a MATLAB matrix.

13.1.1 Import the workflows

First, we import the necessary modules from nipype.

```
import nipy.interfaces.fsl as fsl
import nipy.interfaces.freesurfer as fs # freesurfer
import os.path as op # system functions
import cmp
from nipy.workflows.dmri.camino.group_connectivity import create_group_
↳connectivity_pipeline
from nipy.workflows.dmri.connectivity.group_connectivity import (
    create_merge_networks_by_group_workflow,
    create_merge_group_networks_workflow,
    create_average_networks_by_group_workflow)
```

13.1.2 Set the proper directories

First, we import the necessary modules from nipy.

```
fs_dir = op.abspath('/usr/local/freesurfer')
subjects_dir = op.abspath('groupcondatapackage/subjects/')
data_dir = op.abspath('groupcondatapackage/data/')
fs.FSCommand.set_default_subjects_dir(subjects_dir)
fsl.FSLCommand.set_default_output_type('NIFTI')
```

13.1.3 Define the groups

Here we define the groups for this study. We would like to search for differences between the healthy subject and the two vegetative patients. The group list is defined as a Python dictionary (see <http://docs.python.org/tutorial/datastructures.html>), with group IDs ('controls', 'parkinsons') as keys, and subject/patient names as values. We set the main output directory as 'groupcon'.

```
group_list = {}
group_list['controls'] = ['cont17']
group_list['parkinsons'] = ['pat10', 'pat20']
```

The output directory must be named as well.

```
global output_dir
output_dir = op.abspath('dmri_group_connectivity_camino')
```

13.2 Main processing loop

The title for the final grouped-network connectome file is dependent on the group names. The resulting file for this example is 'parkinsons-controls.cff'. The following code implements the format a-b-c-...x.cff for an arbitrary number of groups.

Warning: The 'info' dictionary below is used to define the input files. In this case, the diffusion weighted image contains the string 'dwi'. The same applies to the b-values and b-vector files, and this must be changed to fit your naming scheme.

This line creates the processing workflow given the information input about the groups and subjects.

See also:

- `nipy/workflows/dmri/mrtrix/group_connectivity.py`
- `nipy/workflows/dmri/camino/connectivity_mapping.py`
- *dmRI: Connectivity - Camino, CMTK, FreeSurfer*

The purpose of the second-level workflow is simple: It is used to merge each subject's CFF file into one, so that there is a single file containing all of the networks for each group. This can be useful for performing Network

Brain Statistics using the NBS plugin in ConnectomeViewer.

See also:

http://www.connectomeviewer.org/documentation/users/tutorials/tut_nbs.html

```

title = ''
for idx, group_id in enumerate(group_list.keys()):
    title += group_id
    if not idx == len(list(group_list.keys())) - 1:
        title += '-'

    info = dict(
        dwi=[['subject_id', 'dti']],
        bvecs=[['subject_id', 'bvecs']],
        bvals=[['subject_id', 'bvals']])

    l1pipeline = create_group_connectivity_pipeline(
        group_list, group_id, data_dir, subjects_dir, output_dir, info)

    # Here we define the parcellation scheme and the number of tracks to produce
    parcellation_scheme = 'NativeFreesurfer'
    cmp_config = cmp.configuration.PipelineConfiguration()
    cmp_config.parcellation_scheme = parcellation_scheme
    l1pipeline.inputs.connectivity.inputnode.resolution_network_file = cmp_config.
    ↪_get_lausanne_parcellation(
        parcellation_scheme)['freesurferaparc']['node_information_graphml']

    l1pipeline.run()
    l1pipeline.write_graph(format='eps', graph2use='flat')

    # The second-level pipeline is created here
    l2pipeline = create_merge_networks_by_group_workflow(
        group_list, group_id, data_dir, subjects_dir, output_dir)
    l2pipeline.run()
    l2pipeline.write_graph(format='eps', graph2use='flat')

```

Now that the for loop is complete there are two grouped CFF files each containing the appropriate subjects. It is also convenient to have every subject in a single CFF file, so that is what the third-level pipeline does.

```

l3pipeline = create_merge_group_networks_workflow(
    group_list, data_dir, subjects_dir, output_dir, title)
l3pipeline.run()
l3pipeline.write_graph(format='eps', graph2use='flat')

```

The fourth and final workflow averages the networks and saves them in another CFF file

```

l4pipeline = create_average_networks_by_group_workflow(
    group_list, data_dir, subjects_dir, output_dir, title)
l4pipeline.run()
l4pipeline.write_graph(format='eps', graph2use='flat')

```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the examples directory.

dMRI: Group connectivity - MRtrix, FSL, FreeSurfer

14.1 Introduction

This script, `dmri_group_connectivity_mrtrix.py`, runs group-based connectivity analysis using the `dmri_mrtrix.connectivity_mapping` Nipype workflow. Further detail on the processing can be found in *dMRI: Connectivity - MRtrix, CMTK, FreeSurfer*. This tutorial can be run using:

```
python dmri_group_connectivity_mrtrix.py
```

We perform this analysis using one healthy subject and two subjects who suffer from Parkinson's disease. The whole package (960 mb as `.tar.gz` / 1.3 gb uncompressed) including the FreeSurfer directories for these subjects, can be acquired from here:

- <http://db.tt/b6F1t0QV>

A data package containing the outputs of this pipeline can be obtained from here:

- <http://db.tt/elmMnIt1>

Along with MRtrix, FSL, and FreeSurfer, you must also have the Connectome File Format library installed as well as the Connectome Mapper (`cmp`).

- MRtrix: <http://www.brain.org.au/software/mrtrix/>
- FSL: <http://www.fmrib.ox.ac.uk/fsl/>
- FreeSurfer: <http://surfer.nmr.mgh.harvard.edu/>
- CMTK: <http://www.cmtk.org/>
- CFF: `sudo apt-get install python-cfflib`

Or on github at:

- CFFlib: <https://github.com/LTS5/cfflib>
- CMP: <https://github.com/LTS5/cmp>

Output data can be visualized in ConnectomeViewer, TrackVis, Gephi, the MRtrix Viewer (`mrview`), and anything that can view Nifti files.

- ConnectomeViewer: <https://github.com/LTS5/connectomeviewer>
- TrackVis: <http://trackvis.org/>
- Gephi: <http://gephi.org/>

The fiber data is available in Numpy arrays, and the connectivity matrix is also produced as a MATLAB matrix.

14.1.1 Import the workflows

First, we import the necessary modules from nipype.

```
import nipy.interfaces.fsl as fsl
import nipy.interfaces.freesurfer as fs # freesurfer
import os.path as op # system functions
import cmp
from nipy.workflows.dmri.mrtrix.group_connectivity import create_group_
    connectivity_pipeline
from nipy.workflows.dmri.connectivity.group_connectivity import (
    create_merge_network_results_by_group_workflow,
    create_merge_group_network_results_workflow,
    create_average_networks_by_group_workflow)
```

14.1.2 Set the proper directories

First, we import the necessary modules from nipy.

```
subjects_dir = op.abspath('groupcondatapackage/subjects/')
data_dir = op.abspath('groupcondatapackage/data/')
fs.FSCommand.set_default_subjects_dir(subjects_dir)
fsl.FSLCommand.set_default_output_type('NIFTI')
```

14.1.3 Define the groups

Here we define the groups for this study. We would like to search for differences between the healthy subject and the two vegetative patients. The group list is defined as a Python dictionary (see <http://docs.python.org/tutorial/datastructures.html>), with group IDs ('controls', 'parkinsons') as keys, and subject/patient names as values. We set the main output directory as 'groupcon'.

```
group_list = {}
group_list['controls'] = ['cont17']
group_list['parkinsons'] = ['pat10', 'pat20']
```

The output directory must be named as well.

```
global output_dir
output_dir = op.abspath('dmri_group_connectivity_mrtrix')
```

14.2 Main processing loop

The title for the final grouped-network connectome file is dependent on the group names. The resulting file for this example is 'parkinsons-controls.cff'. The following code implements the format a-b-c-...x.cff for an arbitrary number of groups.

Warning: The 'info' dictionary below is used to define the input files. In this case, the diffusion weighted image contains the string 'dti'. The same applies to the b-values and b-vector files, and this must be changed to fit your naming scheme.

The workflow is created given the information input about the groups and subjects.

See also:

- `nipy/workflows/dmri/mrtrix/group_connectivity.py`
- `nipy/workflows/dmri/mrtrix/connectivity_mapping.py`
- *dMRI: Connectivity - MRtrix, CMTK, FreeSurfer*

We set values for absolute threshold used on the fractional anisotropy map. This is done in order to identify single-fiber voxels. In brains with more damage, however, it may be necessary to reduce the threshold, since their brains have lower average fractional anisotropy values.

We invert the b-vectors in the encoding file, and set the maximum harmonic order of the pre-tractography spherical deconvolution step. This is done to show how to set inputs that will affect both groups.

Next we create and run the second-level pipeline. The purpose of this workflow is simple: It is used to merge each subject's CFF file into one, so that there is a single file containing all of the networks for each group. This can be useful for performing Network Brain Statistics using the NBS plugin in ConnectomeViewer.

See also:

http://www.connectomeviewer.org/documentation/users/tutorials/tut_nbs.html

```
title = ''
for idx, group_id in enumerate(group_list.keys()):
    title += group_id
    if not idx == len(list(group_list.keys())) - 1:
        title += '-'

    info = dict(
        dwi=[['subject_id', 'dti']],
        bvecs=[['subject_id', 'bvecs']],
        bvals=[['subject_id', 'bvals']])

    l1pipeline = create_group_connectivity_pipeline(
        group_list, group_id, data_dir, subjects_dir, output_dir, info)

    # Here with invert the b-vectors in the Y direction and set the maximum_
    ↪harmonic order of the
    # spherical deconvolution step
    l1pipeline.inputs.connectivity.mapping.fsl2mrtrix.invert_y = True
    l1pipeline.inputs.connectivity.mapping.csdeconv.maximum_harmonic_order = 6

    # Here we define the parcellation scheme and the number of tracks to produce
    parcellation_name = 'scale500'
    l1pipeline.inputs.connectivity.mapping.Parcellate.parcellation_name = _
    ↪parcellation_name
    cmp_config = cmp.configuration.PipelineConfiguration()
    cmp_config.parcellation_scheme = "Lausanne2008"
    l1pipeline.inputs.connectivity.mapping.inputnode_within.resolution_network_
    ↪file = cmp_config._get_lausanne_parcellation(
        'Lausanne2008')[parcellation_name]['node_information_graphml']
    l1pipeline.inputs.connectivity.mapping.probCSDstreamtrack.desired_number_of_
    ↪tracks = 100000

    l1pipeline.run()
    l1pipeline.write_graph(format='eps', graph2use='flat')

    # The second-level pipeline is created here
    l2pipeline = create_merge_network_results_by_group_workflow(
        group_list, group_id, data_dir, subjects_dir, output_dir)
    l2pipeline.inputs.l2inputnode.network_file = cmp_config._get_lausanne_
    ↪parcellation(
        'Lausanne2008')[parcellation_name]['node_information_graphml']
    l2pipeline.run()
    l2pipeline.write_graph(format='eps', graph2use='flat')
```

Now that the for loop is complete there are two grouped CFF files each containing the appropriate subjects. It is also convenient to have every subject in a single CFF file, so that is what the third-level pipeline does.

```
l3pipeline = create_merge_group_network_results_workflow(
    group_list, data_dir, subjects_dir, output_dir, title)
l3pipeline.run()
```

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```
l3pipeline.write_graph(format='eps', graph2use='flat')
```

The fourth and final workflow averages the networks and saves them in another CFF file

```
l4pipeline = create_average_networks_by_group_workflow(  
    group_list, data_dir, subjects_dir, output_dir, title)  
l4pipeline.run()  
l4pipeline.write_graph(format='eps', graph2use='flat')
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

15.1 Introduction

This script, `dmri_mrtrix_dti.py`, demonstrates the ability to perform advanced diffusion analysis in a Nipype pipeline:

```
python dmri_mrtrix_dti.py
```

We perform this analysis using the FSL course data, which can be acquired from here:

- http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz

Import necessary modules from nipype.

```
import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.utility as util # utility
import nipype.pipeline.engine as pe # pypeline engine
import nipype.interfaces.mrtrix as mrtrix # <---- The important new part!
import nipype.interfaces.fsl as fsl
import nipype.algorithms.misc as misc
import os
import os.path as op # system functions

fsl.FSLCommand.set_default_output_type('NIFTI')
```

This needs to point to the `fdt` folder you can find after extracting

- http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz

```
data_dir = op.abspath(op.join(op.curdir, 'exdata/'))
subject_list = ['subj1']
```

Use `infosource` node to loop through the subject list and define the input files. For our purposes, these are the diffusion-weighted MR image, b vectors, and b values.

```
infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")
infosource.iterables = ('subject_id', subject_list)

info = dict(
    dwi=[['subject_id', 'data']],
    bvecs=[['subject_id', 'bvecs']],
```

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```
bvals=[['subject_id', 'bvals']])
```

Use datasource node to perform the actual data grabbing. Templates for the associated images are used to obtain the correct images.

```
datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=list(info.keys()),
        name='datasource')

datasource.inputs.template = "%s/%s"
datasource.inputs.base_directory = data_dir
datasource.inputs.field_template = dict(dwi='%s/%s.nii.gz')
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True
```

An inputnode is used to pass the data obtained by the data grabber to the actual processing functions

```
inputnode = pe.Node(
    interface=util.IdentityInterface(fields=["dwi", "bvecs", "bvals"]),
    name="inputnode")
```

15.1.1 Diffusion processing nodes

See also:

dmri_connectivity_advanced.py Tutorial with further detail on using MRtrix tractography for connectivity analysis

<http://www.brain.org.au/software/mrtrix/index.html> MRtrix's online documentation

b-values and b-vectors stored in FSL's format are converted into a single encoding file for MRTrix.

```
fsl2mrtrix = pe.Node(interface=mrtrix.FSL2MRtrix(), name='fsl2mrtrix')
```

Tensors are fitted to each voxel in the diffusion-weighted image and from these three maps are created:

Major eigenvector in each voxel

Apparent diffusion coefficient

Fractional anisotropy

```
gunzip = pe.Node(interface=misc.Gunzip(), name='gunzip')
dwi2tensor = pe.Node(interface=mrtrix.DWI2Tensor(), name='dwi2tensor')
tensor2vector = pe.Node(interface=mrtrix.Tensor2Vector(), name='tensor2vector')
tensor2adc = pe.Node(
    interface=mrtrix.Tensor2ApparentDiffusion(), name='tensor2adc')
tensor2fa = pe.Node(
    interface=mrtrix.Tensor2FractionalAnisotropy(), name='tensor2fa')
```

These nodes are used to create a rough brain mask from the b0 image. The b0 image is extracted from the original diffusion-weighted image, put through a simple thresholding routine, and smoothed using a 3x3 median filter.

```
MRconvert = pe.Node(interface=mrtrix.MRConvert(), name='MRconvert')
MRconvert.inputs.extract_at_axis = 3
MRconvert.inputs.extract_at_coordinate = [0]
threshold_b0 = pe.Node(interface=mrtrix.Threshold(), name='threshold_b0')
median3d = pe.Node(interface=mrtrix.MedianFilter3D(), name='median3d')
```

The brain mask is also used to help identify single-fiber voxels. This is done by passing the brain mask through two erosion steps, multiplying the remaining mask with the fractional anisotropy map, and thresholding the result to obtain some highly anisotropic within-brain voxels.

```

erode_mask_firstpass = pe.Node(
    interface=mrtrix.Erode(), name='erode_mask_firstpass')
erode_mask_secondpass = pe.Node(
    interface=mrtrix.Erode(), name='erode_mask_secondpass')
MRmultiply = pe.Node(interface=mrtrix.MRMultiply(), name='MRmultiply')
MRmult_merge = pe.Node(interface=util.Merge(2), name='MRmultiply_merge')
threshold_FA = pe.Node(interface=mrtrix.Threshold(), name='threshold_FA')
threshold_FA.inputs.absolute_threshold_value = 0.7

```

For whole-brain tracking we also require a broad white-matter seed mask. This is created by generating a white matter mask, given a brainmask, and thresholding it at a reasonably high level.

```

bet = pe.Node(interface=fsl.BET(mask=True), name='bet_b0')
gen_WM_mask = pe.Node(
    interface=mrtrix.GenerateWhiteMatterMask(), name='gen_WM_mask')
threshold_wmmask = pe.Node(
    interface=mrtrix.Threshold(), name='threshold_wmmask')
threshold_wmmask.inputs.absolute_threshold_value = 0.4

```

The spherical deconvolution step depends on the estimate of the response function in the highly anisotropic voxels we obtained above.

Warning: For damaged or pathological brains one should take care to lower the maximum harmonic order of these steps.

```

estimatereponse = pe.Node(
    interface=mrtrix.EstimateResponseForSH(), name='estimatereponse')
estimatereponse.inputs.maximum_harmonic_order = 6
csdeconv = pe.Node(
    interface=mrtrix.ConstrainedSphericalDeconvolution(), name='csdeconv')
csdeconv.inputs.maximum_harmonic_order = 6

```

Finally, we track probabilistically using the orientation distribution functions obtained earlier. The tracts are then used to generate a tract-density image, and they are also converted to TrackVis format.

```

probCSDstreamtrack = pe.Node(
    interface=mrtrix.ProbabilisticSphericallyDeconvolutedStreamlineTrack(),
    name='probCSDstreamtrack')
probCSDstreamtrack.inputs.inputmodel = 'SD_PROB'
probCSDstreamtrack.inputs.maximum_number_of_tracks = 150000
tracks2prob = pe.Node(interface=mrtrix.Tracks2Prob(), name='tracks2prob')
tracks2prob.inputs.colour = True
tck2trk = pe.Node(interface=mrtrix.MRTrk2TrackVis(), name='tck2trk')

```

15.1.2 Creating the workflow

In this section we connect the nodes for the diffusion processing.

```

tractography = pe.Workflow(name='tractography')

tractography.connect([(inputnode, fsl2mrtrix, [
    ("bvecs", "bvec_file"),
    ("bvals", "bval_file")])])
tractography.connect([(inputnode, gunzip, [
    ("dwi", "in_file")])])
tractography.connect([(gunzip, dwi2tensor, [
    ("out_file", "in_file")])])
tractography.connect([(fsl2mrtrix, dwi2tensor, [
    ("encoding_file",
    "encoding_file")])])

```

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```
tractography.connect([
    (dwi2tensor, tensor2vector, [['tensor', 'in_file']]),
    (dwi2tensor, tensor2adc, [['tensor', 'in_file']]),
    (dwi2tensor, tensor2fa, [['tensor', 'in_file']]),
])
tractography.connect([(tensor2fa, MRmult_merge, [("FA", "in1")])])
```

This block creates the rough brain mask to be multiplied, multiplies it with the fractional anisotropy image, and thresholds it to get the single-fiber voxels.

```
tractography.connect([(gunzip, MRconvert, [("out_file", "in_file")])])
tractography.connect([(MRconvert, threshold_b0, [("converted", "in_file")])])
tractography.connect([(threshold_b0, median3d, [("out_file", "in_file")])])
tractography.connect([(median3d, erode_mask_firstpass, [("out_file",
                                                         "in_file")])])
tractography.connect([(erode_mask_firstpass, erode_mask_secondpass,
                      [("out_file", "in_file")])])
tractography.connect([(erode_mask_secondpass, MRmult_merge, [("out_file",
                                                             "in2")])])
tractography.connect([(MRmult_merge, MRmultiply, [("out", "in_files")])])
tractography.connect([(MRmultiply, threshold_FA, [("out_file", "in_file")])])
```

Here the thresholded white matter mask is created for seeding the tractography.

```
tractography.connect([(gunzip, bet, [("out_file", "in_file")])])
tractography.connect([(gunzip, gen_WM_mask, [("out_file", "in_file")])])
tractography.connect([(bet, gen_WM_mask, [("mask_file", "binary_mask")])])
tractography.connect([(fsl2mrtrix, gen_WM_mask, [("encoding_file",
                                                  "encoding_file")])])
tractography.connect([(gen_WM_mask, threshold_wmmask, [("WMprobabilitymap",
                                                         "in_file")])])
```

Next we estimate the fiber response distribution.

```
tractography.connect([(gunzip, estimatorresponse, [("out_file", "in_file")])])
tractography.connect([(fsl2mrtrix, estimatorresponse, [("encoding_file",
                                                         "encoding_file")])])
tractography.connect([(threshold_FA, estimatorresponse, [("out_file",
                                                         "mask_image")])])
```

Run constrained spherical deconvolution.

```
tractography.connect([(gunzip, csdeconv, [("out_file", "in_file")])])
tractography.connect([(gen_WM_mask, csdeconv, [("WMprobabilitymap",
                                                         "mask_image")])])
tractography.connect([(estimatorresponse, csdeconv, [("response",
                                                         "response_file")])])
tractography.connect([(fsl2mrtrix, csdeconv, [("encoding_file",
                                                         "encoding_file")])])
```

Connect the tractography and compute the tract density image.

```
tractography.connect([(threshold_wmmask, probCSDstreamtrack, [("out_file",
                                                             "seed_file")])])
tractography.connect([(csdeconv, probCSDstreamtrack,
                      [("spherical_harmonics_image", "in_file")])])
tractography.connect([(probCSDstreamtrack, tracks2prob, [("tracked",
                                                         "in_file")])])
```

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```
tractography.connect([(gunzip, tracks2prob, [("out_file", "template_file")])])

tractography.connect([(gunzip, tck2trk, [("out_file", "image_file")])])
tractography.connect([(probCSDstreamtrack, tck2trk, [("tracked", "in_file")])])
```

Finally, we create another higher-level workflow to connect our tractography workflow with the info and data-grabbing nodes declared at the beginning. Our tutorial is now extensible to any arbitrary number of subjects by simply adding their names to the subject list and their data to the proper folders.

```
dwiproc = pe.Workflow(name="dwiproc")
dwiproc.base_dir = os.path.abspath('dmri_mrtrix_dti')
dwiproc.connect([(infosource, datasource, [('subject_id', 'subject_id')]),
                 (datasource, tractography,
                  [('dwi', 'inputnode.dwi'), ('bvals', 'inputnode.bvals'),
                   ('bvecs', 'inputnode.bvecs')])])

if __name__ == '__main__':
    dwiproc.run()
    dwiproc.write_graph()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

16.1 Introduction

This script, `dmri_preprocessing.py`, demonstrates how to prepare dMRI data for tractography and connectivity analysis with `nipype`.

We perform this analysis using the FSL course data, which can be acquired from here: http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz

Can be executed in command line using `python dmri_preprocessing.py`

Import necessary modules from `nipype`.

```
import os # system functions
import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.utility as niu # utility
import nipype.algorithms.misc as misc

import nipype.pipeline.engine as pe # pypeline engine

from nipype.interfaces import fsl
from nipype.interfaces import ants
```

Load specific `nipype`'s workflows for preprocessing of dMRI data: `nipype.workflows.dmri.preprocess.epi.all_peb_pipeline`, as data include a *b0* volume with reverse encoding direction (*P*>>>*A*, or *y*), in contrast with the general acquisition encoding that is *A*>>>*P* or *-y* (in RAS systems).

```
from nipype.workflows.dmri.fsl.artifacts import all_fsl_pipeline, remove_bias
```

Map field names into individual subject runs

```
info = dict(
    dwi=[['subject_id', 'dwidata']],
    bvecs=[['subject_id', 'bvecs']],
    bvals=[['subject_id', 'bvals']],
    dwi_rev=[['subject_id', 'nodif_PA']])

infosource = pe.Node(
    interface=niu.IdentityInterface(fields=['subject_id']), name="infosource")

# Set the subject 1 identifier in subject_list,
```

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```
# we choose the preproc dataset as it contains uncorrected files.
subject_list = ['subj1_preproc']
```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

Now we create a `nipy.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `Node` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```
datasource = pe.Node(
    nio.DataGrabber(infields=['subject_id'], outfields=list(info.keys())),
    name='datasource')

datasource.inputs.template = "%s/%s"

# This needs to point to the fdt folder you can find after extracting
# http://www.fmrib.ox.ac.uk/fslcourse/fsl_course_data2.tar.gz
datasource.inputs.base_directory = os.path.abspath('fdt1')
datasource.inputs.field_template = dict(
    dwi='%s/%s.nii.gz', dwi_rev='%s/%s.nii.gz')
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True
```

An `inputnode` is used to pass the data obtained by the data grabber to the

```
inputnode = pe.Node(
    niu.IdentityInterface(fields=["dwi", "bvecs", "bvals", "dwi_rev"]),
    name="inputnode")
```

16.2 Setup for dMRI preprocessing

In this section we initialize the appropriate workflow for preprocessing of diffusion images.

16.2.1 Artifacts correction

We will use the combination of `topup` and `eddy` as suggested by FSL.

In order to configure the susceptibility distortion correction (SDC), we first write the specific parameters of our echo-planar imaging (EPI) images.

Particularly, we look into the `acqparams.txt` file of the selected subject to gather the encoding direction, acceleration factor (in parallel sequences it is > 1), and readout time or echospacing.

```
epi_AP = {'echospacing': 66.5e-3, 'enc_dir': 'y-'}
epi_PA = {'echospacing': 66.5e-3, 'enc_dir': 'y'}
prep = all_fsl_pipeline(epi_params=epi_AP, altepi_params=epi_PA)
```

16.2.2 Bias field correction

Finally, we set up a node to correct for a single multiplicative bias field from computed on the $b0$ image, as suggested in [Jeurissen2014].

```
bias = remove_bias()
```

16.3 Connect nodes in workflow

We create a higher level workflow to connect the nodes. Please excuse the author for writing the arguments of the `connect` function in a not-standard style with readability aims.

```
wf = pe.Workflow(name="dMRI_Preprocessing")
wf.base_dir = os.path.abspath('preprocessing_dmri_tutorial')
wf.connect([(infosource, datasource, [('subject_id', 'subject_id')]),
            (datasource, prep,
             [('dwi', 'inputnode.in_file'), ('dwi_rev', 'inputnode.alt_file'),
              ('bvals', 'inputnode.in_bval'), ('bvecs', 'inputnode.in_bvec')]),
            (prep, bias, [('outputnode.out_file', 'inputnode.in_file'),
                          ('outputnode.out_mask', 'inputnode.in_mask')]),
            (datasource, bias, [('bvals', 'inputnode.in_bval')])])
```

Run the workflow as command line executable

```
if __name__ == '__main__':
    wf.run()
    wf.write_graph()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

dMRI: TBSS on NKI RS data

A pipeline to do a TBSS analysis on the NKI rockland sample data

```
from nipype.workflows.dmri.fsl.dti import create_eddy_correct_pipeline
from nipype.workflows.dmri.fsl.tbss import create_tbss_non_FA, create_tbss_all
```

Tell python where to find the appropriate functions.

```
import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.fsl as fsl # fsl
import nipype.interfaces.utility as util # utility
import nipype.pipeline.engine as pe # pypeline engine
import os # system functions

fsl.FSLCommand.set_default_output_type('NIFTI')
```

You can get the data from:

http://fcon_1000.projects.nitrc.org/indi/pro/eNKI_RS_TRT/FrontPage.html

```
dataDir = os.path.abspath('nki_rs_data')
workingdir = './tbss_example'
subjects_list = [
    '2475376', '3313349', '3808535', '3893245', '8735778', '9630905'
]

gen_fa = pe.Workflow(name="gen_fa")
gen_fa.base_dir = os.path.join(os.path.abspath(workingdir), '11')

subject_id_infosource = pe.Node(
    util.IdentityInterface(fields=['subject_id']),
    name='subject_id_infosource')
subject_id_infosource.iterables = ('subject_id', subjects_list)

datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=['dwi', 'bvec', 'bval']),
    name='datasource')
datasource.inputs.base_directory = os.path.abspath(dataDir)
datasource.inputs.template = '%s/session2/DTI_mx_137/dti.%s'
```

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```

datasource.inputs.template_args = dict(
    dwi=[['subject_id', 'nii.gz']],
    bvec=[['subject_id', 'bvec']],
    bval=[['subject_id', 'bval']])
datasource.inputs.sort_filelist = True
gen_fa.connect(subject_id_infosource, 'subject_id', datasource, 'subject_id')

eddy_correct = create_eddy_correct_pipeline()
eddy_correct.inputs.inputnode.ref_num = 0
gen_fa.connect(datasource, 'dwi', eddy_correct, 'inputnode.in_file')

bet = pe.Node(interface=fsl.BET(), name='bet')
bet.inputs.mask = True
bet.inputs.frac = 0.34
gen_fa.connect(eddy_correct, 'pick_ref.out', bet, 'in_file')

dtifit = pe.Node(interface=fsl.DTIFit(), name='dtifit')
gen_fa.connect(eddy_correct, 'outputnode.eddy_corrected', dtifit, 'dwi')
gen_fa.connect(subject_id_infosource, 'subject_id', dtifit, 'base_name')
gen_fa.connect(bet, 'mask_file', dtifit, 'mask')
gen_fa.connect(datasource, 'bvec', dtifit, 'bvecs')
gen_fa.connect(datasource, 'bval', dtifit, 'bvals')

datasink = pe.Node(interface=nio.DataSink(), name="datasink")
datasink.inputs.base_directory = os.path.join(
    os.path.abspath(workingdir), '11_results')
datasink.inputs.parameterization = False
gen_fa.connect(dtifit, 'FA', datasink, 'FA')
gen_fa.connect(dtifit, 'MD', datasink, 'MD')

if __name__ == '__main__':
    gen_fa.write_graph()
    gen_fa.run()

```

Here we get the FA list including all the subjects.

```

tbss_source = pe.Node(
    interface=nio.DataGrabber(outfiles=['fa_list', 'md_list']),
    name='tbss_source')
tbss_source.inputs.base_directory = datasink.inputs.base_directory
tbss_source.inputs.template = '%s/%s_%s.nii'
tbss_source.inputs.template_args = dict(
    fa_list=[['FA', subjects_list, 'FA']],
    md_list=[['MD', subjects_list, 'MD']])
tbss_source.inputs.sort_filelist = True

```

TBSS analysis

```

tbss_all = create_tbss_all()
tbss_all.inputs.inputnode.skeleton_thresh = 0.2

tbssproc = pe.Workflow(name="tbssproc")
tbssproc.base_dir = os.path.join(os.path.abspath(workingdir), '12')
tbssproc.connect(tbss_source, 'fa_list', tbss_all, 'inputnode.fa_list')

tbss_MD = create_tbss_non_FA(name='tbss_MD')
tbss_MD.inputs.inputnode.skeleton_thresh = tbss_all.inputs.inputnode.skeleton_
→thresh

```

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```
tbssproc.connect([
    (tbss_all, tbss_MD,
     [('tbss2.outputnode.field_list', 'inputnode.field_list'),
      ('tbss3.outputnode.groupmask', 'inputnode.groupmask'),
      ('tbss3.outputnode.meanfa_file',
       'inputnode.meanfa_file'), ('tbss4.outputnode.distance_map',
       'inputnode.distance_map')]),
    (tbss_source, tbss_MD, [('md_list', 'inputnode.file_list')]),
])

if __name__ == '__main__':
    tbssproc.write_graph()
    tbssproc.run()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

fMRI: OpenfMRI.org data, FSL, ANTS, c3daffine

A growing number of datasets are available on [OpenfMRI](#). This script demonstrates how to use nipy to analyze a data set:

```
python fmri_ants_openfmri.py --datasetdir ds107
```

This workflow also requires 2mm subcortical templates that are available from [MindBoggle](#). Specifically the 2mm version of the [MNI template](#).

Import necessary modules from nipy.

```
from __future__ import division, unicode_literals
from builtins import open, range, str, bytes

from glob import glob
import os

from nipy import config
from nipy import LooseVersion
from nipy import Workflow, Node, MapNode
from nipy.utils.filemanip import filename_to_list
import nipy.pipeline.engine as pe
import nipy.algorithms.modelgen as model
import nipy.algorithms.rapidart as ra
from nipy.algorithms.misc import TSNR, CalculateMedian
from nipy.interfaces.c3 import C3dAffineTool
from nipy.interfaces import fsl, Function, ants, freesurfer as fs
import nipy.interfaces.io as nio
from nipy.interfaces.io import FreeSurferSource
import nipy.interfaces.utility as niu
from nipy.interfaces.utility import Merge, IdentityInterface
from nipy.workflows.fmri.fsl import (create_featreg_preproc,
                                     create_modelfit_workflow,
                                     create_fixed_effects_flow)

from nipy.utils import NUMPY_MMAP

config.enable_provenance()
version = 0
if (fsl.Info.version()
```

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```

    and LooseVersion(fsl.Info.version()) > LooseVersion('5.0.6')):
        version = 507

fsl.FSLCommand.set_default_output_type('NIFTI_GZ')

imports = ['import os',
           'import nibabel as nb',
           'import numpy as np',
           'import scipy as sp',
           'from nipy.utils.filemanip import filename_to_list, list_to_filename,
→ split_filename',
           'from scipy.special import legendre'
          ]

def create_reg_workflow(name='registration'):
    """Create a FEAT preprocessing workflow together with freesurfer

    Parameters
    -----
        name : name of workflow (default: 'registration')

    Inputs:

        inputspec.source_files : files (filename or list of filenames to register)
        inputspec.mean_image : reference image to use
        inputspec.anatomical_image : anatomical image to coregister to
        inputspec.target_image : registration target

    Outputs:

        outputspec.func2anat_transform : FLIRT transform
        outputspec.anat2target_transform : FLIRT+FNIRT transform
        outputspec.transformed_files : transformed files in target space
        outputspec.transformed_mean : mean image in target space

    Example
    -----
        See code below
    """

    register = pe.Workflow(name=name)

    inputnode = pe.Node(
        interface=niu.IdentityInterface(fields=[
            'source_files', 'mean_image', 'anatomical_image', 'target_image',
            'target_image_brain', 'config_file'
        ]),
        name='inputspec')
    outputnode = pe.Node(
        interface=niu.IdentityInterface(fields=[
            'func2anat_transform', 'anat2target_transform',
            'transformed_files', 'transformed_mean', 'anat2target',
            'mean2anat_mask'
        ]),
        name='outputspec')
    """

```

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```
Estimate the tissue classes from the anatomical image. But use spm's segment
as FSL appears to be breaking.
```

```
"""
```

```
stripper = pe.Node(fsl.BET(), name='stripper')
register.connect(inputnode, 'anatomical_image', stripper, 'in_file')
fast = pe.Node(fsl.FAST(), name='fast')
register.connect(stripper, 'out_file', fast, 'in_files')
```

```
"""
```

```
Binarize the segmentation
```

```
"""
```

```
binarize = pe.Node(
    fsl.ImageMaths(op_string='-nan -thr 0.5 -bin'), name='binarize')
pickindex = lambda x, i: x[i]
register.connect(fast, ('partial_volume_files', pickindex, 2), binarize,
                 'in_file')
```

```
"""
```

```
Calculate rigid transform from mean image to anatomical image
```

```
"""
```

```
mean2anat = pe.Node(fsl.FLIRT(), name='mean2anat')
mean2anat.inputs.dof = 6
register.connect(inputnode, 'mean_image', mean2anat, 'in_file')
register.connect(stripper, 'out_file', mean2anat, 'reference')
```

```
"""
```

```
Now use bbr cost function to improve the transform
```

```
"""
```

```
mean2anatbbr = pe.Node(fsl.FLIRT(), name='mean2anatbbr')
mean2anatbbr.inputs.dof = 6
mean2anatbbr.inputs.cost = 'bbr'
mean2anatbbr.inputs.schedule = os.path.join(
    os.getenv('FSLDIR'), 'etc/flirtsch/bbr.sch')
register.connect(inputnode, 'mean_image', mean2anatbbr, 'in_file')
register.connect(binarize, 'out_file', mean2anatbbr, 'wm_seg')
register.connect(inputnode, 'anatomical_image', mean2anatbbr, 'reference')
register.connect(mean2anat, 'out_matrix_file', mean2anatbbr,
                 'in_matrix_file')
```

```
"""
```

```
Create a mask of the median image coregistered to the anatomical image
```

```
"""
```

```
mean2anat_mask = Node(fsl.BET(mask=True), name='mean2anat_mask')
register.connect(mean2anatbbr, 'out_file', mean2anat_mask, 'in_file')
```

```
"""
```

```
Convert the BBRegister transformation to ANTS ITK format
```

```
"""
```

```
convert2itk = pe.Node(C3dAffineTool(), name='convert2itk')
convert2itk.inputs.fsl2ras = True
convert2itk.inputs.itk_transform = True
register.connect(mean2anatbbr, 'out_matrix_file', convert2itk,
                 'transform_file')
register.connect(inputnode, 'mean_image', convert2itk, 'source_file')
register.connect(stripper, 'out_file', convert2itk, 'reference_file')
```

```
"""
```

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```

Compute registration between the subject's structural and MNI template

* All parameters are set using the example from:
#https://github.com/stnava/ANTs/blob/master/Scripts/newAntsExample.sh
* This is currently set to perform a very quick registration. However,
the registration can be made significantly more accurate for cortical
structures by increasing the number of iterations.
"""

reg = pe.Node(ants.Registration(), name='antsRegister')
reg.inputs.output_transform_prefix = "output_"
reg.inputs.transforms = ['Rigid', 'Affine', 'SyN']
reg.inputs.transform_parameters = [(0.1, ), (0.1, ), (0.2, 3.0, 0.0)]
reg.inputs.number_of_iterations = [[10000, 11110, 11110]] * 2 + [[
    100, 30, 20
]]
reg.inputs.dimension = 3
reg.inputs.write_composite_transform = True
reg.inputs.collapse_output_transforms = True
reg.inputs.initial_moving_transform_com = True
reg.inputs.metric = ['Mattes'] * 2 + [['Mattes', 'CC']]
reg.inputs.metric_weight = [1] * 2 + [[0.5, 0.5]]
reg.inputs.radius_or_number_of_bins = [32] * 2 + [[32, 4]]
reg.inputs.sampling_strategy = ['Regular'] * 2 + [[None, None]]
reg.inputs.sampling_percentage = [0.3] * 2 + [[None, None]]
reg.inputs.convergence_threshold = [1.e-8] * 2 + [-0.01]
reg.inputs.convergence_window_size = [20] * 2 + [5]
reg.inputs.smoothing_sigmas = [[4, 2, 1]] * 2 + [[1, 0.5, 0]]
reg.inputs.sigma_units = ['vox'] * 3
reg.inputs.shrink_factors = [[3, 2, 1]] * 2 + [[4, 2, 1]]
reg.inputs.use_estimate_learning_rate_once = [True] * 3
reg.inputs.use_histogram_matching = [False] * 2 + [True]
reg.inputs.winsorize_lower_quantile = 0.005
reg.inputs.winsorize_upper_quantile = 0.995
reg.inputs.args = '--float'
reg.inputs.output_warped_image = 'output_warped_image.nii.gz'
reg.inputs.num_threads = 4
reg.plugin_args = {
    'qsub_args': '-pe orte 4',
    'sbatch_args': '--mem=6G -c 4'
}
register.connect(stripper, 'out_file', reg, 'moving_image')
register.connect(inputnode, 'target_image_brain', reg, 'fixed_image')

```

Concatenate the affine and ants transforms into a list

```

merge = pe.Node(niu.Merge(2), iterfield=['in2'], name='mergexfm')
register.connect(convert2itk, 'itk_transform', merge, 'in2')
register.connect(reg, 'composite_transform', merge, 'in1')

```

Transform the mean image. First to anatomical and then to target

```

warpmean = pe.Node(ants.ApplyTransforms(), name='warpmean')
warpmean.inputs.input_image_type = 0
warpmean.inputs.interpolation = 'Linear'
warpmean.inputs.invert_transform_flags = [False, False]
warpmean.terminal_output = 'file'

```

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```

register.connect(inputnode, 'target_image_brain', warpmean,
                 'reference_image')
register.connect(inputnode, 'mean_image', warpmean, 'input_image')
register.connect(merge, 'out', warpmean, 'transforms')
"""
Transform the remaining images. First to anatomical and then to target
"""

warpall = pe.MapNode(
    ants.ApplyTransforms(), iterfield=['input_image'], name='warpall')
warpall.inputs.input_image_type = 0
warpall.inputs.interpolation = 'Linear'
warpall.inputs.invert_transform_flags = [False, False]
warpall.terminal_output = 'file'

register.connect(inputnode, 'target_image_brain', warpall,
                 'reference_image')
register.connect(inputnode, 'source_files', warpall, 'input_image')
register.connect(merge, 'out', warpall, 'transforms')
"""
Assign all the output files
"""

register.connect(reg, 'warped_image', outputnode, 'anat2target')
register.connect(warpmean, 'output_image', outputnode, 'transformed_mean')
register.connect(warpall, 'output_image', outputnode, 'transformed_files')
register.connect(mean2anatbbr, 'out_matrix_file', outputnode,
                 'func2anat_transform')
register.connect(mean2anat_mask, 'mask_file', outputnode, 'mean2anat_mask')
register.connect(reg, 'composite_transform', outputnode,
                 'anat2target_transform')

return register

def get_aparc_aseg(files):
    """Return the aparc+aseg.mgz file"""

    for name in files:
        if 'aparc+aseg.mgz' in name:
            return name
    raise ValueError('aparc+aseg.mgz not found')

def create_fs_reg_workflow(name='registration'):
    """Create a FEAT preprocessing workflow together with freesurfer

    Parameters
    -----

        name : name of workflow (default: 'registration')

    Inputs:

        inputspec.source_files : files (filename or list of filenames to register)
        inputspec.mean_image : reference image to use
        inputspec.target_image : registration target

```

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Outputs:

```

outputspec.func2anat_transform : FLIRT transform
outputspec.anat2target_transform : FLIRT+FNIRT transform
outputspec.transformed_files : transformed files in target space
outputspec.transformed_mean : mean image in target space

```

Example

See code below

"""

```

register = Workflow(name=name)

inputnode = Node(
    interface=IdentityInterface(fields=[
        'source_files', 'mean_image', 'subject_id', 'subjects_dir',
        'target_image'
    ]),
    name='inputspec')

outputnode = Node(
    interface=IdentityInterface(fields=[
        'func2anat_transform', 'out_reg_file', 'anat2target_transform',
        'transforms', 'transformed_mean', 'transformed_files',
        'min_cost_file', 'anat2target', 'aparc', 'mean2anat_mask'
    ]),
    name='outputspec')

# Get the subject's freesurfer source directory
fssource = Node(FreeSurferSource(), name='fssource')
fssource.run_without_submitting = True
register.connect(inputnode, 'subject_id', fssource, 'subject_id')
register.connect(inputnode, 'subjects_dir', fssource, 'subjects_dir')

convert = Node(freesurfer.MRIConvert(out_type='nii'), name="convert")
register.connect(fssource, 'T1', convert, 'in_file')

# Coregister the median to the surface
bbregister = Node(
    freesurfer.BBRegister(registered_file=True), name='bbregister')
bbregister.inputs.init = 'fsl'
bbregister.inputs.contrast_type = 't2'
bbregister.inputs.out_fsl_file = True
bbregister.inputs.epi_mask = True
register.connect(inputnode, 'subject_id', bbregister, 'subject_id')
register.connect(inputnode, 'mean_image', bbregister, 'source_file')
register.connect(inputnode, 'subjects_dir', bbregister, 'subjects_dir')

# Create a mask of the median coregistered to the anatomical image
mean2anat_mask = Node(fsl.BET(mask=True), name='mean2anat_mask')
register.connect(bbregister, 'registered_file', mean2anat_mask, 'in_file')
"""
use aparc+aseg's brain mask
"""

```

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```

binarize = Node(
    fs.Binarize(min=0.5, out_type="nii.gz", dilate=1),
    name="binarize_aparc")
register.connect(fssource, ("aparc_aseg", get_aparc_aseg), binarize,
                "in_file")

stripper = Node(fsl.ApplyMask(), name='stripper')
register.connect(binarize, "binary_file", stripper, "mask_file")
register.connect(convert, 'out_file', stripper, 'in_file')
"""
Apply inverse transform to aparc file
"""

aparcxfm = Node(
    freesurfer.ApplyVolTransform(inverse=True, interp='nearest'),
    name='aparc_inverse_transform')
register.connect(inputnode, 'subjects_dir', aparcxfm, 'subjects_dir')
register.connect(bbregister, 'out_reg_file', aparcxfm, 'reg_file')
register.connect(fssource, ('aparc_aseg', get_aparc_aseg), aparcxfm,
                'target_file')
register.connect(inputnode, 'mean_image', aparcxfm, 'source_file')
"""
Convert the BBRegister transformation to ANTS ITK format
"""

convert2itk = Node(C3dAffineTool(), name='convert2itk')
convert2itk.inputs.fsl2ras = True
convert2itk.inputs.itk_transform = True
register.connect(bbregister, 'out_fsl_file', convert2itk, 'transform_file')
register.connect(inputnode, 'mean_image', convert2itk, 'source_file')
register.connect(stripper, 'out_file', convert2itk, 'reference_file')
"""
Compute registration between the subject's structural and MNI template

    * All parameters are set using the example from:
      #https://github.com/stnava/ANTs/blob/master/Scripts/newAntsExample.sh
    * This is currently set to perform a very quick registration. However,
      the registration can be made significantly more accurate for cortical
      structures by increasing the number of iterations.
"""

reg = Node(ants.Registration(), name='antsRegister')
reg.inputs.output_transform_prefix = "output_"
reg.inputs.transforms = ['Rigid', 'Affine', 'SyN']
reg.inputs.transform_parameters = [(0.1, ), (0.1, ), (0.2, 3.0, 0.0)]
reg.inputs.number_of_iterations = [[10000, 11110, 11110]] * 2 + [[
    100, 30, 20
]]
reg.inputs.dimension = 3
reg.inputs.write_composite_transform = True
reg.inputs.collapse_output_transforms = True
reg.inputs.initial_moving_transform_com = True
reg.inputs.metric = ['Mattes'] * 2 + [['Mattes', 'CC']]
reg.inputs.metric_weight = [1] * 2 + [[0.5, 0.5]]
reg.inputs.radius_or_number_of_bins = [32] * 2 + [[32, 4]]
reg.inputs.sampling_strategy = ['Regular'] * 2 + [[None, None]]
reg.inputs.sampling_percentage = [0.3] * 2 + [[None, None]]

```

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```
reg.inputs.convergence_threshold = [1.e-8] * 2 + [-0.01]
reg.inputs.convergence_window_size = [20] * 2 + [5]
reg.inputs.smoothing_sigmas = [[4, 2, 1]] * 2 + [[1, 0.5, 0]]
reg.inputs.sigma_units = ['vox'] * 3
reg.inputs.shrink_factors = [[3, 2, 1]] * 2 + [[4, 2, 1]]
reg.inputs.use_estimate_learning_rate_once = [True] * 3
reg.inputs.use_histogram_matching = [False] * 2 + [True]
reg.inputs.winsorize_lower_quantile = 0.005
reg.inputs.winsorize_upper_quantile = 0.995
reg.inputs.float = True
reg.inputs.output_warped_image = 'output_warped_image.nii.gz'
reg.inputs.num_threads = 4
reg.plugin_args = {
    'qsub_args': '-pe orte 4',
    'sbatch_args': '--mem=6G -c 4'
}
register.connect(stripper, 'out_file', reg, 'moving_image')
register.connect(inputnode, 'target_image', reg, 'fixed_image')
```

Concatenate the affine and ants transforms into a list

```
merge = Node(Merge(2), iterfield=['in2'], name='mergexfm')
register.connect(convert2itk, 'itk_transform', merge, 'in2')
register.connect(reg, 'composite_transform', merge, 'in1')
```

Transform the mean image. First to anatomical and then to target

```
warpmean = Node(ants.ApplyTransforms(), name='warpmean')
warpmean.inputs.input_image_type = 0
warpmean.inputs.interpolation = 'Linear'
warpmean.inputs.invert_transform_flags = [False, False]
warpmean.terminal_output = 'file'
warpmean.inputs.args = '--float'
# warpmean.inputs.num_threads = 4
# warpmean.plugin_args = {'sbatch_args': '--mem=4G -c 4'}
```

Transform the remaining images. First to anatomical and then to target

```
warpall = pe.MapNode(
    ants.ApplyTransforms(), iterfield=['input_image'], name='warpall')
warpall.inputs.input_image_type = 0
warpall.inputs.interpolation = 'Linear'
warpall.inputs.invert_transform_flags = [False, False]
warpall.terminal_output = 'file'
warpall.inputs.args = '--float'
warpall.inputs.num_threads = 2
warpall.plugin_args = {'sbatch_args': '--mem=6G -c 2'}
"""
Assign all the output files
"""

register.connect(warpmean, 'output_image', outputnode, 'transformed_mean')
register.connect(warpall, 'output_image', outputnode, 'transformed_files')

register.connect(inputnode, 'target_image', warpmean, 'reference_image')
register.connect(inputnode, 'mean_image', warpmean, 'input_image')
register.connect(merge, 'out', warpmean, 'transforms')
register.connect(inputnode, 'target_image', warpall, 'reference_image')
```

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```

register.connect(inputnode, 'source_files', warpall, 'input_image')
register.connect(merge, 'out', warpall, 'transforms')
"""
Assign all the output files
"""

register.connect(reg, 'warped_image', outputnode, 'anat2target')
register.connect(aparcxfm, 'transformed_file', outputnode, 'aparc')
register.connect(bbregister, 'out_fsl_file', outputnode,
                  'func2anat_transform')
register.connect(bbregister, 'out_reg_file', outputnode, 'out_reg_file')
register.connect(bbregister, 'min_cost_file', outputnode, 'min_cost_file')
register.connect(mean2anat_mask, 'mask_file', outputnode, 'mean2anat_mask')
register.connect(reg, 'composite_transform', outputnode,
                  'anat2target_transform')
register.connect(merge, 'out', outputnode, 'transforms')

return register

```

Get info for a given subject

```

def get_subjectinfo(subject_id, base_dir, task_id, model_id):
    """Get info for a given subject

    Parameters
    -----
    subject_id : string
        Subject identifier (e.g., sub001)
    base_dir : string
        Path to base directory of the dataset
    task_id : int
        Which task to process
    model_id : int
        Which model to process

    Returns
    -----
    run_ids : list of ints
        Run numbers
    conds : list of str
        Condition names
    TR : float
        Repetition time
    """

    from glob import glob
    import os
    import numpy as np
    condition_info = []
    cond_file = os.path.join(base_dir, 'models', 'model%03d' % model_id,
                              'condition_key.txt')
    with open(cond_file, 'rt') as fp:
        for line in fp:
            info = line.strip().split()
            condition_info.append([info[0], info[1], ' '.join(info[2:])])
    if len(condition_info) == 0:
        raise ValueError('No condition info found in %s' % cond_file)

```

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```

taskinfo = np.array(condition_info)
n_tasks = len(np.unique(taskinfo[:, 0]))
conds = []
run_ids = []
if task_id > n_tasks:
    raise ValueError('Task id %d does not exist' % task_id)
for idx in range(n_tasks):
    taskidx = np.where(taskinfo[:, 0] == 'task%03d' % (idx + 1))
    conds.append([
        condition.replace(' ', '_')
        for condition in taskinfo[taskidx[0], 2]
    ]) # if 'junk' not in condition))
    files = sorted(
        glob(
            os.path.join(base_dir, subject_id, 'BOLD',
                          'task%03d_run*' % (idx + 1)))
    )
    runs = [int(val[-3:]) for val in files]
    run_ids.insert(idx, runs)
    json_info = os.path.join(base_dir, subject_id, 'BOLD', 'task%03d_run%03d' %
                             (task_id,
                              run_ids[task_id - 1][0]), 'bold_scaninfo.json')
    if os.path.exists(json_info):
        import json
        with open(json_info, 'rt') as fp:
            data = json.load(fp)
            TR = data['global']['const']['RepetitionTime'] / 1000.
    else:
        task_scan_key = os.path.join(
            base_dir, subject_id, 'BOLD', 'task%03d_run%03d' %
            (task_id, run_ids[task_id - 1][0]), 'scan_key.txt')
        if os.path.exists(task_scan_key):
            TR = np.genfromtxt(task_scan_key)[1]
        else:
            TR = np.genfromtxt(os.path.join(base_dir, 'scan_key.txt'))[1]
    return run_ids[task_id - 1], conds[task_id - 1], TR

```

Analyzes an open fmri dataset

```

def analyze_openfmri_dataset(data_dir,
                             subject=None,
                             model_id=None,
                             task_id=None,
                             output_dir=None,
                             subj_prefix='*',
                             hpcutoff=120.,
                             use_derivatives=True,
                             fwhm=6.0,
                             subjects_dir=None,
                             target=None):
    """Analyzes an open fmri dataset

    Parameters
    -----

    data_dir : str
        Path to the base data directory
    """

```

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```

work_dir : str
    Nipype working directory (defaults to cwd)
    """
    """

Load nipype workflows
    """

preproc = create_featreg_preproc(whichvol='first')
modelfit = create_modelfit_workflow()
fixed_fx = create_fixed_effects_flow()
if subjects_dir:
    registration = create_fs_reg_workflow()
else:
    registration = create_reg_workflow()
    """
    Remove the plotting connection so that plot iterables don't propagate
    to the model stage
    """

preproc.disconnect(
    preproc.get_node('plot_motion'), 'out_file',
    preproc.get_node('outputspec'), 'motion_plots')
    """
    Set up openfmri data specific components
    """

subjects = sorted([
    path.split(os.path.sep)[-1]
    for path in glob(os.path.join(data_dir, subj_prefix))
])

infosource = pe.Node(
    niu.IdentityInterface(fields=['subject_id', 'model_id', 'task_id']),
    name='infosource')
if len(subject) == 0:
    infosource.iterables = [('subject_id', subjects),
                           ('model_id', [model_id]), ('task_id', task_id)]
else:
    infosource.iterables = [('subject_id', [
        subjects[subjects.index(subj)] for subj in subject
    ]), ('model_id', [model_id]), ('task_id', task_id)]

subjinfo = pe.Node(
    niu.Function(
        input_names=['subject_id', 'base_dir', 'task_id', 'model_id'],
        output_names=['run_id', 'conds', 'TR'],
        function=get_subjectinfo),
    name='subjectinfo')
subjinfo.inputs.base_dir = data_dir
    """
    Return data components as anat, bold and behav
    """

contrast_file = os.path.join(data_dir, 'models', 'model%03d' % model_id,
                             'task_contrasts.txt')
has_contrast = os.path.exists(contrast_file)
if has_contrast:

```

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```

datasource = pe.Node(
    nio.DataGrabber(
        infields=['subject_id', 'run_id', 'task_id', 'model_id'],
        outfields=['anat', 'bold', 'behav', 'contrasts']),
    name='datasource')
else:
    datasource = pe.Node(
        nio.DataGrabber(
            infields=['subject_id', 'run_id', 'task_id', 'model_id'],
            outfields=['anat', 'bold', 'behav']),
        name='datasource')
datasource.inputs.base_directory = data_dir
datasource.inputs.template = '*'

if has_contrast:
    datasource.inputs.field_template = {
        'anat': '%s/anatomy/T1_001.nii.gz',
        'bold': '%s/BOLD/task%03d_r*/bold.nii.gz',
        'behav': ('%s/model/model%03d/onsets/task%03d_'
                  'run%03d/cond*.txt'),
        'contrasts': ('models/model%03d/'
                      'task_contrasts.txt')
    }
    datasource.inputs.template_args = {
        'anat': [['subject_id']],
        'bold': [['subject_id', 'task_id']],
        'behav': [['subject_id', 'model_id', 'task_id', 'run_id']],
        'contrasts': [['model_id']]
    }
else:
    datasource.inputs.field_template = {
        'anat': '%s/anatomy/T1_001.nii.gz',
        'bold': '%s/BOLD/task%03d_r*/bold.nii.gz',
        'behav': ('%s/model/model%03d/onsets/task%03d_'
                  'run%03d/cond*.txt')
    }
    datasource.inputs.template_args = {
        'anat': [['subject_id']],
        'bold': [['subject_id', 'task_id']],
        'behav': [['subject_id', 'model_id', 'task_id', 'run_id']]
    }

datasource.inputs.sort_filelist = True
"""
Create meta workflow
"""

wf = pe.Workflow(name='openfmri')
wf.connect(infosource, 'subject_id', subjinfo, 'subject_id')
wf.connect(infosource, 'model_id', subjinfo, 'model_id')
wf.connect(infosource, 'task_id', subjinfo, 'task_id')
wf.connect(infosource, 'subject_id', datasource, 'subject_id')
wf.connect(infosource, 'model_id', datasource, 'model_id')
wf.connect(infosource, 'task_id', datasource, 'task_id')
wf.connect(subjinfo, 'run_id', datasource, 'run_id')
wf.connect([
    (datasource, preproc, [('bold', 'inputspec.func')])),

```

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```

])

def get_highpass(TR, hpcutoff):
    return hpcutoff / (2. * TR)

gethighpass = pe.Node(
    niu.Function(
        input_names=['TR', 'hpcutoff'],
        output_names=['highpass'],
        function=get_highpass),
    name='gethighpass')
wf.connect(subjinfo, 'TR', gethighpass, 'TR')
wf.connect(gethighpass, 'highpass', preproc, 'inputspec.highpass')
"""
Setup a basic set of contrasts, a t-test per condition
"""

def get_contrasts(contrast_file, task_id, conds):
    import numpy as np
    import os
    contrast_def = []
    if os.path.exists(contrast_file):
        with open(contrast_file, 'rt') as fp:
            contrast_def.extend([
                np.array(row.split()) for row in fp.readlines()
                if row.strip()
            ])
    contrasts = []
    for row in contrast_def:
        if row[0] != 'task%03d' % task_id:
            continue
        con = [
            row[1], 'T', ['cond%03d' % (i + 1) for i in range(len(conds))],
            row[2:].astype(float).tolist()
        ]
        contrasts.append(con)
    # add auto contrasts for each column
    for i, cond in enumerate(conds):
        con = [cond, 'T', ['cond%03d' % (i + 1)], [1]]
        contrasts.append(con)
    return contrasts

contrastgen = pe.Node(
    niu.Function(
        input_names=['contrast_file', 'task_id', 'conds'],
        output_names=['contrasts'],
        function=get_contrasts),
    name='contrastgen')

art = pe.MapNode(
    interface=ra.ArtifactDetect(
        use_differences=[True, False],
        use_norm=True,
        norm_threshold=1,
        zintensity_threshold=3,
        parameter_source='FSL',
        mask_type='file'),

```

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```

iterfield=['realigned_files', 'realignment_parameters', 'mask_file'],
name="art")

modelspec = pe.Node(interface=model.SpecifyModel(), name="modelspec")
modelspec.inputs.input_units = 'secs'

def check_behav_list(behav, run_id, conds):
    import numpy as np
    num_conds = len(conds)
    if isinstance(behav, (str, bytes)):
        behav = [behav]
    behav_array = np.array(behav).flatten()
    num_elements = behav_array.shape[0]
    return behav_array.reshape(int(num_elements / num_conds),
                               num_conds).tolist()

reshape_behav = pe.Node(
    niu.Function(
        input_names=['behav', 'run_id', 'conds'],
        output_names=['behav'],
        function=check_behav_list),
    name='reshape_behav')

wf.connect(subjinfo, 'TR', modelspec, 'time_repetition')
wf.connect(datasource, 'behav', reshape_behav, 'behav')
wf.connect(subjinfo, 'run_id', reshape_behav, 'run_id')
wf.connect(subjinfo, 'conds', reshape_behav, 'conds')
wf.connect(reshape_behav, 'behav', modelspec, 'event_files')

wf.connect(subjinfo, 'TR', modelfit, 'inputspec.interscan_interval')
wf.connect(subjinfo, 'conds', contrastgen, 'conds')
if has_contrast:
    wf.connect(datasource, 'contrasts', contrastgen, 'contrast_file')
else:
    contrastgen.inputs.contrast_file = ''
wf.connect(infosource, 'task_id', contrastgen, 'task_id')
wf.connect(contrastgen, 'contrasts', modelfit, 'inputspec.contrasts')

wf.connect([(preproc, art,
              [('outputspec.motion_parameters', 'realignment_parameters'),
               ('outputspec.realigned_files',
                'realigned_files'), ('outputspec.mask', 'mask_file')]),
            (preproc, modelspec,
              [('outputspec.highpassed_files', 'functional_runs'),
               ('outputspec.motion_parameters', 'realignment_parameters')]),
            (art, modelspec,
              [('outlier_files', 'outlier_files')]), (modelspec, modelfit, [
                ('session_info', 'inputspec.session_info')
              ]), (preproc, modelfit, [('outputspec.highpassed_files',
                'inputspec.functional_data')])])

# Compute TSNR on realigned data regressing polynomials upto order 2
tsnr = MapNode(TSNR(regress_poly=2), iterfield=['in_file'], name='tsnr')
wf.connect(preproc, "outputspec.realigned_files", tsnr, "in_file")

# Compute the median image across runs
calc_median = Node(CalculateMedian(), name='median')

```

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```

wf.connect(tsnr, 'detrended_file', calc_median, 'in_files')
"""
Reorder the copes so that now it combines across runs
"""

def sort_copes(copes, varcopes, contrasts):
    import numpy as np
    if not isinstance(copes, list):
        copes = [copes]
        varcopes = [varcopes]
    num_copes = len(contrasts)
    n_runs = len(copes)
    all_copes = np.array(copes).flatten()
    all_varcopes = np.array(varcopes).flatten()
    outcopes = all_copes.reshape(
        int(len(all_copes) / num_copes), num_copes).T.tolist()
    outvarcopes = all_varcopes.reshape(
        int(len(all_varcopes) / num_copes), num_copes).T.tolist()
    return outcopes, outvarcopes, n_runs

cope_sorter = pe.Node(
    niu.Function(
        input_names=['copes', 'varcopes', 'contrasts'],
        output_names=['copes', 'varcopes', 'n_runs'],
        function=sort_copes),
    name='cope_sorter')

pickfirst = lambda x: x[0]

wf.connect(contrastgen, 'contrasts', cope_sorter, 'contrasts')
wf.connect([(preproc, fixed_fx,
    [(['outputspec.mask', pickfirst),
      'flameo.mask_file'])], (modelfit, cope_sorter,
    [(['outputspec.copes', 'copes')]),
    (modelfit, cope_sorter, [(['outputspec.varcopes', 'varcopes')]),
    (cope_sorter, fixed_fx,
    [(['copes', 'inputspec.copes'], ('varcopes',
      'inputspec.varcopes'),
    ('n_runs', 'l2model.num_copes')]), (modelfit, fixed_fx, [
      ('outputspec.dof_file', 'inputspec.dof_files'),
    ]))

wf.connect(calc_median, 'median_file', registration,
    'inputspec.mean_image')
if subjects_dir:
    wf.connect(infosource, 'subject_id', registration,
        'inputspec.subject_id')
    registration.inputs.inputs.spec.subjects_dir = subjects_dir
    registration.inputs.inputs.spec.target_image = fsl.Info.standard_image(
        'MNI152_T1_2mm_brain.nii.gz')
    if target:
        registration.inputs.inputs.spec.target_image = target
else:
    wf.connect(datasource, 'anat', registration,
        'inputspec.anatomical_image')
    registration.inputs.inputs.spec.target_image = fsl.Info.standard_image(
        'MNI152_T1_2mm.nii.gz')

```

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```

        registration.inputs.inputs.spec.target_image_brain = fsl.Info.standard_
↪image(
            'MNI152_T1_2mm_brain.nii.gz')
        registration.inputs.inputs.spec.config_file = 'T1_2_MNI152_2mm'

    def merge_files(copes, varcopes, zstats):
        out_files = []
        splits = []
        out_files.extend(copes)
        splits.append(len(copes))
        out_files.extend(varcopes)
        splits.append(len(varcopes))
        out_files.extend(zstats)
        splits.append(len(zstats))
        return out_files, splits

    mergefunc = pe.Node(
        niu.Function(
            input_names=['copes', 'varcopes', 'zstats'],
            output_names=['out_files', 'splits'],
            function=merge_files),
        name='merge_files')
    wf.connect([(fixed_fx.get_node('outputspec'), mergefunc, [
        ('copes', 'copes'),
        ('varcopes', 'varcopes'),
        ('zstats', 'zstats'),
    ])])
    wf.connect(mergefunc, 'out_files', registration, 'inputs.spec.source_files')

    def split_files(in_files, splits):
        copes = in_files[:splits[0]]
        varcopes = in_files[splits[0]:(splits[0] + splits[1])]
        zstats = in_files[(splits[0] + splits[1]):]
        return copes, varcopes, zstats

    splitfunc = pe.Node(
        niu.Function(
            input_names=['in_files', 'splits'],
            output_names=['copes', 'varcopes', 'zstats'],
            function=split_files),
        name='split_files')
    wf.connect(mergefunc, 'splits', splitfunc, 'splits')
    wf.connect(registration, 'outputs.spec.transformed_files', splitfunc,
        'in_files')

    if subjects_dir:
        get_roi_mean = pe.MapNode(
            fs.SegStats(default_color_table=True),
            iterfield=['in_file'],
            name='get_aparc_means')
        get_roi_mean.inputs.avgwf_txt_file = True
        wf.connect(
            fixed_fx.get_node('outputspec'), 'copes', get_roi_mean, 'in_file')
        wf.connect(registration, 'outputs.spec.aparc', get_roi_mean,
            'segmentation_file')

        get_roi_tsnr = pe.MapNode(

```

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```

        fs.SegStats(default_color_table=True),
        iterfield=['in_file'],
        name='get_aparc_tsnr')
    get_roi_tsnr.inputs.avgwf_txt_file = True
    wf.connect(tsnr, 'tsnr_file', get_roi_tsnr, 'in_file')
    wf.connect(registration, 'outputspec.aparc', get_roi_tsnr,
               'segmentation_file')

    """
    Connect to a datasink
    """

def get_subs(subject_id, conds, run_id, model_id, task_id):
    subs = ['_subject_id_%s' % subject_id, '']
    subs.append('_model_id_%d' % model_id, 'model%03d' % model_id)
    subs.append('_task_id_%d/' % task_id, '/task%03d_' % task_id)
    subs.append('bold_dtype_mcf_mask_smooth_mask_gms_tempfilt_mean_warp',
               'mean'))
    subs.append('bold_dtype_mcf_mask_smooth_mask_gms_tempfilt_mean_flirt',
               'affine'))

    for i in range(len(conds)):
        subs.append('_flameo%d/cope1.' % i, 'cope%02d.' % (i + 1))
        subs.append('_flameo%d/varcope1.' % i, 'varcope%02d.' % (i + 1))
        subs.append('_flameo%d/zstat1.' % i, 'zstat%02d.' % (i + 1))
        subs.append('_flameo%d/tstat1.' % i, 'tstat%02d.' % (i + 1))
        subs.append('_flameo%d/res4d.' % i, 'res4d%02d.' % (i + 1))
        subs.append('_warpall%d/cope1_warp.' % i, 'cope%02d.' % (i + 1))
        subs.append('_warpall%d/varcope1_warp.' % (len(conds) + i),
                   'varcope%02d.' % (i + 1))
        subs.append('_warpall%d/zstat1_warp.' % (2 * len(conds) + i),
                   'zstat%02d.' % (i + 1))
        subs.append('_warpall%d/cope1_trans.' % i, 'cope%02d.' % (i + 1))
        subs.append('_warpall%d/varcope1_trans.' % (len(conds) + i),
                   'varcope%02d.' % (i + 1))
        subs.append('_warpall%d/zstat1_trans.' % (2 * len(conds) + i),
                   'zstat%02d.' % (i + 1))
        subs.append('__get_aparc_means%d/' % i, '/cope%02d_' % (i + 1))

    for i, run_num in enumerate(run_id):
        subs.append('__get_aparc_tsnr%d/' % i, '/run%02d_' % run_num)
        subs.append('__art%d/' % i, '/run%02d_' % run_num)
        subs.append('__dilatemask%d/' % i, '/run%02d_' % run_num)
        subs.append('__realign%d/' % i, '/run%02d_' % run_num)
        subs.append('__modelgen%d/' % i, '/run%02d_' % run_num)
        subs.append('/model%03d/task%03d/' % (model_id, task_id), '/')
        subs.append('/model%03d/task%03d_' % (model_id, task_id), '/')
        subs.append('_bold_dtype_mcf_bet_thresh_dil', '_mask')
        subs.append('_output_warped_image', '_anat2target')
        subs.append('median_flirt_brain_mask', 'median_brain_mask')
        subs.append('median_bbreg_brain_mask', 'median_brain_mask')
    return subs

subsgen = pe.Node(
    niu.Function(
        input_names=[
            'subject_id', 'conds', 'run_id', 'model_id', 'task_id'
        ],

```

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```

        output_names=['substitutions'],
        function=get_subs),
        name='subsgen')
wf.connect(subjinfo, 'run_id', subsgen, 'run_id')

datasink = pe.Node(interface=nio.DataSink(), name="datasink")
wf.connect(infosource, 'subject_id', datasink, 'container')
wf.connect(infosource, 'subject_id', subsgen, 'subject_id')
wf.connect(infosource, 'model_id', subsgen, 'model_id')
wf.connect(infosource, 'task_id', subsgen, 'task_id')
wf.connect(contrastgen, 'contrasts', subsgen, 'conds')
wf.connect(subsgen, 'substitutions', datasink, 'substitutions')
wf.connect([(fixed_fx.get_node('outputspec'), datasink,
        [ ('res4d', 'res4d'), ('copes', 'copes'), ('varcopes',
        'varcopes'),
        ('zstats', 'zstats'), ('tstats', 'tstats') ])]])
wf.connect([(modelfit.get_node('modelgen'), datasink, [
        ('design_cov', 'qa.model'),
        ('design_image', 'qa.model.@matrix_image'),
        ('design_file', 'qa.model.@matrix'),
        ])]])
wf.connect([(preproc, datasink, [ ('outputspec.motion_parameters',
        'qa.motion'), ('outputspec.motion_plots',
        'qa.motion.plots'),
        ('outputspec.mask', 'qa.mask') ])]])
wf.connect(registration, 'outputspec.mean2anat_mask', datasink,
        'qa.mask.mean2anat')
wf.connect(art, 'norm_files', datasink, 'qa.art.@norm')
wf.connect(art, 'intensity_files', datasink, 'qa.art.@intensity')
wf.connect(art, 'outlier_files', datasink, 'qa.art.@outlier_files')
wf.connect(registration, 'outputspec.anat2target', datasink,
        'qa.anat2target')
wf.connect(tsnr, 'tsnr_file', datasink, 'qa.tsnr.@map')
if subjects_dir:
    wf.connect(registration, 'outputspec.min_cost_file', datasink,
        'qa.mincost')
    wf.connect([(get_roi_tsnr, datasink, [ ('avgwf_txt_file', 'qa.tsnr'),
        ('summary_file',
        'qa.tsnr.@summary') ])]])
    wf.connect([(get_roi_mean, datasink, [ ('avgwf_txt_file', 'copes.roi'),
        ('summary_file',
        'copes.roi.@summary') ])]])

wf.connect([(splitfunc, datasink, [
        ('copes', 'copes.mni'),
        ('varcopes', 'varcopes.mni'),
        ('zstats', 'zstats.mni'),
        ])]])
wf.connect(calc_median, 'median_file', datasink, 'mean')
wf.connect(registration, 'outputspec.transformed_mean', datasink,
        'mean.mni')
wf.connect(registration, 'outputspec.func2anat_transform', datasink,
        'xfm.mean2anat')
wf.connect(registration, 'outputspec.anat2target_transform', datasink,
        'xfm.anat2target')

"""
Set processing parameters
"""

```

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```

preproc.inputs.inputs.spec.fwhm = fwhm
gethighpass.inputs.hpcutoff = hpcutoff
modelspec.inputs.high_pass_filter_cutoff = hpcutoff
modelfit.inputs.inputs.spec.bases = {'dgamma': {'derivs': use_derivatives}}
modelfit.inputs.inputs.spec.model_serial_correlations = True
modelfit.inputs.inputs.spec.film_threshold = 1000

datasink.inputs.base_directory = output_dir
return wf

```

The following functions run the whole workflow.

```

if __name__ == '__main__':
    import argparse
    defstr = ' (default %(default)s)'
    parser = argparse.ArgumentParser(
        prog='fmri_openfmri.py', description=__doc__)
    parser.add_argument('-d', '--datasetdir', required=True)
    parser.add_argument(
        '-s',
        '--subject',
        default=[],
        nargs='+',
        type=str,
        help="Subject name (e.g. 'sub001')")
    parser.add_argument(
        '-m', '--model', default=1, help="Model index" + defstr)
    parser.add_argument(
        '-x',
        '--subjectprefix',
        default='sub*',
        help="Subject prefix" + defstr)
    parser.add_argument(
        '-t',
        '--task',
        default=1, # nargs='+',
        type=int,
        help="Task index" + defstr)
    parser.add_argument(
        '--hpfilter',
        default=120.,
        type=float,
        help="High pass filter cutoff (in secs)" + defstr)
    parser.add_argument(
        '--fwhm', default=6., type=float, help="Spatial FWHM" + defstr)
    parser.add_argument(
        '--derivatives', action="store_true", help="Use derivatives" + defstr)
    parser.add_argument(
        "-o", "--output_dir", dest="outdir", help="Output directory base")
    parser.add_argument(
        "-w", "--work_dir", dest="work_dir", help="Output directory base")
    parser.add_argument(
        "-p",
        "--plugin",
        dest="plugin",
        default='Linear',

```

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```

        help="Plugin to use")
    parser.add_argument(
        "--plugin_args", dest="plugin_args", help="Plugin arguments")
    parser.add_argument(
        "--sd",
        dest="subjects_dir",
        help="FreeSurfer subjects directory (if available)")
    parser.add_argument(
        "--target",
        dest="target_file",
        help=("Target in MNI space. Best to use the MindBoggle "
              "template - only used with FreeSurfer "
              "OASIS-30_Atropos_template_in_MNI152_2mm.nii.gz"))
    args = parser.parse_args()
    outdir = args.outdir
    work_dir = os.getcwd()
    if args.work_dir:
        work_dir = os.path.abspath(args.work_dir)
    if outdir:
        outdir = os.path.abspath(outdir)
    else:
        outdir = os.path.join(work_dir, 'output')
    outdir = os.path.join(outdir, 'model%02d' % int(args.model),
                          'task%03d' % int(args.task))
    derivatives = args.derivatives
    if derivatives is None:
        derivatives = False
    wf = analyze_openfmri_dataset(
        data_dir=os.path.abspath(args.datasetdir),
        subject=args.subject,
        model_id=int(args.model),
        task_id=[int(args.task)],
        subj_prefix=args.subjectprefix,
        output_dir=outdir,
        hpcutoff=args.hpfilter,
        use_derivatives=derivatives,
        fwhm=args.fwhm,
        subjects_dir=args.subjects_dir,
        target=args.target_file)
    # wf.config['execution']['remove_unnecessary_outputs'] = False

    wf.base_dir = work_dir
    if args.plugin_args:
        wf.run(args.plugin, plugin_args=eval(args.plugin_args))
    else:
        wf.run(args.plugin)

```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the examples directory.

fMRI: surface smooth - FreeSurfer, SPM

This tutorial illustrates how to perform surface-based smoothing of cortical data using [FreeSurfer](#) and then perform firstlevel model and contrast estimation using [SPM](#). A surface-based second level glm illustrates the use of spherical registration and freesurfer's glm functions.

19.1 Preparing environment

19.1.1 Step 0

In order to run this tutorial you need to have [SPM](#) and [FreeSurfer](#) tools installed and accessible from matlab/command line. Check by calling `mri_info` from the command line.

19.1.2 Step 1

Link the *fsaverage* directory for your freesurfer distribution. To do this type:

```
cd nipy-tutorial/fsdata
ln -s $FREESURFER_HOME/subjects/fsaverage
cd ..
```

19.2 Defining the workflow

```
from __future__ import print_function
from builtins import str
from builtins import range

import os # system functions

import nipy.algorithms.modelgen as model # model generation
import nipy.algorithms.rapidart as ra # artifact detection
import nipy.interfaces.freesurfer as fs # freesurfer
import nipy.interfaces.io as nio # i/o routines
import nipy.interfaces.matlab as mlab # how to run matlab
import nipy.interfaces.spm as spm # spm
```

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```
import nipyne.interfaces.utility as util # utility
import nipyne.pipeline.engine as pe # pypeline engine
```

19.2.1 iminaries

Set any package specific configuration. Setting the subjects directory and the appropriate matlab command to use. if you want to use a different spm version/path, it should also be entered here. These are currently being set at the class level, so every node will inherit these settings. However, these can also be changed or set for an individual

```
# Tell freesurfer what subjects directory to use
subjects_dir = os.path.abspath('fsdata')
fs.FSCommand.set_default_subjects_dir(subjects_dir)

# Set the way matlab should be called
mlab.MatlabCommand.set_default_matlab_cmd("matlab -nodesktop -nosplash")
# If SPM is not in your MATLAB path you should add it here
mlab.MatlabCommand.set_default_paths('/software/spm8')
```

19.2.2 eprocessing workflow

```
preproc = pe.Workflow(name='preproc')
```

Use `nipyne.interfaces.spm.Realign` for motion correction and register all images to the mean image.

```
realign = pe.Node(interface=spm.Realign(), name="realign")
realign.inputs.register_to_mean = True
```

Use `nipyne.algorithms.rapidart` to determine which of the images in the functional series are outliers based on deviations in intensity or movement.

```
art = pe.Node(interface=ra.ArtifactDetect(), name="art")
art.inputs.use_differences = [True, False]
art.inputs.use_norm = True
art.inputs.norm_threshold = 1
art.inputs.zintensity_threshold = 3
art.inputs.mask_type = 'file'
art.inputs.parameter_source = 'SPM'
```

Use `nipyne.interfaces.freesurfer.BBRegister` to coregister the mean functional image generated by `realign` to the subjects' surfaces.

```
surfregister = pe.Node(interface=fs.BBRegister(), name='surfregister')
surfregister.inputs.init = 'fsl'
surfregister.inputs.contrast_type = 't2'
```

Use `nipyne.interfaces.io.FreeSurferSource` to retrieve various image files that are automatically generated by the recon-all process.

```
FreeSurferSource = pe.Node(interface=nio.FreeSurferSource(), name='fssource')
```

Use `nipyne.interfaces.freesurfer.ApplyVolTransform` to convert the brainmask generated by `freesurfer` into the realigned functional space.

```
ApplyVolTransform = pe.Node(interface=fs.ApplyVolTransform(), name='applyreg')
ApplyVolTransform.inputs.inverse = True
```

Use `nipyne.interfaces.freesurfer.Binarize` to extract a binary brain mask.


```
Threshold = pe.Node(interface=fs.Binarize(), name='threshold')
Threshold.inputs.min = 10
Threshold.inputs.out_type = 'nii'
```

Two different types of functional data smoothing are performed in this workflow. The volume smoothing option performs a standard SPM smoothin. using `nipyne.interfaces.spm.Smooth`. In addition, we use a smoothing routine from freesurfer (`nipyne.interfaces.freesurfer.Binarize`) to project the functional data from the volume to the subjects' surface, smooth it on the surface and fit it back into the volume forming the cortical ribbon. The projection uses the average value along a "cortical column". In addition to the surface smoothing, the rest of the volume is smoothed with a 3d gaussian kernel.

Note: It is very important to note that the projection to the surface takes a 3d manifold to a 2d manifold. Hence the reverse projection, simply fills the thickness of cortex with the smoothed data. The smoothing is not performed in a depth specific manner. The output of this branch should only be used for surface-based analysis and visualization.

```
volsmooth = pe.Node(interface=spm.Smooth(), name="volsmooth")
surfsmooth = pe.MapNode(
    interface=fs.Smooth(proj_frac_avg=(0, 1, 0.1)),
    name="surfsmooth",
    iterfield=['in_file'])
```

We connect up the different nodes to implement the preprocessing workflow.

```
preproc.connect([
    (realign, surfregister, [('mean_image', 'source_file')]),
    (FreeSurferSource, ApplyVolTransform, [('brainmask', 'target_file')]),
    (surfregister, ApplyVolTransform, [('out_reg_file', 'reg_file')]),
    (realign, ApplyVolTransform, [('mean_image', 'source_file')]),
    (ApplyVolTransform, Threshold, [('transformed_file', 'in_file')]),
    (realign, art, [('realignment_parameters', 'realignment_parameters'),
        ('realigned_files', 'realigned_files')]),
    (Threshold, art, [('binary_file', 'mask_file')]),
    (realign, volsmooth, [('realigned_files', 'in_files')]),
    (realign, surfsmooth, [('realigned_files', 'in_file')]),
    (surfregister, surfsmooth, [('out_reg_file', 'reg_file')]),
])
```

19.2.3 Set up volume analysis workflow

```
volanalysis = pe.Workflow(name='volanalysis')
```

Generate SPM-specific design information using `nipyne.interfaces.spm.SpecifyModel`.

```
modelspec = pe.Node(interface=model.SpecifySPMModel(), name="modelspec")
modelspec.inputs.concatenate_runs = True
```

Generate a first level SPM.mat file for analysis `nipyne.interfaces.spm.Level1Design`.

```
levelldesign = pe.Node(interface=spm.Level1Design(), name="levelldesign")
levelldesign.inputs.bases = {'hrf': {'derivs': [0, 0]}}
```

Use `nipyne.interfaces.spm.EstimateModel` to determine the parameters of the model.

```
levelleestimate = pe.Node(interface=spm.EstimateModel(), name="levelleestimate")
levelleestimate.inputs.estimate_method = {'Classical': 1}
```

Use `nipyype.interfaces.spm.EstimateContrast` to estimate the first level contrasts specified in a few steps above.

```
contrastestimate = pe.Node(
    interface=spm.EstimateContrast(), name="contrastestimate")

volanalysis.connect([
    (modelspec, levelldesign, [('session_info', 'session_info')]),
    (levelldesign, levellestimate, [('spm_mat_file', 'spm_mat_file')]),
    (levellestimate, contrastestimate,
     [('spm_mat_file', 'spm_mat_file'), ('beta_images', 'beta_images'),
      ('residual_image', 'residual_image')]),
])
```

19.2.4 Set up surface analysis workflow

We simply clone the volume analysis workflow.

```
surfanalysis = volanalysis.clone(name='surfanalysis')
```

19.2.5 Set up volume normalization workflow

The volume analysis is performed in individual space. Therefore, post analysis we normalize the contrast images to MNI space.

```
volnorm = pe.Workflow(name='volnormconimages')
```

Use `nipyype.interfaces.freesurfer.MRISConvert` to convert the brainmask, an mgz file and the contrast images (nifti-1 img/hdr pairs), to single volume nifti images.

```
convert = pe.Node(interface=fs.MRISConvert(out_type='nii'), name='convert2nii')
convert2 = pe.MapNode(
    interface=fs.MRISConvert(out_type='nii'),
    iterfield=['in_file'],
    name='convertimg2nii')
```

Use `nipyype.interfaces.spm.Segment` to segment the structural image and generate the transformation file to MNI space.

Note: Segment takes longer than usual because the nose is wrapped behind the head in the structural image.

```
segment = pe.Node(interface=spm.Segment(), name='segment')
```

Use `nipyype.interfaces.freesurfer.ApplyVolTransform` to convert contrast images into freesurfer space.

```
normwreg = pe.MapNode(
    interface=fs.ApplyVolTransform(),
    iterfield=['source_file'],
    name='applyreg2con')
```

Use `nipyype.interfaces.spm.Normalize` to normalize the contrast images to MNI space

```
normalize = pe.Node(interface=spm.Normalize(jobtype='write'), name='norm2mni')
```

Connect up the volume normalization components

```
volnorm.connect([
    (convert, segment, [('out_file', 'data')]),
    (convert2, normwreg, [('out_file', 'source_file')]),
    (segment, normalize, [('transformation_mat', 'parameter_file')]),
    (normwreg, normalize, [('transformed_file', 'apply_to_files')]),
])
```

19.2.6 Preproc + Analysis + VolumeNormalization workflow

Connect up the lower level workflows into an integrated analysis. In addition, we add an input node that specifies all the inputs needed for this workflow. Thus, one can import this workflow and connect it to their own data sources. An example with the nifti-tutorial data is provided below.

For this workflow the only necessary inputs are the functional images, a freesurfer subject id corresponding to recon-all processed data, the session information for the functional runs and the contrasts to be evaluated.

```
inputnode = pe.Node(
    interface=util.IdentityInterface(
        fields=['func', 'subject_id', 'session_info', 'contrasts']),
    name='inputnode')
```

Connect the components into an integrated workflow.

```
l1pipeline = pe.Workflow(name='firstlevel')
l1pipeline.connect([
    (inputnode, preproc, [
        ('func', 'realigned.in_files'),
        ('subject_id', 'surfregister.subject_id'),
        ('subject_id', 'fssource.subject_id'),
    ]),
    (inputnode, volanalysis, [('session_info', 'modelspec.subject_info'),
                             ('contrasts', 'contrastestimate.contrasts')]),
    (inputnode, surfanalysis, [('session_info', 'modelspec.subject_info'),
                              ('contrasts', 'contrastestimate.contrasts')]),
])

# attach volume and surface model specification and estimation components
l1pipeline.connect([
    (preproc, volanalysis, [
        ('realigned.realignment_parameters', 'modelspec.realignment_parameters'),
        ('volsmooth.smoothed_files', 'modelspec.functional_runs'),
        ('art.outlier_files', 'modelspec.outlier_files'),
        ('threshold.binary_file', 'levelldesign.mask_image')]),
    (preproc, surfanalysis, [
        ('realigned.realignment_parameters', 'modelspec.realignment_parameters'),
        ('surfsmooth.smoothed_file', 'modelspec.functional_runs'),
        ('art.outlier_files', 'modelspec.outlier_files'),
        ('threshold.binary_file', 'levelldesign.mask_image')])])

# attach volume contrast normalization components
l1pipeline.connect([
    (preproc, volnorm, [
        ('fssource.orig', 'convert2nii.in_file'),
        ('surfregister.out_reg_file', 'applyreg2con.reg_file'),
        ('fssource.orig', 'applyreg2con.target_file')]),
    (volanalysis, volnorm, [
        ('contrastestimate.con_images',
```

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```
        'convertimg2nii.in_file'),
    ]))
```

The nipyne tutorial contains data for two subjects. Subject data is in two subdirectories, `s1` and `s2`. Each subject directory contains four functional volumes: `f3.nii`, `f5.nii`, `f7.nii`, `f10.nii`. And mical volume named `struct.nii`. Below we set some variables to inform the `datasource` about the layout of our data. We specify the location of the data, the subject sub-directories and a dictionary that maps each run to a mnemonic (or field) for the run type (`struct` or `func`). These fields become the output fields of the `datasource` node in the pipeline. In the example below, run ‘f3’ is of type ‘func’ and gets mapped to a nifti filename through a template ‘`%s.nii`’. So ‘f3’ would become

```
# Specify the location of the data.
data_dir = os.path.abspath('data')
# Specify the subject directories
subject_list = ['s1', 's3']
# Map field names to individual subject runs.
info = dict(
    func=[['subject_id', ['f3', 'f5', 'f7', 'f10']]],
    struct=[['subject_id', 'struct']])

infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")
```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

Now we create a `nipyne.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipyne.pipeline.NodeWrapper` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```
datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=['func', 'struct']),
    name='datasource')
datasource.inputs.base_directory = data_dir
datasource.inputs.template = '%s/%s.nii'
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True
```

19.2.7 Set preprocessing parameters

```
l1pipeline.inputs.preproc.fsssource.subjects_dir = subjects_dir
l1pipeline.inputs.preproc.volsmooth.fwhm = 4
l1pipeline.inputs.preproc.surfsmooth.surface_fwhm = 5
l1pipeline.inputs.preproc.surfsmooth.vol_fwhm = 4
```

19.2.8 Experimental paradigm specific components

Here we create a function that returns subject-specific information about the experimental paradigm. This is used by the `nipyne.interfaces.spm.SpecifyModel` to create the information necessary to generate an SPM design matrix. In this tutorial, the same paradigm was used for every participant.

```
def subjectinfo(subject_id):
    from nipyne.interfaces.base import Bunch
    from copy import deepcopy
    print("Subject ID: %s\n" % str(subject_id))
    output = []
    names = ['Task-Odd', 'Task-Even']
    for r in range(4):
        onsets = [list(range(15, 240, 60)), list(range(45, 240, 60))]
        output.insert(r,
                      Bunch(
                          conditions=names,
                          onsets=deepcopy(onsets),
                          durations=[[15] for s in names],
                      ))
    return output
```

Setup the contrast structure that needs to be evaluated. This is a list of lists. The inner list specifies the contrasts and has the following format - [Name,Stat,[list of condition names],[weights on those conditions]]. The condition names must match the *names* listed in the *subjectinfo* function described above.

```
cont1 = ('Task>Baseline', 'T', ['Task-Odd', 'Task-Even'], [0.5, 0.5])
cont2 = ('Task-Odd>Task-Even', 'T', ['Task-Odd', 'Task-Even'], [1, -1])
contrasts = [cont1, cont2]
```

19.2.9 Set up node specific inputs

We replicate the modelspec parameters separately for the surface- and volume-based analysis.

```
modelspecref = llpipeline.inputs.volanalysis.modelspec
modelspecref.input_units = 'secs'
modelspecref.time_repetition = 3.
modelspecref.high_pass_filter_cutoff = 120

modelspecref = llpipeline.inputs.surfanalysis.modelspec
modelspecref.input_units = 'secs'
modelspecref.time_repetition = 3.
modelspecref.high_pass_filter_cutoff = 120

l1designref = llpipeline.inputs.volanalysis.level1design
l1designref.timing_units = modelspecref.output_units
l1designref.interscan_interval = modelspecref.time_repetition

l1designref = llpipeline.inputs.surfanalysis.level1design
l1designref.timing_units = modelspecref.output_units
l1designref.interscan_interval = modelspecref.time_repetition

llpipeline.inputs.inputnode.contrasts = contrasts
```

19.2.10 Setup the pipeline

The nodes created above do not describe the flow of data. They merely describe the parameters used for each function. In this section we setup the connections between the nodes such that appropriate outputs from nodes are piped into appropriate inputs of other nodes.

Use the `nipyne.pipeline.engine.Workflow` to create a graph-based execution pipeline for first level analysis.

```

level1 = pe.Workflow(name="level1")
level1.base_dir = os.path.abspath('volsurf_tutorial/workingdir')

level1.connect([
    (infosource, datasource, [('subject_id', 'subject_id')]),
    (datasource, l1pipeline, [('func', 'inputnode.func')]),
    (infosource, l1pipeline, [('subject_id', 'inputnode.subject_id'),
                              (('subject_id', subjectinfo),
                               'inputnode.session_info')]),
])

```

19.2.11 Store the output

Create a datasink node to store the contrast images and registration info

```

datasink = pe.Node(interface=nio.DataSink(), name="datasink")
datasink.inputs.base_directory = os.path.abspath('volsurf_tutorial/l1out')
datasink.inputs.substitutions = []

def getsubs(subject_id):
    subs = [('subject_id_%s/' % subject_id, '')]
    return subs

# store relevant outputs from various stages of the 1st level analysis
level1.connect([(infosource, datasink, [('subject_id', 'container'),
                                         (('subject_id', getsubs),
                                          'substitutions')]),
                (l1pipeline, datasink, [
                    ('surfanalysis.contrastestimate.con_images', 'contrasts'),
                    ('preproc.surfregister.out_reg_file', 'registrations'),
                ])])

```

Run the analysis pipeline and also create a dot+png (if graphviz is available) rkflow.

```

if __name__ == '__main__':
    level1.run()
    level1.write_graph(graph2use='flat')

```

19.2.12 Level2 surface-based pipeline

Create a level2 workflow

```

l2flow = pe.Workflow(name='l2out')
l2flow.base_dir = os.path.abspath('volsurf_tutorial')

```

Setup a dummy node to iterate over contrasts and hemispheres

```

l2inputnode = pe.Node(
    interface=util.IdentityInterface(fields=['contrasts', 'hemi']),
    name='inputnode')
l2inputnode.iterables = [('contrasts', list(range(1,
                                                  len(contrasts) + 1))),
                        ('hemi', ['lh', 'rh'])]

```

Use a datagrabber node to collect contrast images and registration files

```

l2source = pe.Node(
    interface=nio.DataGrabber(infields=['con_id'], outfields=['con', 'reg']),
    name='l2source')
l2source.inputs.base_directory = os.path.abspath('volsurf_tutorial/11out')
l2source.inputs.template = '*'
l2source.inputs.field_template = dict(
    con='*/contrasts/con_%04d.img', reg='*/registrations/*.dat')
l2source.inputs.template_args = dict(con=[['con_id']], reg=[[]])
l2source.inputs.sort_filelist = True

l2flow.connect(l2inputnode, 'contrasts', l2source, 'con_id')

```

Merge contrast images and registration files

```

mergenode = pe.Node(interface=util.Merge(2, axis='hstack'), name='merge')

def ordersubjects(files, subj_list):
    outlist = []
    for s in subj_list:
        for f in files:
            if '/%s/' % s in f:
                outlist.append(f)
            continue
    print(outlist)
    return outlist

l2flow.connect(l2source, ('con', ordersubjects, subject_list), mergenode,
               'in1')
l2flow.connect(l2source, ('reg', ordersubjects, subject_list), mergenode,
               'in2')

```

Concatenate contrast images projected to fsaverage

```

l2concat = pe.Node(interface=fs.MRISPreproc(), name='concat')
l2concat.inputs.target = 'fsaverage'
l2concat.inputs.fwhm = 5

def list2tuple(listoflist):
    return [tuple(x) for x in listoflist]

l2flow.connect(l2inputnode, 'hemi', l2concat, 'hemi')
l2flow.connect(mergenode, ('out', list2tuple), l2concat, 'vol_measure_file')

```

Perform a one sample t-test

```

l2ttest = pe.Node(interface=fs.OneSampleTTest(), name='onesample')
l2flow.connect(l2concat, 'out_file', l2ttest, 'in_file')

```

Run the analysis pipeline and also create a dot+png (if graphviz is available) that visually represents the workflow.

```

if __name__ == '__main__':
    l2flow.run()
    l2flow.write_graph(graph2use='flat')

```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

A workflow that uses fsl to perform a first level analysis on the nipype tutorial data set:

```
python fmri_fsl.py
```

First tell python where to find the appropriate functions.

```
from __future__ import print_function
from __future__ import division
from builtins import str
from builtins import range

import os # system functions

import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.fsl as fsl # fsl
import nipype.interfaces.utility as util # utility
import nipype.pipeline.engine as pe # pypeline engine
import nipype.algorithms.modelgen as model # model generation
import nipype.algorithms.rapidart as ra # artifact detection
```

20.1 Preliminaries

Setup any package specific configuration. The output file format for FSL routines is being set to compressed NIFTI.

```
fsl.FSLCommand.set_default_output_type('NIFTI_GZ')
```

20.2 Setting up workflows

In this tutorial we will be setting up a hierarchical workflow for fsl analysis. This will demonstrate how pre-defined workflows can be setup and shared across users, projects and labs.

20.3 Setup preprocessing workflow

This is a generic fsl feat preprocessing workflow encompassing skull stripping, motion correction and smoothing operations.

```
preproc = pe.Workflow(name='preproc')
```

Set up a node to define all inputs required for the preprocessing workflow

```
inputnode = pe.Node(
    interface=util.IdentityInterface(fields=[
        'func',
        'struct',
    ]),
    name='inputspec')
```

Convert functional images to float representation. Since there can be more than one functional run we use a MapNode to convert each run.

```
img2float = pe.MapNode(
    interface=fsl.ImageMaths(
        out_data_type='float', op_string='', suffix='_dtype'),
    iterfield=['in_file'],
    name='img2float')
preproc.connect(inputnode, 'func', img2float, 'in_file')
```

Extract the middle volume of the first run as the reference

```
extract_ref = pe.Node(interface=fsl.ExtractROI(t_size=1), name='extractref')
```

Define a function to pick the first file from a list of files

```
def pickfirst(files):
    if isinstance(files, list):
        return files[0]
    else:
        return files

preproc.connect(img2float, ('out_file', pickfirst), extract_ref, 'in_file')
```

Define a function to return the 1 based index of the middle volume

```
def getmiddlevolume(func):
    from nibabel import load
    from nipy.utils import NUMPY_MMAP
    funcfile = func
    if isinstance(func, list):
        funcfile = func[0]
    _, _, _, timepoints = load(funcfile, mmap=NUMPY_MMAP).shape
    return int(timepoints / 2) - 1

preproc.connect(inputnode, ('func', getmiddlevolume), extract_ref, 't_min')
```

Realign the functional runs to the middle volume of the first run

```
motion_correct = pe.MapNode(
    interface=fsl.MCFLIRT(save_mats=True, save_plots=True),
    name='realign',
    iterfield=['in_file'])
```

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```
preproc.connect(img2float, 'out_file', motion_correct, 'in_file')
preproc.connect(extract_ref, 'roi_file', motion_correct, 'ref_file')
```

Plot the estimated motion parameters

```
plot_motion = pe.MapNode(
    interface=fsl.PlotMotionParams(in_source='fsl'),
    name='plot_motion',
    iterfield=['in_file'])
plot_motion.iterables = ('plot_type', ['rotations', 'translations'])
preproc.connect(motion_correct, 'par_file', plot_motion, 'in_file')
```

Extract the mean volume of the first functional run

```
meanfunc = pe.Node(
    interface=fsl.ImageMaths(op_string='-Tmean', suffix='_mean'),
    name='meanfunc')
preproc.connect(motion_correct, ('out_file', pickfirst), meanfunc, 'in_file')
```

Strip the skull from the mean functional to generate a mask

```
meanfuncmask = pe.Node(
    interface=fsl.BET(mask=True, no_output=True, frac=0.3),
    name='meanfuncmask')
preproc.connect(meanfunc, 'out_file', meanfuncmask, 'in_file')
```

Mask the functional runs with the extracted mask

```
maskfunc = pe.MapNode(
    interface=fsl.ImageMaths(suffix='_bet', op_string='-mas'),
    iterfield=['in_file'],
    name='maskfunc')
preproc.connect(motion_correct, 'out_file', maskfunc, 'in_file')
preproc.connect(meanfuncmask, 'mask_file', maskfunc, 'in_file2')
```

Determine the 2nd and 98th percentile intensities of each functional run

```
getthresh = pe.MapNode(
    interface=fsl.ImageStats(op_string='-p 2 -p 98'),
    iterfield=['in_file'],
    name='getthreshold')
preproc.connect(maskfunc, 'out_file', getthresh, 'in_file')
```

Threshold the first run of the functional data at 10% of the 98th percentile

```
threshold = pe.Node(
    interface=fsl.ImageMaths(out_data_type='char', suffix='_thresh'),
    name='threshold')
preproc.connect(maskfunc, ('out_file', pickfirst), threshold, 'in_file')
```

Define a function to get 10% of the intensity

```
def getthresshop(thresh):
    return '-thr %.10f -Tmin -bin' % (0.1 * thresh[0][1])

preproc.connect(getthresh, ('out_stat', getthresshop), threshold, 'op_string')
```

Determine the median value of the functional runs using the mask

```
medianval = pe.MapNode(
    interface=fsl.ImageStats(op_string='-k %s -p 50'),
    iterfield=['in_file'],
    name='medianval')
preproc.connect(motion_correct, 'out_file', medianval, 'in_file')
preproc.connect(threshold, 'out_file', medianval, 'mask_file')
```

Dilate the mask

```
dilatemask = pe.Node(
    interface=fsl.ImageMaths(suffix='_dil', op_string='-dilF'),
    name='dilatemask')
preproc.connect(threshold, 'out_file', dilatemask, 'in_file')
```

Mask the motion corrected functional runs with the dilated mask

```
maskfunc2 = pe.MapNode(
    interface=fsl.ImageMaths(suffix='_mask', op_string='-mas'),
    iterfield=['in_file'],
    name='maskfunc2')
preproc.connect(motion_correct, 'out_file', maskfunc2, 'in_file')
preproc.connect(dilatemask, 'out_file', maskfunc2, 'in_file2')
```

Determine the mean image from each functional run

```
meanfunc2 = pe.MapNode(
    interface=fsl.ImageMaths(op_string='-Tmean', suffix='_mean'),
    iterfield=['in_file'],
    name='meanfunc2')
preproc.connect(maskfunc2, 'out_file', meanfunc2, 'in_file')
```

Merge the median values with the mean functional images into a coupled list

```
mergenode = pe.Node(interface=util.Merge(2, axis='hstack'), name='merge')
preproc.connect(meanfunc2, 'out_file', mergenode, 'in1')
preproc.connect(medianval, 'out_stat', mergenode, 'in2')
```

Smooth each run using SUSAN with the brightness threshold set to 75% of the median value for each run and a mask constituting the mean functional

```
smooth = pe.MapNode(
    interface=fsl.SUSAN(),
    iterfield=['in_file', 'brightness_threshold', 'usans'],
    name='smooth')
```

Define a function to get the brightness threshold for SUSAN

```
def getbtthresh(medianvals):
    return [0.75 * val for val in medianvals]

def getusans(x):
    return [[tuple([val[0], 0.75 * val[1]])] for val in x]

preproc.connect(maskfunc2, 'out_file', smooth, 'in_file')
preproc.connect(medianval, ('out_stat', getbtthresh), smooth,
    'brightness_threshold')
preproc.connect(mergenode, ('out', getusans), smooth, 'usans')
```

Mask the smoothed data with the dilated mask

```
maskfunc3 = pe.MapNode(
    interface=fsl.ImageMaths(suffix='_mask', op_string='-mas'),
    iterfield=['in_file'],
    name='maskfunc3')
preproc.connect(smooth, 'smoothed_file', maskfunc3, 'in_file')
preproc.connect(dilatemask, 'out_file', maskfunc3, 'in_file2')
```

Scale each volume of the run so that the median value of the run is set to 10000

```
intnorm = pe.MapNode(
    interface=fsl.ImageMaths(suffix='_intnorm'),
    iterfield=['in_file', 'op_string'],
    name='intnorm')
preproc.connect(maskfunc3, 'out_file', intnorm, 'in_file')
```

Define a function to get the scaling factor for intensity normalization

```
def getinormscale(medianvals):
    return ['-mul %.10f' % (10000. / val) for val in medianvals]

preproc.connect(medianval, ('out_stat', getinormscale), intnorm, 'op_string')
```

Perform temporal highpass filtering on the data

```
highpass = pe.MapNode(
    interface=fsl.ImageMaths(suffix='_tempfilt'),
    iterfield=['in_file'],
    name='highpass')
preproc.connect(intnorm, 'out_file', highpass, 'in_file')
```

Generate a mean functional image from the first run

```
meanfunc3 = pe.MapNode(
    interface=fsl.ImageMaths(op_string='-Tmean', suffix='_mean'),
    iterfield=['in_file'],
    name='meanfunc3')
preproc.connect(highpass, ('out_file', pickfirst), meanfunc3, 'in_file')
```

Strip the structural image and coregister the mean functional image to the structural image

```
nosestrip = pe.Node(interface=fsl.BET(frac=0.3), name='nosestrip')
skullstrip = pe.Node(interface=fsl.BET(mask=True), name='stripstruct')

coregister = pe.Node(interface=fsl.FLIRT(dof=6), name='coregister')
```

Use `nipype.algorithms.rapidart` to determine which of the images in the functional series are outliers based on deviations in intensity and/or movement.

```
art = pe.MapNode(
    interface=ra.ArtifactDetect(
        use_differences=[True, False],
        use_norm=True,
        norm_threshold=1,
        zintensity_threshold=3,
        parameter_source='FSL',
        mask_type='file'),
    iterfield=['realigned_files', 'realignment_parameters'],
    name="art")
```

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```
preproc.connect([
    (inputnode, nosestrip, [('struct', 'in_file')]),
    (nosestrip, skullstrip, [('out_file', 'in_file')]),
    (skullstrip, coregister, [('out_file', 'in_file')]),
    (meanfunc2, coregister, [(['out_file', pickfirst), 'reference']]),
    (motion_correct, art, [(['par_file', 'realignment_parameters')]),
    (maskfunc2, art, [(['out_file', 'realigned_files')]),
    (dilatmask, art, [(['out_file', 'mask_file')]),
])
```

20.4 Set up model fitting workflow

```
modelfit = pe.Workflow(name='modelfit')
```

Use `nipyype.algorithms.modelgen.SpecifyModel` to generate design information.

```
modelspec = pe.Node(interface=model.SpecifyModel(), name="modelspec")
```

Use `nipyype.interfaces.fsl.Level1Design` to generate a run specific fsf file for analysis

```
levelldesign = pe.Node(interface=fsl.Level1Design(), name="levelldesign")
```

Use `nipyype.interfaces.fsl.FEATModel` to generate a run specific mat file for use by FILMGLS

```
modelgen = pe.MapNode(
    interface=fsl.FEATModel(),
    name='modelgen',
    iterfield=['fsf_file', 'ev_files'])
```

Use `nipyype.interfaces.fsl.FILMGLS` to estimate a model specified by a mat file and a functional run

```
modelestimate = pe.MapNode(
    interface=fsl.FILMGLS(smooth_autocorr=True, mask_size=5, threshold=1000),
    name='modelestimate',
    iterfield=['design_file', 'in_file'])
```

Use `nipyype.interfaces.fsl.ContrastMgr` to generate contrast estimates

```
conestimate = pe.MapNode(
    interface=fsl.ContrastMgr(),
    name='conestimate',
    iterfield=[
        'tcon_file', 'param_estimates', 'sigmasquareds', 'corrections',
        'dof_file'
    ])

modelfit.connect([
    (modelspec, levelldesign, [('session_info', 'session_info')]),
    (levelldesign, modelgen, [(['fsf_files', 'fsf_file'), ('ev_files',
                                                                    'ev_files')]),
    (modelgen, modelestimate, [(['design_file', 'design_file')]),
    (modelgen, conestimate, [(['con_file', 'tcon_file')]),
    (modelestimate, conestimate,
        [(['param_estimates', 'param_estimates'), ('sigmasquareds',
                                                                    'sigmasquareds'),
        ('corrections', 'corrections'), ('dof_file', 'dof_file')]),
])
```

20.5 Set up fixed-effects workflow

```
fixed_fx = pe.Workflow(name='fixedfx')
```

Use `nipyre.interfaces.fsl.Merge` to merge the copes and varcopes for each condition

```
copemerge = pe.MapNode(
    interface=fsl.Merge(dimension='t'),
    iterfield=['in_files'],
    name="copemerge")

varcopemerge = pe.MapNode(
    interface=fsl.Merge(dimension='t'),
    iterfield=['in_files'],
    name="varcopemerge")
```

Use `nipyre.interfaces.fsl.L2Model` to generate subject and condition specific level 2 model design files

```
level2model = pe.Node(interface=fsl.L2Model(), name='l2model')
```

Use `nipyre.interfaces.fsl.FLAMEO` to estimate a second level model

```
flameo = pe.MapNode(
    interface=fsl.FLAMEO(run_mode='fe'),
    name="flameo",
    iterfield=['cope_file', 'var_cope_file'])

fixed_fx.connect([
    (copemerge, flameo, [('merged_file', 'cope_file')]),
    (varcopemerge, flameo, [('merged_file', 'var_cope_file')]),
    (level2model, flameo, [('design_mat', 'design_file'),
                          ('design_con', 't_con_file'), ('design_grp',
                                                        'cov_split_file')]),
])
```

20.6 Set up first-level workflow

```
def sort_copes(files):
    numelements = len(files[0])
    outfiles = []
    for i in range(numelements):
        outfiles.insert(i, [])
        for j, elements in enumerate(files):
            outfiles[i].append(elements[i])
    return outfiles

def num_copes(files):
    return len(files)

firstlevel = pe.Workflow(name='firstlevel')
firstlevel.connect(
    [(preproc, modelfit, [('highpass.out_file', 'modelspec.functional_runs'),
                          ('art.outlier_files', 'modelspec.outlier_files'),
```

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```

        ('highpass.out_file', 'modelestimate.in_file'))],
    (preproc, fixed_fx,
     [('coregister.out_file', 'flameo.mask_file')]), (modelfit, fixed_fx, [
        (('conestimate.copes', sort_copes), 'copemerge.in_files'),
        (('conestimate.varcopes', sort_copes), 'varcopemerge.in_files'),
        (('conestimate.copes', num_copes), 'l2model.num_copes'),
    ]))

```

20.7 Experiment specific components

The nipy tutorial contains data for two subjects. Subject data is in two subdirectories, `s1` and `s2`. Each subject directory contains four functional volumes: `f3.nii`, `f5.nii`, `f7.nii`, `f10.nii`. And one anatomical volume named `struct.nii`.

Below we set some variables to inform the `datasource` about the layout of our data. We specify the location of the data, the subject sub-directories and a dictionary that maps each run to a mnemonic (or field) for the run type (`struct` or `func`). These fields become the output fields of the `datasource` node in the pipeline.

In the example below, run 'f3' is of type 'func' and gets mapped to a nifti filename through a template '%s.nii'. So 'f3' would become 'f3.nii'.

```

# Specify the location of the data.
data_dir = os.path.abspath('data')
# Specify the subject directories
subject_list = ['s1'] # , 's3']
# Map field names to individual subject runs.
info = dict(
    func=[['subject_id', ['f3', 'f5', 'f7', 'f10']]],
    struct=[['subject_id', 'struct']])

infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")

```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

Now we create a `nipy.interfaces.io.DataSource` object and fill in the information from above about the layout of our data. The `nipy.pipeline.NodeWrapper` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```

datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=['func', 'struct']),
    name='datasource')
datasource.inputs.base_directory = data_dir
datasource.inputs.template = '%s/%s.nii'
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True

```

Use the `get_node` function to retrieve an internal node by name. Then set the iterables on this node to perform two different extents of smoothing.

```

smoothnode = firstlevel.get_node('preproc.smooth')
assert (str(smoothnode) == 'preproc.smooth')

```

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```
smoothnode.iterables = ('fwhm', [5., 10.])

hpcutoff = 120
TR = 3. # ensure float
firstlevel.inputs.preproc.highpass.suffix = '_hpf'
firstlevel.inputs.preproc.highpass.op_string = '-bptf %d -1' % (hpcutoff / TR)
```

Setup a function that returns subject-specific information about the experimental paradigm. This is used by the `nipy.interfaces.spm.SpecifyModel` to create the information necessary to generate an SPM design matrix. In this tutorial, the same paradigm was used for every participant. Other examples of this function are available in the `doc/examples` folder. Note: Python knowledge required here.

```
def subjectinfo(subject_id):
    from nipy.interfaces.base import Bunch
    from copy import deepcopy
    print("Subject ID: %s\n" % str(subject_id))
    output = []
    names = ['Task-Odd', 'Task-Even']
    for r in range(4):
        onsets = [list(range(15, 240, 60)), list(range(45, 240, 60))]
        output.insert(r,
                      Bunch(
                          conditions=names,
                          onsets=deepcopy(onsets),
                          durations=[[15] for s in names],
                          amplitudes=None,
                          tmod=None,
                          pmod=None,
                          regressor_names=None,
                          regressors=None))

    return output
```

Setup the contrast structure that needs to be evaluated. This is a list of lists. The inner list specifies the contrasts and has the following format - [Name,Stat,[list of condition names],[weights on those conditions]]. The condition names must match the *names* listed in the *subjectinfo* function described above.

```
cont1 = ['Task>Baseline', 'T', ['Task-Odd', 'Task-Even'], [0.5, 0.5]]
cont2 = ['Task-Odd>Task-Even', 'T', ['Task-Odd', 'Task-Even'], [1, -1]]
cont3 = ['Task', 'F', [cont1, cont2]]
contrasts = [cont1, cont2]

firstlevel.inputs.modelfit.modelspec.input_units = 'secs'
firstlevel.inputs.modelfit.modelspec.time_repetition = TR
firstlevel.inputs.modelfit.modelspec.high_pass_filter_cutoff = hpcutoff

firstlevel.inputs.modelfit.level1design.interscan_interval = TR
firstlevel.inputs.modelfit.level1design.bases = {'dgamma': {'derivs': False}}
firstlevel.inputs.modelfit.level1design.contrasts = contrasts
firstlevel.inputs.modelfit.level1design.model_serial_correlations = True
```

20.7.1 Set up complete workflow

```
l1pipeline = pe.Workflow(name="level1")
l1pipeline.base_dir = os.path.abspath('./fsl/workingdir')
l1pipeline.config = {
    "execution": {
```

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```
        "crashdump_dir": os.path.abspath('./fsl/crashdumps')
    }
}

llpipeline.connect([
    (infosource, datasource, [('subject_id', 'subject_id')]),
    (infosource, firstlevel, [('subject_id', subjectinfo,
                                'modelfit.modelspec.subject_info')]),
    (datasource, firstlevel, [
        ('struct', 'preproc.inputs.spec.struct'),
        ('func', 'preproc.inputs.spec.func'),
    ]),
])
```

20.8 Execute the pipeline

The code discussed above sets up all the necessary data structures with appropriate parameters and the connectivity between the processes, but does not generate any output. To actually run the analysis on the data the `nipyne.pipeline.engine.Pipeline.Run` function needs to be called.

```
if __name__ == '__main__':
    lllpipeline.write_graph()
    outgraph = lllpipeline.run()
    # lllpipeline.run(plugin='MultiProc', plugin_args={'n_procs':2})
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

CHAPTER 21

fMRI: FEEDS - FSL

A pipeline example that data from the FSL FEEDS set. Single subject, two stimuli.
You can find it at <http://www.fmrib.ox.ac.uk/fsl/feeds/doc/index.html>

```
from __future__ import division
from builtins import range

import os # system functions
from nipy.interfaces import io as nio # Data i/o
from nipy.interfaces import utility as niu # Utilities
from nipy.interfaces import fsl # fsl
from nipy.pipeline import engine as pe # pypeline engine
from nipy.algorithms import modelgen as model # model generation
from nipy.workflows.fmri.fsl import (
    create_featreg_preproc, create_modelfit_workflow, create_reg_workflow)
from nipy.interfaces.base import Bunch
```

21.1 iminaries

Setup any package specific configuration. The output file format for FSL routines is being set to compressed NIFTI.

```
fsl.FSLCommand.set_default_output_type('NIFTI_GZ')
```

21.2 Experiment specific components

This tutorial does a single subject analysis so we are not using infosource and iterables

```
# Specify the location of the FEEDS data. You can find it at http://www.fmrib.ox.
↪ac.uk/fsl/feeds/doc/index.html

inputnode = pe.Node(
    niu.IdentityInterface(fields=['in_data']), name='inputnode')
# Specify the subject directories
```

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```
# Map field names to individual subject runs.
info = dict(func=[['fmri']], struct=[['structural']])
```

Now we create a `nipy.interfaces.io.DataSource` object and fill in the information from above about the layout of our data. The `nipy.pipeline.Node` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```
datasource = pe.Node(
    interface=nio.DataGrabber(outfields=['func', 'struct']), name='datasource')
datasource.inputs.template = 'feeds/data/%s.nii.gz'
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True

preproc = create_featreg_preproc(whichvol='first')
TR = 3.
preproc.inputs.inputspec.fwhm = 5
preproc.inputs.inputspec.highpass = 100. / TR

modelspec = pe.Node(interface=model.SpecifyModel(), name="modelspec")
modelspec.inputs.input_units = 'secs'
modelspec.inputs.time_repetition = TR
modelspec.inputs.high_pass_filter_cutoff = 100
modelspec.inputs.subject_info = [
    Bunch(
        conditions=['Visual', 'Auditory'],
        onsets=[
            list(range(0, int(180 * TR), 60)),
            list(range(0, int(180 * TR), 90))
        ],
        durations=[[30], [45]],
        amplitudes=None,
        tmod=None,
        pmod=None,
        regressor_names=None,
        regressors=None)
]

modelfit = create_modelfit_workflow(f_contrasts=True)
modelfit.inputs.inputspec.interscan_interval = TR
modelfit.inputs.inputspec.model_serial_correlations = True
modelfit.inputs.inputspec.bases = {'dgamma': {'derivs': True}}
cont1 = ['Visual>Baseline', 'T', ['Visual', 'Auditory'], [1, 0]]
cont2 = ['Auditory>Baseline', 'T', ['Visual', 'Auditory'], [0, 1]]
cont3 = ['Task', 'F', [cont1, cont2]]
modelfit.inputs.inputspec.contrasts = [cont1, cont2, cont3]

registration = create_reg_workflow()
registration.inputs.inputspec.target_image = fsl.Info.standard_image(
    'MNI152_T1_2mm.nii.gz')
registration.inputs.inputspec.target_image_brain = fsl.Info.standard_image(
    'MNI152_T1_2mm_brain.nii.gz')
registration.inputs.inputspec.config_file = 'T1_2_MNI152_2mm'
```

21.2.1 Set up complete workflow

```

llpipeline = pe.Workflow(name="level1")
llpipeline.base_dir = os.path.abspath('./fsl_feeds/workingdir')
llpipeline.config = {
    "execution": {
        "crashdump_dir": os.path.abspath('./fsl_feeds/crashdumps')
    }
}

llpipeline.connect(inputnode, 'in_data', datasource, 'base_directory')
llpipeline.connect(datasource, 'func', preproc, 'inputspec.func')
llpipeline.connect(preproc, 'outputspec.highpassed_files', modelspec,
    'functional_runs')
llpipeline.connect(preproc, 'outputspec.motion_parameters', modelspec,
    'realignment_parameters')
llpipeline.connect(modelspec, 'session_info', modelfit,
    'inputspec.session_info')
llpipeline.connect(preproc, 'outputspec.highpassed_files', modelfit,
    'inputspec.functional_data')
llpipeline.connect(preproc, 'outputspec.mean', registration,
    'inputspec.mean_image')
llpipeline.connect(datasource, 'struct', registration,
    'inputspec.anatomical_image')
llpipeline.connect(modelfit, 'outputspec.zfiles', registration,
    'inputspec.source_files')

```

Setup the datasink

```

datasink = pe.Node(
    interface=nio.DataSink(parameterization=False), name="datasink")
datasink.inputs.base_directory = os.path.abspath('./fsl_feeds/llout')
datasink.inputs.substitutions = [
    ('fmri_dtype_mcf_mask_smooth_mask_gms_mean_warp', 'meanfunc')
]
# store relevant outputs from various stages of the 1st level analysis
llpipeline.connect(registration, 'outputspec.transformed_files', datasink,
    'level1.@Z')
llpipeline.connect(registration, 'outputspec.transformed_mean', datasink,
    'meanfunc')

```

21.3 Execute the pipeline

The code discussed above sets up all the necessary data structures with appropriate parameters and the connectivity between the processes, but does not generate any output. To actually run the analysis on the data the `nipyne.pipeline.engine.Pipeline.Run` function needs to be called.

```

if __name__ == '__main__':
    lllpipeline.inputs.inputnode.in_data = os.path.abspath('feeds/data')
    lllpipeline.run()

```

Example source code

You can download the full source code of this example. This same script is also included in the Nipyne source distribution under the `examples` directory.

fMRI: FSL reuse workflows

A workflow that uses fsl to perform a first level analysis on the nipype tutorial data set:

```
python fmri_fsl_reuse.py
```

First tell python where to find the appropriate functions.

```
from __future__ import print_function
from __future__ import division
from builtins import str
from builtins import range

import os # system functions
import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.fsl as fsl # fsl
from nipype.interfaces import utility as niu # Utilities
import nipype.pipeline.engine as pe # pypeline engine
import nipype.algorithms.modelgen as model # model generation
import nipype.algorithms.rapidart as ra # artifact detection

from nipype.workflows.fmri.fsl import (create_featreg_preproc,
                                       create_modelfit_workflow,
                                       create_fixed_effects_flow)
```

22.1 Preliminaries

Setup any package specific configuration. The output file format for FSL routines is being set to compressed NIFTI.

```
fsl.FSLCommand.set_default_output_type('NIFTI_GZ')

level1_workflow = pe.Workflow(name='level1flow')

preproc = create_featreg_preproc(whichvol='first')

modelfit = create_modelfit_workflow()
```

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```
fixed_fx = create_fixed_effects_flow()
```

Add artifact detection and model specification nodes between the preprocessing and modelfitting workflows.

```
art = pe.MapNode(
    ra.ArtifactDetect(
        use_differences=[True, False],
        use_norm=True,
        norm_threshold=1,
        zintensity_threshold=3,
        parameter_source='FSL',
        mask_type='file'),
    iterfield=['realigned_files', 'realignment_parameters', 'mask_file'],
    name="art")

modelspec = pe.Node(model.SpecifyModel(), name="modelspec")

level1_workflow.connect(
    [(preproc, art,
      [('outputspec.motion_parameters', 'realignment_parameters'),
       ('outputspec.realigned_files', 'realigned_files'), ('outputspec.mask',
                                                            'mask_file')]),
     (preproc, modelspec, [('outputspec.highpassed_files', 'functional_runs'),
                           ('outputspec.motion_parameters',
                            'realignment_parameters')]), (art, modelspec,
                                                            [('outlier_files',
                                                             'outlier_files')]),
     (modelspec, modelfit, [('session_info', 'inputspec.session_info')]),
     (preproc, modelfit, [('outputspec.highpassed_files',
                           'inputspec.functional_data')])])
```

22.2 Set up first-level workflow

```
def sort_copes(files):
    numelements = len(files[0])
    outfiles = []
    for i in range(numelements):
        outfiles.insert(i, [])
        for j, elements in enumerate(files):
            outfiles[i].append(elements[i])
    return outfiles

def num_copes(files):
    return len(files)

pickfirst = lambda x: x[0]

level1_workflow.connect(
    [(preproc, fixed_fx, [('outputspec.mask', pickfirst),
                           'flameo.mask_file']),
     (modelfit, fixed_fx, [
         ('outputspec.copes', sort_copes), 'inputspec.copes'),
         ('outputspec.dof_file', 'inputspec.dof_files'),
```

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```
((('outputspec.varcopes', sort_copes), 'inputspec.varcopes'),
 (('outputspec.copes', num_copes), 'l2model.num_copes'),
 ]))
```

22.3 Experiment specific components

The nipy tutorial contains data for two subjects. Subject data is in two subdirectories, `s1` and `s2`. Each subject directory contains four functional volumes: `f3.nii`, `f5.nii`, `f7.nii`, `f10.nii`. And one anatomical volume named `struct.nii`.

Below we set some variables to inform the `datasource` about the layout of our data. We specify the location of the data, the subject sub-directories and a dictionary that maps each run to a mnemonic (or field) for the run type (`struct` or `func`). These fields become the output fields of the `datasource` node in the pipeline.

In the example below, run 'f3' is of type 'func' and gets mapped to a nifti filename through a template '%s.nii'. So 'f3' would become 'f3.nii'.

```
inputnode = pe.Node(
    niu.IdentityInterface(fields=['in_data']), name='inputnode')

# Specify the subject directories
subject_list = ['s1'] # , 's3']
# Map field names to individual subject runs.
info = dict(
    func=[['subject_id', ['f3', 'f5', 'f7', 'f10']],
    struct=[['subject_id', 'struct']])

infosource = pe.Node(
    niu.IdentityInterface(fields=['subject_id']), name="infosource")
```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

Now we create a `nipy.interfaces.io.DataSource` object and fill in the information from above about the layout of our data. The `nipy.pipeline.NodeWrapper` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```
datasource = pe.Node(
    nio.DataGrabber(infields=['subject_id'], outfields=['func', 'struct']),
    name='datasource')
datasource.inputs.template = 'nipy-tutorial/data/%s/%s.nii'
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True
```

Use the `get_node` function to retrieve an internal node by name. Then set the iterables on this node to perform two different extents of smoothing.

```
featininput = level1_workflow.get_node('featpreproc.inputspec')
featininput.iterables = ('fwhm', [5., 10.])

hpcutoff = 120.
TR = 3.
featininput.inputs.highpass = hpcutoff / (2. * TR)
```

Setup a function that returns subject-specific information about the experimental paradigm. This is used by

the `nipyype.modelgen.SpecifyModel` to create the information necessary to generate an SPM design matrix. In this tutorial, the same paradigm was used for every participant. Other examples of this function are available in the `doc/examples` folder. Note: Python knowledge required here.

```
def subjectinfo(subject_id):
    from nipyype.interfaces.base import Bunch
    from copy import deepcopy
    print("Subject ID: %s\n" % str(subject_id))
    output = []
    names = ['Task-Odd', 'Task-Even']
    for r in range(4):
        onsets = [list(range(15, 240, 60)), list(range(45, 240, 60))]
        output.insert(r,
                      Bunch(
                          conditions=names,
                          onsets=deepcopy(onsets),
                          durations=[[15] for s in names]))
    return output
```

Setup the contrast structure that needs to be evaluated. This is a list of lists. The inner list specifies the contrasts and has the following format - [Name,Stat,[list of condition names],[weights on those conditions]]. The condition names must match the *names* listed in the *subjectinfo* function described above.

```
cont1 = ['Task>Baseline', 'T', ['Task-Odd', 'Task-Even'], [0.5, 0.5]]
cont2 = ['Task-Odd>Task-Even', 'T', ['Task-Odd', 'Task-Even'], [1, -1]]
cont3 = ['Task', 'F', [cont1, cont2]]
contrasts = [cont1, cont2]

modelspec.inputs.input_units = 'secs'
modelspec.inputs.time_repetition = TR
modelspec.inputs.high_pass_filter_cutoff = hpcutoff

modelfit.inputs.inputs.spec.interscan_interval = TR
modelfit.inputs.inputs.spec.bases = {'dgamma': {'derivs': False}}
modelfit.inputs.inputs.spec.contrasts = contrasts
modelfit.inputs.inputs.spec.model_serial_correlations = True
modelfit.inputs.inputs.spec.film_threshold = 1000

levell_workflow.base_dir = os.path.abspath('./fsl/workingdir')
levell_workflow.config['execution'] = dict(
    crashdump_dir=os.path.abspath('./fsl/crashdumps'))

levell_workflow.connect([
    (inputnode, datasource, [('in_data', 'base_directory')]),
    (infosource, datasource, [('subject_id', 'subject_id')]),
    (infosource, modelspec, [([('subject_id', subjectinfo), 'subject_info')]),
    (datasource, preproc, [('func', 'inputspec.func')]),
])
```

22.4 Execute the pipeline

The code discussed above sets up all the necessary data structures with appropriate parameters and the connectivity between the processes, but does not generate any output. To actually run the analysis on the data the `nipyype.pipeline.engine.Pipeline.Run` function needs to be called.

```
if __name__ == '__main__':
    # levell_workflow.write_graph()
```

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```
level1_workflow.run()  
# level1_workflow.run(plugin='MultiProc', plugin_args={'n_procs':2})
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

fMRI: NiPy GLM, SPM

The `fmri_nipy_glm.py` integrates several interfaces to perform a first level analysis on a two-subject data set. It is very similar to the `spm_tutorial` with the difference of using `nipy` for fitting GLM model and estimating contrasts. The tutorial can be found in the examples folder. Run the tutorial from inside the `nipy` tutorial directory:

```
python fmri_nipy_glm.py
```

```
from __future__ import print_function
from builtins import str
from builtins import range

from nipy.interfaces.nipy.model import FitGLM, EstimateContrast
from nipy.interfaces.nipy.preprocess import ComputeMask
```

Import necessary modules from `nipy`.

```
import nipy.interfaces.io as nio # Data i/o
import nipy.interfaces.spm as spm # spm
import nipy.interfaces.matlab as mlab # how to run matlab
import nipy.interfaces.utility as util # utility
import nipy.pipeline.engine as pe # pipeline engine
import nipy.algorithms.rapidart as ra # artifact detection
import nipy.algorithms.modelgen as model # model specification
import os # system functions
```

23.1 Preliminaries

Set any package specific configuration. The output file format for FSL routines is being set to uncompressed NIFTI and a specific version of matlab is being used. The uncompressed format is required because SPM does not handle compressed NIFTI.

```
# Set the way matlab should be called
mlab.MatlabCommand.set_default_matlab_cmd("matlab -nodesktop -nosplash")
```

The `nipy` tutorial contains data for two subjects. Subject data is in two subdirectories, `s1` and `s2`. Each subject directory contains four functional volumes: `f3.nii`, `f5.nii`, `f7.nii`, `f10.nii`. And one anatomical volume

named `struct.nii`. Below we set some variables to inform the `datasource` about the layout of our data. We specify the location of the data, the subject sub-directories and a dictionary that maps each run to a mnemonic (or field) for the run type (`struct` or `func`). These fields become the output fields of the `datasource` node in the pipeline. In the example below, run 'f3' is of type 'func' and gets mapped to a nifti filename through a template '%s.nii'. So 'f3' would become

```
# Specify the location of the data.
data_dir = os.path.abspath('data')
# Specify the subject directories
subject_list = ['s1']
# Map field names to individual subject runs.
info = dict(
    func=[['subject_id', ['f3', 'f5', 'f7', 'f10']],
    struct=[['subject_id', 'struct']])

infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")
```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

23.2 Preprocessing pipeline nodes

Now we create a `nipy.interfaces.io.DataSource` object and fill in the information from above about the layout of our data. The `nipy.pipeline.NodeWrapper` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```
datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=['func', 'struct']),
    name='datasource')
datasource.inputs.base_directory = data_dir
datasource.inputs.template = '%s/%s.nii'
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True
```

Use `nipy.interfaces.spm.Realign` for motion correction and register all images to the mean image.

```
realign = pe.Node(interface=spm.Realign(), name="realign")
realign.inputs.register_to_mean = True

compute_mask = pe.Node(interface=ComputeMask(), name="compute_mask")
```

Use `nipy.algorithms.rapidart` to determine which of the images in the functional series are outliers based on deviations in intensity or movement.

```
art = pe.Node(interface=ra.ArtifactDetect(), name="art")
art.inputs.use_differences = [True, False]
art.inputs.use_norm = True
art.inputs.norm_threshold = 1
art.inputs.zintensity_threshold = 3
art.inputs.mask_type = 'file'
art.inputs.parameter_source = 'SPM'
```

Use `nipyne.interfaces.spm.Coregister` to perform a rigid body registration of the functional data to the structural data.

```
coregister = pe.Node(interface=spm.Coregister(), name="coregister")
coregister.inputs.jobtype = 'estimate'
```

Smooth the functional data using `nipyne.interfaces.spm.Smooth`.

```
smooth = pe.Node(interface=spm.Smooth(), name="smooth")
smooth.inputs.fwhm = 4
```

23.3 Set up analysis components

Here we create a function that returns subject-specific information about the experimental paradigm. This is used by the `nipyne.interfaces.spm.SpecifyModel` to create the information necessary to generate an SPM design matrix. In this tutorial, the same paradigm was used for every participant.

```
def subjectinfo(subject_id):
    from nipyne.interfaces.base import Bunch
    from copy import deepcopy
    print("Subject ID: %s\n" % str(subject_id))
    output = []
    names = ['Task-Odd', 'Task-Even']
    for r in range(4):
        onsets = [list(range(15, 240, 60)), list(range(45, 240, 60))]
        output.insert(r,
                      Bunch(
                          conditions=names,
                          onsets=deepcopy(onsets),
                          durations=[[15] for s in names],
                          amplitudes=None,
                          tmod=None,
                          pmod=None,
                          regressor_names=None,
                          regressors=None))
    return output
```

Setup the contrast structure that needs to be evaluated. This is a list of lists. The inner list specifies the contrasts and has the following format - [Name, Stat, [list of condition names], [weights on those conditions]]. The condition names must match the *names* listed in the *subjectinfo* function described above.

```
cont1 = ('Task>Baseline', 'T', ['Task-Odd', 'Task-Even'], [0.5, 0.5])
cont2 = ('Task-Odd>Task-Even', 'T', ['Task-Odd', 'Task-Even'], [1, -1])
contrasts = [cont1, cont2]
```

Generate design information using `nipyne.interfaces.spm.SpecifyModel`. `nipy` accepts only design specified in seconds so “output_units” has always have to be set to “secs”.

```
modelspec = pe.Node(interface=model.SpecifySPMModel(), name="modelspec")
modelspec.inputs.concatenate_runs = True
modelspec.inputs.input_units = 'secs'
modelspec.inputs.output_units = 'secs'
modelspec.inputs.time_repetition = 3.
modelspec.inputs.high_pass_filter_cutoff = 120
```

Fit the GLM model using `nipy` and ordinary least square method

```

model_estimate = pe.Node(interface=FitGLM(), name="model_estimate")
model_estimate.inputs.TR = 3.
model_estimate.inputs.model = "spherical"
model_estimate.inputs.method = "ols"

```

Estimate the contrasts. The format of the contrasts definition is the same as for FSL and SPM

```

contrast_estimate = pe.Node(
    interface=EstimateContrast(), name="contrast_estimate")
cont1 = ('Task>Baseline', 'T', ['Task-Odd', 'Task-Even'], [0.5, 0.5])
cont2 = ('Task-Odd>Task-Even', 'T', ['Task-Odd', 'Task-Even'], [1, -1])
contrast_estimate.inputs.contrasts = [cont1, cont2]

```

23.4 Setup the pipeline

The nodes created above do not describe the flow of data. They merely describe the parameters used for each function. In this section we setup the connections between the nodes such that appropriate outputs from nodes are piped into appropriate inputs of other nodes.

Use the `nipy.pipeline.engine.Pipeline` to create a graph-based execution pipeline for first level analysis. The config options tells the pipeline engine to use *workdir* as the disk location to use when running the processes and keeping their outputs. The *use_parameterized_dirs* tells the engine to create sub-directories under *workdir* corresponding to the iterables in the pipeline. Thus for this pipeline there will be subject specific sub-directories.

The `nipy.pipeline.engine.Pipeline.connect` function creates the links between the processes, i.e., how data should flow in and out of the processing nodes.

```

l1pipeline = pe.Workflow(name="level1")
l1pipeline.base_dir = os.path.abspath('nipy_tutorial/workingdir')

l1pipeline.connect(
    [(infosource, datasource, [('subject_id', 'subject_id')]),
     (datasource, realign, [('func', 'in_files')]), (realign, compute_mask, [
         ('mean_image', 'mean_volume')
     ]), (realign, coregister, [('mean_image', 'source'),
                               ('realigned_files',
                                'apply_to_files')]), (datasource, coregister,
                                                         [
                                                             ('struct', 'target')]),
     (coregister, smooth,
      [
          ('coregistered_files', 'in_files')]), (realign, modelspec, [
          ('realignment_parameters', 'realignment_parameters')
      ]), (smooth, modelspec,
          [
              ('smoothed_files', 'functional_runs')]), (realign, art, [
              ('realignment_parameters', 'realignment_parameters')
          ]), (coregister, art, [
              ('coregistered_files', 'realigned_files')]),
     (compute_mask, art, [
         ('brain_mask', 'mask_file')]), (art, modelspec, [
         ('outlier_files', 'outlier_files')
     ]), (infosource, modelspec, [
         ("subject_id", subjectinfo), "subject_info"
     ]), (modelspec, model_estimate,
          [
              ('session_info', 'session_info')]), (compute_mask, model_estimate,
          [
              ('brain_mask', 'mask')]),
     (model_estimate, contrast_estimate,
      [
          ("beta", "beta"), ("nvbeta", "nvbeta"), ("s2", "s2"), ("dof", "dof"),
          ("axis", "axis"), ("constants", "constants"), ("reg_names",
                                                         "reg_names")
      ]))

```

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```
if __name__ == '__main__':  
    llpipeline.run()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipyype source distribution under the `examples` directory.

Example source code

You can download the full source code of this example. This same script is also included in the Nipyype source distribution under the `examples` directory.

fmRI: Coregistration - Slicer, BRAINS

This is currently not working and will raise an exception in release 0.3. It will be fixed in a later release:

```
python fmri_slicer_coregistration.py
```

```
# raise RuntimeError, 'Slicer not fully implemented'
from nipy.interfaces.slicer import BRAINSFit, BRAINSResample
```

Import necessary modules from nipy.

```
import nipy.interfaces.io as nio # Data i/o
import nipy.interfaces.utility as util # utility
import nipy.pipeline.engine as pe # pypeline engine
import os # system functions
```

24.1 Preliminaries

Confirm package dependencies are installed. (This is only for the tutorial, rarely would you put this in your own code.)

```
from nipy.utils.misc import package_check

package_check('numpy', '1.3', 'tutorial1')
package_check('scipy', '0.7', 'tutorial1')
package_check('IPython', '0.10', 'tutorial1')
```

The nipy tutorial contains data for two subjects. Subject data is in two subdirectories, `s1` and `s2`. Each subject directory contains four functional volumes: `f3.nii`, `f5.nii`, `f7.nii`, `f10.nii`. And one anatomical volume named `struct.nii`.

Below we set some variables to inform the `datasource` about the layout of our data. We specify the location of the data, the subject sub-directories and a dictionary that maps each run to a mnemonic (or field) for the run type (`struct` or `func`). These fields become the output fields of the `datasource` node in the pipeline.

In the example below, run ‘f3’ is of type ‘func’ and gets mapped to a nifti filename through a template ‘%s.nii’. So ‘f3’ would become ‘f3.nii’.

```
# Specify the location of the data.
data_dir = os.path.abspath('data')
```

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```
# Specify the subject directories
subject_list = ['s1', 's3']
# Map field names to individual subject runs.
info = dict(func=[['subject_id', 'f3']], struct=[['subject_id', 'struct']])

infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")
```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

24.2 Preprocessing pipeline nodes

Now we create a `nipy.interfaces.io.DataSource` object and fill in the information from above about the layout of our data. The `nipy.pipeline.NodeWrapper` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```
datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=['func', 'struct']),
    name='datasource')
datasource.inputs.base_directory = data_dir
datasource.inputs.template = '%s/%s.nii'
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True

coregister = pe.Node(interface=BRAINSFit(), name="coregister")
coregister.inputs.outputTransform = True
coregister.inputs.outputVolume = True
coregister.inputs.transformType = ["Affine"]

reslice = pe.Node(interface=BRAINSResample(), name="reslice")
reslice.inputs.outputVolume = True

pipeline = pe.Workflow(name="pipeline")
pipeline.base_dir = os.path.abspath('slicer_tutorial/workingdir')

pipeline.connect([(infosource, datasource, [('subject_id', 'subject_id')]),
                  (datasource, coregister, [('func', 'movingVolume')]),
                  (datasource, coregister,
                   [('struct', 'fixedVolume')]), (coregister, reslice, [
                   ('outputTransform', 'warpTransform')
                   ]), (datasource, reslice, [('func', 'inputVolume')]),
                  (datasource, reslice, [('struct', 'referenceVolume')])])

if __name__ == '__main__':
    pipeline.run()
    pipeline.write_graph()
```

Example source code

You can download the full source code of this example. This same script is also included in

the Nipyte source distribution under the `examples` directory.

The `fmri_spm.py` integrates several interfaces to perform a first and second level analysis on a two-subject data set. The tutorial can be found in the examples folder. Run the tutorial from inside the nipype tutorial directory:

```
python fmri_spm.py
```

Import necessary modules from nipype.

```
from __future__ import print_function
from builtins import str
from builtins import range

import os # system functions

from nipype import config
# config.enable_provenance()

from nipype.interfaces import spm, fsl

# In order to use this example with SPM's matlab common runtime
# matlab_cmd = ('/Users/satra/Downloads/spm8/run_spm8.sh '
#              '/Applications/MATLAB/MATLAB_Compiler_Runtime/v713/ script')
# spm.SPMCommand.set_mlab_paths(matlab_cmd=matlab_cmd, use_mcr=True)

import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.utility as util # utility
import nipype.pipeline.engine as pe # pipeline engine
import nipype.algorithms.rapidart as ra # artifact detection
import nipype.algorithms.modelgen as model # model specification
import nipype.interfaces.matlab as mlab
```

25.1 Preliminaries

Set any package specific configuration. The output file format for FSL routines is being set to uncompressed NIFTI and a specific version of matlab is being used. The uncompressed format is required because SPM does not handle compressed NIFTI.

```
# Tell fsl to generate all output in uncompressed nifti format
fsl.FSLCommand.set_default_output_type('NIFTI')

# Set the way matlab should be called
# import nipy.interfaces.matlab as mlab          # how to run matlab
# mlab.MatlabCommand.set_default_matlab_cmd("matlab -nodesktop -nosplash")

# In case a different path is required
# mlab.MatlabCommand.set_default_paths('/software/matlab/spm12b/spm12b_r5918')
```

The nipy tutorial contains data for two subjects. Subject data is in two subdirectories, `s1` and `s2`. Each subject directory contains four functional volumes: `f3.nii`, `f5.nii`, `f7.nii`, `f10.nii`. And one anatomical volume named `struct.nii`. Below we set some variables to inform the `datasource` about the layout of our data. We specify the location of the data, the subject sub-directories and a dictionary that maps each run to a mnemonic (or field) for the run type (`struct` or `func`). These fields become the output fields of the `datasource` node in the pipeline. In the example below, run `'f3'` is of type `'func'` and gets mapped to a nifti filename through a template `'%s.nii'`. So `'f3'` would become

```
# Specify the location of the data.
data_dir = os.path.abspath('data')
# Specify the subject directories
subject_list = ['s1', 's3']
# Map field names to individual subject runs.
info = dict(
    func=[['subject_id', ['f3', 'f5', 'f7', 'f10']]],
    struct=[['subject_id', 'struct']])

infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")
```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

25.2 Preprocessing pipeline nodes

Now we create a `nipy.interfaces.io.DataSource` object and fill in the information from above about the layout of our data. The `nipy.pipeline.NodeWrapper` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```
datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=['func', 'struct']),
    name='datasource')
datasource.inputs.base_directory = data_dir
datasource.inputs.template = '%s/%s.nii'
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True
```

Use `nipy.interfaces.spm.Realign` for motion correction and register all images to the mean image.

```
realign = pe.Node(interface=spm.Realign(), name="realign")
realign.inputs.register_to_mean = True
```


Use `nipy.algorithms.rapidart` to determine which of the images in the functional series are outliers based on deviations in intensity or movement.

```
art = pe.Node(interface=ra.ArtifactDetect(), name="art")
art.inputs.use_differences = [True, False]
art.inputs.use_norm = True
art.inputs.norm_threshold = 1
art.inputs.zintensity_threshold = 3
art.inputs.mask_type = 'file'
art.inputs.parameter_source = 'SPM'
```

Skull strip structural images using `nipy.interfaces.fsl.BET`.

```
skullstrip = pe.Node(interface=fsl.BET(), name="skullstrip")
skullstrip.inputs.mask = True
```

Use `nipy.interfaces.spm.Coregister` to perform a rigid body registration of the functional data to the structural data.

```
coregister = pe.Node(interface=spm.Coregister(), name="coregister")
coregister.inputs.jobtype = 'estimate'
```

Warp functional and structural data to SPM's T1 template using `nipy.interfaces.spm.Normalize`. The tutorial data set includes the template image, `T1.nii`.

```
normalize = pe.Node(interface=spm.Normalize(), name="normalize")
normalize.inputs.template = os.path.abspath('data/T1.nii')
```

Smooth the functional data using `nipy.interfaces.spm.Smooth`.

```
smooth = pe.Node(interface=spm.Smooth(), name="smooth")
fwhmlist = [4]
smooth.iterables = ('fwhm', fwhmlist)
```

25.3 Set up analysis components

Here we create a function that returns subject-specific information about the experimental paradigm. This is used by the `nipy.interfaces.spm.SpecifyModel` to create the information necessary to generate an SPM design matrix. In this tutorial, the same paradigm was used for every participant.

```
def subjectinfo(subject_id):
    from nipy.interfaces.base import Bunch
    from copy import deepcopy
    print("Subject ID: %s\n" % str(subject_id))
    output = []
    names = ['Task-Odd', 'Task-Even']
    for r in range(4):
        onsets = [list(range(15, 240, 60)), list(range(45, 240, 60))]
        output.insert(r,
                      Bunch(
                          conditions=names,
                          onsets=deepcopy(onsets),
                          durations=[[15] for s in names]))
    return output
```

Setup the contrast structure that needs to be evaluated. This is a list of lists. The inner list specifies the contrasts and has the following format - [Name,Stat,[list of condition names],[weights on those conditions]]. The condition names must match the *names* listed in the *subjectinfo* function described above.

```
cont1 = ('Task>Baseline', 'T', ['Task-Odd', 'Task-Even'], [0.5, 0.5])
cont2 = ('Task-Odd>Task-Even', 'T', ['Task-Odd', 'Task-Even'], [1, -1])
contrasts = [cont1, cont2]
```

Generate SPM-specific design information using `nipyype.interfaces.spm.SpecifyModel`.

```
modelspec = pe.Node(interface=model.SpecifySPMModel(), name="modelspec")
modelspec.inputs.concatenate_runs = False
modelspec.inputs.input_units = 'secs'
modelspec.inputs.output_units = 'secs'
modelspec.inputs.time_repetition = 3.
modelspec.inputs.high_pass_filter_cutoff = 120
```

Generate a first level SPM.mat file for analysis `nipyype.interfaces.spm.Level1Design`.

```
levelldesign = pe.Node(interface=spm.Level1Design(), name="levelldesign")
levelldesign.inputs.timing_units = modelspec.inputs.output_units
levelldesign.inputs.interscan_interval = modelspec.inputs.time_repetition
levelldesign.inputs.bases = {'hrf': {'derivs': [0, 0]}}
```

Use `nipyype.interfaces.spm.EstimateModel` to determine the parameters of the model.

```
levelleestimate = pe.Node(interface=spm.EstimateModel(), name="levelleestimate")
levelleestimate.inputs.estimate_method = {'Classical': 1}
```

Use `nipyype.interfaces.spm.EstimateContrast` to estimate the first level contrasts specified in a few steps above.

```
contrastestimate = pe.Node(
    interface=spm.EstimateContrast(), name="contrastestimate")
contrastestimate.inputs.contrasts = contrasts
contrastestimate.overwrite = True
contrastestimate.config = {'execution': {'remove_unnecessary_outputs': False}}
```

25.4 Setup the pipeline

The nodes created above do not describe the flow of data. They merely describe the parameters used for each function. In this section we setup the connections between the nodes such that appropriate outputs from nodes are piped into appropriate inputs of other nodes.

Use the `nipyype.pipeline.engine.Pipeline` to create a graph-based execution pipeline for first level analysis. The config options tells the pipeline engine to use *workdir* as the disk location to use when running the processes and keeping their outputs. The *use_parameterized_dirs* tells the engine to create sub-directories under *workdir* corresponding to the iterables in the pipeline. Thus for this pipeline there will be subject specific sub-directories.

The `nipyype.pipeline.engine.Pipeline.connect` function creates the links between the processes, i.e., how data should flow in and out of the processing nodes.

```
l1pipeline = pe.Workflow(name="level1")
l1pipeline.base_dir = os.path.abspath('spm_tutorial/workingdir')

l1pipeline.connect([
    (infosource, datasource, [('subject_id', 'subject_id')]),
    (datasource, realign, [('func', 'in_files')]),
    (realign, coregister, [('mean_image', 'source'), ('realigned_files',
                                                                'apply_to_files')]),
    (datasource, coregister, [('struct', 'target')]),
    (datasource, normalize, [('struct', 'source')]),
```

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```

(coregister, normalize, [('coregistered_files', 'apply_to_files')]),
(normalize, smooth, [('normalized_files', 'in_files')]),
(infosource, modelspec, [('subject_id', subjectinfo), 'subject_info']),
(realign, modelspec, [('realignment_parameters',
                      'realignment_parameters')]),
(smooth, modelspec, [('smoothed_files', 'functional_runs')]),
(normalize, skullstrip, [('normalized_source', 'in_file')]),
(realign, art, [('realignment_parameters', 'realignment_parameters')]),
(normalize, art, [('normalized_files', 'realigned_files')]),
(skullstrip, art, [('mask_file', 'mask_file')]),
(art, modelspec, [('outlier_files', 'outlier_files')]),
(modelspec, levelldesign, [('session_info', 'session_info')]),
(skullstrip, levelldesign, [('mask_file', 'mask_image')]),
(levelldesign, levelleestimate, [('spm_mat_file', 'spm_mat_file')]),
(levelleestimate, contrastestimate,
 [('spm_mat_file', 'spm_mat_file'), ('beta_images', 'beta_images'),
  ('residual_image', 'residual_image')]),
])

```

25.5 Setup storage results

Use `nipy.interfaces.io.DataSink` to store selected outputs from the pipeline in a specific location. This allows the user to selectively choose important output bits from the analysis and keep them.

The first step is to create a datasink node and then to connect outputs from the modules above to storage locations. These take the following form `directory_name[@subdir]` where parts between `[]` are optional. For example `'realign.@mean'` below creates a directory called `realign` in `'l1output/subject_id/'` and stores the mean image output from the Realign process in the `realign` directory. If the `@` is left out, then a sub-directory with the name `'mean'` would be created and the mean image would be copied to that directory.

```

datasink = pe.Node(interface=nio.DataSink(), name="datasink")
datasink.inputs.base_directory = os.path.abspath('spm_tutorial/l1output')

def getstripdir(subject_id):
    import os
    return os.path.join(
        os.path.abspath('spm_tutorial/workingdir'),
        '_subject_id_%s' % subject_id)

# store relevant outputs from various stages of the 1st level analysis
l1pipeline.connect([
    (infosource, datasink, [('subject_id', 'container'),
                           (('subject_id', getstripdir), 'strip_dir')]),
    (realign, datasink, [('mean_image', 'realign.@mean'),
                        ('realignment_parameters', 'realign.@param')]),
    (art, datasink, [('outlier_files', 'art.@outliers'), ('statistic_files',
                                                           'art.@stats')]),
    (levelldesign, datasink, [('spm_mat_file', 'model.pre-estimate')]),
    (levelleestimate, datasink,
     [('spm_mat_file', 'model.@spm'), ('beta_images', 'model.@beta'),
      ('mask_image', 'model.@mask'), ('residual_image', 'model.@res'),
      ('RPVimage', 'model.@rpv')]),
    (contrastestimate, datasink, [('con_images', 'contrasts.@con'),
                                  ('spmT_images', 'contrasts.@T')]),

```

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```
l)
```

Use `nipyype.interfaces.io.DataGrabber` to extract the contrast ges across a group of first level subjects. Unlike the previous pipeline that iterated over subjects, this pipeline will iterate over

```
# collect all the con images for each contrast.
contrast_ids = list(range(1, len(contrasts) + 1))
l2source = pe.Node(nio.DataGrabber(infields=['fwhm', 'con']), name="l2source")
# we use .*i* to capture both .img (SPM8) and .nii (SPM12)
l2source.inputs.template = os.path.abspath(
    'spm_tutorial/l1output/*/con*/*_fwhm_%d/con_%04d.*i*')
# iterate over all contrast images
l2source.iterables = [('fwhm', fwhmlist), ('con', contrast_ids)]
l2source.inputs.sort_filelist = True
```

Use `nipyype.interfaces.spm.OneSampleTTestDesign` to perform a simple statistical analysis of the contrasts from the group of n this example).

```
# setup a 1-sample t-test node
onesampltestdes = pe.Node(
    interface=spm.OneSampleTTestDesign(), name="onesampttestdes")
l2estimate = pe.Node(interface=spm.EstimateModel(), name="level2estimate")
l2estimate.inputs.estimate_method = {'Classical': 1}
l2conestimate = pe.Node(
    interface=spm.EstimateContrast(), name="level2conestimate")
cont1 = ('Group', 'T', ['mean'], [1])
l2conestimate.inputs.contrasts = [cont1]
l2conestimate.inputs.group_contrast = True
```

As before, we setup a pipeline to connect these two nodes (l2source lettest).

```
l2pipeline = pe.Workflow(name="level2")
l2pipeline.base_dir = os.path.abspath('spm_tutorial/l2output')
l2pipeline.connect([
    (l2source, onesampltestdes, [('outfiles', 'in_files')]),
    (onesampltestdes, l2estimate, [('spm_mat_file', 'spm_mat_file')]),
    (l2estimate, l2conestimate,
     [('spm_mat_file', 'spm_mat_file'), ('beta_images', 'beta_images'),
      ('residual_image', 'residual_image')]),
])
```

25.6 Execute the pipeline

The code discussed above sets up all the necessary data structures with appropriate parameters and the connectivity between the processes, but does not generate any output. To actually run the analysis on the data the `nipyype.pipeline.engine.Pipeline.Run` function needs to be called.

```
if __name__ == '__main__':
    l1pipeline.run('MultiProc')
    l2pipeline.run('MultiProc')
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipyype source distribution under the examples directory.

fMRI: SPM Auditory dataset

26.1 Introduction

The `fmri_spm_auditory.py` recreates the classical workflow described in the [SPM8 manual](http://www.fil.ion.ucl.ac.uk/spm/data/auditory/) using auditory dataset that can be downloaded from <http://www.fil.ion.ucl.ac.uk/spm/data/auditory/>:

```
python fmri_spm_auditory.py
```

Import necessary modules from `nipype`.

```
from builtins import range

import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.spm as spm # spm
import nipype.interfaces.fsl as fsl # fsl
import nipype.interfaces.matlab as mlab # how to run matlab
import nipype.interfaces.utility as util # utility
import nipype.pipeline.engine as pe # pypeline engine
import nipype.algorithms.modelgen as model # model specification
import os # system functions
```

26.1.1 Preliminaries

```
# Set the way matlab should be called
mlab.MatlabCommand.set_default_matlab_cmd("matlab -nodesktop -nosplash")
```

26.1.2 IOWs

In this tutorial we will be setting up a hierarchical workflow for `spm` analysis. This will demonstrate how pre-defined workflows can be setup and shared across users, projects and labs. `eprocessing` workflow ————— This is a generic preprocessing workflow that can be used by different analyses

```
preproc = pe.Workflow(name='preproc')
```

We strongly encourage to use 4D files instead of series of 3D for fMRI analyses for many reasons (cleanness and saving and filesystem inodes are among them). However, the the workflow presented in the SPM8 manual which this tutorial is based on uses 3D files. Therefore we leave converting to 4D as an option. We are using

merge_to_4d variable, because switching between 3d and 4d requires some additional steps (explained later on). Use `nipyype.interfaces.fsl.Merge` to merge a series of 3D files along the time dimension creating a 4d file.

```
merge_to_4d = True

if merge_to_4d:
    merge = pe.Node(interface=fsl.Merge(), name="merge")
    merge.inputs.dimension = "t"
```

Use `nipyype.interfaces.spm.Realign` for motion correction and register all images to the mean image.

```
realign = pe.Node(interface=spm.Realign(), name="realign")
```

Use `nipyype.interfaces.spm.Coregister` to perform a rigid body registration of the functional data to the structural data.

```
coregister = pe.Node(interface=spm.Coregister(), name="coregister")
coregister.inputs.jobtype = 'estimate'

segment = pe.Node(interface=spm.Segment(), name="segment")
```

Uncomment the following line for faster execution

```
# segment.inputs.gaussians_per_class = [1, 1, 1, 4]
```

Warp functional and structural data to SPM's T1 template using `nipyype.interfaces.spm.Normalize`. The tutorial data set emplate image, T1.nii.

```
normalize_func = pe.Node(interface=spm.Normalize(), name="normalize_func")
normalize_func.inputs.jobtype = "write"

normalize_struc = pe.Node(interface=spm.Normalize(), name="normalize_struc")
normalize_struc.inputs.jobtype = "write"
```

Smooth the functional data using `nipyype.interfaces.spm.Smooth`.

```
smooth = pe.Node(interface=spm.Smooth(), name="smooth")
```

write_voxel_sizes is the input of the normalize interface that is recommended to be set to the voxel sizes of the target volume. There is no need to set it manually since we can infer it from data using the following function:

```
def get_vox_dims(volume):
    import nibabel as nb
    from nipyype.utils import NUMPY_MMAP
    if isinstance(volume, list):
        volume = volume[0]
    nii = nb.load(volume, mmap=NUMPY_MMAP)
    hdr = nii.header
    voxdims = hdr.get_zooms()
    return [float(voxdims[0]), float(voxdims[1]), float(voxdims[2])]
```

Here we are connecting all the nodes together. Notice that we add the merge node only if you choose to use 4D. Also *get_vox_dims* function is passed along the input volume of normalise to set the optimal voxel sizes.

```
if merge_to_4d:
    preproc.connect([(merge, realign, [('merged_file', 'in_files')])])

preproc.connect([
    (realign, coregister, [('mean_image', 'target')]),
    (coregister, segment, [('coregistered_source', 'data')]),
```

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```

(segment, normalize_func, [('transformation_mat', 'parameter_file')]),
(segment, normalize_struc,
 [ ('transformation_mat', 'parameter_file'), ('modulated_input_image',
                                             'apply_to_files'),
  (('modulated_input_image', get_vox_dims), 'write_voxel_sizes')]),
(realign, normalize_func, [('realigned_files', 'apply_to_files'),
                           (('realigned_files', get_vox_dims),
                            'write_voxel_sizes')]),
(normalize_func, smooth, [('normalized_files', 'in_files')]),
])

```

26.1.3 Set up analysis workflow

```
l1analysis = pe.Workflow(name='analysis')
```

Generate SPM-specific design information using `nipy.interfaces.spm.SpecifyModel`.

```
modelspec = pe.Node(interface=model.SpecifySPMModel(), name="modelspec")
```

Generate a first level SPM.mat file for analysis `nipy.interfaces.spm.Level1Design`.

```

levelldesign = pe.Node(interface=spm.Level1Design(), name="levelldesign")
levelldesign.inputs.bases = {'hrf': {'derivs': [0, 0]}}

```

Use `nipy.interfaces.spm.EstimateModel` to determine the parameters of the model.

```

levelleestimate = pe.Node(interface=spm.EstimateModel(), name="levelleestimate")
levelleestimate.inputs.estimate_method = {'Classical': 1}

threshold = pe.Node(interface=spm.Threshold(), name="threshold")

```

Use `nipy.interfaces.spm.EstimateContrast` to estimate the first level contrasts specified in a few steps above.

```

contrastestimate = pe.Node(
    interface=spm.EstimateContrast(), name="contrastestimate")

l1analysis.connect([
    (modelspec, levelldesign, [('session_info', 'session_info')]),
    (levelldesign, levelleestimate, [('spm_mat_file', 'spm_mat_file')]),
    (levelleestimate, contrastestimate,
     [('spm_mat_file', 'spm_mat_file'), ('beta_images', 'beta_images'),
      ('residual_image', 'residual_image')]),
    (contrastestimate, threshold, [('spm_mat_file', 'spm_mat_file'),
                                   ('spmT_images', 'stat_image')]),
])

```

26.1.4 Preproc + Analysis pipeline

```

l1pipeline = pe.Workflow(name='firstlevel')
l1pipeline.connect([ (preproc, l1analysis,
                     [ ('realign.realignment_parameters',
                        'modelspec.realignment_parameters') ] ) ])

```

Plugging in *functional_runs* is a bit more complicated, because model spec expects a list of *runs*. Every run can be a 4D file or a list of 3D files. Therefore for 3D analysis we need a list of lists and to make one we need a helper function.

```

if merge_to_4d:
    llpipeline.connect([(preproc, llanalysis,
                        [(['smooth.smoothed_files',
                          'modelspec.functional_runs'])])])
else:
    def makelist(item):
        return [item]

    llpipeline.connect([(preproc, llanalysis,
                        [(['smooth.smoothed_files', makelist),
                          'modelspec.functional_runs'])])])

```

26.1.5 Data specific components

In this tutorial there is only one subject *M00223*. Below we set some variables to inform the `datasource` about the layout of our data. We specify the location of the data, the subject sub-directories and a dictionary that maps each run to a mnemonic (or field) for the run type (struct or func). These fields become the output fields of the `datasource` node in the pipeline.

```

# Specify the location of the data downloaded from http://www.fil.ion.ucl.ac.uk/
↳spm/data/auditory/
data_dir = os.path.abspath('spm_auditory_data')
# Specify the subject directories
subject_list = ['M00223']
# Map field names to individual subject runs.
info = dict(
    func=[['f', 'subject_id', 'f', 'subject_id',
            list(range(16, 100))]],
    struct=[['s', 'subject_id', 's', 'subject_id', 2]])

infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")

```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

Now we create a `nipy.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipy.pipeline.NodeWrapper` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```

datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=['func', 'struct']),
    name='datasource')
datasource.inputs.base_directory = data_dir
datasource.inputs.template = '%s%s/%s%s_%03d.img'
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True

```


26.1.6 Experimental paradigm specific components

Here we create a structure that provides information about the experimental paradigm. This is used by the `nipyne.interfaces.spm.SpecifyModel` to create the information necessary to generate an SPM design matrix.

```
from nipyne.interfaces.base import Bunch
subjectinfo = [
    Bunch(
        conditions=['Task'], onsets=[list(range(6, 84, 12))], durations=[[6]])
]
```

Setup the contrast structure that needs to be evaluated. This is a list of lists. The inner list specifies the contrasts and has the following format - [Name,Stat,[list of condition names],[weights on those conditions]]. The condition names must match the *names* listed in the *subjectinfo* function described above.

```
cont1 = ('active > rest', 'T', ['Task'], [1])
contrasts = [cont1]

# set up node specific inputs
modelspecref = llpipeline.inputs.analysis.modelspec
modelspecref.input_units = 'scans'
modelspecref.output_units = 'scans'
modelspecref.time_repetition = 7
modelspecref.high_pass_filter_cutoff = 120

l1designref = llpipeline.inputs.analysis.level1design
l1designref.timing_units = modelspecref.output_units
l1designref.interscan_interval = modelspecref.time_repetition

llpipeline.inputs.preproc.smooth.fwhm = [6, 6, 6]
llpipeline.inputs.analysis.modelspec.subject_info = subjectinfo
llpipeline.inputs.analysis.contrastestimate.contrasts = contrasts
llpipeline.inputs.analysis.threshold.contrast_index = 1
```

26.1.7 Setup the pipeline

The nodes created above do not describe the flow of data. They merely describe the parameters used for each function. In this section we setup the connections between the nodes such that appropriate outputs from nodes are piped into appropriate inputs of other nodes.

Use the `nipyne.pipeline.engine.Pipeline` to create a graph-based execution pipeline for first level analysis. The `config` options tells the pipeline engine to use *workdir* as the disk location to use when running the processes and keeping their outputs. The `use_parameterized_dirs` tells the engine to create sub-directories under *workdir* corresponding to the iterables in the pipeline. Thus for this pipeline there will be subject specific sub-directories.

The `nipyne.pipeline.engine.Pipeline.connect` function creates the links between the processes, i.e., how data should flow in and out of the processing nodes.

```
level1 = pe.Workflow(name="level1")
level1.base_dir = os.path.abspath('spm_auditory_tutorial/workingdir')

level1.connect([(infosource, datasource, [('subject_id', 'subject_id')]),
                (datasource, llpipeline, [('struct',
                'preproc.coregister.source')])])

if merge_to_4d:
    level1.connect([(datasource, llpipeline, [('func',
                'preproc.merge.in_files')])])
```

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```

else:
    levell.connect([(datasource, llpipeline, [('func',
                                              'preproc.realign.in_files')])])

```

26.1.8 Setup storage results

Use `nipy.interfaces.io.DataSink` to store selected outputs from the pipeline in a specific location. This allows the user to selectively choose important output bits from the analysis and keep them.

The first step is to create a datasink node and then to connect outputs from the modules above to storage locations. These take the following form `directory_name[@subdir]` where parts between `[]` are optional. For example `'realign.@mean'` below creates a directory called `realign` in `'lloutput/subject_id/'` and stores the mean image output from the `Realign` process in the `realign` directory. If the `@` is left out, then a sub-directory with the name `'mean'` would be created and the mean image would be copied to that directory.

```

datasink = pe.Node(interface=nio.DataSink(), name="datasink")
datasink.inputs.base_directory = os.path.abspath(
    'spm_auditory_tutorial/lloutput')

def getstripdir(subject_id):
    import os
    return os.path.join(
        os.path.abspath('spm_auditory_tutorial/workingdir'),
        '_subject_id_%s' % subject_id)

# store relevant outputs from various stages of the 1st level analysis
levell.connect([
    (infosource, datasink, [('subject_id', 'container'),
                            (('subject_id', getstripdir), 'strip_dir')]),
    (llpipeline, datasink,
     [('analysis.contrastestimate.con_images', 'contrasts.@con'),
      ('analysis.contrastestimate.spmT_images', 'contrasts.@T')]),
])

code discussed above sets up all the necessary data structures

```

opriate parameters and the connectivity between the sses, but does not generate any output. To actually run the sis on the data the `nipy.pipeline.engine.Pipeline.Run`

```

if __name__ == '__main__':
    levell.run()
    levell.write_graph()

```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

fMRI: DARTEL, SPM

The `fmri_spm_dartel.py` integrates several interfaces to perform a first and second level analysis on a two-subject data set. The tutorial can be found in the examples folder. Run the tutorial from inside the nipyre tutorial directory:

```
python fmri_spm_dartel.py
```

Import necessary modules from nipyre.

```
from __future__ import print_function
from builtins import str
from builtins import range

import nipyre.interfaces.io as nio # Data i/o
import nipyre.interfaces.spm as spm # spm
import nipyre.workflows.fmri.spm as spm_wf # spm
import nipyre.interfaces.fsl as fsl # fsl
from nipyre.interfaces import utility as niu # Utilities
import nipyre.pipeline.engine as pe # pypeline engine
import nipyre.algorithms.rapidart as ra # artifact detection
import nipyre.algorithms.modelgen as model # model specification
import os # system functions
```

27.1 Preliminaries

Set any package specific configuration. The output file format for FSL routines is being set to uncompressed NIFTI and a specific version of matlab is being used. The uncompressed format is required because SPM does not handle compressed NIFTI.

```
# Tell fsl to generate all output in uncompressed nifti format
fsl.FSLCommand.set_default_output_type('NIFTI')

# Set the way matlab should be called
# mlab.MatlabCommand.set_default_matlab_cmd("matlab -nodesktop -nosplash")
# mlab.MatlabCommand.set_default_paths('/software/spm8')
```

27.2 lows

In this tutorial we will be setting up a hierarchical workflow for spm analysis. This will demonstrate how pre-defined workflows can be setup and shared across users, projects and labs. eprocessing workflow

This is a generic preprocessing workflow that can be used by different analyses

```
preproc = pe.Workflow(name='preproc')
```

Use `nipype.interfaces.spm.Realign` for motion correction and register all images to the mean image.

```
realign = pe.Node(spm.Realign(), name="realign")
realign.inputs.register_to_mean = True
```

Use `nipype.algorithms.rapidart` to determine which of the images in the functional series are outliers based on deviations in intensity or movement.

```
art = pe.Node(ra.ArtifactDetect(), name="art")
art.inputs.use_differences = [True, False]
art.inputs.use_norm = True
art.inputs.norm_threshold = 1
art.inputs.zintensity_threshold = 3
art.inputs.mask_type = 'file'
art.inputs.parameter_source = 'SPM'
```

Skull strip structural images using `nipype.interfaces.fsl.BET`.

```
skullstrip = pe.Node(fsl.BET(), name="skullstrip")
skullstrip.inputs.mask = True
```

Use `nipype.interfaces.spm.Coregister` to perform a rigid body registration of the functional data to the structural data.

```
coregister = pe.Node(spm.Coregister(), name="coregister")
coregister.inputs.jobtype = 'estimate'
```

Normalize and smooth functional data using DARTEL template

```
normalize_and_smooth_func = pe.Node(
    spm.DARTENorm2MNI(modulate=True), name='normalize_and_smooth_func')
fwhmlist = [4]
normalize_and_smooth_func.iterables = ('fwhm', fwhmlist)
```

Normalize structural data using DARTEL template

```
normalize_struct = pe.Node(
    spm.DARTENorm2MNI(modulate=True), name='normalize_struct')
normalize_struct.inputs.fwhm = 2

preproc.connect([
    (realign, coregister, [('mean_image', 'source'), ('realigned_files',
                                                         'apply_to_files')]),
    (coregister, normalize_and_smooth_func, [('coregistered_files',
                                                         'apply_to_files')]),
    (normalize_struct, skullstrip, [('normalized_files', 'in_file')]),
    (realign, art, [('realignment_parameters', 'realignment_parameters')]),
    (normalize_and_smooth_func, art, [('normalized_files',
                                                         'realigned_files')]),
    (skullstrip, art, [('mask_file', 'mask_file')]),
])
```

27.3 Set up analysis workflow

```
l1analysis = pe.Workflow(name='analysis')
```

Generate SPM-specific design information using `nipy.interfaces.spm.SpecifyModel`.

```
modelspec = pe.Node(model.SpecifySPMModel(), name="modelspec")
modelspec.inputs.concatenate_runs = True
```

Generate a first level SPM.mat file for analysis `nipy.interfaces.spm.Level1Design`.

```
level1design = pe.Node(spm.Level1Design(), name="level1design")
level1design.inputs.bases = {'hrf': {'derivs': [0, 0]}}
```

Use `nipy.interfaces.spm.EstimateModel` to determine the parameters of the model.

```
levelleestimate = pe.Node(spm.EstimateModel(), name="levelleestimate")
levelleestimate.inputs.estimate_method = {'Classical': 1}
```

Use `nipy.interfaces.spm.EstimateContrast` to estimate the first level contrasts specified in a few steps above.

```
contrastestimate = pe.Node(spm.EstimateContrast(), name="contrastestimate")
```

Use `:class: nipy.interfaces.utility.Select` to select each contrast for reporting.

```
selectcontrast = pe.Node(niu.Select(), name="selectcontrast")
```

Use `nipy.interfaces.fsl.Overlay` to combine the statistical output of the contrast estimate and a background image into one volume.

```
overlaystats = pe.Node(fsl.Overlay(), name="overlaystats")
overlaystats.inputs.stat_thresh = (3, 10)
overlaystats.inputs.show_negative_stats = True
overlaystats.inputs.auto_thresh_bg = True
```

Use `nipy.interfaces.fsl.Slicer` to create images of the overlaid statistical volumes for a report of the first-level results.

```
slicestats = pe.Node(fsl.Slicer(), name="slicestats")
slicestats.inputs.all_axial = True
slicestats.inputs.image_width = 750

l1analysis.connect([(modelspec, level1design,
                      [ ('session_info',
                          'session_info') ]), (level1design, levelleestimate,
                      [ ('spm_mat_file', 'spm_mat_file') ]),
                    (levelleestimate, contrastestimate,
                      [ ('spm_mat_file', 'spm_mat_file'), ('beta_images',
                                                              'beta_images'),
                      ('residual_image',
                       'residual_image') ]), (contrastestimate, selectcontrast,
                      [ ('spmT_images', 'inlist') ]),
                    (selectcontrast, overlaystats,
                      [ ('out', 'stat_image') ]), (overlaystats, slicestats,
                      [ ('out_file', 'in_file') ])]])
```

27.4 Preproc + Analysis pipeline

```
llpipeline = pe.Workflow(name='firstlevel')
llpipeline.connect([
    (preproc, llanalysis,
     [('realign.realignment_parameters', 'modelspec.realignment_parameters'),
      ('normalize_and_smooth_func.normalized_files',
       'modelspec.functional_runs'), ('art.outlier_files',
                                     'modelspec.outlier_files'),
      ('skullstrip.mask_file',
       'level1design.mask_image'), ('normalize_struct.normalized_files',
                                   'overlaystats.background_image')]),
])
```

27.5 Data specific components

The nipyype tutorial contains data for two subjects. Subject data is in two subdirectories, `s1` and `s2`. Each subject directory contains four functional volumes: `f3.nii`, `f5.nii`, `f7.nii`, `f10.nii`. And one anatomical volume named `struct.nii`.

Below we set some variables to inform the `datasource` about the layout of our data. We specify the location of the data, the subject sub-directories and a dictionary that maps each run to a mnemonic (or field) for the run type (`struct` or `func`). These fields become the output fields of the `datasource` node in the pipeline.

In the example below, run 'f3' is of type 'func' and gets mapped to a nifti filename through a template '%s.nii'. So 'f3' would become 'f3.nii'.

```
# Specify the location of the data.
# data_dir = os.path.abspath('data')
# Specify the subject directories
subject_list = ['s1', 's3']
# Map field names to individual subject runs.
info = dict(
    func=[['subject_id', ['f3', 'f5', 'f7', 'f10']]],
    struct=[['subject_id', 'struct']])

infosource = pe.Node(
    niu.IdentityInterface(fields=['subject_id']), name="infosource")
```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

Now we create a `nipyype.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipyype.pipeline.NodeWrapper` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```
inputnode = pe.Node(
    niu.IdentityInterface(fields=['in_data']), name='inputnode')
datasource = pe.Node(
    nio.DataGrabber(infields=['subject_id'], outfields=['func', 'struct']),
    name='datasource')
datasource.inputs.template = 'nipyype-tutorial/data/%s/%s.nii'
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True
```

We need to create a separate workflow to make the DARTEL template

```
datasource_dartel = pe.MapNode(
    nio.DataGrabber(infields=['subject_id'], outfields=['struct']),
    name='datasource_dartel',
    iterfield=['subject_id'])
datasource_dartel.inputs.template = 'nipyne-tutorial/data/%s/%s.nii'
datasource_dartel.inputs.template_args = dict(
    struct=[['subject_id', 'struct']])
datasource_dartel.inputs.sort_filelist = True
datasource_dartel.inputs.subject_id = subject_list
```

Here we make sure that struct files have names corresponding to the subject ids. This way we will be able to pick the right field flows later.

```
rename_dartel = pe.MapNode(
    niu.Rename(format_string="subject_id_%(subject_id)s_struct"),
    iterfield=['in_file', 'subject_id'],
    name='rename_dartel')
rename_dartel.inputs.subject_id = subject_list
rename_dartel.inputs.keep_ext = True

dartel_workflow = spm_wf.create_DARTEL_template(name='dartel_workflow')
dartel_workflow.inputs.inputspec.template_prefix = "template"
```

This function will allow to pick the right field flow for each subject

```
def pickFieldFlow(dartel_flow_fields, subject_id):
    from nipyne.utils.filemanip import split_filename
    for f in dartel_flow_fields:
        _, name, _ = split_filename(f)
        if name.find("subject_id_%s" % subject_id):
            return f

    raise Exception

pick_flow = pe.Node(
    niu.Function(
        input_names=['dartel_flow_fields', 'subject_id'],
        output_names=['dartel_flow_field'],
        function=pickFieldFlow),
    name="pick_flow")
```

27.6 Experimental paradigm specific components

Here we create a function that returns subject-specific information about the experimental paradigm. This is used by the `nipyne.interfaces.spm.SpecifyModel` to create the information necessary to generate an SPM design matrix. In this tutorial, the same paradigm was used for every participant.

```
def subjectinfo(subject_id):
    from nipyne.interfaces.base import Bunch
    from copy import deepcopy
    print("Subject ID: %s\n" % str(subject_id))
    output = []
    names = ['Task-Odd', 'Task-Even']
    for r in range(4):
```

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```

onsets = [list(range(15, 240, 60)), list(range(45, 240, 60))]
output.insert(r,
              Bunch(
                  conditions=names,
                  onsets=deepcopy(onsets),
                  durations=[[15] for s in names],
                  amplitudes=None,
                  tmod=None,
                  pmod=None,
                  regressor_names=None,
                  regressors=None))

return output

```

Setup the contrast structure that needs to be evaluated. This is a list of lists. The inner list specifies the contrasts and has the following format - [Name,Stat,[list of condition names],[weights on those conditions]]. The condition names must match the *names* listed in the *subjectinfo* function described above.

```

cont1 = ('Task>Baseline', 'T', ['Task-Odd', 'Task-Even'], [0.5, 0.5])
cont2 = ('Task-Odd>Task-Even', 'T', ['Task-Odd', 'Task-Even'], [1, -1])
contrasts = [cont1, cont2]

# set up node specific inputs
modelspecref = llpipeline.inputs.analysis.modelspec
modelspecref.input_units = 'secs'
modelspecref.output_units = 'secs'
modelspecref.time_repetition = 3.
modelspecref.high_pass_filter_cutoff = 120

l1designref = llpipeline.inputs.analysis.level1design
l1designref.timing_units = modelspecref.output_units
l1designref.interscan_interval = modelspecref.time_repetition

llpipeline.inputs.analysis.contrastestimate.contrasts = contrasts

# Iterate over each contrast and create report images.
selectcontrast.iterables = ('index', [[i] for i in range(len(contrasts))])

```

The nodes created above do not describe the flow of data. They merely describe the parameters used for each function. In this section we setup the connections between the nodes such that appropriate outputs from nodes are piped into appropriate inputs of other nodes. Use the `nipy.pipeline.engine.Pipeline` to create a graph-based execution pipeline for first level analysis. The config options tells the pipeline engine to use *workdir* as the disk location to use when running the processes and keeping their outputs. The *use_parameterized_dirs* tells the engine to create sub-directories under *workdir* corresponding to the iterables in the pipeline. Thus for this pipeline there will be subject specific The `nipy.pipeline.engine.Pipeline.connect` function creates the links between the processes, i.e., how data should flow in and out of

```

level1 = pe.Workflow(name="level1")
level1.base_dir = os.path.abspath('spm_dartel_tutorial/workingdir')

level1.connect([
    (inputnode, datasource, [('in_data', 'base_directory')]),
    (inputnode, datasource_dartel, [('in_data', 'base_directory')]),
    (datasource_dartel, rename_dartel, [('struct', 'in_file')]),
    (rename_dartel, dartel_workflow, [('out_file',
                                         'inputspec.structural_files')]),
    (infosource, datasource, [('subject_id', 'subject_id')]),

```

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```

(datasource, llpipeline,
 [ ('func', 'preproc.realign.in_files'), ('struct',
                                         'preproc.coregister.target'),
   ('struct', 'preproc.normalize_struct.apply_to_files') ]),
(dartel_workflow, llpipeline,
 [ ('outputspec.template_file', 'preproc.normalize_struct.template_file'),
   ('outputspec.template_file',
    'preproc.normalize_and_smooth_func.template_file') ]),
(infosource, pick_flow, [ ('subject_id', 'subject_id') ]),
(dartel_workflow, pick_flow, [ ('outputspec.flow_fields',
                               'dartel_flow_fields') ]),

(pick_flow, llpipeline,
 [ ('dartel_flow_field', 'preproc.normalize_struct.flowfield_files'),
   ('dartel_flow_field',
    'preproc.normalize_and_smooth_func.flowfield_files') ]),
(infosource, llpipeline, [ (('subject_id', subjectinfo),
                           'analysis.modelspec.subject_info') ]),
])

```

27.7 Setup storage results

Use `nipy.interfaces.io.DataSink` to store selected outputs from the pipeline in a specific location. This allows the user to selectively choose important output bits from the analysis and keep them.

The first step is to create a datasink node and then to connect outputs from the modules above to storage locations. These take the following form `directory_name[.@]subdir` where parts between `[]` are optional. For example `'realign.@mean'` below creates a directory called `realign` in `'l1output/subject_id/'` and stores the mean image output from the Realign process in the `realign` directory. If the `@` is left out, then a sub-directory with the name `'mean'` would be created and the mean image would be copied to that directory.

```

datasink = pe.Node(nio.DataSink(), name="datasink")
datasink.inputs.base_directory = os.path.abspath(
    'spm_dartel_tutorial/l1output')
report = pe.Node(nio.DataSink(), name='report')
report.inputs.base_directory = os.path.abspath('spm_dartel_tutorial/report')
report.inputs.parameterization = False

def getstripdir(subject_id):
    import os
    return os.path.join(
        os.path.abspath('spm_dartel_tutorial/workingdir'),
        '_subject_id_%s' % subject_id)

# store relevant outputs from various stages of the 1st level analysis
levell.connect([
    (infosource, datasink, [ ('subject_id', 'container'),
                             (('subject_id', getstripdir), 'strip_dir') ]),
    (llpipeline, datasink,
     [ ('analysis.contrastestimate.con_images', 'contrasts.@con'),
       ('analysis.contrastestimate.spmT_images', 'contrasts.@T') ]),
    (infosource, report, [ ('subject_id', 'container'),
                           (('subject_id', getstripdir), 'strip_dir') ]),
    (llpipeline, report, [ ('analysis.slicestats.out_file', '@report') ]),
])

```

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code discussed above sets up `all` the necessary data structures

opriate parameters and the connectivity between the sses, but does not generate any output. To actually run the sis on the data the `nipyype.pipeline.engine.Pipeline.Run`

```
if __name__ == '__main__':
    level1.run(plugin_args={'n_procs': 4})
    level1.write_graph()
```

27.8 Setup level 2 pipeline

Use `nipyype.interfaces.io.DataGrabber` to extract the contrast images across a group of first level subjects. Unlike the previous pipeline that iterated over subjects, this pipeline will iterate over contrasts.

```
# collect all the con images for each contrast.
contrast_ids = list(range(1, len(contrasts) + 1))
l2source = pe.Node(nio.DataGrabber(infields=['fwhm', 'con']), name="l2source")
# we use .*i* to capture both .img (SPM8) and .nii (SPM12)
l2source.inputs.template = os.path.abspath(
    'spm_dartel_tutorial/l1output/*/con*/*_fwhm_%d/con_%04d.*i*')
# iterate over all contrast images
l2source.iterables = [('fwhm', fwhmlist), ('con', contrast_ids)]
l2source.inputs.sort_filelist = True
```

Use `nipyype.interfaces.spm.OneSampleTTestDesign` to perform a simple statistical analysis of the contrasts from the group of `n` this example).

```
# setup a 1-sample t-test node
onesampttestdes = pe.Node(spm.OneSampleTTestDesign(), name="onesampttestdes")
l2estimate = pe.Node(spm.EstimateModel(), name="level2estimate")
l2estimate.inputs.estimate_method = {'Classical': 1}
l2conestimate = pe.Node(spm.EstimateContrast(), name="level2conestimate")
cont1 = ('Group', 'T', ['mean'], [1])
l2conestimate.inputs.contrasts = [cont1]
l2conestimate.inputs.group_contrast = True
```

As before, we setup a pipeline to connect these two nodes (l2source lettest).

```
l2pipeline = pe.Workflow(name="level2")
l2pipeline.base_dir = os.path.abspath('spm_dartel_tutorial/l2output')
l2pipeline.connect([
    (l2source, onesampttestdes, [('outfiles', 'in_files')]),
    (onesampttestdes, l2estimate, [('spm_mat_file', 'spm_mat_file')]),
    (l2estimate, l2conestimate,
     [('spm_mat_file', 'spm_mat_file'), ('beta_images', 'beta_images'),
      ('residual_image', 'residual_image')]),
])
```

27.9 Execute the second level pipeline

```
if __name__ == '__main__':
    l2pipeline.run()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipyte source distribution under the `examples` directory.

fMRI: Famous vs non-famous faces, SPM

28.1 Introduction

The `fmri_spm_face.py` recreates the classical workflow described in the [SPM8 manual](http://www.fil.ion.ucl.ac.uk/spm/data/face_rep/) using face dataset that can be downloaded from http://www.fil.ion.ucl.ac.uk/spm/data/face_rep/:

```
python fmri_spm.py
```

Import necessary modules from `nipype`.

```
from __future__ import division
from builtins import range

import os # system functions
import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.spm as spm # spm
import nipype.interfaces.matlab as mlab # how to run matlab
import nipype.interfaces.utility as util # utility
import nipype.pipeline.engine as pe # pypeline engine
import nipype.algorithms.modelgen as model # model specification
```

28.1.1 iminaries

Set any package specific configuration. The output file format for FSL routines is being set to uncompressed NIFTI and a specific version of matlab is being used. The uncompressed format is required because SPM does not handle compressed NIFTI.

```
# Set the way matlab should be called
mlab.MatlabCommand.set_default_matlab_cmd("matlab -nodesktop -nosplash")
# If SPM is not in your MATLAB path you should add it here
# mlab.MatlabCommand.set_default_paths('/path/to/your/spm8')
```

28.1.2 lows

In this tutorial we will be setting up a hierarchical workflow for `spm` analysis. It one is slightly different then the one used in `spm_tutorial2`. `eprocessing` workflow ————— This is a generic preprocessing workflow that can be used by different analyses

```
preproc = pe.Workflow(name='preproc')
```

Use `nipyne.interfaces.spm.Realign` for motion correction and register all images to the mean image.

```
realign = pe.Node(interface=spm.Realign(), name="realign")
```

```
slice_timing = pe.Node(interface=spm.SliceTiming(), name="slice_timing")
```

Use `nipyne.interfaces.spm.Coregister` to perform a rigid body registration of the functional data to the structural data.

```
coregister = pe.Node(interface=spm.Coregister(), name="coregister")
coregister.inputs.jobtype = 'estimate'
```

```
segment = pe.Node(interface=spm.Segment(), name="segment")
segment.inputs.save_bias_corrected = True
```

Uncomment the following line for faster execution

```
# segment.inputs.gaussians_per_class = [1, 1, 1, 4]
```

Warp functional and structural data to SPM's T1 template using `nipyne.interfaces.spm.Normalize`. The tutorial data set emplate image, T1.nii.

```
normalize_func = pe.Node(interface=spm.Normalize(), name="normalize_func")
normalize_func.inputs.jobtype = "write"
```

```
normalize_struc = pe.Node(interface=spm.Normalize(), name="normalize_struc")
normalize_struc.inputs.jobtype = "write"
```

Smooth the functional data using `nipyne.interfaces.spm.Smooth`.

```
smooth = pe.Node(interface=spm.Smooth(), name="smooth")
```

`write_voxel_sizes` is the input of the normalize interface that is recommended to be set to the voxel sizes of the target volume. There is no need to set it manually since we can infer it from data using the following function:

```
def get_vox_dims(volume):
    import nibabel as nb
    from nipyne.utils import NUMPY_MMAP
    if isinstance(volume, list):
        volume = volume[0]
    nii = nb.load(volume, mmap=NUMPY_MMAP)
    hdr = nii.header
    voxdims = hdr.get_zooms()
    return [float(voxdims[0]), float(voxdims[1]), float(voxdims[2])]
```

Here we are connecting all the nodes together. Notice that we add the merge node only if you choose to use 4D. Also `get_vox_dims` function is passed along the input volume of normalise to set the optimal voxel sizes.

```
preproc.connect([
    (realign, coregister, [('mean_image', 'target')]),
    (coregister, segment, [('coregistered_source', 'data')]),
    (segment, normalize_func, [('transformation_mat', 'parameter_file')]),
    (segment, normalize_struc,
     [('transformation_mat', 'parameter_file'), ('bias_corrected_image',
                                                'apply_to_files')]),
    ((('bias_corrected_image', get_vox_dims), 'write_voxel_sizes')),
    (realign, slice_timing, [('realigned_files', 'in_files')]),
    (slice_timing, normalize_func, [('timecorrected_files', 'apply_to_files'),
                                    (('timecorrected_files', get_vox_dims),
```

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```

        'write_voxel_sizes'])),
    (normalize_func, smooth, [('normalized_files', 'in_files')]),
])

```

28.1.3 Set up analysis workflow

```
l1analysis = pe.Workflow(name='analysis')
```

Generate SPM-specific design information using `nipy.interfaces.spm.SpecifyModel`.

```
modelspec = pe.Node(interface=model.SpecifySPMModel(), name="modelspec")
```

Generate a first level SPM.mat file for analysis `nipy.interfaces.spm.Level1Design`.

```
level1design = pe.Node(interface=spm.Level1Design(), name="level1design")
```

Use `nipy.interfaces.spm.EstimateModel` to determine the parameters of the model.

```

level1estimate = pe.Node(interface=spm.EstimateModel(), name="level1estimate")
level1estimate.inputs.estimate_method = {'Classical': 1}

threshold = pe.Node(interface=spm.Threshold(), name="threshold")

```

Use `nipy.interfaces.spm.EstimateContrast` to estimate the first level contrasts specified in a few steps above.

```

contrastestimate = pe.Node(
    interface=spm.EstimateContrast(), name="contrastestimate")

def pickfirst(l):
    return l[0]

l1analysis.connect([
    (modelspec, level1design, [('session_info', 'session_info')]),
    (level1design, level1estimate, [('spm_mat_file', 'spm_mat_file')]),
    (level1estimate, contrastestimate,
     [('spm_mat_file', 'spm_mat_file'), ('beta_images', 'beta_images'),
      ('residual_image', 'residual_image')]),
    (contrastestimate, threshold, [('spm_mat_file', 'spm_mat_file'),
                                   (('spmT_images', pickfirst),
                                    'stat_image')]),
])

```

28.1.4 Preproc + Analysis pipeline

```

l1pipeline = pe.Workflow(name='firstlevel')
l1pipeline.connect([(preproc, l1analysis,
                     [('realignment_parameters',
                      'modelspec.realignment_parameters')])])

```

Plugging in *functional_runs* is a bit more complicated, because model spec expects a list of *runs*. Every run can be a 4D file or a list of 3D files. Therefore for 3D analysis we need a list of lists and to make one we need a helper function.

```
def makelist(item):
    return [item]

l1pipeline.connect([(preproc, l1analysis, [(['smooth.smoothed_files',
                                             makelist),
                                             'modelspec.functional_runs'])])])
```

28.1.5 Data specific components

In this tutorial there is only one subject *M03953*.

Below we set some variables to inform the `datasource` about the layout of our data. We specify the location of the data, the subject sub-directories and a dictionary that maps each run to a mnemonic (or field) for the run type (struct or func). These fields become the output fields of the `datasource` node in the pipeline.

```
# Specify the location of the data downloaded from http://www.fil.ion.ucl.ac.uk/
↳spm/data/face_rep/face_rep_SPM5.html
data_dir = os.path.abspath('spm_face_data')
# Specify the subject directories
subject_list = ['M03953']
# Map field names to individual subject runs.
info = dict(
    func=[['RawEPI', 'subject_id', 5, ["_%04d" % i for i in range(6, 357)]]],
    struct=[['Structural', 'subject_id', 7, '']]

infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")
```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```

Now we create a `nipyne.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipyne.pipeline.NodeWrapper` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```
datasource = pe.Node(
    interface=nio.DataGrabber(
        infields=['subject_id'], outfields=['func', 'struct']),
    name='datasource')
datasource.inputs.base_directory = data_dir
datasource.inputs.template = '%s/s%s_%04d%s.img'
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True
```

28.1.6 Experimental paradigm specific components

Here we create a structure that provides information about the experimental paradigm. This is used by the `nipyne.interfaces.spm.SpecifyModel` to create the information necessary to generate an SPM design matrix.

```
from nipyne.interfaces.base import Bunch
```

We're importing the onset times from a mat file (found on http://www.fil.ion.ucl.ac.uk/spm/data/face_rep/)


```

from scipy.io.matlab import loadmat
mat = loadmat(os.path.join(data_dir, "sots.mat"), struct_as_record=False)
sot = mat['sot'][0]
itemlag = mat['itemlag'][0]

subjectinfo = [
    Bunch(
        conditions=['N1', 'N2', 'F1', 'F2'],
        onsets=[sot[0], sot[1], sot[2], sot[3]],
        durations=[[0], [0], [0], [0]],
        amplitudes=None,
        tmod=None,
        pmod=None,
        regressor_names=None,
        regressors=None)
]

```

Setup the contrast structure that needs to be evaluated. This is a list of lists. The inner list specifies the contrasts and has the following format - [Name,Stat,[list of condition names],[weights on those conditions]]. The condition names must match the *names* listed in the *subjectinfo* function described above.

```

cond1 = ('positive effect of condition', 'T',
        ['N1*bf(1)', 'N2*bf(1)', 'F1*bf(1)', 'F2*bf(1)'], [1, 1, 1, 1])
cond2 = ('positive effect of condition_dtemp', 'T',
        ['N1*bf(2)', 'N2*bf(2)', 'F1*bf(2)', 'F2*bf(2)'], [1, 1, 1, 1])
cond3 = ('positive effect of condition_ddisp', 'T',
        ['N1*bf(3)', 'N2*bf(3)', 'F1*bf(3)', 'F2*bf(3)'], [1, 1, 1, 1])
# non-famous > famous
fam1 = ('positive effect of Fame', 'T',
        ['N1*bf(1)', 'N2*bf(1)', 'F1*bf(1)', 'F2*bf(1)'], [1, 1, -1, -1])
fam2 = ('positive effect of Fame_dtemp', 'T',
        ['N1*bf(2)', 'N2*bf(2)', 'F1*bf(2)', 'F2*bf(2)'], [1, 1, -1, -1])
fam3 = ('positive effect of Fame_ddisp', 'T',
        ['N1*bf(3)', 'N2*bf(3)', 'F1*bf(3)', 'F2*bf(3)'], [1, 1, -1, -1])
# rep1 > rep2
rep1 = ('positive effect of Rep', 'T',
        ['N1*bf(1)', 'N2*bf(1)', 'F1*bf(1)', 'F2*bf(1)'], [1, -1, 1, -1])
rep2 = ('positive effect of Rep_dtemp', 'T',
        ['N1*bf(2)', 'N2*bf(2)', 'F1*bf(2)', 'F2*bf(2)'], [1, -1, 1, -1])
rep3 = ('positive effect of Rep_ddisp', 'T',
        ['N1*bf(3)', 'N2*bf(3)', 'F1*bf(3)', 'F2*bf(3)'], [1, -1, 1, -1])
int1 = ('positive interaction of Fame x Rep', 'T',
        ['N1*bf(1)', 'N2*bf(1)', 'F1*bf(1)', 'F2*bf(1)'], [-1, -1, -1, 1])
int2 = ('positive interaction of Fame x Rep_dtemp', 'T',
        ['N1*bf(2)', 'N2*bf(2)', 'F1*bf(2)', 'F2*bf(2)'], [1, -1, -1, 1])
int3 = ('positive interaction of Fame x Rep_ddisp', 'T',
        ['N1*bf(3)', 'N2*bf(3)', 'F1*bf(3)', 'F2*bf(3)'], [1, -1, -1, 1])

contf1 = ['average effect condition', 'F', [cond1, cond2, cond3]]
contf2 = ['main effect Fam', 'F', [fam1, fam2, fam3]]
contf3 = ['main effect Rep', 'F', [rep1, rep2, rep3]]
contf4 = ['interaction: Fam x Rep', 'F', [int1, int2, int3]]
contrasts = [
    cond1, cond2, cond3, fam1, fam2, fam3, rep1, rep2, rep3, int1, int2, int3,
    contf1, contf2, contf3, contf4
]

```

Setting up nodes inputs

```

num_slices = 24
TR = 2.

slice_timingref = l1pipeline.inputs.preproc.slice_timing
slice_timingref.num_slices = num_slices
slice_timingref.time_repetition = TR
slice_timingref.time_acquisition = TR - TR / float(num_slices)
slice_timingref.slice_order = list(range(num_slices, 0, -1))
slice_timingref.ref_slice = int(num_slices / 2)

l1pipeline.inputs.preproc.smooth.fwhm = [8, 8, 8]

# set up node specific inputs
modelspecref = l1pipeline.inputs.analysis.modelspec
modelspecref.input_units = 'scans'
modelspecref.output_units = 'scans'
modelspecref.time_repetition = TR
modelspecref.high_pass_filter_cutoff = 120

l1designref = l1pipeline.inputs.analysis.level1design
l1designref.timing_units = modelspecref.output_units
l1designref.interscan_interval = modelspecref.time_repetition
l1designref.microtime_resolution = slice_timingref.num_slices
l1designref.microtime_onset = slice_timingref.ref_slice
l1designref.bases = {'hrf': {'derivs': [1, 1]}}
```

The following lines automatically inform SPM to create a default set of contrasts for a factorial design.

```

# l1designref.factor_info = [dict(name = 'Fame', levels = 2),
#                           dict(name = 'Rep', levels = 2)]

l1pipeline.inputs.analysis.modelspec.subject_info = subjectinfo
l1pipeline.inputs.analysis.contrastestimate.contrasts = contrasts
l1pipeline.inputs.analysis.threshold.contrast_index = 1
```

Use derivative estimates in the non-parametric model

```
l1pipeline.inputs.analysis.contrastestimate.use_derivs = True
```

Setting up parametricvariation of the model

```

subjectinfo_param = [
    Bunch(
        conditions=['N1', 'N2', 'F1', 'F2'],
        onsets=[sot[0], sot[1], sot[2], sot[3]],
        durations=[[0], [0], [0], [0]],
        amplitudes=None,
        tmod=None,
        pmod=[
            None,
            Bunch(name=['Lag'], param=itemlag[1].tolist(), poly=[2]), None,
            Bunch(name=['Lag'], param=itemlag[3].tolist(), poly=[2])
        ],
        regressor_names=None,
        regressors=None)
]

cont1 = ('Famous_lag1', 'T', ['F2xLag^1'], [1])
cont2 = ('Famous_lag2', 'T', ['F2xLag^2'], [1])
```

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```
fcont1 = ('Famous Lag', 'F', [cont1, cont2])
paramcontrasts = [cont1, cont2, fcont1]

paramanalysis = llanalysis.clone(name='paramanalysis')

paramanalysis.inputs.level1design.bases = {'hrf': {'derivs': [0, 0]}}
paramanalysis.inputs.modelspec.subject_info = subjectinfo_param
paramanalysis.inputs.contrastestimate.contrasts = paramcontrasts
paramanalysis.inputs.contrastestimate.use_derivs = False

llpipeline.connect(
    [(preproc, paramanalysis,
      [('realn.realignment_parameters', 'modelspec.realignment_parameters'),
       (('smooth.smoothed_files', makelist), 'modelspec.functional_runs')])])])
```

28.1.7 Setup the pipeline

The nodes created above do not describe the flow of data. They merely describe the parameters used for each function. In this section we setup the connections between the nodes such that appropriate outputs from nodes are piped into appropriate inputs of other nodes.

Use the `nipyype.pipeline.engine.Pipeline` to create a graph-based execution pipeline for first level analysis. The config options tells the pipeline engine to use *workdir* as the disk location to use when running the processes and keeping their outputs. The *use_parameterized_dirs* tells the engine to create sub-directories under *workdir* corresponding to the iterables in the pipeline. Thus for this pipeline there will be subject specific sub-directories.

The `nipyype.pipeline.engine.Pipeline.connect` function creates the links between the processes, i.e., how data should flow in and out of the processing nodes.

```
level1 = pe.Workflow(name="level1")
level1.base_dir = os.path.abspath('spm_face_tutorial/workingdir')

level1.connect([(infosource, datasource, [('subject_id', 'subject_id')]),
               (datasource, llpipeline,
                [('struct', 'preproc.coregister.source'),
                 ('func', 'preproc.realn.in_files')])])])
```

28.1.8 Setup storage results

Use `nipyype.interfaces.io.DataSink` to store selected outputs from the pipeline in a specific location. This allows the user to selectively choose important output bits from the analysis and keep them.

The first step is to create a `datasink` node and then to connect outputs from the modules above to storage locations. These take the following form `directory_name[.@]subdir` where parts between `[]` are optional. For example `'realn.@mean'` below creates a directory called `realn` in `'11output/subject_id/'` and stores the mean image output from the `Realign` process in the `realn` directory. If the `@` is left out, then a sub-directory with the name `'mean'` would be created and the mean image would be copied to that directory.

```
datasink = pe.Node(interface=nio.DataSink(), name="datasink")
datasink.inputs.base_directory = os.path.abspath(
    'spm_auditory_tutorial/11output')

def getstripdir(subject_id):
    import os
    return os.path.join(
```

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```
os.path.abspath('spm_auditory_tutorial/workingdir'),
'_subject_id_%s' % subject_id)

# store relevant outputs from various stages of the 1st level analysis
level1.connect([
    (infosource, datasink, [('subject_id', 'container'),
                            (('subject_id', getstripdir), 'strip_dir')]),
    (l1pipeline, datasink,
     [('analysis.contrastestimate.con_images', 'contrasts.@con'),
      ('analysis.contrastestimate.spmT_images', 'contrasts.@T'),
      ('paramanalysis.contrastestimate.con_images',
       'paramcontrasts.@con'), ('paramanalysis.contrastestimate.spmT_images',
                               'paramcontrasts.@T')]),
])
```

code discussed above sets up **all** the necessary data structures

opriate parameters and the connectivity between the sses, but does not generate any output. To actually run the sis on the data the `nipype.pipeline.engine.Pipeline.Run`

```
if __name__ == '__main__':
    level1.run()
    level1.write_graph()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

fMRI: SPM nested workflows

The `fmri_spm.py` integrates several interfaces to perform a first and second level analysis on a two-subject data set. The tutorial can be found in the examples folder. Run the tutorial from inside the `nipype` tutorial directory:

```
python fmri_spm_nested.py
```

Import necessary modules from `nipype`.

```
from __future__ import print_function
from builtins import str
from builtins import range
import os.path as op # system functions

from nipype.interfaces import io as nio # Data i/o
from nipype.interfaces import spm as spm # spm
# from nipype.interfaces import matlab as mlab # how to run matlab
from nipype.interfaces import fsl as fsl # fsl
from nipype.interfaces import utility as niu # utility
from nipype.pipeline import engine as pe # pypeline engine
from nipype.algorithms import rapidart as ra # artifact detection
from nipype.algorithms import modelgen as model # model specification
```

29.1 Preliminaries

Set any package specific configuration. The output file format for FSL routines is being set to uncompressed NIFTI and a specific version of matlab is being used. The uncompressed format is required because SPM does not handle compressed NIFTI.

```
# Tell fsl to generate all output in uncompressed nifti format
fsl.FSLCommand.set_default_output_type('NIFTI')

# Set the way matlab should be called
# mlab.MatlabCommand.set_default_matlab_cmd("matlab -nodesktop -nosplash")
# mlab.MatlabCommand.set_default_paths('/software/spm8')
```

29.2 lows

In this tutorial we will be setting up a hierarchical workflow for spm analysis. This will demonstrate how pre-defined workflows can be setup and shared across users, projects and labs. Example of how to inline functions in connect() —————

```
def _template_path(in_data):
    import os.path as op
    return op.abspath(op.join(in_data, 'nipyne-tutorial/data/T1.nii'))
```

29.3 Set-up preprocessing workflow

This is a generic preprocessing workflow that can be used by different analyses

```
preproc = pe.Workflow(name='preproc')
```

A node called inputnode is set to designate the path in which input data are located:

```
inputnode = pe.Node(
    niu.IdentityInterface(fields=['in_data']), name='inputnode')
```

Use `nipyne.interfaces.spm.Realign` for motion correction and register all images to the mean image.

```
realign = pe.Node(spm.Realign(), name="realign")
realign.inputs.register_to_mean = True
```

Use `nipyne.algorithms.rapidart` to determine which of the images in the functional series are outliers based on deviations in intensity or movement.

```
art = pe.Node(ra.ArtifactDetect(), name="art")
art.inputs.use_differences = [True, False]
art.inputs.use_norm = True
art.inputs.norm_threshold = 1
art.inputs.zintensity_threshold = 3
art.inputs.mask_type = 'file'
art.inputs.parameter_source = 'SPM'
```

Skull strip structural images using `nipyne.interfaces.fsl.BET`.

```
skullstrip = pe.Node(fsl.BET(), name="skullstrip")
skullstrip.inputs.mask = True
```

Use `nipyne.interfaces.spm.Coregister` to perform a rigid body registration of the functional data to the structural data.

```
coregister = pe.Node(spm.Coregister(), name="coregister")
coregister.inputs.jobtype = 'estimate'
```

Warp functional and structural data to SPM's T1 template using `nipyne.interfaces.spm.Normalize`. The tutorial data set includes the template image, T1.nii.

```
normalize = pe.Node(spm.Normalize(), name="normalize")
```

Smooth the functional data using `nipyne.interfaces.spm.Smooth`.

```
smooth = pe.Node(spm.Smooth(), name="smooth")
fwhmlist = [4]
smooth.iterables = ('fwhm', fwhmlist)
```

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```

preproc.connect([
    (inputnode, normalize, [(['in_data', _template_path), 'template'])),
    (realign, coregister, [(['mean_image', 'source'), ('realigned_files',
                                                                    'apply_to_files')]),
    (coregister, normalize, [(['coregistered_files', 'apply_to_files')]),
    (normalize, smooth, [(['normalized_files', 'in_files')]),
    (normalize, skullstrip, [(['normalized_source', 'in_file')]),
    (realign, art, [(['realignment_parameters', 'realignment_parameters')]),
    (normalize, art, [(['normalized_files', 'realigned_files')]),
    (skullstrip, art, [(['mask_file', 'mask_file')]),
])

```

29.4 Set up analysis workflow

```
l1analysis = pe.Workflow(name='analysis')
```

Generate SPM-specific design information using `nipy.interfaces.spm.SpecifyModel`.

```

modelspec = pe.Node(model.SpecifySPMModel(), name="modelspec")
modelspec.inputs.concatenate_runs = True

```

Generate a first level SPM.mat file for analysis `nipy.interfaces.spm.Level1Design`.

```

levelldesign = pe.Node(spm.Level1Design(), name="levelldesign")
levelldesign.inputs.bases = {'hrf': {'derivs': [0, 0]}}

```

Use `nipy.interfaces.spm.EstimateModel` to determine the parameters of the model.

```

levellestimate = pe.Node(spm.EstimateModel(), name="levellestimate")
levellestimate.inputs.estimate_method = {'Classical': 1}

```

Use `nipy.interfaces.spm.EstimateContrast` to estimate the first level contrasts specified in a few steps above.

```
contrastestimate = pe.Node(spm.EstimateContrast(), name="contrastestimate")
```

Use `:class: nipy.interfaces.utility.Select` to select each contrast for reporting.

```
selectcontrast = pe.Node(niu.Select(), name="selectcontrast")
```

Use `nipy.interfaces.fsl.Overlay` to combine the statistical output of the contrast estimate and a background image into one volume.

```

overlaystats = pe.Node(fsl.Overlay(), name="overlaystats")
overlaystats.inputs.stat_thresh = (3, 10)
overlaystats.inputs.show_negative_stats = True
overlaystats.inputs.auto_thresh_bg = True

```

Use `nipy.interfaces.fsl.Slicer` to create images of the overlaid statistical volumes for a report of the first-level results.

```

slicestats = pe.Node(fsl.Slicer(), name="slicestats")
slicestats.inputs.all_axial = True
slicestats.inputs.image_width = 750

l1analysis.connect([ (modelspec, levelldesign,
                      [(['session_info',
                        'session_info')]), (levelldesign, levellestimate,

```

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```

[('spm_mat_file', 'spm_mat_file')]],
(levelleestimate, contrastestimate,
[('spm_mat_file', 'spm_mat_file'), ('beta_images',
'beta_images'),
('residual_image',
'residual_image')]), (contrastestimate, selectcontrast,
[('spmT_images', 'inlist')]),
(selectcontrast, overlaystats,
[('out', 'stat_image')]), (overlaystats, slicestats,
[('out_file', 'in_file')]))

```

29.5 Preproc + Analysis pipeline

```

l1pipeline = pe.Workflow(name='firstlevel')
l1pipeline.connect([
    (preproc, l1analysis,
    [('realign.realignment_parameters', 'modelspec.realignment_parameters'),
    ('smooth.smoothed_files',
    'modelspec.functional_runs'), ('art.outlier_files',
    'modelspec.outlier_files'),
    ('skullstrip.mask_file',
    'levelldesign.mask_image'), ('normalize.normalized_source',
    'overlaystats.background_image')]),
])

```

29.6 Data specific components

The nipy tutorial contains data for two subjects. Subject data is in two subdirectories, `s1` and `s2`. Each subject directory contains four functional volumes: `f3.nii`, `f5.nii`, `f7.nii`, `f10.nii`. And one anatomical volume named `struct.nii`.

Below we set some variables to inform the `datasource` about the layout of our data. We specify the location of the data, the subject sub-directories and a dictionary that maps each run to a mnemonic (or field) for the run type (`struct` or `func`). These fields become the output fields of the `datasource` node in the pipeline.

In the example below, run 'f3' is of type 'func' and gets mapped to a nifti filename through a template '%s.nii'. So 'f3' would become 'f3.nii'.

```

# Specify the subject directories
subject_list = ['s1', 's3']
# Map field names to individual subject runs.
info = dict(
    func=[('subject_id', ['f3', 'f5', 'f7', 'f10'])],
    struct=[('subject_id', 'struct')])

infosource = pe.Node(
    niu.IdentityInterface(fields=['subject_id']), name="infosource")

```

Here we set up iteration over all the subjects. The following line is a particular example of the flexibility of the system. The `datasource` attribute `iterables` tells the pipeline engine that it should repeat the analysis on each of the items in the `subject_list`. In the current example, the entire first level preprocessing and estimation will be repeated for each subject contained in `subject_list`.

```
infosource.iterables = ('subject_id', subject_list)
```


Now we create a `nipyre.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipyre.pipeline.NodeWrapper` module wraps the interface object and provides additional housekeeping and pipeline specific functionality.

```
datasource = pe.Node(
    nio.DataGrabber(infields=['subject_id'], outfields=['func', 'struct']),
    name='datasource')
datasource.inputs.template = 'nipyre-tutorial/data/%s/%s.nii'
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True
```

29.7 Experimental paradigm specific components

Here we create a function that returns subject-specific information about the experimental paradigm. This is used by the `nipyre.interfaces.spm.SpecifyModel` to create the information necessary to generate an SPM design matrix. In this tutorial, the same paradigm was used for every participant.

```
def subjectinfo(subject_id):
    from nipyre.interfaces.base import Bunch
    from copy import deepcopy
    print("Subject ID: %s\n" % str(subject_id))
    output = []
    names = ['Task-Odd', 'Task-Even']
    for r in range(4):
        onsets = [list(range(15, 240, 60)), list(range(45, 240, 60))]
        output.insert(r,
            Bunch(
                conditions=names,
                onsets=deepcopy(onsets),
                durations=[[15] for s in names],
                amplitudes=None,
                tmod=None,
                pmod=None,
                regressor_names=None,
                regressors=None))
    return output
```

Setup the contrast structure that needs to be evaluated. This is a list of lists. The inner list specifies the contrasts and has the following format - [Name,Stat,[list of condition names],[weights on those conditions]]. The condition names must match the *names* listed in the *subjectinfo* function described above.

```
cont1 = ('Task>Baseline', 'T', ['Task-Odd', 'Task-Even'], [0.5, 0.5])
cont2 = ('Task-Odd>Task-Even', 'T', ['Task-Odd', 'Task-Even'], [1, -1])
contrasts = [cont1, cont2]

# set up node specific inputs
modelspecref = llpipeline.inputs.analysis.modelspec
modelspecref.input_units = 'secs'
modelspecref.output_units = 'secs'
modelspecref.time_repetition = 3.
modelspecref.high_pass_filter_cutoff = 120

l1designref = llpipeline.inputs.analysis.level1design
l1designref.timing_units = modelspecref.output_units
l1designref.interscan_interval = modelspecref.time_repetition

llpipeline.inputs.analysis.contrastestimate.contrasts = contrasts
```

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```
# Iterate over each contrast and create report images.
selectcontrast.iterables = ('index', [[i] for i in range(len(contrasts))])
```

The nodes created above do not describe the flow of data. They merely describe the parameters used for each function. In this section we setup the connections between the nodes such that appropriate outputs from nodes are piped into appropriate inputs of other nodes. Use the `nipype.pipeline.engine.Pipeline` to create a graph-based execution pipeline for first level analysis. The config options tells the pipeline engine to use *workdir* as the disk location to use when running the processes and keeping their outputs. The *use_parameterized_dirs* tells the engine to create sub-directories under *workdir* corresponding to the iterables in the pipeline. Thus for this pipeline there will be subject specific The `nipype.pipeline.engine.Pipeline.connect` function creates the links between the processes, i.e., how data should flow in and out of

```
level1 = pe.Workflow(name="level1")
level1.base_dir = op.abspath('spm_tutorial2/workingdir')

level1.connect([
    (inputnode, datasource, [('in_data', 'base_directory')]),
    (infosource, datasource, [('subject_id', 'subject_id')]),
    (datasource, llpipeline, [('func', 'preproc.realign.in_files'),
                              ('struct', 'preproc.coregister.target'),
                              ('struct', 'preproc.normalize.source')]),
    (infosource, llpipeline, [(['subject_id', subjectinfo),
                              'analysis.modelspec.subject_info'])),
])
```

29.8 Setup storage results

Use `nipype.interfaces.io.DataSink` to store selected outputs from the pipeline in a specific location. This allows the user to selectively choose important output bits from the analysis and keep them.

The first step is to create a datasink node and then to connect outputs from the modules above to storage locations. These take the following form `directory_name[.@]subdir` where parts between `[]` are optional. For example `'realign.@mean'` below creates a directory called `realign` in `'l1output/subject_id/'` and stores the mean image output from the `Realign` process in the `realign` directory. If the `@` is left out, then a sub-directory with the name `'mean'` would be created and the mean image would be copied to that directory.

```
datasink = pe.Node(nio.DataSink(), name="datasink")
datasink.inputs.base_directory = op.abspath('spm_tutorial2/l1output')
report = pe.Node(nio.DataSink(), name='report')
report.inputs.base_directory = op.abspath('spm_tutorial2/report')
report.inputs.parameterization = False

def getstripdir(subject_id):
    import os.path as op
    return op.join(
        op.abspath('spm_tutorial2/workingdir'), '_subject_id_%s' % subject_id)

# store relevant outputs from various stages of the 1st level analysis
level1.connect([
    (infosource, datasink, [(['subject_id', 'container'),
                            (('subject_id', getstripdir), 'strip_dir')]),
```

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```

(l1pipeline, datasink,
 [ ('analysis.contrastestimate.con_images', 'contrasts.@con'),
   ('analysis.contrastestimate.spmT_images', 'contrasts.@T') ]),
 (infosource, report, [ ('subject_id', 'container'),
                        (('subject_id', getstripdir), 'strip_dir') ]),
 (l1pipeline, report, [ ('analysis.slicestats.out_file', '@report') ]),
 ])

```

code discussed above sets up `all` the necessary data structures

opriate parameters and the connectivity between the sses, but does not generate any output. To actually run the sis on the data the `nipyne.pipeline.engine.Pipeline.Run`

```

if __name__ == '__main__':
    level1.run('MultiProc')
    level1.write_graph()

```

29.9 Setup level 2 pipeline

Use `nipyne.interfaces.io.DataGrabber` to extract the contrast images across a group of first level subjects. Unlike the previous pipeline that iterated over subjects, this pipeline will iterate over contrasts.

```

# collect all the con images for each contrast.
contrast_ids = list(range(1, len(contrasts) + 1))
l2source = pe.Node(nio.DataGrabber(infields=['fwhm', 'con']), name="l2source")
# we use .*i* to capture both .img (SPM8) and .nii (SPM12)
l2source.inputs.template = op.abspath(
    'spm_tutorial2/l1output/*/con*/*/_fwhm_%d/con_%04d.*i*')
# iterate over all contrast images
l2source.iterables = [ ('fwhm', fwhmlist), ('con', contrast_ids) ]
l2source.inputs.sort_filelist = True

```

Use `nipyne.interfaces.spm.OneSampleTTestDesign` to perform a simple statistical analysis of the contrasts from the group of `n` this example).

```

# setup a 1-sample t-test node
onesampttestdes = pe.Node(spm.OneSampleTTestDesign(), name="onesampttestdes")
l2estimate = pe.Node(spm.EstimateModel(), name="level2estimate")
l2estimate.inputs.estimation_method = {'Classical': 1}
l2conestimate = pe.Node(spm.EstimateContrast(), name="level2conestimate")
cont1 = ('Group', 'T', ['mean'], [1])
l2conestimate.inputs.contrasts = [cont1]
l2conestimate.inputs.group_contrast = True

```

As before, we setup a pipeline to connect these two nodes (l2source lettest).

```

l2pipeline = pe.Workflow(name="level2")
l2pipeline.base_dir = op.abspath('spm_tutorial2/l2output')
l2pipeline.connect([
    (l2source, onesampttestdes, [ ('outfiles', 'in_files') ]),
    (onesampttestdes, l2estimate, [ ('spm_mat_file', 'spm_mat_file') ]),
    (l2estimate, l2conestimate,
     [ ('spm_mat_file', 'spm_mat_file'), ('beta_images', 'beta_images'),
       ('residual_image', 'residual_image') ]),
])

```

29.10 Execute the second level pipeline

```
if __name__ == '__main__':  
    l2pipeline.run('MultiProc')
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

HOWTO: Using caching without using Workflow

Using nipy in an imperative way: caching without workflow

Note that in the following example, we are calling command-lines with disk I/O that persists across runs, but we never have to worry about the file names or the directories.

The disk location of the persistence is encoded by hashes. To find out where an operation has been persisted, simply look in it's output variable:

```
out.runtime.cwd
```

```
from nipy.interfaces import fsl
fsl.FSLCommand.set_default_output_type('NIFTI')

from nipy.caching import Memory

import glob

# First retrieve the list of files that we want to work upon
in_files = glob.glob('data/*/f3.nii')

# Create a memory context
mem = Memory('.')

# Apply an arbitrary (and pointless, here) threshold to the files
threshold = [
    mem.cache(fsl.Threshold)(in_file=f, thresh=i)
    for i, f in enumerate(in_files)
]

# Merge all these files along the time dimension
out_merge = mem.cache(fsl.Merge)(
    dimension="t",
    in_files=[t.outputs.out_file for t in threshold],
)

# And finally compute the mean
out_mean = mem.cache(fsl.MeanImage)(in_file=out_merge.outputs.merged_file)

# To avoid having increasing disk size we can keep only what was touched
```

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```
# in this run
# mem.clear_previous_runs()

# or what wasn't used since the start of 2011
# mem.clear_runs_since(year=2011)
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

rsfMRI: ANTS, FS, FSL, SPM, aCompCor

A preprocessing workflow for Siemens resting state data.

This workflow makes use of:

- ANTS
- FreeSurfer
- FSL
- SPM
- CompCor

For example:

```
python rsfmri_preprocessing.py -d /data/12345-34-1.dcm -f /data/Resting.nii
-s subj001 -o output -p PBS --plugin_args "dict(qsub_args='-q many')"
```

or

```
python rsfmri_vol_surface_preprocessing.py -f SUB_1024011/E?/func/rest.nii
-t OASIS-30_Atropos_template_in_MNI152_2mm.nii.gz --TR 2 -s SUB_1024011
--subjects_dir fsdata --slice_times 0 17 1 18 2 19 3 20 4 21 5 22 6 23
7 24 8 25 9 26 10 27 11 28 12 29 13 30 14 31 15 32 16 -o .
```

This workflow takes resting timeseries and a Siemens dicom file corresponding to it and preprocesses it to produce timeseries coordinates or grayordinates.

This workflow also requires 2mm subcortical atlas and templates that are available from:

<http://mindboggle.info/data.html>

specifically the 2mm versions of:

- Joint Fusion Atlas
- MNI template

```
from __future__ import division, unicode_literals
from builtins import open, range, str

import os

from nipype.interfaces.base import CommandLine
CommandLine.set_default_terminal_output('allatonce')

from dicom import read_file
```

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```

from nipyype.interfaces import (spm, fsl, Function, ants, freesurfer)
from nipyype.interfaces.c3 import C3dAffineTool

fsl.FSLCommand.set_default_output_type('NIFTI')

from nipyype import Workflow, Node, MapNode
from nipyype.interfaces import matlab as mlab

mlab.MatlabCommand.set_default_matlab_cmd("matlab -nodisplay")
# If SPM is not in your MATLAB path you should add it here
# mlab.MatlabCommand.set_default_paths('/software/matlab/spm12')

from nipyype.algorithms.rapidart import ArtifactDetect
from nipyype.algorithms.misc import TSNR, CalculateMedian
from nipyype.interfaces.utility import Rename, Merge, IdentityInterface
from nipyype.utils.filemanip import filename_to_list
from nipyype.interfaces.io import DataSink, FreeSurferSource

import numpy as np
import scipy as sp
import nibabel as nb

imports = [
    'import os', 'import nibabel as nb', 'import numpy as np',
    'import scipy as sp',
    'from nipyype.utils.filemanip import filename_to_list, list_to_filename, split_
    ↪filename',
    'from scipy.special import legendre'
]

def get_info(dicom_files):
    from dcmstack.extract import default_extractor
    """Given a Siemens dicom file return metadata

    Returns
    -----
    RepetitionTime
    Slice Acquisition Times
    Spacing between slices
    """
    meta = default_extractor(
        read_file(
            filename_to_list(dicom_files)[0],
            stop_before_pixels=True,
            force=True))
    return (meta['RepetitionTime'] / 1000., meta['CsaImage.MosaicRefAcqTimes'],
            meta['SpacingBetweenSlices'])

def median(in_files):
    """Computes an average of the median of each realigned timeseries

    Parameters
    -----

```

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```

in_files: one or more realigned Nifti 4D time series

Returns
-----

out_file: a 3D Nifti file
"""
import numpy as np
import nibabel as nb
from nipy.utils import NUMPY_MMAP
average = None
for idx, filename in enumerate(filename_to_list(in_files)):
    img = nb.load(filename, mmap=NUMPY_MMAP)
    data = np.median(img.get_data(), axis=3)
    if average is None:
        average = data
    else:
        average = average + data
median_img = nb.Nifti1Image(average / float(idx + 1), img.affine,
                             img.header)
filename = os.path.join(os.getcwd(), 'median.nii.gz')
median_img.to_filename(filename)
return filename

def bandpass_filter(files, lowpass_freq, highpass_freq, fs):
    """Bandpass filter the input files

    Parameters
    -----
    files: list of 4d nifti files
    lowpass_freq: cutoff frequency for the low pass filter (in Hz)
    highpass_freq: cutoff frequency for the high pass filter (in Hz)
    fs: sampling rate (in Hz)
    """
    from nipy.utils.filemanip import split_filename, list_to_filename
    import numpy as np
    import nibabel as nb
    from nipy.utils import NUMPY_MMAP
    out_files = []
    for filename in filename_to_list(files):
        path, name, ext = split_filename(filename)
        out_file = os.path.join(os.getcwd(), name + '_bp' + ext)
        img = nb.load(filename, mmap=NUMPY_MMAP)
        timepoints = img.shape[-1]
        F = np.zeros((timepoints))
        lowidx = int(timepoints / 2) + 1
        if lowpass_freq > 0:
            lowidx = np.round(lowpass_freq / fs * timepoints)
        highidx = 0
        if highpass_freq > 0:
            highidx = np.round(highpass_freq / fs * timepoints)
        F[highidx:lowidx] = 1
        F = ((F + F[::-1]) > 0).astype(int)
        data = img.get_data()
        if np.all(F == 1):
            filtered_data = data

```

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```

        else:
            filtered_data = np.real(np.fft.ifftn(np.fft.fftn(data) * F))
            img_out = nb.Nifti1Image(filtered_data, img.affine, img.header)
            img_out.to_filename(out_file)
            out_files.append(out_file)
    return list_to_filename(out_files)

def motion_regressors(motion_params, order=0, derivatives=1):
    """Compute motion regressors upto given order and derivative

    motion + d(motion)/dt + d2(motion)/dt2 (linear + quadratic)
    """
    import numpy as np
    out_files = []
    for idx, filename in enumerate(filename_to_list(motion_params)):
        params = np.genfromtxt(filename)
        out_params = params
        for d in range(1, derivatives + 1):
            cparams = np.vstack((np.repeat(params[0, :], None, :), d, axis=0),
                                params))
            out_params = np.hstack((out_params, np.diff(cparams, d, axis=0)))
        out_params2 = out_params
        for i in range(2, order + 1):
            out_params2 = np.hstack((out_params2, np.power(out_params, i)))
        filename = os.path.join(os.getcwd(), "motion_regressor%02d.txt" % idx)
        np.savetxt(filename, out_params2, fmt=b"%10f")
        out_files.append(filename)
    return out_files

def build_filter1(motion_params, comp_norm, outliers, detrend_poly=None):
    """Builds a regressor set comprising motion parameters, composite norm and
    outliers

    The outliers are added as a single time point column for each outlier

    Parameters
    -----

    motion_params: a text file containing motion parameters and its derivatives
    comp_norm: a text file containing the composite norm
    outliers: a text file containing 0-based outlier indices
    detrend_poly: number of polynomials to add to detrend

    Returns
    -----

    components_file: a text file containing all the regressors
    """
    import numpy as np
    import nibabel as nb
    from scipy.special import legendre
    out_files = []
    for idx, filename in enumerate(filename_to_list(motion_params)):
        params = np.genfromtxt(filename)
        norm_val = np.genfromtxt(filename_to_list(comp_norm)[idx])

```

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```

out_params = np.hstack((params, norm_val[:, None]))
try:
    outlier_val = np.genfromtxt(filename_to_list(outliers)[idx])
except IOError:
    outlier_val = np.empty((0))
for index in np.atleast_1d(outlier_val):
    outlier_vector = np.zeros((out_params.shape[0], 1))
    outlier_vector[index] = 1
    out_params = np.hstack((out_params, outlier_vector))
if detrend_poly:
    timepoints = out_params.shape[0]
    X = np.empty((timepoints, 0))
    for i in range(detrend_poly):
        X = np.hstack((X, legendre(i + 1)(np.linspace(
            -1, 1, timepoints))[:, None]))
    out_params = np.hstack((out_params, X))
filename = os.path.join(os.getcwd(), "filter_regressor%02d.txt" % idx)
np.savetxt(filename, out_params, fmt=b"%10f")
out_files.append(filename)
return out_files

def extract_noise_components(realigned_file,
                             mask_file,
                             num_components=5,
                             extra_regressors=None):
    """Derive components most reflective of physiological noise

    Parameters
    -----
    realigned_file: a 4D Nifti file containing realigned volumes
    mask_file: a 3D Nifti file containing white matter + ventricular masks
    num_components: number of components to use for noise decomposition
    extra_regressors: additional regressors to add

    Returns
    -----
    components_file: a text file containing the noise components
    """
    from scipy.linalg.decomp_svd import svd
    import numpy as np
    import nibabel as nb
    from nipy.utils import NUMPY_MMAP
    import os
    imgseries = nb.load(realigned_file, mmap=NUMPY_MMAP)
    components = None
    for filename in filename_to_list(mask_file):
        mask = nb.load(filename, mmap=NUMPY_MMAP).get_data()
        if len(np.nonzero(mask > 0)[0]) == 0:
            continue
        voxel_timecourses = imgseries.get_data()[mask > 0]
        voxel_timecourses[np.isnan(np.sum(voxel_timecourses, axis=1)), :] = 0
        # remove mean and normalize by variance
        # voxel_timecourses.shape == [nvoxels, time]
        X = voxel_timecourses.T
        stdX = np.std(X, axis=0)
        stdX[stdX == 0] = 1.

```

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```

        stdX[np.isnan(stdX)] = 1.
        stdX[np.isinf(stdX)] = 1.
        X = (X - np.mean(X, axis=0)) / stdX
        u, _, _ = svd(X, full_matrices=False)
        if components is None:
            components = u[:, :num_components]
        else:
            components = np.hstack((components, u[:, :num_components]))
    if extra_regressors:
        regressors = np.genfromtxt(extra_regressors)
        components = np.hstack((components, regressors))
    components_file = os.path.join(os.getcwd(), 'noise_components.txt')
    np.savetxt(components_file, components, fmt=b"%10f")
    return components_file

def rename(in_files, suffix=None):
    from nipy.utils.filemanip import (filename_to_list, split_filename,
                                       list_to_filename)

    out_files = []
    for idx, filename in enumerate(filename_to_list(in_files)):
        _, name, ext = split_filename(filename)
        if suffix is None:
            out_files.append(name + ('_%03d' % idx) + ext)
        else:
            out_files.append(name + suffix + ext)
    return list_to_filename(out_files)

def get_aparc_aseg(files):
    """Return the aparc+aseg.mgz file"""
    for name in files:
        if 'aparc+aseg.mgz' in name:
            return name
    raise ValueError('aparc+aseg.mgz not found')

def extract_subrois(timeseries_file, label_file, indices):
    """Extract voxel time courses for each subcortical roi index

    Parameters
    -----

    timeseries_file: a 4D Nifti file
    label_file: a 3D file containing rois in the same space/size of the 4D file
    indices: a list of indices for ROIs to extract.

    Returns
    -----

    out_file: a text file containing time courses for each voxel of each roi
    The first four columns are: freesurfer index, i, j, k positions in the
    label file
    """
    from nipy.utils.filemanip import split_filename
    import nibabel as nb
    from nipy.utils import NUMPY_MMAP
    import os

```

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img = nb.load(timeseries_file, mmap=NUMPY_MMAP)
data = img.get_data()
roiimg = nb.load(label_file, mmap=NUMPY_MMAP)
rois = roiimg.get_data()
prefix = split_filename(timeseries_file)[1]
out_ts_file = os.path.join(os.getcwd(), '%s_subcortical_ts.txt' % prefix)
with open(out_ts_file, 'wt') as fp:
    for fsindex in indices:
        ijk = np.nonzero(rois == fsindex)
        ts = data[ijk]
        for i0, row in enumerate(ts):
            fp.write('%d,%d,%d,%d,' % (
                fsindex, ijk[0][i0], ijk[1][i0],
                ijk[2][i0]) + ','.join(['%.10f' % val
                                        for val in row]) + '\n')
    return out_ts_file

def combine_hemi(left, right):
    """Combine left and right hemisphere time series into a single text file
    """
    import os
    import numpy as np
    from nipy.utils import NUMPY_MMAP
    lh_data = nb.load(left, mmap=NUMPY_MMAP).get_data()
    rh_data = nb.load(right, mmap=NUMPY_MMAP).get_data()

    indices = np.vstack((1000000 + np.arange(0, lh_data.shape[0])[:, None],
                        2000000 + np.arange(0, rh_data.shape[0])[:, None]))
    all_data = np.hstack((indices,
                        np.vstack((lh_data.squeeze(), rh_data.squeeze()))))
    filename = left.split('.')[1] + '_combined.txt'
    np.savetxt(
        filename,
        all_data,
        fmt=''.join(['%d'] + ['%.10f'] * (all_data.shape[1] - 1)))
    return os.path.abspath(filename)

def create_reg_workflow(name='registration'):
    """Create a FEAT preprocessing workflow together with freesurfer

    Parameters
    -----

    name : name of workflow (default: 'registration')

    Inputs::

        inputspec.source_files : files (filename or list of filenames to register)
        inputspec.mean_image : reference image to use
        inputspec.anatomical_image : anatomical image to coregister to
        inputspec.target_image : registration target

    Outputs::

        outputspec.func2anat_transform : FLIRT transform

```

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        outputspec.anat2target_transform : FLIRT+FNIRT transform
        outputspec.transformed_files : transformed files in target space
        outputspec.transformed_mean : mean image in target space
    """

    register = Workflow(name=name)

    inputnode = Node(
        interface=IdentityInterface(fields=[
            'source_files', 'mean_image', 'subject_id', 'subjects_dir',
            'target_image'
        ]),
        name='inputspec')

    outputnode = Node(
        interface=IdentityInterface(fields=[
            'func2anat_transform', 'out_reg_file', 'anat2target_transform',
            'transforms', 'transformed_mean', 'segmentation_files',
            'anat2target', 'aparc'
        ]),
        name='outputspec')

    # Get the subject's freesurfer source directory
    fssource = Node(FreeSurferSource(), name='fssource')
    fssource.run_without_submitting = True
    register.connect(inputnode, 'subject_id', fssource, 'subject_id')
    register.connect(inputnode, 'subjects_dir', fssource, 'subjects_dir')

    convert = Node(freesurfer.MRIConvert(out_type='nii'), name="convert")
    register.connect(fssource, 'T1', convert, 'in_file')

    # Coregister the median to the surface
    bbregister = Node(freesurfer.BBRegister(), name='bbregister')
    bbregister.inputs.init = 'fsl'
    bbregister.inputs.contrast_type = 't2'
    bbregister.inputs.out_fsl_file = True
    bbregister.inputs.epi_mask = True
    register.connect(inputnode, 'subject_id', bbregister, 'subject_id')
    register.connect(inputnode, 'mean_image', bbregister, 'source_file')
    register.connect(inputnode, 'subjects_dir', bbregister, 'subjects_dir')
    """
    Estimate the tissue classes from the anatomical image. But use spm's segment
    as FSL appears to be breaking.
    """

    stripper = Node(fsl.BET(), name='stripper')
    register.connect(convert, 'out_file', stripper, 'in_file')
    fast = Node(fsl.FAST(), name='fast')
    register.connect(stripper, 'out_file', fast, 'in_files')
    """
    Binarize the segmentation
    """

    binarize = MapNode(
        fsl.ImageMaths(op_string='-nan -thr 0.9 -ero -bin'),
        iterfield=['in_file'],
        name='binarize')

```

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register.connect(fast, 'partial_volume_files', binarize, 'in_file')
"""
Apply inverse transform to take segmentations to functional space
"""

applyxfm = MapNode(
    freesurfer.ApplyVolTransform(inverse=True, interp='nearest'),
    iterfield=['target_file'],
    name='inverse_transform')
register.connect(inputnode, 'subjects_dir', applyxfm, 'subjects_dir')
register.connect(bregister, 'out_reg_file', applyxfm, 'reg_file')
register.connect(binarize, 'out_file', applyxfm, 'target_file')
register.connect(inputnode, 'mean_image', applyxfm, 'source_file')
"""
Apply inverse transform to aparc file
"""

aparcxfm = Node(
    freesurfer.ApplyVolTransform(inverse=True, interp='nearest'),
    name='aparc_inverse_transform')
register.connect(inputnode, 'subjects_dir', aparcxfm, 'subjects_dir')
register.connect(bregister, 'out_reg_file', aparcxfm, 'reg_file')
register.connect(fssource, ('aparc_aseg', get_aparc_aseg), aparcxfm,
                  'target_file')
register.connect(inputnode, 'mean_image', aparcxfm, 'source_file')
"""
Convert the BBRegister transformation to ANTS ITK format
"""

convert2itk = Node(C3dAffineTool(), name='convert2itk')
convert2itk.inputs.fsl2ras = True
convert2itk.inputs.itk_transform = True
register.connect(bregister, 'out_fsl_file', convert2itk, 'transform_file')
register.connect(inputnode, 'mean_image', convert2itk, 'source_file')
register.connect(stripper, 'out_file', convert2itk, 'reference_file')
"""
Compute registration between the subject's structural and MNI template
This is currently set to perform a very quick registration. However, the
registration can be made significantly more accurate for cortical
structures by increasing the number of iterations
All parameters are set using the example from:
#https://github.com/stnava/ANTs/blob/master/Scripts/newAntsExample.sh
"""

reg = Node(ants.Registration(), name='antsRegister')
reg.inputs.output_transform_prefix = "output_"
reg.inputs.transforms = ['Rigid', 'Affine', 'SyN']
reg.inputs.transform_parameters = [(0.1, ), (0.1, ), (0.2, 3.0, 0.0)]
reg.inputs.number_of_iterations = [[10000, 11110, 11110]] * 2 + [[
    100, 30, 20
]]
reg.inputs.dimension = 3
reg.inputs.write_composite_transform = True
reg.inputs.collapse_output_transforms = True
reg.inputs.initial_moving_transform_com = True
reg.inputs.metric = ['Mattes'] * 2 + [['Mattes', 'CC']]
reg.inputs.metric_weight = [1] * 2 + [[0.5, 0.5]]

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reg.inputs.radius_or_number_of_bins = [32] * 2 + [[32, 4]]
reg.inputs.sampling_strategy = ['Regular'] * 2 + [[None, None]]
reg.inputs.sampling_percentage = [0.3] * 2 + [[None, None]]
reg.inputs.convergence_threshold = [1.e-8] * 2 + [-0.01]
reg.inputs.convergence_window_size = [20] * 2 + [5]
reg.inputs.smoothing_sigmas = [[4, 2, 1]] * 2 + [[1, 0.5, 0]]
reg.inputs.sigma_units = ['vox'] * 3
reg.inputs.shrink_factors = [[3, 2, 1]] * 2 + [[4, 2, 1]]
reg.inputs.use_estimate_learning_rate_once = [True] * 3
reg.inputs.use_histogram_matching = [False] * 2 + [True]
reg.inputs.winsorize_lower_quantile = 0.005
reg.inputs.winsorize_upper_quantile = 0.995
reg.inputs.float = True
reg.inputs.output_warped_image = 'output_warped_image.nii.gz'
reg.inputs.num_threads = 4
reg.plugin_args = {'qsub_args': '-l nodes=1:ppn=4'}
register.connect(stripper, 'out_file', reg, 'moving_image')
register.connect(inputnode, 'target_image', reg, 'fixed_image')
"""
Concatenate the affine and ants transforms into a list
"""

merge = Node(Merge(2), iterfield=['in2'], name='mergexfm')
register.connect(convert2itk, 'itk_transform', merge, 'in2')
register.connect(reg, 'composite_transform', merge, 'in1')
"""
Transform the mean image. First to anatomical and then to target
"""

warpmean = Node(ants.ApplyTransforms(), name='warpmean')
warpmean.inputs.input_image_type = 3
warpmean.inputs.interpolation = 'Linear'
warpmean.inputs.invert_transform_flags = [False, False]
warpmean.terminal_output = 'file'
warpmean.inputs.args = '--float'
warpmean.inputs.num_threads = 4

register.connect(inputnode, 'target_image', warpmean, 'reference_image')
register.connect(inputnode, 'mean_image', warpmean, 'input_image')
register.connect(merge, 'out', warpmean, 'transforms')
"""
Assign all the output files
"""

register.connect(reg, 'warped_image', outputnode, 'anat2target')
register.connect(warpmean, 'output_image', outputnode, 'transformed_mean')
register.connect(applyxfm, 'transformed_file', outputnode,
                 'segmentation_files')
register.connect(aparcxfm, 'transformed_file', outputnode, 'aparc')
register.connect(bbregister, 'out_fsl_file', outputnode,
                 'func2anat_transform')
register.connect(bbregister, 'out_reg_file', outputnode, 'out_reg_file')
register.connect(reg, 'composite_transform', outputnode,
                 'anat2target_transform')
register.connect(merge, 'out', outputnode, 'transforms')

return register

```


Creates the main preprocessing workflow

```
def create_workflow(files,
                    target_file,
                    subject_id,
                    TR,
                    slice_times,
                    norm_threshold=1,
                    num_components=5,
                    vol_fwhm=None,
                    surf_fwhm=None,
                    lowpass_freq=-1,
                    highpass_freq=-1,
                    subjects_dir=None,
                    sink_directory=os.getcwd(),
                    target_subject=['fsaverage3', 'fsaverage4'],
                    name='resting'):

    wf = Workflow(name=name)

    # Rename files in case they are named identically
    name_unique = MapNode(
        Rename(format_string='rest_%(run)02d'),
        iterfield=['in_file', 'run'],
        name='rename')
    name_unique.inputs.keep_ext = True
    name_unique.inputs.run = list(range(1, len(files) + 1))
    name_unique.inputs.in_file = files

    realign = Node(interface=spm.Realign(), name="realign")
    realign.inputs.jobtype = 'estwrite'

    num_slices = len(slice_times)
    slice_timing = Node(interface=spm.SliceTiming(), name="slice_timing")
    slice_timing.inputs.num_slices = num_slices
    slice_timing.inputs.time_repetition = TR
    slice_timing.inputs.time_acquisition = TR - TR / float(num_slices)
    slice_timing.inputs.slice_order = (np.argsort(slice_times) + 1).tolist()
    slice_timing.inputs.ref_slice = int(num_slices / 2)

    # Compute TSNR on realigned data regressing polynomials upto order 2
    tsnr = MapNode(TSNR(regress_poly=2), iterfield=['in_file'], name='tsnr')
    wf.connect(slice_timing, 'timecorrected_files', tsnr, 'in_file')

    # Compute the median image across runs
    calc_median = Node(CalculateMedian(), name='median')
    wf.connect(tsnr, 'detrended_file', calc_median, 'in_files')
    """Segment and Register
    """

    registration = create_reg_workflow(name='registration')
    wf.connect(calc_median, 'median_file', registration,
              'inputspec.mean_image')
    registration.inputs.inputspec.subject_id = subject_id
    registration.inputs.inputspec.subjects_dir = subjects_dir
    registration.inputs.inputspec.target_image = target_file
    """Use :class:`nipy.algorithms.rapidart` to determine which of the
    images in the functional series are outliers based on deviations in
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intensity or movement.
"""

art = Node(interface=ArtifactDetect(), name="art")
art.inputs.use_differences = [True, True]
art.inputs.use_norm = True
art.inputs.norm_threshold = norm_threshold
art.inputs.zintensity_threshold = 9
art.inputs.mask_type = 'spm_global'
art.inputs.parameter_source = 'SPM'
"""Here we are connecting all the nodes together. Notice that we add the
↪merge node only if you choose
   to use 4D. Also `get_vox_dims` function is passed along the input volume of
↪normalise to set the optimal
   voxel sizes.
"""

wf.connect([
    (name_unique, realign, [('out_file', 'in_files')]),
    (realign, slice_timing, [('realigned_files', 'in_files')]),
    (slice_timing, art, [('timecorrected_files', 'realigned_files')]),
    (realign, art, [('realignment_parameters', 'realignment_parameters')]),
])

def selectindex(files, idx):
    import numpy as np
    from nipy.utils.filemanip import filename_to_list, list_to_filename
    return list_to_filename(
        np.array(filename_to_list(files))[idx].tolist())

mask = Node(fsl.BET(), name='getmask')
mask.inputs.mask = True
wf.connect(calc_median, 'median_file', mask, 'in_file')

# get segmentation in normalized functional space

def merge_files(in1, in2):
    out_files = filename_to_list(in1)
    out_files.extend(filename_to_list(in2))
    return out_files

# filter some noise

# Compute motion regressors
motreg = Node(
    Function(
        input_names=['motion_params', 'order', 'derivatives'],
        output_names=['out_files'],
        function=motion_regressors,
        imports=imports),
    name='getmotionregress')
wf.connect(realign, 'realignment_parameters', motreg, 'motion_params')

# Create a filter to remove motion and art confounds
createfilter1 = Node(
    Function(
        input_names=[

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        'motion_params', 'comp_norm', 'outliers', 'detrend_poly'
    ],
    output_names=['out_files'],
    function=build_filter1,
    imports=imports),
    name='makemotionbasedfilter')
createfilter1.inputs.detrend_poly = 2
wf.connect(motreg, 'out_files', createfilter1, 'motion_params')
wf.connect(art, 'norm_files', createfilter1, 'comp_norm')
wf.connect(art, 'outlier_files', createfilter1, 'outliers')

filter1 = MapNode(
    fsl.GLM(
        out_f_name='F_mcart.nii', out_pf_name='pF_mcart.nii', demean=True),
    iterfield=['in_file', 'design', 'out_res_name'],
    name='filtermotion')

wf.connect(slice_timing, 'timecorrected_files', filter1, 'in_file')
wf.connect(slice_timing, ('timecorrected_files', rename, '_filtermotart'),
            filter1, 'out_res_name')
wf.connect(createfilter1, 'out_files', filter1, 'design')

createfilter2 = MapNode(
    Function(
        input_names=[
            'realigned_file', 'mask_file', 'num_components',
            'extra_regressors'
        ],
        output_names=['out_files'],
        function=extract_noise_components,
        imports=imports),
    iterfield=['realigned_file', 'extra_regressors'],
    name='makecompcorrfilter')
createfilter2.inputs.num_components = num_components

wf.connect(createfilter1, 'out_files', createfilter2, 'extra_regressors')
wf.connect(filter1, 'out_res', createfilter2, 'realigned_file')
wf.connect(registration,
            ('outputspec.segmentation_files', selectindex, [0, 2]),
            createfilter2, 'mask_file')

filter2 = MapNode(
    fsl.GLM(out_f_name='F.nii', out_pf_name='pF.nii', demean=True),
    iterfield=['in_file', 'design', 'out_res_name'],
    name='filter_noise_nosmooth')
wf.connect(filter1, 'out_res', filter2, 'in_file')
wf.connect(filter1, ('out_res', rename, '_cleaned'), filter2,
            'out_res_name')
wf.connect(createfilter2, 'out_files', filter2, 'design')
wf.connect(mask, 'mask_file', filter2, 'mask')

bandpass = Node(
    Function(
        input_names=['files', 'lowpass_freq', 'highpass_freq', 'fs'],
        output_names=['out_files'],
        function=bandpass_filter,
        imports=imports),

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        name='bandpass_unsmooth')
bandpass.inputs.fs = 1. / TR
bandpass.inputs.highpass_freq = highpass_freq
bandpass.inputs.lowpass_freq = lowpass_freq
wf.connect(filter2, 'out_res', bandpass, 'files')
"""Smooth the functional data using
:class:`nipy.interfaces.spm.Smooth`.
"""

smooth = Node(interface=spm.Smooth(), name="smooth")
smooth.inputs.fwhm = vol_fwhm

wf.connect(bandpass, 'out_files', smooth, 'in_files')

collector = Node(Merge(2), name='collect_streams')
wf.connect(smooth, 'smoothed_files', collector, 'in1')
wf.connect(bandpass, 'out_files', collector, 'in2')
"""
Transform the remaining images. First to anatomical and then to target
"""

warpall = MapNode(
    ants.ApplyTransforms(), iterfield=['input_image'], name='warpall')
warpall.inputs.input_image_type = 3
warpall.inputs.interpolation = 'Linear'
warpall.inputs.invert_transform_flags = [False, False]
warpall.terminal_output = 'file'
warpall.inputs.reference_image = target_file
warpall.inputs.args = '--float'
warpall.inputs.num_threads = 1

# transform to target
wf.connect(collector, 'out', warpall, 'input_image')
wf.connect(registration, 'outputs.spec.transforms', warpall, 'transforms')

mask_target = Node(fsl.ImageMaths(op_string='-bin'), name='target_mask')

wf.connect(registration, 'outputs.spec.anat2target', mask_target, 'in_file')

maskts = MapNode(fsl.ApplyMask(), iterfield=['in_file'], name='ts_masker')
wf.connect(warpall, 'output_image', maskts, 'in_file')
wf.connect(mask_target, 'out_file', maskts, 'mask_file')

# map to surface
# extract aparc+aseg ROIs
# extract subcortical ROIs
# extract target space ROIs
# combine subcortical and cortical rois into a single cifti file

#####
# Convert aparc to subject functional space

# Sample the average time series in aparc ROIs
sampleaparc = MapNode(
    freesurfer.SegStats(default_color_table=True),
    iterfield=['in_file', 'summary_file', 'avgwf_txt_file'],
    name='aparc_ts')

```

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```

sampleaparc.inputs.segment_id = (
    [8] + list(range(10, 14)) + [17, 18, 26, 47] + list(range(49, 55)) +
    [58] + list(range(1001, 1036)) + list(range(2001, 2036)))

wf.connect(registration, 'outputspec.aparc', sampleaparc,
            'segmentation_file')
wf.connect(collector, 'out', sampleaparc, 'in_file')

def get_names(files, suffix):
    """Generate appropriate names for output files
    """
    from nipy.utils.filemanip import (split_filename, filename_to_list,
                                      list_to_filename)

    out_names = []
    for filename in files:
        _, name, _ = split_filename(filename)
        out_names.append(name + suffix)
    return list_to_filename(out_names)

wf.connect(collector, ('out', get_names, '_avgwf.txt'), sampleaparc,
            'avgwf_txt_file')
wf.connect(collector, ('out', get_names, '_summary.stats'), sampleaparc,
            'summary_file')

# Sample the time series onto the surface of the target surface. Performs
# sampling into left and right hemisphere
target = Node(IdentityInterface(fields=['target_subject']), name='target')
target.iterables = ('target_subject', filename_to_list(target_subject))

samplerlh = MapNode(
    freesurfer.SampleToSurface(),
    iterfield=['source_file'],
    name='sampler_lh')
samplerlh.inputs.sampling_method = "average"
samplerlh.inputs.sampling_range = (0.1, 0.9, 0.1)
samplerlh.inputs.sampling_units = "frac"
samplerlh.inputs.interp_method = "trilinear"
samplerlh.inputs.smooth_surf = surf_fwhm
# samplerlh.inputs.cortex_mask = True
samplerlh.inputs.out_type = 'niigz'
samplerlh.inputs.subjects_dir = subjects_dir

samplerlh = samplerlh.clone('sampler_rh')

samplerlh.inputs.hemi = 'lh'
wf.connect(collector, 'out', samplerlh, 'source_file')
wf.connect(registration, 'outputspec.out_reg_file', samplerlh, 'reg_file')
wf.connect(target, 'target_subject', samplerlh, 'target_subject')

samplerlh.set_input('hemi', 'rh')
wf.connect(collector, 'out', samplerlh, 'source_file')
wf.connect(registration, 'outputspec.out_reg_file', samplerlh, 'reg_file')
wf.connect(target, 'target_subject', samplerlh, 'target_subject')

# Combine left and right hemisphere to text file
combiner = MapNode(
    Function(

```

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```

        input_names=['left', 'right'],
        output_names=['out_file'],
        function=combine_hemi,
        imports=imports),
        iterfield=['left', 'right'],
        name="combiner")
wf.connect(samplerlh, 'out_file', combiner, 'left')
wf.connect(samplerlh, 'out_file', combiner, 'right')

# Sample the time series file for each subcortical roi
ts2txt = MapNode(
    Function(
        input_names=['timeseries_file', 'label_file', 'indices'],
        output_names=['out_file'],
        function=extract_subrois,
        imports=imports),
        iterfield=['timeseries_file'],
        name='getsubcortts')
ts2txt.inputs.indices = [8] + list(range(10, 14)) + [17, 18, 26, 47] + \
    list(range(49, 55)) + [58]
ts2txt.inputs.label_file = \
    os.path.abspath(('OASIS-TRT-20_jointfusion_DKT31_CMA_labels_in_MNI152_'
                    '2mm_v2.nii.gz'))
wf.connect(maskts, 'out_file', ts2txt, 'timeseries_file')

#####

substitutions = [('_target_subject_',
                  ''), ('_filtermotart_cleaned_bp_trans_masked', ''),
                  ('_filtermotart_cleaned_bp', '')]

regex_subs = [
    ('_ts_masker.*/sar', '/smooth/'),
    ('_ts_masker.*/ar', '/unsmooth/'),
    ('_combiner.*/sar', '/smooth/'),
    ('_combiner.*/ar', '/unsmooth/'),
    ('_aparc_ts.*/sar', '/smooth/'),
    ('_aparc_ts.*/ar', '/unsmooth/'),
    ('_getsubcortts.*/sar', '/smooth/'),
    ('_getsubcortts.*/ar', '/unsmooth/'),
    ('series/sar', 'series/smooth/'),
    ('series/ar', 'series/unsmooth/'),
    ('_inverse_transform./', ''),
]

# Save the relevant data into an output directory
datasink = Node(interface=DataSink(), name="datasink")
datasink.inputs.base_directory = sink_directory
datasink.inputs.container = subject_id
datasink.inputs.substitutions = substitutions
datasink.inputs.regexp_substitutions = regex_subs # (r'(/_.*(\d+))', r'/'
→run\2')
wf.connect(realign, 'realignment_parameters', datasink,
            'resting.qa.motion')
wf.connect(art, 'norm_files', datasink, 'resting.qa.art.@norm')
wf.connect(art, 'intensity_files', datasink, 'resting.qa.art.@intensity')
wf.connect(art, 'outlier_files', datasink, 'resting.qa.art.@outlier_files')
wf.connect(registration, 'outputspec.segmentation_files', datasink,
            'resting.mask_files')

```

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```

wf.connect(registration, 'outputspec.anat2target', datasink,
            'resting.qa.ants')
wf.connect(mask, 'mask_file', datasink, 'resting.mask_files.@brainmask')
wf.connect(mask_target, 'out_file', datasink, 'resting.mask_files.target')
wf.connect(filter1, 'out_f', datasink, 'resting.qa.compmaps.@mc_F')
wf.connect(filter1, 'out_pf', datasink, 'resting.qa.compmaps.@mc_pF')
wf.connect(filter2, 'out_f', datasink, 'resting.qa.compmaps')
wf.connect(filter2, 'out_pf', datasink, 'resting.qa.compmaps.@p')
wf.connect(bandpass, 'out_files', datasink,
            'resting.timeseries.@bandpassed')
wf.connect(smooth, 'smoothed_files', datasink,
            'resting.timeseries.@smoothed')
wf.connect(createfilter1, 'out_files', datasink,
            'resting.regress.@regressors')
wf.connect(createfilter2, 'out_files', datasink,
            'resting.regress.@compcorr')
wf.connect(maskts, 'out_file', datasink, 'resting.timeseries.target')
wf.connect(sampleaparc, 'summary_file', datasink,
            'resting.parcellations.aparc')
wf.connect(sampleaparc, 'avgwf_txt_file', datasink,
            'resting.parcellations.aparc.@avgwf')
wf.connect(ts2txt, 'out_file', datasink,
            'resting.parcellations.grayo.@subcortical')

datasink2 = Node(interface=DataSink(), name="datasink2")
datasink2.inputs.base_directory = sink_directory
datasink2.inputs.container = subject_id
datasink2.inputs.substitutions = substitutions
datasink2.inputs.regexp_substitutions = regex_subs # (r'(/_.*(\d+))', r'/'
→run\2')
wf.connect(combiner, 'out_file', datasink2,
            'resting.parcellations.grayo.@surface')
return wf

```

Creates the full workflow including getting information from dicom files

```

def create_resting_workflow(args, name=None):
    TR = args.TR
    slice_times = args.slice_times
    if args.dicom_file:
        TR, slice_thickness = get_info(args.dicom_file)
        slice_times = (np.array(slice_times) / 1000.).tolist()
    if name is None:
        name = 'resting_' + args.subject_id
    kwargs = dict(
        files=[os.path.abspath(filename) for filename in args.files],
        target_file=os.path.abspath(args.target_file),
        subject_id=args.subject_id,
        TR=TR,
        slice_times=slice_times,
        vol_fwhm=args.vol_fwhm,
        surf_fwhm=args.surf_fwhm,
        norm_threshold=2.,
        subjects_dir=os.path.abspath(args.fmdir),
        target_subject=args.target_surfs,
        lowpass_freq=args.lowpass_freq,
        highpass_freq=args.highpass_freq,

```

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```

        sink_directory=os.path.abspath(args.sink),
        name=name)
    wf = create_workflow(**kwargs)
    return wf

if __name__ == "__main__":
    from argparse import ArgumentParser, RawTextHelpFormatter
    defstr = ' (default %(default)s) '
    parser = ArgumentParser(
        description=__doc__, formatter_class=RawTextHelpFormatter)
    parser.add_argument(
        "-d",
        "--dicom_file",
        dest="dicom_file",
        help="an example dicom file from the resting series")
    parser.add_argument(
        "-f",
        "--files",
        dest="files",
        nargs="+",
        help="4d nifti files for resting state",
        required=True)
    parser.add_argument(
        "-t",
        "--target",
        dest="target_file",
        help=("Target in MNI space. Best to use the MindBoggle "
              "template - "
              "OASIS-30_Atropos_template_in_MNI152_2mm.nii.gz"),
        required=True)
    parser.add_argument(
        "-s",
        "--subject_id",
        dest="subject_id",
        help="FreeSurfer subject id",
        required=True)
    parser.add_argument(
        "--subjects_dir",
        dest="fsdir",
        help="FreeSurfer subject directory",
        required=True)
    parser.add_argument(
        "--target_surfaces",
        dest="target_surfs",
        nargs="+",
        default=['fsaverage5'],
        help="FreeSurfer target surfaces" + defstr)
    parser.add_argument(
        "--TR",
        dest="TR",
        default=None,
        type=float,
        help="TR if dicom not provided in seconds")
    parser.add_argument(
        "--slice_times",
        dest="slice_times",

```

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```

        nargs="+",
        type=float,
        help="Slice onset times in seconds")
    parser.add_argument(
        '--vol_fwhm',
        default=6.,
        dest='vol_fwhm',
        type=float,
        help="Spatial FWHM" + defstr)
    parser.add_argument(
        '--surf_fwhm',
        default=15.,
        dest='surf_fwhm',
        type=float,
        help="Spatial FWHM" + defstr)
    parser.add_argument(
        "-l",
        "--lowpass_freq",
        dest="lowpass_freq",
        default=0.1,
        type=float,
        help="Low pass frequency (Hz)" + defstr)
    parser.add_argument(
        "-u",
        "--highpass_freq",
        dest="highpass_freq",
        default=0.01,
        type=float,
        help="High pass frequency (Hz)" + defstr)
    parser.add_argument(
        "-o",
        "--output_dir",
        dest="sink",
        help="Output directory base",
        required=True)
    parser.add_argument(
        "-w", "--work_dir", dest="work_dir", help="Output directory base")
    parser.add_argument(
        "-p",
        "--plugin",
        dest="plugin",
        default='Linear',
        help="Plugin to use")
    parser.add_argument(
        "--plugin_args", dest="plugin_args", help="Plugin arguments")
    args = parser.parse_args()

    wf = create_resting_workflow(args)

    if args.work_dir:
        work_dir = os.path.abspath(args.work_dir)
    else:
        work_dir = os.getcwd()

    wf.base_dir = work_dir
    if args.plugin_args:
        wf.run(args.plugin, plugin_args=eval(args.plugin_args))

```

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```
else:
    wf.run(args.plugin)
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

rsfMRI: ANTS, FS, FSL, NiPy, aCompCor

A preprocessing workflow for Siemens resting state data.

This workflow makes use of:

- ANTS
- FreeSurfer
- FSL
- NiPy
- CompCor

For example:

```
python rsfmri_preprocessing.py -d /data/12345-34-1.dcm -f /data/Resting.nii
-s subj001 -o output -p PBS --plugin_args "dict(qsub_args='-q many')"
```

or:

```
python rsfmri_vol_surface_preprocessing.py -f SUB_1024011/E?/func/rest.nii
-t OASIS-30_Atropos_template_in_MNI152_2mm.nii.gz --TR 2 -s SUB_1024011
--subjects_dir fsdata --slice_times 0 17 1 18 2 19 3 20 4 21 5 22 6 23
7 24 8 25 9 26 10 27 11 28 12 29 13 30 14 31 15 32 16 -o .
```

This workflow takes resting timeseries and a Siemens dicom file corresponding to it and preprocesses it to produce timeseries coordinates or grayordinates.

For non-Siemens dicoms, provide slice times instead, since the dicom extractor is not guaranteed to work.

This workflow also requires 2mm subcortical atlas and templates that are available from:

<http://mindboggle.info/data.html>

specifically the 2mm versions of:

- Joint Fusion Atlas
- MNI template

Import necessary modules from nipype.

```
from __future__ import division, unicode_literals
from builtins import open, range, str

import os

from nipype.interfaces.base import CommandLine
CommandLine.set_default_terminal_output('allatonce')
```

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```
# https://github.com/moloney/dcmstack
from dcmstack.extract import default_extractor
# pip install pydicom
from dicom import read_file

from nipy.interfaces import (fsl, Function, ants, freesurfer, nipy)
from nipy.interfaces.c3 import C3dAffineTool

fsl.FSLCommand.set_default_output_type('NIFTI_GZ')

from nipy import Workflow, Node, MapNode

from nipy.algorithms.rapidart import ArtifactDetect
from nipy.algorithms.misc import TSNR, CalculateMedian
from nipy.algorithms.confounds import ACompCor
from nipy.interfaces.utility import Rename, Merge, IdentityInterface
from nipy.utils.filemanip import filename_to_list
from nipy.interfaces.io import DataSink, FreeSurferSource
import nipy.interfaces.freesurfer as fs

import numpy as np
import scipy as sp
import nibabel as nb
from nipy.utils.config import NUMPY_MMAP
```

A list of modules and functions to import inside of nodes

```
imports = [
    'import os',
    'import nibabel as nb',
    'import numpy as np',
    'import scipy as sp',
    'from nipy.utils.filemanip import filename_to_list, list_to_filename, split_
    ↪filename',
    'from scipy.special import legendre'
]
```

Define utility functions for use in workflow nodes

```
def get_info(dicom_files):
    """Given a Siemens dicom file return metadata

    Returns
    -----
    RepetitionTime
    Slice Acquisition Times
    Spacing between slices
    """
    meta = default_extractor(
        read_file(
            filename_to_list(dicom_files)[0],
            stop_before_pixels=True,
            force=True))
    return (meta['RepetitionTime'] / 1000., meta['CsaImage.MosaicRefAcqTimes'],
            meta['SpacingBetweenSlices'])

def median(in_files):
```

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```

"""Computes an average of the median of each realigned timeseries

Parameters
-----

in_files: one or more realigned Nifti 4D time series

Returns
-----

out_file: a 3D Nifti file
"""
average = None
for idx, filename in enumerate(filename_to_list(in_files)):
    img = nb.load(filename, mmap=NUMPY_MMAP)
    data = np.median(img.get_data(), axis=3)
    if average is None:
        average = data
    else:
        average = average + data
median_img = nb.Nifti1Image(average / float(idx + 1), img.affine,
                           img.header)
filename = os.path.join(os.getcwd(), 'median.nii.gz')
median_img.to_filename(filename)
return filename

def bandpass_filter(files, lowpass_freq, highpass_freq, fs):
    """Bandpass filter the input files

    Parameters
    -----
    files: list of 4d nifti files
    lowpass_freq: cutoff frequency for the low pass filter (in Hz)
    highpass_freq: cutoff frequency for the high pass filter (in Hz)
    fs: sampling rate (in Hz)
    """
    out_files = []
    for filename in filename_to_list(files):
        path, name, ext = split_filename(filename)
        out_file = os.path.join(os.getcwd(), name + '_bp' + ext)
        img = nb.load(filename, mmap=NUMPY_MMAP)
        timepoints = img.shape[-1]
        F = np.zeros((timepoints))
        lowidx = int(timepoints / 2) + 1
        if lowpass_freq > 0:
            lowidx = np.round(float(lowpass_freq) / fs * timepoints)
            highidx = 0
        if highpass_freq > 0:
            highidx = np.round(float(highpass_freq) / fs * timepoints)
        F[highidx:lowidx] = 1
        F = ((F + F[::-1]) > 0).astype(int)
        data = img.get_data()
        if np.all(F == 1):
            filtered_data = data
        else:
            filtered_data = np.real(np.fft.ifftn(np.fft.fftn(data) * F))

```

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```

        img_out = nb.Nifti1Image(filtered_data, img.affine, img.header)
        img_out.to_filename(out_file)
        out_files.append(out_file)
    return list_to_filename(out_files)

def motion_regressors(motion_params, order=0, derivatives=1):
    """Compute motion regressors upto given order and derivative

    motion + d(motion)/dt + d2(motion)/dt2 (linear + quadratic)
    """
    out_files = []
    for idx, filename in enumerate(filename_to_list(motion_params)):
        params = np.genfromtxt(filename)
        out_params = params
        for d in range(1, derivatives + 1):
            cparams = np.vstack((np.repeat(params[0, :][None, :], d, axis=0),
                                params))
            out_params = np.hstack((out_params, np.diff(cparams, d, axis=0)))
        out_params2 = out_params
        for i in range(2, order + 1):
            out_params2 = np.hstack((out_params2, np.power(out_params, i)))
        filename = os.path.join(os.getcwd(), "motion_regressor%02d.txt" % idx)
        np.savetxt(filename, out_params2, fmt=b"%10f")
        out_files.append(filename)
    return out_files

def build_filter1(motion_params, comp_norm, outliers, detrend_poly=None):
    """Builds a regressor set comprising motion parameters, composite norm and
    outliers

    The outliers are added as a single time point column for each outlier

    Parameters
    -----

    motion_params: a text file containing motion parameters and its derivatives
    comp_norm: a text file containing the composite norm
    outliers: a text file containing 0-based outlier indices
    detrend_poly: number of polynomials to add to detrend

    Returns
    -----

    components_file: a text file containing all the regressors
    """
    out_files = []
    for idx, filename in enumerate(filename_to_list(motion_params)):
        params = np.genfromtxt(filename)
        norm_val = np.genfromtxt(filename_to_list(comp_norm)[idx])
        out_params = np.hstack((params, norm_val[:, None]))
        try:
            outlier_val = np.genfromtxt(filename_to_list(outliers)[idx])
        except IOError:
            outlier_val = np.empty((0))
        for index in np.atleast_1d(outlier_val):

```

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```

        outlier_vector = np.zeros((out_params.shape[0], 1))
        outlier_vector[index] = 1
        out_params = np.hstack((out_params, outlier_vector))
    if detrend_poly:
        timepoints = out_params.shape[0]
        X = np.empty((timepoints, 0))
        for i in range(detrend_poly):
            X = np.hstack((X, legendre(i + 1)(np.linspace(
                -1, 1, timepoints))[:, None])))
        out_params = np.hstack((out_params, X))
        filename = os.path.join(os.getcwd(), "filter_regressor%02d.txt" % idx)
        np.savetxt(filename, out_params, fmt=b"%10f")
        out_files.append(filename)
    return out_files

def rename(in_files, suffix=None):
    from nipy.utils.filemanip import (filename_to_list, split_filename,
                                      list_to_filename)

    out_files = []
    for idx, filename in enumerate(filename_to_list(in_files)):
        _, name, ext = split_filename(filename)
        if suffix is None:
            out_files.append(name + ('_%03d' % idx) + ext)
        else:
            out_files.append(name + suffix + ext)
    return list_to_filename(out_files)

def get_aparc_aseg(files):
    """Return the aparc+aseg.mgz file"""
    for name in files:
        if 'aparc+aseg.mgz' in name:
            return name
    raise ValueError('aparc+aseg.mgz not found')

def extract_subrois(timeseries_file, label_file, indices):
    """Extract voxel time courses for each subcortical roi index

    Parameters
    -----

    timeseries_file: a 4D Nifti file
    label_file: a 3D file containing rois in the same space/size of the 4D file
    indices: a list of indices for ROIs to extract.

    Returns
    -----

    out_file: a text file containing time courses for each voxel of each roi
    The first four columns are: freesurfer index, i, j, k positions in the
    label file
    """
    img = nb.load(timeseries_file, mmap=NUMPY_MMAP)
    data = img.get_data()
    roiimg = nb.load(label_file, mmap=NUMPY_MMAP)
    rois = roiimg.get_data()

```

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```

prefix = split_filename(timeseries_file)[1]
out_ts_file = os.path.join(os.getcwd(), '%s_subcortical_ts.txt' % prefix)
with open(out_ts_file, 'wt') as fp:
    for fsindex in indices:
        ijk = np.nonzero(rois == fsindex)
        ts = data[ijk]
        for i0, row in enumerate(ts):
            fp.write('%d,%d,%d,%d,' % (
                fsindex, ijk[0][i0], ijk[1][i0],
                ijk[2][i0]) + ','.join(['%.10f' % val
                                        for val in row]) + '\n')
    return out_ts_file

def combine_hemi(left, right):
    """Combine left and right hemisphere time series into a single text file
    """
    lh_data = nb.load(left, mmap=NUMPY_MMAP).get_data()
    rh_data = nb.load(right, mmap=NUMPY_MMAP).get_data()

    indices = np.vstack((1000000 + np.arange(0, lh_data.shape[0])[:, None],
                        2000000 + np.arange(0, rh_data.shape[0])[:, None]))
    all_data = np.hstack((indices,
                        np.vstack((lh_data.squeeze(), rh_data.squeeze()))))
    filename = left.split('.')[1] + '_combined.txt'
    np.savetxt(
        filename,
        all_data,
        fmt=','.join(['%d'] + ['%.10f'] * (all_data.shape[1] - 1)))
    return os.path.abspath(filename)

```

Create a Registration Workflow

```

def create_reg_workflow(name='registration'):
    """Create a FEAT preprocessing workflow together with freesurfer

    Parameters
    -----
        name : name of workflow (default: 'registration')

    Inputs:

        inputspec.source_files : files (filename or list of filenames to register)
        inputspec.mean_image : reference image to use
        inputspec.anatomical_image : anatomical image to coregister to
        inputspec.target_image : registration target

    Outputs:

        outputspec.func2anat_transform : FLIRT transform
        outputspec.anat2target_transform : FLIRT+FNIRT transform
        outputspec.transformed_files : transformed files in target space
        outputspec.transformed_mean : mean image in target space

    Example
    -----
        See code below

```

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```

"""

register = Workflow(name=name)

inputnode = Node(
    interface=IdentityInterface(fields=[
        'source_files', 'mean_image', 'subject_id', 'subjects_dir',
        'target_image'
    ]),
    name='inputspec')

outputnode = Node(
    interface=IdentityInterface(fields=[
        'func2anat_transform', 'out_reg_file', 'anat2target_transform',
        'transforms', 'transformed_mean', 'segmentation_files',
        'anat2target', 'aparc', 'min_cost_file'
    ]),
    name='outputspec')

# Get the subject's freesurfer source directory
fssource = Node(FreeSurferSource(), name='fssource')
fssource.run_without_submitting = True
register.connect(inputnode, 'subject_id', fssource, 'subject_id')
register.connect(inputnode, 'subjects_dir', fssource, 'subjects_dir')

convert = Node(freesurfer.MRIConvert(out_type='nii'), name="convert")
register.connect(fssource, 'T1', convert, 'in_file')

# Coregister the median to the surface
bbregister = Node(freesurfer.BBRegister(), name='bbregister')
bbregister.inputs.init = 'fsl'
bbregister.inputs.contrast_type = 't2'
bbregister.inputs.out_fsl_file = True
bbregister.inputs.epi_mask = True
register.connect(inputnode, 'subject_id', bbregister, 'subject_id')
register.connect(inputnode, 'mean_image', bbregister, 'source_file')
register.connect(inputnode, 'subjects_dir', bbregister, 'subjects_dir')
"""

Estimate the tissue classes from the anatomical image. But use aparc+aseg's_
→brain mask
"""

binarize = Node(
    fs.Binarize(min=0.5, out_type="nii.gz", dilate=1),
    name="binarize_aparc")
register.connect(fssource, ("aparc_aseg", get_aparc_aseg), binarize,
                "in_file")
stripper = Node(fsl.ApplyMask(), name='stripper')
register.connect(binimize, "binary_file", stripper, "mask_file")
register.connect(convert, 'out_file', stripper, 'in_file')

fast = Node(fsl.FAST(), name='fast')
register.connect(stripper, 'out_file', fast, 'in_files')
"""

Binimize the segmentation
"""

```

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```

binarize = MapNode(
    fsl.ImageMaths(op_string='-nan -thr 0.9 -ero -bin'),
    iterfield=['in_file'],
    name='binarize')
register.connect(fast, 'partial_volume_files', binarize, 'in_file')
"""
Apply inverse transform to take segmentations to functional space
"""

applyxfm = MapNode(
    freesurfer.ApplyVolTransform(inverse=True, interp='nearest'),
    iterfield=['target_file'],
    name='inverse_transform')
register.connect(inputnode, 'subjects_dir', applyxfm, 'subjects_dir')
register.connect(bbregister, 'out_reg_file', applyxfm, 'reg_file')
register.connect(binarize, 'out_file', applyxfm, 'target_file')
register.connect(inputnode, 'mean_image', applyxfm, 'source_file')
"""
Apply inverse transform to aparc file
"""

aparcxfm = Node(
    freesurfer.ApplyVolTransform(inverse=True, interp='nearest'),
    name='aparc_inverse_transform')
register.connect(inputnode, 'subjects_dir', aparcxfm, 'subjects_dir')
register.connect(bbregister, 'out_reg_file', aparcxfm, 'reg_file')
register.connect(fssource, ('aparc_aseg', get_aparc_aseg), aparcxfm,
    'target_file')
register.connect(inputnode, 'mean_image', aparcxfm, 'source_file')
"""
Convert the BBRegister transformation to ANTS ITK format
"""

convert2itk = Node(C3dAffineTool(), name='convert2itk')
convert2itk.inputs.fsl2ras = True
convert2itk.inputs.itk_transform = True
register.connect(bbregister, 'out_fsl_file', convert2itk, 'transform_file')
register.connect(inputnode, 'mean_image', convert2itk, 'source_file')
register.connect(stripper, 'out_file', convert2itk, 'reference_file')
"""
Compute registration between the subject's structural and MNI template

    * All parameters are set using the example from:
      #https://github.com/stnava/ANTs/blob/master/Scripts/newAntsExample.sh
    * This is currently set to perform a very quick registration. However,
      the registration can be made significantly more accurate for cortical
      structures by increasing the number of iterations.
"""

reg = Node(ants.Registration(), name='antsRegister')
reg.inputs.output_transform_prefix = "output_"
reg.inputs.transforms = ['Rigid', 'Affine', 'SyN']
reg.inputs.transform_parameters = [(0.1, ), (0.1, ), (0.2, 3.0, 0.0)]
reg.inputs.number_of_iterations = [[10000, 11110, 11110]] * 2 + [[
    100, 30, 20
]]
reg.inputs.dimension = 3

```

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```

reg.inputs.write_composite_transform = True
reg.inputs.collapse_output_transforms = True
reg.inputs.initial_moving_transform_com = True
reg.inputs.metric = ['Mattes'] * 2 + [['Mattes', 'CC']]
reg.inputs.metric_weight = [1] * 2 + [[0.5, 0.5]]
reg.inputs.radius_or_number_of_bins = [32] * 2 + [[32, 4]]
reg.inputs.sampling_strategy = ['Regular'] * 2 + [[None, None]]
reg.inputs.sampling_percentage = [0.3] * 2 + [[None, None]]
reg.inputs.convergence_threshold = [1.e-8] * 2 + [-0.01]
reg.inputs.convergence_window_size = [20] * 2 + [5]
reg.inputs.smoothing_sigmas = [[4, 2, 1]] * 2 + [[1, 0.5, 0]]
reg.inputs.sigma_units = ['vox'] * 3
reg.inputs.shrink_factors = [[3, 2, 1]] * 2 + [[4, 2, 1]]
reg.inputs.use_estimate_learning_rate_once = [True] * 3
reg.inputs.use_histogram_matching = [False] * 2 + [True]
reg.inputs.winsorize_lower_quantile = 0.005
reg.inputs.winsorize_upper_quantile = 0.995
reg.inputs.float = True
reg.inputs.output_warped_image = 'output_warped_image.nii.gz'
reg.inputs.num_threads = 4
reg.plugin_args = {'sbatch_args': '-c%d' % 4}
register.connect(stripper, 'out_file', reg, 'moving_image')
register.connect(inputnode, 'target_image', reg, 'fixed_image')

```

Concatenate the affine and ants transforms into a list

```

merge = Node(Merge(2), iterfield=['in2'], name='mergexfm')
register.connect(convert2itk, 'itk_transform', merge, 'in2')
register.connect(reg, ('composite_transform', pickfirst), merge, 'in1')

```

Transform the mean image. First to anatomical and then to target

```

warpmean = Node(ants.ApplyTransforms(), name='warpmean')
warpmean.inputs.input_image_type = 3
warpmean.inputs.interpolation = 'Linear'
warpmean.inputs.invert_transform_flags = [False, False]
warpmean.terminal_output = 'file'
warpmean.inputs.args = '--float'
warpmean.inputs.num_threads = 4
warpmean.plugin_args = {'sbatch_args': '-c%d' % 4}

register.connect(inputnode, 'target_image', warpmean, 'reference_image')
register.connect(inputnode, 'mean_image', warpmean, 'input_image')
register.connect(merge, 'out', warpmean, 'transforms')

```

Assign all the output files

```

register.connect(reg, 'warped_image', outputnode, 'anat2target')
register.connect(warpmean, 'output_image', outputnode, 'transformed_mean')
register.connect(applyxfm, 'transformed_file', outputnode,
                 'segmentation_files')
register.connect(aparcxfm, 'transformed_file', outputnode, 'aparc')
register.connect(bbregister, 'out_fsl_file', outputnode,
                 'func2anat_transform')
register.connect(bbregister, 'out_reg_file', outputnode, 'out_reg_file')
register.connect(reg, 'composite_transform', outputnode,
                 'anat2target_transform')
register.connect(merge, 'out', outputnode, 'transforms')

```

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```
register.connect(bregister, 'min_cost_file', outputnode, 'min_cost_file')

return register
```

Creates the main preprocessing workflow

```
def create_workflow(files,
                    target_file,
                    subject_id,
                    TR,
                    slice_times,
                    norm_threshold=1,
                    num_components=5,
                    vol_fwhm=None,
                    surf_fwhm=None,
                    lowpass_freq=-1,
                    highpass_freq=-1,
                    subjects_dir=None,
                    sink_directory=os.getcwd(),
                    target_subject=['fsaverage3', 'fsaverage4'],
                    name='resting'):

    wf = Workflow(name=name)

    # Rename files in case they are named identically
    name_unique = MapNode(
        Rename(format_string='rest_%(run)02d'),
        iterfield=['in_file', 'run'],
        name='rename')
    name_unique.inputs.keep_ext = True
    name_unique.inputs.run = list(range(1, len(files) + 1))
    name_unique.inputs.in_file = files

    realign = Node(nipy.SpaceTimeRealigner(), name="spacetime_realign")
    realign.inputs.slice_times = slice_times
    realign.inputs.tr = TR
    realign.inputs.slice_info = 2
    realign.plugin_args = {'sbatch_args': '-c%d' % 4}

    # Compute TSNR on realigned data regressing polynomials up to order 2
    tsnr = MapNode(TSNR(regress_poly=2), iterfield=['in_file'], name='tsnr')
    wf.connect(realign, "out_file", tsnr, "in_file")

    # Compute the median image across runs
    calc_median = Node(CalculateMedian(), name='median')
    wf.connect(tsnr, 'detrended_file', calc_median, 'in_files')
```

Segment and Register

```
registration = create_reg_workflow(name='registration')
wf.connect(calc_median, 'median_file', registration,
          'inputspec.mean_image')
registration.inputs.inputspec.subject_id = subject_id
registration.inputs.inputspec.subjects_dir = subjects_dir
registration.inputs.inputspec.target_image = target_file
```

Quantify TSNR in each freesurfer ROI

```

get_roi_tsnr = MapNode(
    fs.SegStats(default_color_table=True),
    iterfield=['in_file'],
    name='get_aparc_tsnr')
get_roi_tsnr.inputs.avgwf_txt_file = True
wf.connect(tsnr, 'tsnr_file', get_roi_tsnr, 'in_file')
wf.connect(registration, 'outputspec.aparc', get_roi_tsnr,
            'segmentation_file')

```

Use `nipy.algorithms.rapidart` to determine which of the images in the functional series are outliers based on deviations in intensity or movement.

```

art = Node(interface=ArtifactDetect(), name="art")
art.inputs.use_differences = [True, True]
art.inputs.use_norm = True
art.inputs.norm_threshold = norm_threshold
art.inputs.zintensity_threshold = 9
art.inputs.mask_type = 'spm_global'
art.inputs.parameter_source = 'NiPy'

```

Here we are connecting all the nodes together. Notice that we add the merge node only if you choose to use 4D. Also `get_vox_dims` function is passed along the input volume of normalise to set the optimal voxel sizes.

```

wf.connect([
    (name_unique, realign, [('out_file', 'in_file')]),
    (realign, art, [('out_file', 'realigned_files')]),
    (realign, art, [('par_file', 'realignment_parameters')]),
])

def selectindex(files, idx):
    import numpy as np
    from nipy.utils.filemanip import filename_to_list, list_to_filename
    return list_to_filename(
        np.array(filename_to_list(files))[idx].tolist())

mask = Node(fsl.BET(), name='getmask')
mask.inputs.mask = True
wf.connect(calc_median, 'median_file', mask, 'in_file')

# get segmentation in normalized functional space

def merge_files(in1, in2):
    out_files = filename_to_list(in1)
    out_files.extend(filename_to_list(in2))
    return out_files

# filter some noise

# Compute motion regressors
motreg = Node(
    Function(
        input_names=['motion_params', 'order', 'derivatives'],
        output_names=['out_files'],
        function=motion_regressors,
        imports=imports),
    name='getmotionregress')
wf.connect(realign, 'par_file', motreg, 'motion_params')

```

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```

# Create a filter to remove motion and art confounds
createfilter1 = Node(
    Function(
        input_names=[
            'motion_params', 'comp_norm', 'outliers', 'detrend_poly'
        ],
        output_names=['out_files'],
        function=build_filter1,
        imports=imports),
    name='makemotionbasedfilter')
createfilter1.inputs.detrend_poly = 2
wf.connect(motreg, 'out_files', createfilter1, 'motion_params')
wf.connect(art, 'norm_files', createfilter1, 'comp_norm')
wf.connect(art, 'outlier_files', createfilter1, 'outliers')

filter1 = MapNode(
    fsl.GLM(
        out_f_name='F_mcart.nii.gz',
        out_pf_name='pF_mcart.nii.gz',
        demean=True),
    iterfield=['in_file', 'design', 'out_res_name'],
    name='filtermotion')

wf.connect(realign, 'out_file', filter1, 'in_file')
wf.connect(realign, ('out_file', rename, '_filtermotart'), filter1,
            'out_res_name')
wf.connect(createfilter1, 'out_files', filter1, 'design')

createfilter2 = MapNode(
    ACompCor(),
    iterfield=['realigned_file', 'extra_regressors'],
    name='makecompcorrfilter')
createfilter2.inputs.components_file = 'noise_components.txt'
createfilter2.inputs.num_components = num_components

wf.connect(createfilter1, 'out_files', createfilter2, 'extra_regressors')
wf.connect(filter1, 'out_res', createfilter2, 'realigned_file')
wf.connect(registration,
            ('outputspec.segmentation_files', selectindex, [0, 2]),
            createfilter2, 'mask_file')

filter2 = MapNode(
    fsl.GLM(out_f_name='F.nii.gz', out_pf_name='pF.nii.gz', demean=True),
    iterfield=['in_file', 'design', 'out_res_name'],
    name='filter_noise_nosmooth')
wf.connect(filter1, 'out_res', filter2, 'in_file')
wf.connect(filter1, ('out_res', rename, '_cleaned'), filter2,
            'out_res_name')
wf.connect(createfilter2, 'components_file', filter2, 'design')
wf.connect(mask, 'mask_file', filter2, 'mask')

bandpass = Node(
    Function(
        input_names=['files', 'lowpass_freq', 'highpass_freq', 'fs'],
        output_names=['out_files'],
        function=bandpass_filter,
        imports=imports),

```

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```

        name='bandpass_unsmooth')
bandpass.inputs.fs = 1. / TR
bandpass.inputs.highpass_freq = highpass_freq
bandpass.inputs.lowpass_freq = lowpass_freq
wf.connect(filter2, 'out_res', bandpass, 'files')
"""Smooth the functional data using
:class:`nipy.interfaces.fsl.IsotropicSmooth`.
"""

smooth = MapNode(
    interface=fsl.IsotropicSmooth(), name="smooth", iterfield=["in_file"])
smooth.inputs.fwhm = vol_fwhm

wf.connect(bandpass, 'out_files', smooth, 'in_file')

collector = Node(Merge(2), name='collect_streams')
wf.connect(smooth, 'out_file', collector, 'in1')
wf.connect(bandpass, 'out_files', collector, 'in2')
"""
Transform the remaining images. First to anatomical and then to target
"""

warpall = MapNode(
    ants.ApplyTransforms(), iterfield=['input_image'], name='warpall')
warpall.inputs.input_image_type = 3
warpall.inputs.interpolation = 'Linear'
warpall.inputs.invert_transform_flags = [False, False]
warpall.terminal_output = 'file'
warpall.inputs.reference_image = target_file
warpall.inputs.args = '--float'
warpall.inputs.num_threads = 2
warpall.plugin_args = {'sbatch_args': '-c%d' % 2}

# transform to target
wf.connect(collector, 'out', warpall, 'input_image')
wf.connect(registration, 'outputspec.transforms', warpall, 'transforms')

mask_target = Node(fsl.ImageMaths(op_string='-bin'), name='target_mask')

wf.connect(registration, 'outputspec.anat2target', mask_target, 'in_file')

maskts = MapNode(fsl.ApplyMask(), iterfield=['in_file'], name='ts_masker')
wf.connect(warpall, 'output_image', maskts, 'in_file')
wf.connect(mask_target, 'out_file', maskts, 'mask_file')

# map to surface
# extract aparc+aseg ROIs
# extract subcortical ROIs
# extract target space ROIs
# combine subcortical and cortical rois into a single cifti file

#####
# Convert aparc to subject functional space

# Sample the average time series in aparc ROIs
sampleaparc = MapNode(
    freesurfer.SegStats(default_color_table=True),

```

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```

    iterfield=['in_file', 'summary_file', 'avgwf_txt_file'],
    name='aparc_ts')
sampleaparc.inputs.segment_id = (
    [8] + list(range(10, 14)) + [17, 18, 26, 47] + list(range(49, 55)) +
    [58] + list(range(1001, 1036)) + list(range(2001, 2036)))

wf.connect(registration, 'outputspec.aparc', sampleaparc,
            'segmentation_file')
wf.connect(collector, 'out', sampleaparc, 'in_file')

def get_names(files, suffix):
    """Generate appropriate names for output files
    """
    from nipy.utils.filemanip import (split_filename, filename_to_list,
                                      list_to_filename)

    import os
    out_names = []
    for filename in files:
        path, name, _ = split_filename(filename)
        out_names.append(os.path.join(path, name + suffix))
    return list_to_filename(out_names)

wf.connect(collector, ('out', get_names, '_avgwf.txt'), sampleaparc,
            'avgwf_txt_file')
wf.connect(collector, ('out', get_names, '_summary.stats'), sampleaparc,
            'summary_file')

# Sample the time series onto the surface of the target surface. Performs
# sampling into left and right hemisphere
target = Node(IdentityInterface(fields=['target_subject']), name='target')
target.iterables = ('target_subject', filename_to_list(target_subject))

samplerlh = MapNode(
    freesurfer.SampleToSurface(),
    iterfield=['source_file'],
    name='sampler_lh')
samplerlh.inputs.sampling_method = "average"
samplerlh.inputs.sampling_range = (0.1, 0.9, 0.1)
samplerlh.inputs.sampling_units = "frac"
samplerlh.inputs.interp_method = "trilinear"
samplerlh.inputs.smooth_surf = surf_fwhm
# samplerlh.inputs.cortex_mask = True
samplerlh.inputs.out_type = 'niigz'
samplerlh.inputs.subjects_dir = subjects_dir

samplerrh = samplerlh.clone('sampler_rh')

samplerlh.inputs.hemi = 'lh'
wf.connect(collector, 'out', samplerlh, 'source_file')
wf.connect(registration, 'outputspec.out_reg_file', samplerlh, 'reg_file')
wf.connect(target, 'target_subject', samplerlh, 'target_subject')

samplerrh.set_input('hemi', 'rh')
wf.connect(collector, 'out', samplerrh, 'source_file')
wf.connect(registration, 'outputspec.out_reg_file', samplerrh, 'reg_file')
wf.connect(target, 'target_subject', samplerrh, 'target_subject')

```

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```

# Combine left and right hemisphere to text file
combiner = MapNode(
    Function(
        input_names=['left', 'right'],
        output_names=['out_file'],
        function=combine_hemi,
        imports=imports),
    iterfield=['left', 'right'],
    name="combiner")
wf.connect(samplerlh, 'out_file', combiner, 'left')
wf.connect(samplerlh, 'out_file', combiner, 'right')

# Sample the time series file for each subcortical roi
ts2txt = MapNode(
    Function(
        input_names=['timeseries_file', 'label_file', 'indices'],
        output_names=['out_file'],
        function=extract_subrois,
        imports=imports),
    iterfield=['timeseries_file'],
    name='getsubcortts')
ts2txt.inputs.indices = [8] + list(range(10, 14)) + [17, 18, 26, 47] + \
    list(range(49, 55)) + [58]
ts2txt.inputs.label_file = \
    os.path.abspath(('OASIS-TRT-20_jointfusion_DKT31_CMA_labels_in_MNI152_'
        '2mm_v2.nii.gz'))
wf.connect(maskts, 'out_file', ts2txt, 'timeseries_file')

#####

substitutions = [
    ('_target_subject_', ''),
    ('_filtermotart_cleaned_bp_trans_masked', ''),
    ('_filtermotart_cleaned_bp', ''),
]
substitutions += [("_smooth%d" % i, "") for i in range(11)[::-1]]
substitutions += [("_ts_masker%d" % i, "") for i in range(11)[::-1]]
substitutions += [("_getsubcortts%d" % i, "") for i in range(11)[::-1]]
substitutions += [("_combiner%d" % i, "") for i in range(11)[::-1]]
substitutions += [("_filtermotion%d" % i, "") for i in range(11)[::-1]]
substitutions += [("_filter_noise_nosmooth%d" % i, "")
    for i in range(11)[::-1]]
substitutions += [("_makecompcofilter%d" % i, "")
    for i in range(11)[::-1]]
substitutions += [("_get_aparc_tsnr%d/" % i, "run%d_" % (i + 1))
    for i in range(11)[::-1]]

substitutions += [("T1_out_brain_pve_0_maths_warped", "compcor_csf"),
    ("T1_out_brain_pve_1_maths_warped",
        "compcor_gm"), ("T1_out_brain_pve_2_maths_warped",
        "compcor_wm"),
    ("output_warped_image_maths",
        "target_brain_mask"), ("median_brain_mask",
        "native_brain_mask"), ("corr_",
        "")]

regex_subs = [

```

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```

    ('_combiner.*/sar', '/smooth/'),
    ('_combiner.*/ar', '/unsmooth/'),
    ('_aparc_ts.*/sar', '/smooth/'),
    ('_aparc_ts.*/ar', '/unsmooth/'),
    ('_getsubcortts.*/sar', '/smooth/'),
    ('_getsubcortts.*/ar', '/unsmooth/'),
    ('series/sar', 'series/smooth/'),
    ('series/ar', 'series/unsmooth/'),
    ('_inverse_transform./', ''),
]
# Save the relevant data into an output directory
datasink = Node(interface=DataSink(), name="datasink")
datasink.inputs.base_directory = sink_directory
datasink.inputs.container = subject_id
datasink.inputs.substitutions = substitutions
datasink.inputs.regexp_substitutions = regex_subs # (r'(/_.*(\d+))', r'/run\2')
wf.connect(realign, 'par_file', datasink, 'resting.qa.motion')
wf.connect(art, 'norm_files', datasink, 'resting.qa.art.@norm')
wf.connect(art, 'intensity_files', datasink, 'resting.qa.art.@intensity')
wf.connect(art, 'outlier_files', datasink, 'resting.qa.art.@outlier_files')
wf.connect(registration, 'outputspec.segmentation_files', datasink,
            'resting.mask_files')
wf.connect(registration, 'outputspec.anat2target', datasink,
            'resting.qa.ants')
wf.connect(mask, 'mask_file', datasink, 'resting.mask_files.@brainmask')
wf.connect(mask_target, 'out_file', datasink, 'resting.mask_files.target')
wf.connect(filter1, 'out_f', datasink, 'resting.qa.compmaps.@mc_F')
wf.connect(filter1, 'out_pf', datasink, 'resting.qa.compmaps.@mc_pF')
wf.connect(filter2, 'out_f', datasink, 'resting.qa.compmaps')
wf.connect(filter2, 'out_pf', datasink, 'resting.qa.compmaps.@p')
wf.connect(registration, 'outputspec.min_cost_file', datasink,
            'resting.qa.mincost')
wf.connect(tsnr, 'tsnr_file', datasink, 'resting.qa.tsnr.@map')
wf.connect([(get_roi_tsnr,
              [('avgwf_txt_file', 'resting.qa.tsnr'),
               ('summary_file', 'resting.qa.tsnr.@summary')])])

wf.connect(bandpass, 'out_files', datasink,
            'resting.timeseries.@bandpassed')
wf.connect(smooth, 'out_file', datasink, 'resting.timeseries.@smoothed')
wf.connect(createfilter1, 'out_files', datasink,
            'resting.regress.@regressors')
wf.connect(createfilter2, 'components_file', datasink,
            'resting.regress.@compcorr')
wf.connect(maskts, 'out_file', datasink, 'resting.timeseries.target')
wf.connect(sampleaparc, 'summary_file', datasink,
            'resting.parcellations.aparc')
wf.connect(sampleaparc, 'avgwf_txt_file', datasink,
            'resting.parcellations.aparc.@avgwf')
wf.connect(ts2txt, 'out_file', datasink,
            'resting.parcellations.grayo.@subcortical')

datasink2 = Node(interface=DataSink(), name="datasink2")
datasink2.inputs.base_directory = sink_directory
datasink2.inputs.container = subject_id
datasink2.inputs.substitutions = substitutions
datasink2.inputs.regexp_substitutions = regex_subs # (r'(/_.*(\d+))', r'/run\2')

```

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```
wf.connect(combiner, 'out_file', datasink2,
           'resting.parcellations.grayo.@surface')
return wf
```

Creates the full workflow including getting information from dicom files

```
def create_resting_workflow(args, name=None):
    TR = args.TR
    slice_times = args.slice_times
    if args.dicom_file:
        TR, slice_times, slice_thickness = get_info(args.dicom_file)
        slice_times = (np.array(slice_times) / 1000.).tolist()

    if name is None:
        name = 'resting_' + args.subject_id
    kwargs = dict(
        files=[os.path.abspath(filename) for filename in args.files],
        target_file=os.path.abspath(args.target_file),
        subject_id=args.subject_id,
        TR=TR,
        slice_times=slice_times,
        vol_fwhm=args.vol_fwhm,
        surf_fwhm=args.surf_fwhm,
        norm_threshold=2.,
        subjects_dir=os.path.abspath(args.fsd_dir),
        target_subject=args.target_surfs,
        lowpass_freq=args.lowpass_freq,
        highpass_freq=args.highpass_freq,
        sink_directory=os.path.abspath(args.sink),
        name=name)
    wf = create_workflow(**kwargs)
    return wf

if __name__ == "__main__":
    from argparse import ArgumentParser, RawTextHelpFormatter
    defstr = ' (default %(default)s) '
    parser = ArgumentParser(
        description=__doc__, formatter_class=RawTextHelpFormatter)
    parser.add_argument(
        "-d",
        "--dicom_file",
        dest="dicom_file",
        help="a SIEMENS example dicom file from the resting series")
    parser.add_argument(
        "-f",
        "--files",
        dest="files",
        nargs="+",
        help="4d nifti files for resting state",
        required=True)
    parser.add_argument(
        "-t",
        "--target",
        dest="target_file",
        help=("Target in MNI space. Best to use the MindBoggle "
              "template - "
```

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```

        "OASIS-30_Atropos_template_in_MNI152_2mm.nii.gz"),
        required=True)
parser.add_argument(
    "-s",
    "--subject_id",
    dest="subject_id",
    help="FreeSurfer subject id",
    required=True)
parser.add_argument(
    "--subjects_dir",
    dest="fsdir",
    help="FreeSurfer subject directory",
    required=True)
parser.add_argument(
    "--target_surfaces",
    dest="target_surfs",
    nargs="+",
    default=['fsaverage5'],
    help="FreeSurfer target surfaces" + defstr)
parser.add_argument(
    "--TR",
    dest="TR",
    default=None,
    type=float,
    help="TR if dicom not provided in seconds")
parser.add_argument(
    "--slice_times",
    dest="slice_times",
    nargs="+",
    type=float,
    help="Slice onset times in seconds")
parser.add_argument(
    "--vol_fwhm",
    default=6.,
    dest='vol_fwhm',
    type=float,
    help="Spatial FWHM" + defstr)
parser.add_argument(
    "--surf_fwhm",
    default=15.,
    dest='surf_fwhm',
    type=float,
    help="Spatial FWHM" + defstr)
parser.add_argument(
    "-l",
    "--lowpass_freq",
    dest="lowpass_freq",
    default=0.1,
    type=float,
    help="Low pass frequency (Hz)" + defstr)
parser.add_argument(
    "-u",
    "--highpass_freq",
    dest="highpass_freq",
    default=0.01,
    type=float,
    help="High pass frequency (Hz)" + defstr)

```

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```
parser.add_argument(
    "-o",
    "--output_dir",
    dest="sink",
    help="Output directory base",
    required=True)
parser.add_argument(
    "-w", "--work_dir", dest="work_dir", help="Output directory base")
parser.add_argument(
    "-p",
    "--plugin",
    dest="plugin",
    default='Linear',
    help="Plugin to use")
parser.add_argument(
    "--plugin_args", dest="plugin_args", help="Plugin arguments")
args = parser.parse_args()

wf = create_resting_workflow(args)

if args.work_dir:
    work_dir = os.path.abspath(args.work_dir)
else:
    work_dir = os.getcwd()

wf.base_dir = work_dir
if args.plugin_args:
    wf.run(args.plugin, plugin_args=eval(args.plugin_args))
else:
    wf.run(args.plugin)
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

Paper: Smoothing comparison

```

from builtins import range

import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.spm as spm # spm
import nipype.interfaces.freesurfer as fs # freesurfer
import nipype.interfaces.nipy as nipy
import nipype.interfaces.utility as util
import nipype.pipeline.engine as pe # pypeline engine
import nipype.algorithms.modelgen as model # model specification
import nipype.workflows.fmri.fsl as fsl_wf
from nipype.interfaces.base import Bunch
import os # system functions

preprocessing = pe.Workflow(name="preprocessing")

iter_fwhm = pe.Node(
    interface=util.IdentityInterface(fields=["fwhm"]), name="iter_fwhm")
iter_fwhm.iterables = [('fwhm', [4, 8])]

iter_smoothing_method = pe.Node(
    interface=util.IdentityInterface(fields=["smoothing_method"]),
    name="iter_smoothing_method")
iter_smoothing_method.iterables = [('smoothing_method', [
    'isotropic_voxel', 'anisotropic_voxel', 'isotropic_surface'
])]

realign = pe.Node(interface=spm.Realign(), name="realign")
realign.inputs.register_to_mean = True

isotropic_voxel_smooth = pe.Node(
    interface=spm.Smooth(), name="isotropic_voxel_smooth")
preprocessing.connect(realign, "realigned_files", isotropic_voxel_smooth,
    "in_files")
preprocessing.connect(iter_fwhm, "fwhm", isotropic_voxel_smooth, "fwhm")

compute_mask = pe.Node(interface=nipy.ComputeMask(), name="compute_mask")

```

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```

preprocessing.connect(realign, "mean_image", compute_mask, "mean_volume")

anisotropic_voxel_smooth = fsl_wf.create_susan_smooth(
    name="anisotropic_voxel_smooth", separate_masks=False)
anisotropic_voxel_smooth.inputs.smooth.output_type = 'NIFTI'
preprocessing.connect(realign, "realigned_files", anisotropic_voxel_smooth,
    "inputnode.in_files")
preprocessing.connect(iter_fwhm, "fwhm", anisotropic_voxel_smooth,
    "inputnode.fwhm")
preprocessing.connect(compute_mask, "brain_mask", anisotropic_voxel_smooth,
    "inputnode.mask_file")

recon_all = pe.Node(interface=fs.ReconAll(), name="recon_all")

surfregister = pe.Node(interface=fs.BBRegister(), name='surfregister')
surfregister.inputs.init = 'fsl'
surfregister.inputs.contrast_type = 't2'
preprocessing.connect(realign, 'mean_image', surfregister, 'source_file')
preprocessing.connect(recon_all, 'subject_id', surfregister, 'subject_id')
preprocessing.connect(recon_all, 'subjects_dir', surfregister, 'subjects_dir')

isotropic_surface_smooth = pe.MapNode(
    interface=fs.Smooth(proj_frac_avg=(0, 1, 0.1)),
    iterfield=['in_file'],
    name="isotropic_surface_smooth")
preprocessing.connect(surfregister, 'out_reg_file', isotropic_surface_smooth,
    'reg_file')
preprocessing.connect(realign, "realigned_files", isotropic_surface_smooth,
    "in_file")
preprocessing.connect(iter_fwhm, "fwhm", isotropic_surface_smooth,
    "surface_fwhm")
preprocessing.connect(iter_fwhm, "fwhm", isotropic_surface_smooth, "vol_fwhm")
preprocessing.connect(recon_all, 'subjects_dir', isotropic_surface_smooth,
    'subjects_dir')

merge_smoothed_files = pe.Node(
    interface=util.Merge(3), name='merge_smoothed_files')
preprocessing.connect(isotropic_voxel_smooth, 'smoothed_files',
    merge_smoothed_files, 'in1')
preprocessing.connect(anisotropic_voxel_smooth, 'outputnode.smoothed_files',
    merge_smoothed_files, 'in2')
preprocessing.connect(isotropic_surface_smooth, 'smoothed_file',
    merge_smoothed_files, 'in3')

select_smoothed_files = pe.Node(
    interface=util.Select(), name="select_smoothed_files")
preprocessing.connect(merge_smoothed_files, 'out', select_smoothed_files,
    'inlist')

def chooseindex(roi):
    return {
        'isotropic_voxel': list(range(0, 4)),
        'anisotropic_voxel': list(range(4, 8)),
        'isotropic_surface': list(range(8, 12))
    }[roi]

```

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```

preprocessing.connect(iter_smoothing_method, ("smoothing_method", chooseindex),
                      select_smoothed_files, 'index')

rename = pe.MapNode(
    util.Rename(format_string="%(orig)s"),
    name="rename",
    iterfield=['in_file'])
rename.inputs.parse_string = "(?P<orig>.*)"

preprocessing.connect(select_smoothed_files, 'out', rename, 'in_file')

specify_model = pe.Node(interface=model.SpecifyModel(), name="specify_model")
specify_model.inputs.input_units = 'secs'
specify_model.inputs.time_repetition = 3.
specify_model.inputs.high_pass_filter_cutoff = 120
specify_model.inputs.subject_info = [
    Bunch(
        conditions=['Task-Odd', 'Task-Even'],
        onsets=[list(range(15, 240, 60)),
                list(range(45, 240, 60))],
        durations=[[15], [15]])
] * 4

levelldesign = pe.Node(interface=spm.Level1Design(), name="levelldesign")
levelldesign.inputs.bases = {'hrf': {'derivs': [0, 0]}}
levelldesign.inputs.timing_units = 'secs'
levelldesign.inputs.interscan_interval = specify_model.inputs.time_repetition

levelleestimate = pe.Node(interface=spm.EstimateModel(), name="levelleestimate")
levelleestimate.inputs.estimate_method = {'Classical': 1}

contrastestimate = pe.Node(
    interface=spm.EstimateContrast(), name="contrastestimate")
contrastestimate.inputs.contrasts = [('Task>Baseline', 'T',
                                     ['Task-Odd', 'Task-Even'], [0.5, 0.5])]

modelling = pe.Workflow(name="modelling")
modelling.connect(specify_model, 'session_info', levelldesign, 'session_info')
modelling.connect(levelldesign, 'spm_mat_file', levelleestimate, 'spm_mat_file')
modelling.connect(levelleestimate, 'spm_mat_file', contrastestimate,
                  'spm_mat_file')
modelling.connect(levelleestimate, 'beta_images', contrastestimate,
                  'beta_images')
modelling.connect(levelleestimate, 'residual_image', contrastestimate,
                  'residual_image')

main_workflow = pe.Workflow(name="main_workflow")
main_workflow.base_dir = "smoothing_comparison_workflow"
main_workflow.connect(preprocessing, "realignment_parameters",
                      modelling, "specify_model.realignment_parameters")
main_workflow.connect(preprocessing, "select_smoothed_files.out", modelling,
                      "specify_model.functional_runs")
main_workflow.connect(preprocessing, "compute_mask.brain_mask", modelling,
                      "levelldesign.mask_image")

datasource = pe.Node(

```

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```
interface=nio.DataGrabber(
    infields=['subject_id'], outfields=['func', 'struct']),
    name='datasource')
datasource.inputs.base_directory = os.path.abspath('data')
datasource.inputs.template = '%s/%s.nii'
datasource.inputs.template_args = info = dict(
    func=[['subject_id', ['f3', 'f5', 'f7', 'f10']],
    struct=[['subject_id', 'struct']])
datasource.inputs.subject_id = 's1'
datasource.inputs.sort_filelist = True

main_workflow.connect(datasource, 'func', preprocessing, 'realigned_files')
main_workflow.connect(datasource, 'struct', preprocessing,
    'recon_all.T1_files')

datasink = pe.Node(interface=nio.DataSink(), name="datasink")
datasink.inputs.base_directory = os.path.abspath(
    'smoothing_comparison_workflow/output')
datasink.inputs.regexp_substitutions = [("_rename[0-9]", "")]

main_workflow.connect(modelling, 'contrastestimate.spmT_images', datasink,
    'contrasts')
main_workflow.connect(preprocessing, 'rename.out_file', datasink,
    'smoothed_epi')

main_workflow.run()
main_workflow.write_graph()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the examples directory.

smRI: Using new ANTS for creating a T1 template

In this tutorial we will use ANTS (old version aka “ANTS”) based workflow to create a template out of multiple T1 volumes.

1. Tell python where to find the appropriate functions.

```
from __future__ import print_function, unicode_literals
from builtins import open
from future import standard_library
standard_library.install_aliases()

import os
import nipype.interfaces.utility as util
import nipype.interfaces.ants as ants
import nipype.interfaces.io as io
import nipype.pipeline.engine as pe  # pypeline engine

from nipype.workflows.smri.ants import ANTSTemplateBuildSingleIterationWF
```

2. Download T1 volumes into home directory

```
import urllib.request
import urllib.error
import urllib.parse
homeDir = os.getenv("HOME")
requestedPath = os.path.join(homeDir, 'nipypeTestPath')
mydatadir = os.path.realpath(requestedPath)
if not os.path.exists(mydatadir):
    os.makedirs(mydatadir)
print(mydatadir)

MyFileURLs = [
    ('http://slicer.kitware.com/midas3/download?bitstream=13121',
     '01_T1_half.nii.gz'),
    ('http://slicer.kitware.com/midas3/download?bitstream=13122',
     '02_T1_half.nii.gz'),
    ('http://slicer.kitware.com/midas3/download?bitstream=13124',
     '03_T1_half.nii.gz'),
    ('http://slicer.kitware.com/midas3/download?bitstream=13128',
```

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```

    '01_T1_inv_half.nii.gz'),
    ('http://slicer.kitware.com/midas3/download?bitstream=13123',
     '02_T1_inv_half.nii.gz'),
    ('http://slicer.kitware.com/midas3/download?bitstream=13125',
     '03_T1_inv_half.nii.gz'),
]
for tt in MyFileURLs:
    myURL = tt[0]
    localFilename = os.path.join(mydatadir, tt[1])
    if not os.path.exists(localFilename):
        remotefile = urllib.request.urlopen(myURL)

        localFile = open(localFilename, 'wb')
        localFile.write(remotefile.read())
        localFile.close()
        print("Downloaded file: {0}".format(localFilename))
    else:
        print("File previously downloaded {0}".format(localFilename))

input_images = [
    os.path.join(mydatadir, '01_T1_half.nii.gz'),
    os.path.join(mydatadir, '02_T1_half.nii.gz'),
    os.path.join(mydatadir, '03_T1_half.nii.gz')
]
input_passive_images = [{
    'INV_T1':
        os.path.join(mydatadir, '01_T1_inv_half.nii.gz')
}, {
    'INV_T1':
        os.path.join(mydatadir, '02_T1_inv_half.nii.gz')
}, {
    'INV_T1':
        os.path.join(mydatadir, '03_T1_inv_half.nii.gz')
}]

```

3. Define the workflow and its working directory

```

tbuilder = pe.Workflow(name="ANTSTemplateBuilder")
tbuilder.base_dir = requestedPath

```

4. Define data sources. In real life these would be replace by DataGrabbers

```

datasource = pe.Node(
    interface=util.IdentityInterface(
        fields=['imageList', 'passiveImagesDictionariesList']),
    run_without_submitted=True,
    name='InputImages')
datasource.inputs.imageList = input_images
datasource.inputs.passiveImagesDictionariesList = input_passive_images
datasource.inputs.sort_filelist = True

```

5. Template is initialized by a simple average

```

initAvg = pe.Node(interface=ants.AverageImages(), name='initAvg')
initAvg.inputs.dimension = 3
initAvg.inputs.normalize = True

tbuilder.connect(datasource, "imageList", initAvg, "images")

```

6. Define the first iteration of template building

```
buildTemplateIteration1 = ANTSTemplateBuildSingleIterationWF('iteration01')
tbuilder.connect(initAvg, 'output_average_image', buildTemplateIteration1,
                 'inputspec.fixed_image')
tbuilder.connect(datasource, 'imageList', buildTemplateIteration1,
                 'inputspec.images')
tbuilder.connect(datasource, 'passiveImagesDictionariesList',
                 buildTemplateIteration1,
                 'inputspec.ListOfPassiveImagesDictionaries')
```

7. Define the second iteration of template building

```
buildTemplateIteration2 = ANTSTemplateBuildSingleIterationWF('iteration02')
tbuilder.connect(buildTemplateIteration1, 'outputspec.template',
                 buildTemplateIteration2, 'inputspec.fixed_image')
tbuilder.connect(datasource, 'imageList', buildTemplateIteration2,
                 'inputspec.images')
tbuilder.connect(datasource, 'passiveImagesDictionariesList',
                 buildTemplateIteration2,
                 'inputspec.ListOfPassiveImagesDictionaries')
```

8. Move selected files to a designated results folder

```
datasink = pe.Node(io.DataSink(), name="datasink")
datasink.inputs.base_directory = os.path.join(requestedPath, "results")

tbuilder.connect(buildTemplateIteration2, 'outputspec.template', datasink,
                 'PrimaryTemplate')
tbuilder.connect(buildTemplateIteration2,
                 'outputspec.passive_deformed_templates', datasink,
                 'PassiveTemplate')
tbuilder.connect(initAvg, 'output_average_image', datasink,
                 'PreRegisterAverage')
```

8. Run the workflow

```
tbuilder.run()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipyre source distribution under the `examples` directory.

sMRI: Using ANTS for registration

In this simple tutorial we will use the Registration interface from ANTS to coregister two T1 volumes.

1. Tell python where to find the appropriate functions.

```
from __future__ import print_function, unicode_literals
from builtins import open

from future import standard_library
standard_library.install_aliases()

import os
import urllib.request
import urllib.error
import urllib.parse
from nipy.interfaces.ants import Registration
from nipy.testing import example_data
```

2. Download T1 volumes into home directory

```
homeDir = os.getenv("HOME")
requestedPath = os.path.join(homeDir, 'nipyTestPath')
mydatadir = os.path.realpath(requestedPath)
if not os.path.exists(mydatadir):
    os.makedirs(mydatadir)
print(mydatadir)

MyFileURLs = [
    ('http://slicer.kitware.com/midas3/download?bitstream=13121',
     '01_T1_half.nii.gz'),
    ('http://slicer.kitware.com/midas3/download?bitstream=13122',
     '02_T1_half.nii.gz'),
]
for tt in MyFileURLs:
    myURL = tt[0]
    localFilename = os.path.join(mydatadir, tt[1])
    if not os.path.exists(localFilename):
        remotefile = urllib.request.urlopen(myURL)
```

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```

        localFile = open(localFilename, 'wb')
        localFile.write(remotefile.read())
        localFile.close()
        print("Downloaded file: {0}".format(localFilename))
    else:
        print("File previously downloaded {0}".format(localFilename))

input_images = [
    os.path.join(mydatadir, '01_T1_half.nii.gz'),
    os.path.join(mydatadir, '02_T1_half.nii.gz'),
]

```

3. Define the parameters of the registration. Settings are found in the file `smri_ants_registration_settings.json` distributed with the example_data of *nipy*.

```

reg = Registration(
    from_file=example_data('smri_ants_registration_settings.json'))
reg.inputs.fixed_image = input_images[0]
reg.inputs.moving_image = input_images[1]

```

Alternatively to the use of the `from_file` feature to load ANTs settings, the user can manually set all those inputs instead:

```

reg.inputs.output_transform_prefix = 'thisTransform'
reg.inputs.output_warped_image = 'INTERNAL_WARPED.nii.gz'
reg.inputs.output_transform_prefix = "output_"
reg.inputs.transforms = ['Translation', 'Rigid', 'Affine', 'SyN']
reg.inputs.transform_parameters = [(0.1,), (0.1,), (0.1,), (0.2, 3.0, 0.0)]
reg.inputs.number_of_iterations = ([10000, 111110, 11110] * 3 +
                                   [[100, 50, 30]])

reg.inputs.dimension = 3
reg.inputs.write_composite_transform = True
reg.inputs.collapse_output_transforms = False
reg.inputs.metric = ['Mattes'] * 3 + [['Mattes', 'CC']]
reg.inputs.metric_weight = [1] * 3 + [[0.5, 0.5]]
reg.inputs.radius_or_number_of_bins = [32] * 3 + [[32, 4]]
reg.inputs.sampling_strategy = ['Regular'] * 3 + [[None, None]]
reg.inputs.sampling_percentage = [0.3] * 3 + [[None, None]]
reg.inputs.convergence_threshold = [1.e-8] * 3 + [-0.01]
reg.inputs.convergence_window_size = [20] * 3 + [5]
reg.inputs.smoothing_sigmas = [[4, 2, 1]] * 3 + [[1, 0.5, 0]]
reg.inputs.sigma_units = ['vox'] * 4
reg.inputs.shrink_factors = [[6, 4, 2]] + [[3, 2, 1]] * 2 + [[4, 2, 1]]
reg.inputs.use_estimate_learning_rate_once = [True] * 4
reg.inputs.use_histogram_matching = [False] * 3 + [True]
reg.inputs.initial_moving_transform_com = True

```

```
print(reg.cmdline)
```

3. Run the registration

```
reg.run()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipy source distribution under the `examples` directory.

smMRI: Using new ANTS for creating a T1 template (ITK4)

In this tutorial we will use ANTS (new ITK4 version aka “antsRegistration”) based workflow to create a template out of multiple T1 volumes. We will also showcase how to fine tune SGE jobs requirements.

1. Tell python where to find the appropriate functions.

```
from __future__ import print_function
from future import standard_library
standard_library.install_aliases()

import os
import nipype.interfaces.utility as util
import nipype.interfaces.ants as ants
import nipype.interfaces.io as io
import nipype.pipeline.engine as pe # pypeline engine

from nipype.workflows.smri.ants import _
↪ antsRegistrationTemplateBuildSingleIterationWF
```

2. Download T1 volumes into home directory

```
import urllib.request
import urllib.error
import urllib.parse
homeDir = os.getenv("HOME")
requestedPath = os.path.join(homeDir, 'nipypeTestPath')
mydatadir = os.path.realpath(requestedPath)
if not os.path.exists(mydatadir):
    os.makedirs(mydatadir)
print(mydatadir)

MyFileURLs = [
    ('http://slicer.kitware.com/midas3/download?bitstream=13121',
     '01_T1_half.nii.gz'),
    ('http://slicer.kitware.com/midas3/download?bitstream=13122',
     '02_T1_half.nii.gz'),
    ('http://slicer.kitware.com/midas3/download?bitstream=13124',
     '03_T1_half.nii.gz'),
    ('http://slicer.kitware.com/midas3/download?bitstream=13128',
```

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```

    '01_T1_inv_half.nii.gz'),
    ('http://slicer.kitware.com/midas3/download?bitstream=13123',
     '02_T1_inv_half.nii.gz'),
    ('http://slicer.kitware.com/midas3/download?bitstream=13125',
     '03_T1_inv_half.nii.gz'),
]
for tt in MyFileURLs:
    myURL = tt[0]
    localFilename = os.path.join(mydatadir, tt[1])
    if not os.path.exists(localFilename):
        remotefile = urllib.request.urlopen(myURL)

        localFile = open(localFilename, 'wb')
        localFile.write(remotefile.read())
        localFile.close()
        print("Downloaded file: {}".format(localFilename))
    else:
        print("File previously downloaded {}".format(localFilename))

```

ListOfImagesDictionaries - a list of dictionaries where each dictionary is for one scan session, and the mappings in the dictionary are for all the co-aligned images for that one scan session

```

ListOfImagesDictionaries = [{
    'T1':
        os.path.join(mydatadir, '01_T1_half.nii.gz'),
    'INV_T1':
        os.path.join(mydatadir, '01_T1_inv_half.nii.gz'),
    'LABEL_MAP':
        os.path.join(mydatadir, '01_T1_inv_half.nii.gz')
}, {
    'T1':
        os.path.join(mydatadir, '02_T1_half.nii.gz'),
    'INV_T1':
        os.path.join(mydatadir, '02_T1_inv_half.nii.gz'),
    'LABEL_MAP':
        os.path.join(mydatadir, '02_T1_inv_half.nii.gz')
}, {
    'T1':
        os.path.join(mydatadir, '03_T1_half.nii.gz'),
    'INV_T1':
        os.path.join(mydatadir, '03_T1_inv_half.nii.gz'),
    'LABEL_MAP':
        os.path.join(mydatadir, '03_T1_inv_half.nii.gz')
}]
input_passive_images = [{
    'INV_T1':
        os.path.join(mydatadir, '01_T1_inv_half.nii.gz')
}, {
    'INV_T1':
        os.path.join(mydatadir, '02_T1_inv_half.nii.gz')
}, {
    'INV_T1':
        os.path.join(mydatadir, '03_T1_inv_half.nii.gz')
}]

```

registrationImageTypes - A list of the image types to be used actively during the estimation process of registration, any image type not in this list will be passively resampled with the estimated transforms. ['T1','T2']

```
registrationImageTypes = ['T1']
```

interpolationMap - A map of image types to interpolation modes. If an image type is not listed, it will be linearly interpolated. { 'labelmap': 'NearestNeighbor', 'FLAIR': 'WindowedSinc' }

```
interpolationMapping = {
    'INV_T1': 'LanczosWindowedSinc',
    'LABEL_MAP': 'NearestNeighbor',
    'T1': 'Linear'
}
```

3. Define the workflow and its working directory

```
tbuilder = pe.Workflow(name="antsRegistrationTemplateBuilder")
tbuilder.base_dir = requestedPath
```

4. Define data sources. In real life these would be replace by DataGrabbers

```
InitialTemplateInputs = [mdict['T1'] for mdict in ListOfImagesDictionaries]

datasource = pe.Node(
    interface=util.IdentityInterface(fields=[
        'InitialTemplateInputs', 'ListOfImagesDictionaries',
        'registrationImageTypes', 'interpolationMapping'
    ]),
    run_without_submitting=True,
    name='InputImages')
datasource.inputs.InitialTemplateInputs = InitialTemplateInputs
datasource.inputs.ListOfImagesDictionaries = ListOfImagesDictionaries
datasource.inputs.registrationImageTypes = registrationImageTypes
datasource.inputs.interpolationMapping = interpolationMapping
datasource.inputs.sort_filelist = True
```

5. Template is initialized by a simple average in this simple example, any reference image could be used (i.e. a previously created template)

```
initAvg = pe.Node(interface=ants.AverageImages(), name='initAvg')
initAvg.inputs.dimension = 3
initAvg.inputs.normalize = True

tbuilder.connect(datasource, "InitialTemplateInputs", initAvg, "images")
```

6. Define the first iteration of template building

```
buildTemplateIteration1 = antsRegistrationTemplateBuildSingleIterationWF(
    'iteration01')
```

Here we are fine tuning parameters of the SGE job (memory limit, numebr of cores etc.)

```
BeginANTS = buildTemplateIteration1.get_node("BeginANTS")
BeginANTS.plugin_args = {
    'qsub_args':
        '-S /bin/bash -pe smpl 8-12 -l mem_free=6000M -o /dev/null -e /dev/null queue_
↪name',
    'overwrite':
        True
}

tbuilder.connect(initAvg, 'output_average_image', buildTemplateIteration1,
    'inputspec.fixed_image')
```

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```

tbuilder.connect(datasource, 'ListOfImagesDictionaries',
                  buildTemplateIteration1, 'inputspec.ListOfImagesDictionaries')
tbuilder.connect(datasource, 'registrationImageTypes', buildTemplateIteration1,
                  'inputspec.registrationImageTypes')
tbuilder.connect(datasource, 'interpolationMapping', buildTemplateIteration1,
                  'inputspec.interpolationMapping')

```

7. Define the second iteration of template building

```

buildTemplateIteration2 = antsRegistrationTemplateBuildSingleIterationWF(
    'iteration02')
BeginANTS = buildTemplateIteration2.get_node("BeginANTS")
BeginANTS.plugin_args = {
    'qsub_args':
        '-S /bin/bash -pe smpl 8-12 -l mem_free=6000M -o /dev/null -e /dev/null queue_
↪name',
    'overwrite':
        True
}
tbuilder.connect(buildTemplateIteration1, 'outputspec.template',
                  buildTemplateIteration2, 'inputspec.fixed_image')
tbuilder.connect(datasource, 'ListOfImagesDictionaries',
                  buildTemplateIteration2, 'inputspec.ListOfImagesDictionaries')
tbuilder.connect(datasource, 'registrationImageTypes', buildTemplateIteration2,
                  'inputspec.registrationImageTypes')
tbuilder.connect(datasource, 'interpolationMapping', buildTemplateIteration2,
                  'inputspec.interpolationMapping')

```

8. Move selected files to a designated results folder

```

datasink = pe.Node(io.DataSink(), name="datasink")
datasink.inputs.base_directory = os.path.join(requestedPath, "results")

tbuilder.connect(buildTemplateIteration2, 'outputspec.template', datasink,
                  'PrimaryTemplate')
tbuilder.connect(buildTemplateIteration2,
                  'outputspec.passive_deformed_templates', datasink,
                  'PassiveTemplate')
tbuilder.connect(initAvg, 'output_average_image', datasink,
                  'PreRegisterAverage')

```

9. Run the workflow

```

tbuilder.run(plugin="SGE")

```

Example source code

You can download the full source code of this example. This same script is also included in the Nipy source distribution under the `examples` directory.

sMRI: USing CBS Tools for skullstripping

This simple workflow uses SPECTRE2010 algorithm to skullstrip an MP2RAGE anatomical scan.

```
import nipype.pipeline.engine as pe
from nipype.interfaces.mipav.developer import (JistIntensityMp2rageMasking,
                                                MedicAlgorithmSPECTRE2010)

wf = pe.Workflow("skullstripping")

mask = pe.Node(JistIntensityMp2rageMasking(), name="masking")
folder_path = '/Users/filo/7t_trt/niftis/sub001/session_1/'
mask.inputs.inSecond = folder_path + "MP2RAGE_INV2.nii.gz"
mask.inputs.inQuantitative = folder_path + "MP2RAGE_UNI.nii.gz"
mask.inputs.inT1weighted = folder_path + "MP2RAGE_T1.nii.gz"
mask.inputs.outMasked = True
mask.inputs.outMasked2 = True
mask.inputs.outSignal = True
mask.inputs.outSignal2 = True

skullstrip = pe.Node(MedicAlgorithmSPECTRE2010(), name="skullstrip")
skullstrip.inputs.outStripped = True
skullstrip.inputs.xDefaultMem = 6000

wf.connect(mask, 'outMasked', skullstrip, 'inInput')
wf.run()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the examples directory.

sMRI: FreeSurfer

This script, `smri_freesurfer.py`, demonstrates the ability to call `reconall` on a set of subjects and then make an average subject:

```
python smri_freesurfer.py
```

Import necessary modules from `nipype`.

```
import os

import nipype.pipeline.engine as pe
import nipype.interfaces.io as nio
from nipype.interfaces.freesurfer.preprocess import ReconAll
from nipype.interfaces.freesurfer.utils import MakeAverageSubject

subject_list = ['s1', 's3']
data_dir = os.path.abspath('data')
subjects_dir = os.path.abspath('amri_freesurfer_tutorial/subjects_dir')

wf = pe.Workflow(name="11workflow")
wf.base_dir = os.path.abspath('amri_freesurfer_tutorial/workdir')
```

Grab data

```
datasource = pe.MapNode(
    interface=nio.DataGrabber(infields=['subject_id'], outfields=['struct']),
    name='datasource',
    iterfield=['subject_id'])
datasource.inputs.base_directory = data_dir
datasource.inputs.template = '%s/%s.nii'
datasource.inputs.template_args = dict(struct=[['subject_id', 'struct']])
datasource.inputs.subject_id = subject_list
datasource.inputs.sort_filelist = True
```

Run recon-all

```
recon_all = pe.MapNode(
    interface=ReconAll(),
    name='recon_all',
    iterfield=['subject_id', 'T1_files'])
```

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```
recon_all.inputs.subject_id = subject_list
if not os.path.exists(subjects_dir):
    os.mkdir(subjects_dir)
recon_all.inputs.subjects_dir = subjects_dir

wf.connect(datasource, 'struct', recon_all, 'T1_files')
```

Make average subject

```
average = pe.Node(interface=MakeAverageSubject(), name="average")
average.inputs.subjects_dir = subjects_dir

wf.connect(recon_all, 'subject_id', average, 'subjects_ids')

wf.run("MultiProc", plugin_args={'n_procs': 4})
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

sMRI: FSReconAll

This script, `smri_fsreconall.py`, demonstrates the ability to use the `create_reconall_workflow` function to create a workflow and then run it on a set of subjects and then make an average subject:

```
python smri_fsreconall.py
```

For an example on how to call FreeSurfer's reconall script in Nipype see `smri_freesurfer.py`.
Import necessary modules from nipype.

```
import os

import nipype.pipeline.engine as pe
import nipype.interfaces.io as nio
from nipype.workflows.smri.freesurfer import create_reconall_workflow
from nipype.interfaces.freesurfer.utils import MakeAverageSubject
from nipype.interfaces.utility import IdentityInterface
```

Assign the tutorial directory

```
tutorial_dir = os.path.abspath('smri_fsreconall_tutorial')
if not os.path.isdir(tutorial_dir):
    os.mkdir(tutorial_dir)
```

Define the workflow directories

```
subject_list = ['s1', 's3']
data_dir = os.path.abspath('data')
subjects_dir = os.path.join(tutorial_dir, 'subjects_dir')
if not os.path.exists(subjects_dir):
    os.mkdir(subjects_dir)

wf = pe.Workflow(name="11workflow")
wf.base_dir = os.path.join(tutorial_dir, 'workdir')
```

Create inputspec

```
inputspec = pe.Node(
    interface=IdentityInterface(['subject_id']), name="inputspec")
inputspec.iterables = ("subject_id", subject_list)
```

Grab data

```
datasource = pe.Node(
    interface=nio.DataGrabber(infields=['subject_id'], outfields=['struct']),
    name='datasource')
datasource.inputs.base_directory = data_dir
datasource.inputs.template = '%s/%s.nii'
datasource.inputs.template_args = dict(struct=[['subject_id', 'struct']])
datasource.inputs.subject_id = subject_list
datasource.inputs.sort_filelist = True

wf.connect(inputspec, 'subject_id', datasource, 'subject_id')
```

Run recon-all

```
recon_all = create_reconall_workflow()
recon_all.inputs.inputspec.subjects_dir = subjects_dir

wf.connect(datasource, 'struct', recon_all, 'inputspec.T1_files')
wf.connect(inputspec, 'subject_id', recon_all, 'inputspec.subject_id')
```

Make average subject

```
average = pe.JoinNode(
    interface=MakeAverageSubject(),
    joinsource="inputspec",
    joinfield="subjects_ids",
    name="average")
average.inputs.subjects_dir = subjects_dir

wf.connect(recon_all, 'postdatasink_outputspec.subject_id', average,
            'subjects_ids')

wf.run("MultiProc", plugin_args={'n_procs': 4})
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

sMRI: Regional Tessellation and Surface Smoothing

40.1 Introduction

This script, `tessellation_tutorial.py`, demonstrates the use of `create_tessellation_flow` from `nipype.workflows.smri.freesurfer`, and it can be run with:

```
python tessellation_tutorial.py
```

This example requires that the user has Freesurfer installed, and that the Freesurfer directory for 'fsaverage' is present.

See also:

ConnectomeViewer The Connectome Viewer connects Multi-Modal Multi-Scale Neuroimaging and Network Datasets For Analysis and Visualization in Python.

<http://www.geuz.org/gmsh/> Gmsh: a three-dimensional finite element mesh generator with built-in pre- and post-processing facilities

<http://www.blender.org/> Blender is the free open source 3D content creation suite, available for all major operating systems under the GNU General Public License.

Warning: This workflow will take several hours to finish entirely, since smoothing the larger cortical surfaces is very time consuming.

40.2 Packages and Data Setup

Import the necessary modules and workflow from `nipype`.

```
import nipype.pipeline.engine as pe # pipeline engine
import nipype.interfaces.cmtk as cmtk
import nipype.interfaces.io as nio # Data i/o
import os
import os.path as op
from nipype.workflows.smri.freesurfer import create_tessellation_flow
```


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```
tesspipe.run()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

Example source code

You can download the full source code of this example. This same script is also included in the Nipype source distribution under the `examples` directory.

Workflow from scratch

```

from builtins import range

import nipype.interfaces.io as nio # Data i/o
import nipype.interfaces.spm as spm # spm
import nipype.pipeline.engine as pe # pipeline engine
import nipype.algorithms.modelgen as model # model specification
from nipype.interfaces.base import Bunch
import os # system functions

```

In the following section, to showcase NiPyPe, we will describe how to create and extend a typical fMRI processing pipeline. We will begin with a basic processing layout and follow with extending it by adding/exchanging different components. Most fMRI pipeline can be divided into two sections - preprocessing and modelling. First one deals with cleaning data from confounds and noise and the second one fits a model based on the experimental design. Preprocessing stage in our first iteration of a pipeline will consist of only two steps: realignment and smoothing. In NiPyPe Every processing step consist of an Interface (which defines how to execute corresponding software) encapsulated in a Node (which defines for example a unique name). For realignment (motion correction achieved by coregistering all volumes to the mean) and smoothing (convolution with 3D Gaussian kernel) we will use SPM implementation. Definition of appropriate nodes can be found in Listing 1 (TODO). Inputs (such as `register_to_mean` from listing 1) of nodes are accessible through the `inputs` property. Upon setting any input its type is verified to avoid errors during the execution.

```

realign = pe.Node(interface=spm.Realign(), name="realign")
realign.inputs.register_to_mean = True

smooth = pe.Node(interface=spm.Smooth(), name="smooth")
smooth.inputs.fwhm = 4

```

To connect two nodes a Workflow has to be created. `connect()` method of a Workflow allows to specify which outputs of which Nodes should be connected to which inputs of which Nodes (see Listing 2). By connecting `realigned_files` output of `realign` to `in_files` input of `Smooth` we have created a simple preprocessing workflow (see Figure TODO).

```

preprocessing = pe.Workflow(name="preprocessing")
preprocessing.connect(realign, "realigned_files", smooth, "in_files")

```

Creating a modelling workflow which will define the design, estimate model and contrasts follows the same suite. We will again use SPM implementations. NiPyPe, however, adds extra abstraction layer to model def-

inition which allows using the same definition for many model estimation implementations (for example one from FSL or nippy). Therefore we will need four nodes: SpecifyModel (NiPyPe specific abstraction layer), Level1Design (SPM design definition), ModelEstimate, and ContrastEstimate. The connected modelling Workflow can be seen on Figure TODO. Model specification supports block, event and sparse designs. Contrasts provided to ContrastEstimate are defined using the same names of regressors as defined in the SpecifyModel.

```
specify_model = pe.Node(interface=model.SpecifyModel(), name="specify_model")
specify_model.inputs.input_units = 'secs'
specify_model.inputs.time_repetition = 3.
specify_model.inputs.high_pass_filter_cutoff = 120
specify_model.inputs.subject_info = [
    Bunch(
        conditions=['Task-Odd', 'Task-Even'],
        onsets=[list(range(15, 240, 60)),
                list(range(45, 240, 60))],
        durations=[[15], [15]])
] * 4

level1design = pe.Node(interface=spm.Level1Design(), name="level1design")
level1design.inputs.bases = {'hrf': {'derivs': [0, 0]}}
level1design.inputs.timing_units = 'secs'
level1design.inputs.interscan_interval = specify_model.inputs.time_repetition

level1estimate = pe.Node(interface=spm.EstimateModel(), name="level1estimate")
level1estimate.inputs.estimate_method = {'Classical': 1}

contrastestimate = pe.Node(
    interface=spm.EstimateContrast(), name="contrastestimate")
cont1 = ('Task>Baseline', 'T', ['Task-Odd', 'Task-Even'], [0.5, 0.5])
cont2 = ('Task-Odd>Task-Even', 'T', ['Task-Odd', 'Task-Even'], [1, -1])
contrastestimate.inputs.contrasts = [cont1, cont2]

modelling = pe.Workflow(name="modelling")
modelling.connect(specify_model, 'session_info', level1design, 'session_info')
modelling.connect(level1design, 'spm_mat_file', level1estimate, 'spm_mat_file')
modelling.connect(level1estimate, 'spm_mat_file', contrastestimate,
                  'spm_mat_file')
modelling.connect(level1estimate, 'beta_images', contrastestimate,
                  'beta_images')
modelling.connect(level1estimate, 'residual_image', contrastestimate,
                  'residual_image')
```

Having preprocessing and modelling workflows we need to connect them together, add data grabbing facility and save the results. For this we will create a master Workflow which will host preprocessing and model Workflows as well as DataGrabber and DataSink Nodes. NiPyPe allows connecting Nodes between Workflows. We will use this feature to connect realignment_parameters and smoothed_files to modelling workflow.

```
main_workflow = pe.Workflow(name="main_workflow")
main_workflow.base_dir = "workflow_from_scratch"
main_workflow.connect(preprocessing, "realignment_parameters",
                     modelling, "specify_model.realignment_parameters")
main_workflow.connect(preprocessing, "smooth.smoothed_files", modelling,
                     "specify_model.functional_runs")
```

DataGrabber allows to define flexible search patterns which can be parameterized by user defined inputs (such as subject ID, session etc.). This allows to adapt to a wide range of file layouts. In our case we will parameterize it with subject ID. In this way we will be able to run it for different subjects. We can automate this by iterating over a list of subject IDs, by setting an iterables property on the subject_id input of DataGrabber. Its output will be connected to realignment node from preprocessing workflow.


```
datasource = pe.Node(
    interface=nio.DataGrabber(infields=['subject_id'], outfields=['func']),
    name='datasource')
datasource.inputs.base_directory = os.path.abspath('data')
datasource.inputs.template = '%s/%s.nii'
datasource.inputs.template_args = dict(
    func=[['subject_id', ['f3', 'f5', 'f7', 'f10']]])
datasource.inputs.subject_id = 's1'
datasource.inputs.sort_filelist = True

main_workflow.connect(datasource, 'func', preprocessing, 'realigned_files')
```

DataSink on the other side provides means to storing selected results to a specified location. It supports automatic creation of folder stricter and regular expression based substitutions. In this example we will store T maps.

```
datasink = pe.Node(interface=nio.DataSink(), name="datasink")
datasink.inputs.base_directory = os.path.abspath(
    'workflow_from_scratch/output')

main_workflow.connect(modelling, 'contrastestimate.spmT_images', datasink,
    'contrasts.@T')

main_workflow.run()
main_workflow.write_graph()
```

Example source code

You can download the full source code of this example. This same script is also included in the Nipyne source distribution under the `examples` directory.

Workshop: Dartmouth College 2010

First lets go to the directory with the data we'll be working on and start the interactive python interpreter (with some nipytype specific configuration). Note that nipytype does not need to be run through ipython - it is just much nicer to do interactive work in it.

```
cd $TDPATH
ipython -p nipytype
```

For every neuroimaging procedure supported by nipytype there exists a wrapper - a small piece of code managing the underlying software (FSL, SPM, AFNI etc.). We call those interfaces. They are standardised so we can hook them up together. Lets have a look at some of them.

```
In [1]: import nipytype.interfaces.fsl as fsl

In [2]: fsl.BET.help()
Inputs
-----

Mandatory:
  in_file: input file to skull strip

Optional:
  args: Additional parameters to the command
  center: center of gravity in voxels
  environ: Environment variables (default={})
  frac: fractional intensity threshold
  functional: apply to 4D fMRI data
  mutually exclusive: functional, reduce_bias
  mask: create binary mask image
  mesh: generate a vtk mesh brain surface
  no_output: Don't generate segmented output
  out_file: name of output skull stripped image
  outline: create surface outline image
  output_type: FSL output type
  radius: head radius
  reduce_bias: bias field and neck cleanup
  mutually exclusive: functional, reduce_bias
  skull: create skull image
```

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```

threshold: apply thresholding to segmented brain image and mask
vertical_gradient: vertical gradient in fractional intensity threshold (-1, 1)

Outputs
-----
mask_file: path/name of binary brain mask (if generated)
meshfile: path/name of vtk mesh file (if generated)
out_file: path/name of skullstripped file
outline_file: path/name of outline file (if generated)

In [3]: import nipy.interfaces.freesurfer as fs

In [4]: fs.Smooth.help()
Inputs
-----

Mandatory:
  in_file: source volume
  num_iters: number of iterations instead of fwhm
  mutually exclusive: surface_fwhm
  reg_file: registers volume to surface anatomical
  surface_fwhm: surface FWHM in mm
  mutually exclusive: num_iters
  requires: reg_file

Optional:
  args: Additional parameters to the command
  environ: Environment variables (default={})
  proj_frac: project frac of thickness a long surface normal
  mutually exclusive: proj_frac_avg
  proj_frac_avg: average a long normal min max delta
  mutually exclusive: proj_frac
  smoothed_file: output volume
  subjects_dir: subjects directory
  vol_fwhm: volumesmoothing outside of surface

Outputs
-----
args: Additional parameters to the command
environ: Environment variables
smoothed_file: smoothed input volume
subjects_dir: subjects directory

```

You can read about all of the interfaces implemented in nipy at our online documentation at <http://nipy.sourceforge.net/nipy/documentation.html#documentation> . Check it out now.

42.1 Using interfaces

Having interfaces allows us to use third party software (like FSL BET) as function. Look how simple it is.

```

from __future__ import print_function
from builtins import str

import nipy.interfaces.fsl as fsl
result = fsl.BET(in_file='data/s1/struct.nii').run()
print(result)

```

Running a single program is not much of a breakthrough. Lets run motion correction followed by smoothing (isotropic - in other words not using SUSAN). Notice that in the first line we are setting the output data type for all FSL interfaces.

```
fsl.FSLCommand.set_default_output_type('NIFTI_GZ')
result1 = fsl.MCFLIRT(in_file='data/s1/f3.nii').run()
result2 = fsl.Smooth(in_file='f3_mcf.nii.gz', fwhm=6).run()
```

42.2 Simple workflow

In the previous example we knew that fsl.MCFLIRT will produce a file called f3_mcf.nii.gz and we have hard coded this as an input to fsl.Smooth. This is quite limited, but luckily nipy supports joining interfaces in pipelines. This way output of one interface will be used as an input of another without having to hard code anything. Before connecting Interfaces we need to put them into (separate) Nodes and give them unique names. This way every interface will process data in a separate folder.

```
import nipy.pipeline.engine as pe
import os

motion_correct = pe.Node(
    interface=fsl.MCFLIRT(in_file=os.path.abspath('data/s1/f3.nii')),
    name="motion_correct")
smooth = pe.Node(interface=fsl.Smooth(fwhm=6), name="smooth")

motion_correct_and_smooth = pe.Workflow(name="motion_correct_and_smooth")
motion_correct_and_smooth.base_dir = os.path.abspath(
    '.') # define where will be the root folder for the workflow
motion_correct_and_smooth.connect([(motion_correct, smooth, [('out_file',
                                                                'in_file')])])

# we are connecting 'out_file' output of motion_correct to 'in_file' input of
↪ smooth
motion_correct_and_smooth.run()
```

42.3 Another workflow

Another example of a simple workflow (calculate the mean of fMRI signal and subtract it). This time we'll be assigning inputs after defining the workflow.

```
calc_mean = pe.Node(interface=fsl.ImageMaths(), name="calc_mean")
calc_mean.inputs.op_string = "-Tmean"
subtract = pe.Node(interface=fsl.ImageMaths(), name="subtract")
subtract.inputs.op_string = "-sub"

demean = pe.Workflow(name="demean")
demean.base_dir = os.path.abspath('.')
demean.connect([(calc_mean, subtract, [('out_file', 'in_file2')])])

demean.inputs.calc_mean.in_file = os.path.abspath('data/s1/f3.nii')
demean.inputs.subtract.in_file = os.path.abspath('data/s1/f3.nii')
demean.run()
```

42.4 Reusing workflows

The beauty of the workflows is that they are reusable. We can just import a workflow made by someone else and feed it with our data.

```
from fmri_fsl import preproc
preproc.base_dir = os.path.abspath('.')
preproc.inputs.inputs.spec.func = os.path.abspath('data/s1/f3.nii')
preproc.inputs.inputs.spec.struct = os.path.abspath('data/s1/struct.nii')
preproc.run()
```

... and we can run it again and it won't actually rerun anything because none of the parameters have changed.

```
preproc.run()
```

... and we can change a parameter and run it again. Only the dependent nodes are rerun and that too only if the input state has changed.

```
preproc.inputs.meanfuncmask.frac = 0.5
preproc.run()
```

42.5 Visualizing workflows 1

So what did we run in this precanned workflow

```
preproc.write_graph()
```

42.6 Datasink

Datasink is a special interface for copying and arranging results.

```
import nipy.interfaces.io as nio

preproc.inputs.inputs.spec.func = os.path.abspath('data/s1/f3.nii')
preproc.inputs.inputs.spec.struct = os.path.abspath('data/s1/struct.nii')
datasink = pe.Node(interface=nio.DataSink(), name='sink')
preprocess = pe.Workflow(name='preprocout')
preprocess.base_dir = os.path.abspath('.')
preprocess.connect([(preproc, datasink, [
    ('meanfunc2.out_file', 'meanfunc'),
    ('maskfunc3.out_file', 'funcruns')])])

preprocess.run()
```

42.7 Datagrabber

Datagrabber is (surprise, surprise) an interface for collecting files from hard drive. It is very flexible and supports almost any file organisation of your data you can imagine.

```
datasource1 = nio.DataGrabber()
datasource1.inputs.template = 'data/s1/f3.nii'
datasource1.inputs.sort_filelist = True
results = datasource1.run()
print(results.outputs)

datasource2 = nio.DataGrabber()
```

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```

datasource2.inputs.template = 'data/s*/f*.nii'
datasource2.inputs.sort_filelist = True
results = datasource2.run()
print(results.outputs)

datasource3 = nio.DataGrabber(infields=['run'])
datasource3.inputs.template = 'data/s1/f%d.nii'
datasource3.inputs.sort_filelist = True
datasource3.inputs.run = [3, 7]
results = datasource3.run()
print(results.outputs)

datasource4 = nio.DataGrabber(infields=['subject_id', 'run'])
datasource4.inputs.template = 'data/%s/f%d.nii'
datasource4.inputs.sort_filelist = True
datasource4.inputs.run = [3, 7]
datasource4.inputs.subject_id = ['s1', 's3']
results = datasource4.run()
print(results.outputs)

```

42.8 Iterables

Iterables is a special field of the Node class that enables to iterate all workflows/nodes connected to it over some parameters. Here we'll use it to iterate over two subjects.

```

import nipy.interfaces.utility as util
infosource = pe.Node(
    interface=util.IdentityInterface(fields=['subject_id']), name="infosource")
infosource.iterables = ('subject_id', ['s1', 's3'])

datasource = pe.Node(
    nio.DataGrabber(infields=['subject_id'], outfields=['func', 'struct']),
    name="datasource")
datasource.inputs.template = '%s/%s.nii'
datasource.inputs.base_directory = os.path.abspath('data')
datasource.inputs.template_args = dict(
    func=[['subject_id', 'f3']], struct=[['subject_id', 'struct']])
datasource.inputs.sort_filelist = True

my_workflow = pe.Workflow(name="my_workflow")
my_workflow.base_dir = os.path.abspath('.')

my_workflow.connect([(infosource, datasource, [('subject_id', 'subject_id')]),
                    (datasource, preproc, [('func', 'inputspec.func'),
                                             ('struct', 'inputspec.struct')])])

my_workflow.run()

```

and we can change a node attribute and run it again

```

smoothnode = my_workflow.get_node('preproc.smooth')
assert (str(smoothnode) == 'preproc.smooth')
smoothnode.iterables = ('fwhm', [5., 10.])
my_workflow.run()

```

42.9 Visualizing workflows 2

In the case of nested workflows, we might want to look at expanded forms of the workflow.

Example source code

You can download the full source code of this example. This same script is also included in the Nipytype source distribution under the `examples` directory.

- Interfaces

43.1 ACompCor

[Link to code](#)

Anatomical compcor: for inputs and outputs, see CompCor. When the mask provided is an anatomical mask, then CompCor is equivalent to ACompCor.

Inputs:

```
[Mandatory]
realigned_file: (a pathlike object or string representing an existing
                 file)
                 already realigned brain image (4D)

[Optional]
mask_files: (a list of items which are a pathlike object or string
             representing an existing file)
             One or more mask files that determines ROI (3D). When more than one
             file is provided `merge_method` or `merge_index` must be provided
merge_method: ('union' or 'intersect' or 'none')
             Merge method if multiple masks are present - `union` uses voxels
             included in at least one input mask, `intersect` uses only voxels
             present in all input masks, `none` performs CompCor on each mask
             individually
             mutually_exclusive: mask_index
             requires: mask_files
mask_index: (a long integer >= 0)
             Position of mask in `mask_files` to use - first is the default.
             mutually_exclusive: merge_method
             requires: mask_files
mask_names: (a list of items which are a unicode string)
             Names for provided masks (for printing into metadata). If provided,
             it must be as long as the final mask list (after any merge and
             indexing operations).
components_file: (a unicode string, nipype default value:
                  components_file.txt)
                  Filename to store physiological components
num_components: (a long integer >= 1 or 'all')
```

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```

        Number of components to return from the decomposition. If
        `num_components` is `all`, then all components will be retained.
        mutually_exclusive: variance_threshold
variance_threshold: (0.0 < a floating point number < 1.0)
        Select the number of components to be returned automatically based
        on their ability to explain variance in the dataset.
        `variance_threshold` is a fractional value between 0 and 1; the
        number of components retained will be equal to the minimum number of
        components necessary to explain the provided fraction of variance in
        the masked time series.
        mutually_exclusive: num_components
pre_filter: ('polynomial' or 'cosine' or False, nipy default value:
            polynomial)
        Detrend time series prior to component extraction
use_regress_poly: (a boolean)
        use polynomial regression pre-component extraction
regress_poly_degree: (a long integer >= 1, nipy default value: 1)
        the degree polynomial to use
header_prefix: (a unicode string)
        the desired header for the output tsv file (one column). If
        undefined, will default to "CompCor"
high_pass_cutoff: (a float, nipy default value: 128)
        Cutoff (in seconds) for "cosine" pre-filter
repetition_time: (a float)
        Repetition time (TR) of series - derived from image header if
        unspecified
save_pre_filter: (a boolean or a pathlike object or string
        representing a file, nipy default value: False)
        Save pre-filter basis as text file
save_metadata: (a boolean or a pathlike object or string representing
        a file, nipy default value: False)
        Save component metadata as text file
ignore_initial_volumes: (a long integer >= 0, nipy default value:
        0)
        Number of volumes at start of series to ignore
failure_mode: ('error' or 'NaN', nipy default value: error)
        When no components are found or convergence fails, raise an error or
        silently return columns of NaNs.

```

Outputs:

```

components_file: (a pathlike object or string representing an
        existing file)
        text file containing the noise components
pre_filter_file: (a pathlike object or string representing a file)
        text file containing high-pass filter basis
metadata_file: (a pathlike object or string representing a file)
        text file containing component metadata

```

43.1.1 References:

None

43.2 CompCor[Link to code](#)

Interface with core CompCor computation, used in aCompCor and tCompCor

CompCor provides three pre-filter options, all of which include per-voxel mean removal:

- polynomial: Legendre polynomial basis
- cosine: Discrete cosine basis
- False: mean-removal only

In the case of polynomial and cosine filters, a pre-filter file may be saved with a row for each volume/timepoint, and a column for each non-constant regressor. If no non-constant (mean-removal) columns are used, this file may be empty.

If `ignore_initial_volumes` is set, then the specified number of initial volumes are excluded both from pre-filtering and CompCor component extraction. Each column in the components and pre-filter files are prefixed with zeros for each excluded volume so that the number of rows continues to match the number of volumes in the input file. In addition, for each excluded volume, a column is added to the pre-filter file with a 1 in the corresponding row.

43.2.1 Example

```
>>> ccinterface = CompCor()
>>> ccinterface.inputs.realigned_file = 'functional.nii'
>>> ccinterface.inputs.mask_files = 'mask.nii'
>>> ccinterface.inputs.num_components = 1
>>> ccinterface.inputs.pre_filter = 'polynomial'
>>> ccinterface.inputs.regress_poly_degree = 2
```

Inputs:

```
[Mandatory]
realigned_file: (a pathlike object or string representing an existing
                 file)
                 already realigned brain image (4D)

[Optional]
mask_files: (a list of items which are a pathlike object or string
             representing an existing file)
             One or more mask files that determines ROI (3D). When more than one
             file is provided `merge_method` or `merge_index` must be provided
merge_method: ('union' or 'intersect' or 'none')
             Merge method if multiple masks are present - `union` uses voxels
             included in at least one input mask, `intersect` uses only voxels
             present in all input masks, `none` performs CompCor on each mask
             individually
             mutually_exclusive: mask_index
             requires: mask_files
mask_index: (a long integer >= 0)
             Position of mask in `mask_files` to use - first is the default.
             mutually_exclusive: merge_method
             requires: mask_files
mask_names: (a list of items which are a unicode string)
             Names for provided masks (for printing into metadata). If provided,
             it must be as long as the final mask list (after any merge and
             indexing operations).
components_file: (a unicode string, nipy default value:
                  components_file.txt)
                  Filename to store physiological components
num_components: (a long integer >= 1 or 'all')
                 Number of components to return from the decomposition. If
                 `num_components` is `all`, then all components will be retained.
```

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```

    mutually_exclusive: variance_threshold
variance_threshold: (0.0 < a floating point number < 1.0)
    Select the number of components to be returned automatically based
    on their ability to explain variance in the dataset.
    `variance_threshold` is a fractional value between 0 and 1; the
    number of components retained will be equal to the minimum number of
    components necessary to explain the provided fraction of variance in
    the masked time series.
    mutually_exclusive: num_components
pre_filter: ('polynomial' or 'cosine' or False, nipy default value:
    polynomial)
    Detrend time series prior to component extraction
use_regress_poly: (a boolean)
    use polynomial regression pre-component extraction
regress_poly_degree: (a long integer >= 1, nipy default value: 1)
    the degree polynomial to use
header_prefix: (a unicode string)
    the desired header for the output tsv file (one column). If
    undefined, will default to "CompCor"
high_pass_cutoff: (a float, nipy default value: 128)
    Cutoff (in seconds) for "cosine" pre-filter
repetition_time: (a float)
    Repetition time (TR) of series - derived from image header if
    unspecified
save_pre_filter: (a boolean or a pathlike object or string
    representing a file, nipy default value: False)
    Save pre-filter basis as text file
save_metadata: (a boolean or a pathlike object or string representing
    a file, nipy default value: False)
    Save component metadata as text file
ignore_initial_volumes: (a long integer >= 0, nipy default value:
    0)
    Number of volumes at start of series to ignore
failure_mode: ('error' or 'NaN', nipy default value: error)
    When no components are found or convergence fails, raise an error or
    silently return columns of NaNs.

```

Outputs:

```

components_file: (a pathlike object or string representing an
    existing file)
    text file containing the noise components
pre_filter_file: (a pathlike object or string representing a file)
    text file containing high-pass filter basis
metadata_file: (a pathlike object or string representing a file)
    text file containing component metadata

```

43.2.2 References:

None

43.3 ComputeDVARs[Link to code](#)

Computes the DVARs.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        functional data, after HMC
in_mask: (a pathlike object or string representing an existing file)
        a brain mask

[Optional]
remove_zerovariance: (a boolean, nipy default value: True)
        remove voxels with zero variance
save_std: (a boolean, nipy default value: True)
        save standardized DVARS
save_nstd: (a boolean, nipy default value: False)
        save non-standardized DVARS
save_vxstd: (a boolean, nipy default value: False)
        save voxel-wise standardized DVARS
save_all: (a boolean, nipy default value: False)
        output all DVARS
series_tr: (a float)
        repetition time in sec.
save_plot: (a boolean, nipy default value: False)
        write DVARS plot
figdpi: (an integer (int or long), nipy default value: 100)
        output dpi for the plot
figsize: (a tuple of the form: (a float, a float), nipy default
        value: (11.7, 2.3))
        output figure size
figformat: ('png' or 'pdf' or 'svg', nipy default value: png)
        output format for figures
intensity_normalization: (a float, nipy default value: 1000.0)
        Divide value in each voxel at each timepoint by the median
        calculated across all voxels and timepoints within the mask (if
        specified) and then multiply by the value specified by this parameter.
        By using the default (1000) output DVARS will be expressed in x10 %
        BOLD units compatible with Power et al. 2012. Set this to 0 to
        disable intensity normalization altogether.

```

Outputs:

```

out_std: (a pathlike object or string representing an existing file)
        output text file
out_nstd: (a pathlike object or string representing an existing file)
        output text file
out_vxstd: (a pathlike object or string representing an existing
        file)
        output text file
out_all: (a pathlike object or string representing an existing file)
        output text file
avg_std: (a float)
avg_nstd: (a float)
avg_vxstd: (a float)
fig_std: (a pathlike object or string representing an existing file)
        output DVARS plot
fig_nstd: (a pathlike object or string representing an existing file)
        output DVARS plot
fig_vxstd: (a pathlike object or string representing an existing
        file)
        output DVARS plot

```

43.3.1 References:

None None

43.4 FramewiseDisplacement

[Link to code](#)

Calculate the FD (framewise displacement) as in [Power2012]. This implementation reproduces the calculation in fsl_motion_outliers

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        motion parameters
parameter_source: ('FSL' or 'AFNI' or 'SPM' or 'FSFAST' or 'NIPY')
                  Source of movement parameters

[Optional]
radius: (a float, nipy default value: 50)
        radius in mm to calculate angular FDs, 50mm is the default since it
        is used in Power et al. 2012
out_file: (a pathlike object or string representing a file, nipy default value: fd_power_2012.txt)
          output file name
out_figure: (a pathlike object or string representing a file, nipy default value: fd_power_2012.pdf)
            output figure name
series_tr: (a float)
            repetition time in sec.
save_plot: (a boolean, nipy default value: False)
            write FD plot
normalize: (a boolean, nipy default value: False)
            calculate FD in mm/s
figdpi: (an integer (int or long), nipy default value: 100)
         output dpi for the FD plot
figsize: (a tuple of the form: (a float, a float), nipy default value: (11.7, 2.3))
         output figure size
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
          calculated FD per timestep
out_figure: (a pathlike object or string representing a file)
            output image file
fd_average: (a float)
            average FD
```

43.4.1 References:

None

43.5 NonSteadyStateDetector

[Link to code](#)

Returns the number of non-steady state volumes detected at the beginning of the scan.

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        4D NIFTI EPI file
```

Outputs:

```
n_volumes_to_discard: (an integer (int or long))
        Number of non-steady state volumes detected in the beginning of the
        scan.
```

43.6 TCompCor

[Link to code](#)

Interface for tCompCor. Computes a ROI mask based on variance of voxels.

43.6.1 Example

```
>>> ccinterface = TCompCor()
>>> ccinterface.inputs.realigned_file = 'functional.nii'
>>> ccinterface.inputs.mask_files = 'mask.nii'
>>> ccinterface.inputs.num_components = 1
>>> ccinterface.inputs.pre_filter = 'polynomial'
>>> ccinterface.inputs.regress_poly_degree = 2
>>> ccinterface.inputs.percentile_threshold = .03
```

Inputs:

```
[Mandatory]
realigned_file: (a pathlike object or string representing an existing
                file)
                already realigned brain image (4D)

[Optional]
percentile_threshold: (0.0 < a floating point number < 1.0, nipy
                    default value: 0.02)
                    the percentile used to select highest-variance voxels, represented
                    by a number between 0 and 1, exclusive. By default, this value is
                    set to .02. That is, the 2% of voxels with the highest variance are
                    used.
mask_files: (a list of items which are a pathlike object or string
            representing an existing file)
            One or more mask files that determines ROI (3D). When more than one
            file is provided `merge_method` or `merge_index` must be provided
merge_method: ('union' or 'intersect' or 'none')
            Merge method if multiple masks are present - `union` uses voxels
            included in at least one input mask, `intersect` uses only voxels
            present in all input masks, `none` performs CompCor on each mask
            individually
mutually_exclusive: mask_index
requires: mask_files
mask_index: (a long integer >= 0)
            Position of mask in `mask_files` to use - first is the default.
mutually_exclusive: merge_method
requires: mask_files
mask_names: (a list of items which are a unicode string)
            Names for provided masks (for printing into metadata). If provided,
```

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```

        it must be as long as the final mask list (after any merge and
        indexing operations).
components_file: (a unicode string, nipy default value:
    components_file.txt)
    Filename to store physiological components
num_components: (a long integer >= 1 or 'all')
    Number of components to return from the decomposition. If
    `num_components` is `all`, then all components will be retained.
    mutually_exclusive: variance_threshold
variance_threshold: (0.0 < a floating point number < 1.0)
    Select the number of components to be returned automatically based
    on their ability to explain variance in the dataset.
    `variance_threshold` is a fractional value between 0 and 1; the
    number of components retained will be equal to the minimum number of
    components necessary to explain the provided fraction of variance in
    the masked time series.
    mutually_exclusive: num_components
pre_filter: ('polynomial' or 'cosine' or False, nipy default value:
    polynomial)
    Detrend time series prior to component extraction
use_regress_poly: (a boolean)
    use polynomial regression pre-component extraction
regress_poly_degree: (a long integer >= 1, nipy default value: 1)
    the degree polynomial to use
header_prefix: (a unicode string)
    the desired header for the output tsv file (one column). If
    undefined, will default to "CompCor"
high_pass_cutoff: (a float, nipy default value: 128)
    Cutoff (in seconds) for "cosine" pre-filter
repetition_time: (a float)
    Repetition time (TR) of series - derived from image header if
    unspecified
save_pre_filter: (a boolean or a pathlike object or string
    representing a file, nipy default value: False)
    Save pre-filter basis as text file
save_metadata: (a boolean or a pathlike object or string representing
    a file, nipy default value: False)
    Save component metadata as text file
ignore_initial_volumes: (a long integer >= 0, nipy default value:
    0)
    Number of volumes at start of series to ignore
failure_mode: ('error' or 'NaN', nipy default value: error)
    When no components are found or convergence fails, raise an error or
    silently return columns of NaNs.

```

Outputs:

```

high_variance_masks: (a list of items which are a pathlike object or
    string representing an existing file)
    voxels exceeding the variance threshold
components_file: (a pathlike object or string representing an
    existing file)
    text file containing the noise components
pre_filter_file: (a pathlike object or string representing a file)
    text file containing high-pass filter basis
metadata_file: (a pathlike object or string representing a file)
    text file containing component metadata

```


43.6.2 References:

None

43.7 TSNR

[Link to code](#)

Computes the time-course SNR for a time series

Typically you want to run this on a realigned time-series.

43.7.1 Example

```
>>> tsnr = TSNR()
>>> tsnr.inputs.in_file = 'functional.nii'
>>> res = tsnr.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a list of items which are a pathlike object or string
         representing an existing file)
         realigned 4D file or a list of 3D files

[Optional]
regress_poly: (a long integer >= 1)
              Remove polynomials
tsnr_file: (a pathlike object or string representing a file, nipy
           default value: tsnr.nii.gz)
           output tSNR file
mean_file: (a pathlike object or string representing a file, nipy
           default value: mean.nii.gz)
           output mean file
stddev_file: (a pathlike object or string representing a file, nipy
             default value: stddev.nii.gz)
             output tSNR file
detrended_file: (a pathlike object or string representing a file,
               nipy default value: detrend.nii.gz)
               input file after detrending
```

Outputs:

```
tsnr_file: (a pathlike object or string representing an existing
           file)
           tsnr image file
mean_file: (a pathlike object or string representing an existing
           file)
           mean image file
stddev_file: (a pathlike object or string representing an existing
             file)
             std dev image file
detrended_file: (a pathlike object or string representing a file)
               detrended input file
```

43.8 combine_mask_files()

[Link to code](#)

Combines input mask files into a single nibabel image

A helper function for CompCor

mask_files: a list one or more binary mask files

mask_method: enum ('union', 'intersect', 'none') determines how to combine masks

mask_index: an integer determines which file to return (mutually exclusive with mask_method)

returns: a list of nibabel images

43.9 compute_dvars()

[Link to code](#)

Compute the DVARS (D referring to temporal derivative of timecourses, VARS referring to RMS variance over voxels) [Power2012].

Particularly, the *standardized* DVARS [Nichols2013] are computed.

Note: Implementation details

Uses the implementation of the [Yule-Walker equations](#) from `nitime` for the AR (auto-regressive) filtering of the fMRI signal.

param numpy.ndarray func functional data, after head-motion-correction.

param numpy.ndarray mask a 3D mask of the brain

param bool output_all write out all dvars

param str out_file a path to which the standardized dvars should be saved.

return the standardized DVARS

43.10 compute_noise_components()

[Link to code](#)

Compute the noise components from the imgseries for each mask

43.10.1 Parameters

imgseries: nibabel image Time series data to be decomposed.

mask_images: list List of nibabel images. Time series data from *img_series* is subset according to the spatial extent of each mask, and the subset data is then decomposed using principal component analysis. Masks should be coextensive with either anatomical or spatial noise ROIs.

components_criterion: float Number of noise components to return. If this is a decimal value between 0 and 1, then *create_noise_components* will instead return the smallest number of components necessary to explain the indicated fraction of variance. If *components_criterion* is *all*, then all components will be returned.

filter_type: str

Type of filter to apply to time series before computing noise components.

'polynomial' - Legendre polynomial basis 'cosine' - Discrete cosine (DCT) basis False - None (mean-removal only)

failure_mode: str Action to be taken in the event that any decomposition fails to identify any components. *error* indicates that the routine should raise an exception and exit, while any other value indicates that the routine should return a matrix of NaN values equal in size to the requested decomposition matrix.

mask_names: list or None List of names for each image in *mask_images*. This should be equal in length to *mask_images*, with the *i*th element of *mask_names* naming the *i*th element of *mask_images*.

Filter options:

degree: int Order of polynomial used to remove trends from the timeseries

period_cut: float Minimum period (in sec) for DCT high-pass filter

repetition_time: float Time (in sec) between volume acquisitions. This must be defined if the *filter_type* is *cosine*.

43.10.2 Returns

components: numpy array Numpy array containing the requested set of noise components

basis: numpy array Numpy array containing the (non-constant) filter regressors

metadata: OrderedDict{str: numpy array} Dictionary of eigenvalues, fractional explained variances, and cumulative explained variances.

43.11 cosine_filter()

[Link to code](#)

43.12 fallback_svd()

[Link to code](#)

43.13 is_outlier()

[Link to code](#)

Returns a boolean array with True if points are outliers and False otherwise.

param nparray points an numobservations by numdimensions numpy array of observations

param float thresh the modified z-score to use as a threshold. Observations with a modified z-score (based on the median absolute deviation) greater than this value will be classified as outliers.

return A boolean mask, of size numobservations-length array.

Note: References

Boris Iglewicz and David Hoaglin (1993), “Volume 16: How to Detect and Handle Outliers”, The ASQC Basic References in Quality Control: Statistical Techniques, Edward F. Mykytka, Ph.D., Editor.

43.14 plot_confound()

[Link to code](#)

A helper function to plot FMRI (functional MRI) confounds.

43.15 regress_poly()

[Link to code](#)

Returns data with degree polynomial regressed out.

param bool remove_mean whether or not demean data (i.e. degree 0),

param int axis numpy array axes along which regression is performed

44.1 ICC

[Link to code](#)

Calculates Interclass Correlation Coefficient (3,1) as defined in P. E. Shrout & Joseph L. Fleiss (1979). “Intra-class Correlations: Uses in Assessing Rater Reliability”. Psychological Bulletin 86 (2): 420-428. This particular implementation is aimed at reliability (test-retest) studies.

Inputs:

```
[Mandatory]
subjects_sessions: (a list of items which are a list of items which
                    are a pathlike object or string representing an existing file)
                    n subjects m sessions 3D stat files
mask: (a pathlike object or string representing an existing file)
```

Outputs:

```
icc_map: (a pathlike object or string representing an existing file)
session_var_map: (a pathlike object or string representing an
                 existing file)
                 variance between sessions
subject_var_map: (a pathlike object or string representing an
                 existing file)
                 variance between subjects
```

44.2 ICC_rep_anova()

[Link to code](#)

the data Y are entered as a ‘table’ ie subjects are in rows and repeated measures in columns

One Sample Repeated measure ANOVA

$Y = XB + E$ with $X = [\text{FaTor} / \text{Subjects}]$

45.1 ComputeMeshWarp

[Link to code](#)

Calculates a the vertex-wise warping to get surface2 from surface1. It also reports the average distance of vertices, using the norm specified as input.

Example:

```
import nipy.algorithms.mesh as m
dist = m.ComputeMeshWarp()
dist.inputs.surface1 = 'surf1.vtk'
dist.inputs.surface2 = 'surf2.vtk'
res = dist.run()
```

Inputs:

```
[Mandatory]
surface1: (a pathlike object or string representing an existing file)
    Reference surface (vtk format) to which compute distance.
surface2: (a pathlike object or string representing an existing file)
    Test surface (vtk format) from which compute distance.

[Optional]
metric: ('euclidean' or 'sqeuclidean', nipy default value:
    euclidean)
    norm used to report distance
weighting: ('none' or 'area', nipy default value: none)
    "none": no weighting is performed, surface": edge distance is
    weighted by the corresponding surface area
out_warp: (a pathlike object or string representing a file, nipy
    default value: surfwarp.vtk)
    vtk file based on surface1 and warplings mapping it to surface2
out_file: (a pathlike object or string representing a file, nipy
    default value: distance.npy)
    numpy file keeping computed distances and weights
```

Outputs:

```
distance: (a float)
    computed distance
out_warp: (a pathlike object or string representing an existing file)
    vtk file with the vertex-wise mapping of surface1 to surface2
out_file: (a pathlike object or string representing an existing file)
    numpy file keeping computed distances and weights
```

45.2 MeshWarpMaths

[Link to code](#)

Performs the most basic mathematical operations on the warping field defined at each vertex of the input surface. A surface with scalar or vector data can be used as operator for non-uniform operations.

Example:

```
import nipyype.algorithms.mesh as m
mmath = m.MeshWarpMaths()
mmath.inputs.in_surf = 'surf1.vtk'
mmath.inputs.operator = 'surf2.vtk'
mmath.inputs.operation = 'mul'
res = mmath.run()
```

Inputs:

```
[Mandatory]
in_surf: (a pathlike object or string representing an existing file)
    Input surface in vtk format, with associated warp field as point
    data (ie. from ComputeMeshWarp)
operator: (a float or a tuple of the form: (a float, a float, a
    float) or a pathlike object or string representing an existing
    file, nipyype default value: 1.0)
    image, float or tuple of floats to act as operator

[Optional]
float_trait: (a float or a tuple of the form: (a float, a float, a
    float))
operation: ('sum' or 'sub' or 'mul' or 'div', nipyype default value:
    sum)
    operation to be performed
out_warp: (a pathlike object or string representing a file, nipyype
    default value: warp_maths.vtk)
    vtk file based on in_surf and warpings mapping it to out_file
out_file: (a pathlike object or string representing a file, nipyype
    default value: warped_surf.vtk)
    vtk with surface warped
```

Outputs:

```
out_warp: (a pathlike object or string representing an existing file)
    vtk file with the vertex-wise mapping of surface1 to surface2
out_file: (a pathlike object or string representing an existing file)
    vtk with surface warped
```

45.3 P2PDistance

[Link to code](#)

Calculates a point-to-point (p2p) distance between two corresponding VTK-readable meshes or contours.

A point-to-point correspondence between nodes is required
 Deprecated since version 1.0-dev: Use ComputeMeshWarp instead.
 Inputs:

```
[Mandatory]
surface1: (a pathlike object or string representing an existing file)
           Reference surface (vtk format) to which compute distance.
surface2: (a pathlike object or string representing an existing file)
           Test surface (vtk format) from which compute distance.

[Optional]
metric: ('euclidean' or 'sqeuclidean', nipyre default value:
         euclidean)
         norm used to report distance
weighting: ('none' or 'area', nipyre default value: none)
            "none": no weighting is performed, surface": edge distance is
            weighted by the corresponding surface area
out_warp: (a pathlike object or string representing a file, nipyre
           default value: surfwarp.vtk)
           vtk file based on surface1 and warpings mapping it to surface2
out_file: (a pathlike object or string representing a file, nipyre
           default value: distance.npy)
           numpy file keeping computed distances and weights
```

Outputs:

```
distance: (a float)
           computed distance
out_warp: (a pathlike object or string representing an existing file)
           vtk file with the vertex-wise mapping of surface1 to surface2
out_file: (a pathlike object or string representing an existing file)
           numpy file keeping computed distances and weights
```

45.4 TVTKBaseInterface

[Link to code](#)

A base class for interfaces using VTK

Inputs:

None

Outputs:

None

45.5 WarpPoints

[Link to code](#)

Applies a displacement field to a point set given in vtk format. Any discrete deformation field, given in physical coordinates and which volume covers the extent of the vtk point set, is a valid warp file. FSL interfaces are compatible, for instance any field computed with `nipyre.interfaces.fsl.utils.ConvertWarp`.

Example:

```
from nipyre.algorithms.mesh import WarpPoints
wp = WarpPoints()
```

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```
wp.inputs.points = 'surfl.vtk'
wp.inputs.warp = 'warpfield.nii'
res = wp.run()
```

Inputs:

```
[Mandatory]
points: (a pathlike object or string representing an existing file)
        file containing the point set
warp: (a pathlike object or string representing an existing file)
       dense deformation field to be applied
interp: ('cubic' or 'nearest' or 'linear', nipy default value:
         cubic)
         interpolation

[Optional]
out_points: (a pathlike object or string representing a file)
            the warped point set
```

Outputs:

```
out_points: (a pathlike object or string representing a file)
            the warped point set
```

46.1 Distance

[Link to code](#)

Calculates distance between two volumes.

Inputs:

```
[Mandatory]
volume1: (a pathlike object or string representing an existing file)
         Has to have the same dimensions as volume2.
volume2: (a pathlike object or string representing an existing file)
         Has to have the same dimensions as volume1.

[Optional]
method: ('eucl_min' or 'eucl_cog' or 'eucl_mean' or 'eucl_wmean' or
         'eucl_max', nipype default value: eucl_min)
        "eucl_min": Euclidean distance between two closest points
        "eucl_cog": mean Euclidian distance between the Center of Gravity of
        volume1 and CoGs of volume2 "eucl_mean": mean Euclidian minimum
        distance of all volume2 voxels to volume1 "eucl_wmean": mean
        Euclidian minimum distance of all volume2 voxels to volume1 weighted
        by their values "eucl_max": maximum over minimum Euclidian distances
        of all volume2 voxels to volume1 (also known as the Hausdorff
        distance)
mask_volume: (a pathlike object or string representing an existing
              file)
              calculate overlap only within this mask.
```

Outputs:

```
distance: (a float)
point1: (an array with shape (3,))
point2: (an array with shape (3,))
histogram: (a pathlike object or string representing a file)
```

46.2 ErrorMap

[Link to code](#)

Calculates the error (distance) map between two input volumes.

46.2.1 Example

```
>>> errormap = ErrorMap()
>>> errormap.inputs.in_ref = 'cont1.nii'
>>> errormap.inputs.in_tst = 'cont2.nii'
>>> res = errormap.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_ref: (a pathlike object or string representing an existing file)
        Reference image. Requires the same dimensions as in_tst.
in_tst: (a pathlike object or string representing an existing file)
        Test image. Requires the same dimensions as in_ref.
metric: ('squeuclidean' or 'euclidean', nipy default value:
        squeuclidean)
        error map metric (as implemented in scipy cdist)

[Optional]
mask: (a pathlike object or string representing an existing file)
       calculate overlap only within this mask.
out_map: (a pathlike object or string representing a file)
         Name for the output file
```

Outputs:

```
out_map: (a pathlike object or string representing an existing file)
         resulting error map
distance: (a float)
         Average distance between volume 1 and 2
```

46.3 FuzzyOverlap

[Link to code](#)

Calculates various overlap measures between two maps, using the fuzzy definition proposed in: Crum et al., Generalized Overlap Measures for Evaluation and Validation in Medical Image Analysis, IEEE Trans. Med. Ima. 25(11),pp 1451-1461, Nov. 2006.

in_ref and in_tst are lists of 2/3D images, each element on the list containing one volume fraction map of a class in a fuzzy partition of the domain.

46.3.1 Example

```
>>> overlap = FuzzyOverlap()
>>> overlap.inputs.in_ref = [ 'ref_class0.nii', 'ref_class1.nii' ]
>>> overlap.inputs.in_tst = [ 'tst_class0.nii', 'tst_class1.nii' ]
>>> overlap.inputs.weighting = 'volume'
>>> res = overlap.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_ref: (a list of items which are a pathlike object or string
        representing an existing file)
        Reference image. Requires the same dimensions as in_tst.
in_tst: (a list of items which are a pathlike object or string
        representing an existing file)
        Test image. Requires the same dimensions as in_ref.

[Optional]
in_mask: (a pathlike object or string representing an existing file)
        calculate overlap only within mask
weighting: ('none' or 'volume' or 'squared_vol', nipy default
            value: none)
            'none': no class-overlap weighting is performed. 'volume': computed
            class-overlaps are weighted by class volume 'squared_vol': computed
            class-overlaps are weighted by the squared volume of the class
out_file: (a pathlike object or string representing a file, nipy
            default value: diff.nii)
            alternative name for resulting difference-map
```

Outputs:

```
jaccard: (a float)
        Fuzzy Jaccard Index (fJI), all the classes
dice: (a float)
        Fuzzy Dice Index (fDI), all the classes
class_fji: (a list of items which are a float)
        Array containing the fJIs of each computed class
class_fdi: (a list of items which are a float)
        Array containing the fDIs of each computed class
```

46.4 Overlap

[Link to code](#)

Calculates Dice and Jaccard's overlap measures between two ROI maps. The interface is backwards compatible with the former version in which only binary files were accepted.

The averaged values of overlap indices can be weighted. Volumes now can be reported in mm^3 , although they are given in voxels to keep backwards compatibility.

46.4.1 Example

```
>>> overlap = Overlap()
>>> overlap.inputs.volume1 = 'cont1.nii'
>>> overlap.inputs.volume2 = 'cont2.nii'
>>> res = overlap.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
volume1: (a pathlike object or string representing an existing file)
        Has to have the same dimensions as volume2.
volume2: (a pathlike object or string representing an existing file)
        Has to have the same dimensions as volume1.
bg_overlap: (a boolean, nipy default value: False)
            consider zeros as a label
```

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```

vol_units: ('voxel' or 'mm', nipy default value: voxel)
           units for volumes

[Optional]
mask_volume: (a pathlike object or string representing an existing
              file)
              calculate overlap only within this mask.
out_file: (a pathlike object or string representing a file, nipy
           default value: diff.nii)
weighting: ('none' or 'volume' or 'squared_vol', nipy default
            value: none)
            'none': no class-overlap weighting is performed. 'volume': computed
            class-overlaps are weighted by class volume 'squared_vol': computed
            class-overlaps are weighted by the squared volume of the class

```

Outputs:

```

jaccard: (a float)
         averaged jaccard index
dice: (a float)
      averaged dice index
roi_ji: (a list of items which are a float)
        the Jaccard index (JI) per ROI
roi_di: (a list of items which are a float)
        the Dice index (DI) per ROI
volume_difference: (a float)
                  averaged volume difference
roi_voldiff: (a list of items which are a float)
              volume differences of ROIs
labels: (a list of items which are an integer (int or long))
        detected labels
diff_file: (a pathlike object or string representing an existing
            file)
            error map of differences

```

46.5 Similarity

[Link to code](#)

Calculates similarity between two 3D or 4D volumes. Both volumes have to be in the same coordinate system, same space within that coordinate system and with the same voxel dimensions.

Note: This interface is an extension of `nipy.interfaces.nipy.utils.Similarity` to support 4D files. Requires `nipy`

46.5.1 Example

```

>>> from nipy.algorithms.metrics import Similarity
>>> similarity = Similarity()
>>> similarity.inputs.volume1 = 'rcls1.nii'
>>> similarity.inputs.volume2 = 'rcls2.nii'
>>> similarity.inputs.mask1 = 'mask.nii'
>>> similarity.inputs.mask2 = 'mask.nii'
>>> similarity.inputs.metric = 'cr'

```

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```
>>> res = similarity.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
volume1: (a pathlike object or string representing an existing file)
         3D/4D volume
volume2: (a pathlike object or string representing an existing file)
         3D/4D volume

[Optional]
mask1: (a pathlike object or string representing an existing file)
       3D volume
mask2: (a pathlike object or string representing an existing file)
       3D volume
metric: ('cc' or 'cr' or 'crl1' or 'mi' or 'nmi' or 'slr' or a
         callable value, nipype default value: None)
         str or callable
         Cost-function for assessing image similarity. If a string,
         one of 'cc': correlation coefficient, 'cr': correlation
         ratio, 'crl1': L1-norm based correlation ratio, 'mi': mutual
         information, 'nmi': normalized mutual information, 'slr':
         supervised log-likelihood ratio. If a callable, it should
         take a two-dimensional array representing the image joint
         histogram as an input and return a float.
```

Outputs:

```
similarity: (a list of items which are a float)
```


47.1 AddCSVColumn

[Link to code](#)

Short interface to add an extra column and field to a text file

47.1.1 Example

```
>>> from nipy.algorithms import misc
>>> addcol = misc.AddCSVColumn()
>>> addcol.inputs.in_file = 'degree.csv'
>>> addcol.inputs.extra_column_heading = 'group'
>>> addcol.inputs.extra_field = 'male'
>>> addcol.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         Input comma-separated value (CSV) files

[Optional]
out_file: (a pathlike object or string representing a file, nipy
         default value: extra_heading.csv)
         Output filename for merged CSV file
extra_column_heading: (a unicode string)
         New heading to add for the added field.
extra_field: (a unicode string)
         New field to add to each row. This is useful for saving the group or
         subject ID in the file.
```

Outputs:

```
csv_file: (a pathlike object or string representing a file)
         Output CSV file containing columns
```

47.2 AddCSVRow

[Link to code](#)

Simple interface to add an extra row to a csv file

Note: Requires `pandas`

Warning: Multi-platform thread-safe execution is possible with `lockfile`. Please recall that (1) this module is alpha software; and (2) it should be installed for thread-safe writing. If `lockfile` is not installed, then the interface is not thread-safe.

47.2.1 Example

```
>>> from nipyne.algorithms import misc
>>> addrow = misc.AddCSVRow()
>>> addrow.inputs.in_file = 'scores.csv'
>>> addrow.inputs.si = 0.74
>>> addrow.inputs.di = 0.93
>>> addrow.inputs.subject_id = 'S400'
>>> addrow.inputs.list_of_values = [ 0.4, 0.7, 0.3 ]
>>> addrow.run() # doctest: +SKIP
```

Inputs:

[Mandatory]

`in_file`: (a pathlike `object` **or** string representing a file)
Input comma-separated value (CSV) files

[Optional]

`_outputs`: (a dictionary **with** keys which are `any` value **and with** values which are `any` value, nipyne default value: {})

Outputs:

`csv_file`: (a pathlike `object` **or** string representing a file)
Output CSV file containing rows

47.3 AddNoise

[Link to code](#)

Corrupts with noise the input image

47.3.1 Example

```
>>> from nipyne.algorithms.misc import AddNoise
>>> noise = AddNoise()
>>> noise.inputs.in_file = 'T1.nii'
>>> noise.inputs.in_mask = 'mask.nii'
>>> noise.snr = 30.0
>>> noise.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input image that will be corrupted with noise
dist: ('normal' or 'rician', nipy default value: normal)
      desired noise distribution
bg_dist: ('normal' or 'rayleigh', nipy default value: normal)
         desired noise distribution, currently only normal is implemented

[Optional]
in_mask: (a pathlike object or string representing an existing file)
         input mask, voxels outside this mask will be considered background
snr: (a float, nipy default value: 10.0)
     desired output SNR in dB
out_file: (a pathlike object or string representing a file)
          desired output filename
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          corrupted image
```

47.4 CalculateMedian

[Link to code](#)

Computes an average of the median across one or more 4D Nifti timeseries

47.4.1 Example

```
>>> from nipy.algorithms.misc import CalculateMedian
>>> mean = CalculateMedian()
>>> mean.inputs.in_files = 'functional.nii'
>>> mean.run() # doctest: +SKIP
```

Inputs:

```
[Optional]
in_files: (a list of items which are a pathlike object or string
          representing an existing file)
median_file: (a unicode string)
             Filename prefix to store median images
median_per_file: (a boolean, nipy default value: False)
                 Calculate a median file for each Nifti
```

Outputs:

```
median_files: (a list of items which are a pathlike object or string
              representing an existing file)
              One or more median images
```

47.5 CalculateNormalizedMoments

[Link to code](#)

Calculates moments of timeseries.

47.5.1 Example

```
>>> from nipyype.algorithms import misc
>>> skew = misc.CalculateNormalizedMoments()
>>> skew.inputs.moment = 3
>>> skew.inputs.timeseries_file = 'timeseries.txt'
>>> skew.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
timeseries_file: (a pathlike object or string representing an
                  existing file)
                  Text file with timeseries in columns and timepoints in rows,
                  whitespace separated
moment: (an integer (int or long))
        Define which moment should be calculated, 3 for skewness, 4 for
        kurtosis.
```

Outputs:

```
moments: (a list of items which are a float)
          Moments
```

47.6 CreateNifti

[Link to code](#)

Creates a nifti volume

Inputs:

```
[Mandatory]
data_file: (a pathlike object or string representing an existing
            file)
            ANALYZE img file
header_file: (a pathlike object or string representing an existing
              file)
              corresponding ANALYZE hdr file

[Optional]
affine: (an array)
         affine transformation array
```

Outputs:

```
nifti_file: (a pathlike object or string representing an existing
             file)
```

47.7 Distance

[Link to code](#)

Calculates distance between two volumes.

Deprecated since version 0.10.0: Use `nipyype.algorithms.metrics.Distance` instead.

Inputs:

```
[Mandatory]
volume1: (a pathlike object or string representing an existing file)
```

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```

        Has to have the same dimensions as volume2.
volume2: (a pathlike object or string representing an existing file)
        Has to have the same dimensions as volume1.

[Optional]
method: ('eucl_min' or 'eucl_cog' or 'eucl_mean' or 'eucl_wmean' or
        'eucl_max', nipype default value: eucl_min)
    "eucl_min": Euclidean distance between two closest points
    "eucl_cog": mean Euclidian distance between the Center of Gravity of
    volume1 and CoGs of volume2 "eucl_mean": mean Euclidian minimum
    distance of all volume2 voxels to volume1 "eucl_wmean": mean
    Euclidian minimum distance of all volume2 voxels to volume1 weighted
    by their values "eucl_max": maximum over minimum Euclidian distances
    of all volume2 voxels to volume1 (also known as the Hausdorff
    distance)
mask_volume: (a pathlike object or string representing an existing
    file)
    calculate overlap only within this mask.

```

Outputs:

```

distance: (a float)
point1: (an array with shape (3,))
point2: (an array with shape (3,))
histogram: (a pathlike object or string representing a file)

```

47.8 FuzzyOverlap

[Link to code](#)

Calculates various overlap measures between two maps, using a fuzzy definition.

Deprecated since version 0.10.0: Use `nipyype.algorithms.metrics.FuzzyOverlap` instead.**Inputs:**

```

[Mandatory]
in_ref: (a list of items which are a pathlike object or string
    representing an existing file)
    Reference image. Requires the same dimensions as in_tst.
in_tst: (a list of items which are a pathlike object or string
    representing an existing file)
    Test image. Requires the same dimensions as in_ref.

[Optional]
in_mask: (a pathlike object or string representing an existing file)
    calculate overlap only within mask
weighting: ('none' or 'volume' or 'squared_vol', nipype default
    value: none)
    'none': no class-overlap weighting is performed. 'volume': computed
    class-overlaps are weighted by class volume 'squared_vol': computed
    class-overlaps are weighted by the squared volume of the class
out_file: (a pathlike object or string representing a file, nipype
    default value: diff.nii)
    alternative name for resulting difference-map

```

Outputs:

```
jaccard: (a float)
    Fuzzy Jaccard Index (fJI), all the classes
dice: (a float)
    Fuzzy Dice Index (fDI), all the classes
class_fji: (a list of items which are a float)
    Array containing the fJIs of each computed class
class_fdi: (a list of items which are a float)
    Array containing the fDIs of each computed class
```

47.9 Gunzip

[Link to code](#)

Gunzip wrapper

```
>>> from nipy.algorithms.misc import Gunzip
>>> gunzip = Gunzip(in_file='tpms_msk.nii.gz')
>>> res = gunzip.run()
>>> res.outputs.out_file # doctest: +ELLIPSIS
'.../tpms_msk.nii'
```

```
>>> os.unlink('tpms_msk.nii')
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

47.10 Matlab2CSV

[Link to code](#)

Simple interface to save the components of a MATLAB .mat file as a text file with comma-separated values (CSVs).

CSV files are easily loaded in R, for use in statistical processing. For further information, see cran.r-project.org/doc/manuals/R-data.pdf

47.10.1 Example

```
>>> from nipy.algorithms import misc
>>> mat2csv = misc.Matlab2CSV()
>>> mat2csv.inputs.in_file = 'cmatrix.mat'
>>> mat2csv.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Input MATLAB .mat file
```

```
[Optional]
reshape_matrix: (a boolean, nipy default value: True)
```

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The output of this interface **is** meant **for** R, so matrices will be reshaped to vectors by default.

Outputs:

csv_files: (a **list** of items which are a pathlike **object** **or** string representing a file)

47.11 MergeCSVFiles

[Link to code](#)

This interface is designed to facilitate data loading in the R environment. It takes input CSV files and merges them into a single CSV file. If provided, it will also incorporate column heading names into the resulting CSV file.

CSV files are easily loaded in R, for use in statistical processing. For further information, see cran.r-project.org/doc/manuals/R-data.pdf

47.11.1 Example

```
>>> from nipy.algorithms import misc
>>> mat2csv = misc.MergeCSVFiles()
>>> mat2csv.inputs.in_files = ['degree.mat','clustering.mat']
>>> mat2csv.inputs.column_headings = ['degree','clustering']
>>> mat2csv.run() # doctest: +SKIP
```

Inputs:

[Mandatory]
in_files: (a **list** of items which are a pathlike **object** **or** string representing an existing file)
Input comma-separated value (CSV) files

[Optional]
out_file: (a pathlike **object** **or** string representing a file, nipy default value: merged.csv)
Output filename **for** merged CSV file
column_headings: (a **list** of items which are a unicode string)
List of column headings to save **in** merged CSV file (must be equal to number of **input** files). If left undefined, these will be pulled **from the input** filenames.
row_headings: (a **list** of items which are a unicode string)
List of row headings to save **in** merged CSV file (must be equal to number of rows **in** the **input** files).
row_heading_title: (a unicode string, nipy default value: label)
Column heading **for** the row headings added
extra_column_heading: (a unicode string)
New heading to add **for** the added field.
extra_field: (a unicode string)
New field to add to each row. This **is** useful **for** saving the group **or** subject ID **in** the file.

Outputs:

csv_file: (a pathlike **object** **or** string representing a file)
Output CSV file containing columns

47.12 MergeROIs

[Link to code](#)

Splits a 3D image in small chunks to enable parallel processing. ROIs keep time series structure in 4D images.

47.12.1 Example

```
>>> from nipy.algorithms import misc
>>> rois = misc.MergeROIs()
>>> rois.inputs.in_files = ['roi%02d.nii' % i for i in range(1, 6)]
>>> rois.inputs.in_reference = 'mask.nii'
>>> rois.inputs.in_index = ['roi%02d_idx.npz' % i for i in range(1, 6)]
>>> rois.run() # doctest: +SKIP
```

Inputs:

```
[Optional]
in_files: (a list of items which are a pathlike object or string
           representing an existing file)
in_index: (a list of items which are a pathlike object or string
           representing an existing file)
           array keeping original locations
in_reference: (a pathlike object or string representing an existing
              file)
              reference file
```

Outputs:

```
merged_file: (a pathlike object or string representing an existing
              file)
              the recomposed file
```

47.13 ModifyAffine

[Link to code](#)

Left multiplies the affine matrix with a specified values. Saves the volume as a nifti file.

Inputs:

```
[Mandatory]
volumes: (a list of items which are a pathlike object or string
          representing an existing file)
          volumes which affine matrices will be modified

[Optional]
transformation_matrix: (an array with shape (4, 4), nipy default
                        value: (<bound method AbstractArray.copy_default_value of
                                <traits.trait_numeric.Array object at 0x7f32d995d160>>,
                                (array([[1., 0., 0., 0.],
                                      [0., 1., 0., 0.],
                                      [0., 0., 1., 0.],
                                      [0., 0., 0., 1.])), None))
                        transformation matrix that will be left multiplied by the affine
                        matrix
```

Outputs:

```
transformed_volumes: (a list of items which are a pathlike object or
                      string representing a file)
```


47.14 NormalizeProbabilityMapSet

[Link to code](#)

Returns the input tissue probability maps (tpms, aka volume fractions) normalized to sum up 1.0 at each voxel within the mask.

Note: Please recall this is not a spatial normalization algorithm

47.14.1 Example

```
>>> from nipy.algorithms import misc
>>> normalize = misc.NormalizeProbabilityMapSet()
>>> normalize.inputs.in_files = [ 'tpm_00.nii.gz', 'tpm_01.nii.gz', 'tpm_02.nii.gz'
↪ ]
>>> normalize.inputs.in_mask = 'tpms_msk.nii.gz'
>>> normalize.run() # doctest: +SKIP
```

Inputs:

```
[Optional]
in_files: (a list of items which are a pathlike object or string
           representing an existing file)
in_mask: (a pathlike object or string representing an existing file)
          Masked voxels must sum up 1.0, 0.0 otherwise.
```

Outputs:

```
out_files: (a list of items which are a pathlike object or string
            representing an existing file)
            normalized maps
```

47.15 Overlap

[Link to code](#)

Calculates various overlap measures between two maps.

Deprecated since version 0.10.0: Use `nipy.algorithms.metrics.Overlap` instead.

Inputs:

```
[Mandatory]
volume1: (a pathlike object or string representing an existing file)
          Has to have the same dimensions as volume2.
volume2: (a pathlike object or string representing an existing file)
          Has to have the same dimensions as volume1.
bg_overlap: (a boolean, nipy default value: False)
             consider zeros as a label
vol_units: ('voxel' or 'mm', nipy default value: voxel)
            units for volumes

[Optional]
mask_volume: (a pathlike object or string representing an existing
              file)
              calculate overlap only within this mask.
out_file: (a pathlike object or string representing a file, nipy
           default value: diff.nii)
```

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```
weighting: ('none' or 'volume' or 'squared_vol', nipy default
            value: none)
            'none': no class-overlap weighting is performed. 'volume': computed
            class-overlaps are weighted by class volume 'squared_vol': computed
            class-overlaps are weighted by the squared volume of the class
```

Outputs:

```
jaccard: (a float)
          averaged jaccard index
dice: (a float)
       averaged dice index
roi_ji: (a list of items which are a float)
        the Jaccard index (JI) per ROI
roi_di: (a list of items which are a float)
        the Dice index (DI) per ROI
volume_difference: (a float)
                   averaged volume difference
roi_voldiff: (a list of items which are a float)
              volume differences of ROIs
labels: (a list of items which are an integer (int or long))
         detected labels
diff_file: (a pathlike object or string representing an existing
            file)
            error map of differences
```

47.16 PickAtlas

[Link to code](#)

Returns ROI masks given an atlas and a list of labels. Supports dilation and left right masking (assuming the atlas is properly aligned).

Inputs:

```
[Mandatory]
atlas: (a pathlike object or string representing an existing file)
        Location of the atlas that will be used.
labels: (an integer (int or long) or a list of items which are an
         integer (int or long))
         Labels of regions that will be included in the mask. Must be
         compatible with the atlas used.

[Optional]
hemi: ('both' or 'left' or 'right', nipy default value: both)
       Restrict the mask to only one hemisphere: left or right
dilation_size: (an integer (int or long), nipy default value: 0)
                Defines how much the mask will be dilated (expanded in 3D).
output_file: (a pathlike object or string representing a file)
              Where to store the output mask.
```

Outputs:

```
mask_file: (a pathlike object or string representing an existing
            file)
            output mask file
```

47.17 SimpleThreshold

[Link to code](#)

Applies a threshold to input volumes

Inputs:

```
[Mandatory]
volumes: (a list of items which are a pathlike object or string
          representing an existing file)
          volumes to be thresholded
threshold: (a float)
           volumes to be thresholded everything below this value will be set to
           zero
```

Outputs:

```
thresholded_volumes: (a list of items which are a pathlike object or
                      string representing an existing file)
                      thresholded volumes
```

47.18 SplitROIs

[Link to code](#)

Splits a 3D image in small chunks to enable parallel processing. ROIs keep time series structure in 4D images.

47.18.1 Example

```
>>> from nipy.algorithms import misc
>>> rois = misc.SplitROIs()
>>> rois.inputs.in_file = 'diffusion.nii'
>>> rois.inputs.in_mask = 'mask.nii'
>>> rois.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         file to be splitted

[Optional]
in_mask: (a pathlike object or string representing an existing file)
         only process files inside mask
roi_size: (a tuple of the form: (an integer (int or long), an integer
                                (int or long), an integer (int or long)))
         desired ROI size
```

Outputs:

```
out_files: (a list of items which are a pathlike object or string
            representing an existing file)
            the resulting ROIs
out_masks: (a list of items which are a pathlike object or string
            representing an existing file)
            a mask indicating valid values
out_index: (a list of items which are a pathlike object or string
            representing an existing file)
            arrays keeping original locations
```

47.19 TSNR

[Link to code](#)

Deprecated since version 0.12.1: Use `nipyype.algorithms.confounds.TSNR` instead

Inputs:

```
[Mandatory]
in_file: (a list of items which are a pathlike object or string
         representing an existing file)
         realigned 4D file or a list of 3D files

[Optional]
regress_poly: (a long integer >= 1)
              Remove polynomials
tsnr_file: (a pathlike object or string representing a file, nipyype
           default value: tsnr.nii.gz)
           output tSNR file
mean_file: (a pathlike object or string representing a file, nipyype
           default value: mean.nii.gz)
           output mean file
stddev_file: (a pathlike object or string representing a file, nipyype
            default value: stddev.nii.gz)
            output tSNR file
detrended_file: (a pathlike object or string representing a file,
               nipyype default value: detrend.nii.gz)
               input file after detrending
```

Outputs:

```
tsnr_file: (a pathlike object or string representing an existing
           file)
           tsnr image file
mean_file: (a pathlike object or string representing an existing
           file)
           mean image file
stddev_file: (a pathlike object or string representing an existing
            file)
            std dev image file
detrended_file: (a pathlike object or string representing a file)
               detrended input file
```

47.20 calc_moments()

[Link to code](#)

Returns nth moment (3 for skewness, 4 for kurtosis) of timeseries (list of values; one per timeseries).

Keyword arguments: `timeseries_file` – text file with white space separated timepoints in rows

47.21 makefmtlist()

[Link to code](#)

47.22 maketypelist()

[Link to code](#)

47.23 `matlab2csv()`

[Link to code](#)

47.24 `merge_csvs()`

[Link to code](#)

47.25 `merge_rois()`

[Link to code](#)

Re-builds an image resulting from a parallelized processing

47.26 `normalize_tpms()`

[Link to code](#)

Returns the input tissue probability maps (tpms, aka volume fractions) normalized to sum up 1.0 at each voxel within the mask.

47.27 `remove_identical_paths()`

[Link to code](#)

47.28 `replaceext()`

[Link to code](#)

47.29 `split_rois()`

[Link to code](#)

Splits an image in ROIs for parallel processing

48.1 SpecifyModel

[Link to code](#)

Makes a model specification compatible with spm/fsl designers.

The `subject_info` field should contain paradigm information in the form of a Bunch or a list of Bunch. The Bunch should contain the following information:

```
[Mandatory]
- conditions : list of names
- onsets : lists of onsets corresponding to each condition
- durations : lists of durations corresponding to each condition. Should be
left to a single 0 if all events are being modelled as impulses.

[Optional]
- regressor_names : list of str
    list of names corresponding to each column. Should be None if
    automatically assigned.
- regressors : list of lists
    values for each regressor - must correspond to the number of
    volumes in the functional run
- amplitudes : lists of amplitudes for each event. This will be ignored by
SPM's Level1Design.

The following two (tmod, pmod) will be ignored by any Level1Design class
other than SPM:

- tmod : lists of conditions that should be temporally modulated. Should
default to None if not being used.
- pmod : list of Bunch corresponding to conditions
    - name : name of parametric modulator
    - param : values of the modulator
    - poly : degree of modulation
```

Alternatively, you can provide information through event files.

The event files have to be in 1, 2 or 3 column format with the columns corresponding to Onsets, Durations and Amplitudes and they have to have the name `event_name.runXXX...` e.g.: `Words.run001.txt`. The `event_name` part will be used to create the condition names.

48.1.1 Examples

```
>>> from nipy.algorithms import modelgen
>>> from nipy.interfaces.base import Bunch
>>> s = modelgen.SpecifyModel()
>>> s.inputs.input_units = 'secs'
>>> s.inputs.functional_runs = ['functional2.nii', 'functional3.nii']
>>> s.inputs.time_repetition = 6
>>> s.inputs.high_pass_filter_cutoff = 128.
>>> evs_run2 = Bunch(conditions=['cond1'], onsets=[[2, 50, 100, 180]],
↳ durations=[[1]])
>>> evs_run3 = Bunch(conditions=['cond1'], onsets=[[30, 40, 100, 150]],
↳ durations=[[1]])
>>> s.inputs.subject_info = [evs_run2, evs_run3]
```

Using pmod:

```
>>> evs_run2 = Bunch(conditions=['cond1', 'cond2'], onsets=[[2, 50], [100, 180]],
↳ durations=[[0], [0]], pmod=[Bunch(name=['amp'], poly=[2], param=[[1, 2]]),
↳ None])
>>> evs_run3 = Bunch(conditions=['cond1', 'cond2'], onsets=[[20, 120], [80, 160]],
↳ durations=[[0], [0]], pmod=[Bunch(name=['amp'], poly=[2], param=[[1, 2]]),
↳ None])
>>> s.inputs.subject_info = [evs_run2, evs_run3]
```

Inputs:

```
[Mandatory]
subject_info: (a list of items which are a Bunch or None)
    Bunch or List(Bunch) subject-specific condition information. see
    :ref:`SpecifyModel` or SpecifyModel.__doc__ for details
    mutually_exclusive: subject_info, event_files, bids_event_file
event_files: (a list of items which are a list of items which are a
    pathlike object or string representing an existing file)
    List of event description files 1, 2 or 3 column format
    corresponding to onsets, durations and amplitudes
    mutually_exclusive: subject_info, event_files, bids_event_file
bids_event_file: (a list of items which are a pathlike object or
    string representing an existing file)
    TSV event file containing common BIDS fields: `onset`, `duration`,
    and categorization and amplitude columns
    mutually_exclusive: subject_info, event_files, bids_event_file
functional_runs: (a list of items which are a list of items which are
    a pathlike object or string representing an existing file or a
    pathlike object or string representing an existing file)
    Data files for model. List of 4D files or list of list of 3D files
    per session
input_units: ('secs' or 'scans')
    Units of event onsets and durations (secs or scans). Output units
    are always in secs
high_pass_filter_cutoff: (a float)
    High-pass filter cutoff in secs
time_repetition: (a float)
    Time between the start of one volume to the start of the next image
    volume.

[Optional]
bids_condition_column: (a unicode string, nipy default value:
    trial_type)
```

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```

        Column of the file passed to `bids_event_file` to the unique values
        of which events will be assigned to regressors
bids_amplitude_column: (a unicode string)
        Column of the file passed to `bids_event_file` according to which to
        assign amplitudes to events
realignment_parameters: (a list of items which are a pathlike object
        or string representing an existing file)
        Realignment parameters returned by motion correction algorithm
parameter_source: ('SPM' or 'FSL' or 'AFNI' or 'FSFAST' or 'NIPY',
        nipy default value: SPM)
        Source of motion parameters
outlier_files: (a list of items which are a pathlike object or string
        representing an existing file)
        Files containing scan outlier indices that should be tossed

```

Outputs:

```

session_info: (any value)
        Session info for level1 designs

```

48.2 SpecifySPMModel

[Link to code](#)

Adds SPM specific options to SpecifyModel

adds:

```

concatenate_runs
output_units

```

48.2.1 Examples

```

>>> from nipy.algorithms import modelgen
>>> from nipy.interfaces.base import Bunch
>>> s = modelgen.SpecifySPMModel()
>>> s.inputs.input_units = 'secs'
>>> s.inputs.output_units = 'scans'
>>> s.inputs.high_pass_filter_cutoff = 128.
>>> s.inputs.functional_runs = ['functional2.nii', 'functional3.nii']
>>> s.inputs.time_repetition = 6
>>> s.inputs.concatenate_runs = True
>>> evs_run2 = Bunch(conditions=['cond1'], onsets=[[2, 50, 100, 180]],
↳durations=[[1]])
>>> evs_run3 = Bunch(conditions=['cond1'], onsets=[[30, 40, 100, 150]],
↳durations=[[1]])
>>> s.inputs.subject_info = [evs_run2, evs_run3]

```

Inputs:

```

[Mandatory]
subject_info: (a list of items which are a Bunch or None)
        Bunch or List(Bunch) subject-specific condition information. see
        :ref:`SpecifyModel` or SpecifyModel.__doc__ for details
mutually_exclusive: subject_info, event_files, bids_event_file
event_files: (a list of items which are a list of items which are a
        pathlike object or string representing an existing file)
        List of event description files 1, 2 or 3 column format

```

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```

        corresponding to onsets, durations and amplitudes
        mutually_exclusive: subject_info, event_files, bids_event_file
bids_event_file: (a list of items which are a pathlike object or
        string representing an existing file)
        TSV event file containing common BIDS fields: `onset`, `duration`,
        and categorization and amplitude columns
        mutually_exclusive: subject_info, event_files, bids_event_file
functional_runs: (a list of items which are a list of items which are
        a pathlike object or string representing an existing file or a
        pathlike object or string representing an existing file)
        Data files for model. List of 4D files or list of list of 3D files
        per session
input_units: ('secs' or 'scans')
        Units of event onsets and durations (secs or scans). Output units
        are always in secs
high_pass_filter_cutoff: (a float)
        High-pass filter cutoff in secs
time_repetition: (a float)
        Time between the start of one volume to the start of the next image
        volume.

[Optional]
concatenate_runs: (a boolean, nipy default value: False)
        Concatenate all runs to look like a single session.
output_units: ('secs' or 'scans', nipy default value: secs)
        Units of design event onsets and durations (secs or scans)
bids_condition_column: (a unicode string, nipy default value:
        trial_type)
        Column of the file passed to `bids_event_file` to the unique values
        of which events will be assigned to regressors
bids_amplitude_column: (a unicode string)
        Column of the file passed to `bids_event_file` according to which to
        assign amplitudes to events
realignment_parameters: (a list of items which are a pathlike object
        or string representing an existing file)
        Realignment parameters returned by motion correction algorithm
parameter_source: ('SPM' or 'FSL' or 'AFNI' or 'FSFAST' or 'NIPY',
        nipy default value: SPM)
        Source of motion parameters
outlier_files: (a list of items which are a pathlike object or string
        representing an existing file)
        Files containing scan outlier indices that should be tossed

```

Outputs:

```

session_info: (any value)
        Session info for level1 designs

```

48.3 SpecifySparseModel

[Link to code](#)

Specify a sparse model that is compatible with spm/fsl designers

48.3.1 References

sparse-sampling fMRI experiments. Front. Neurosci. 7:55 <http://journal.frontiersin.org/Journal/10.3389/fnins.2013.00055/abstract>

48.3.2 Examples

```
>>> from nipy.algorithms import modelgen
>>> from nipy.interfaces.base import Bunch
>>> s = modelgen.SpecifySparseModel()
>>> s.inputs.input_units = 'secs'
>>> s.inputs.functional_runs = ['functional2.nii', 'functional3.nii']
>>> s.inputs.time_repetition = 6
>>> s.inputs.time_acquisition = 2
>>> s.inputs.high_pass_filter_cutoff = 128.
>>> s.inputs.model_hrf = True
>>> evs_run2 = Bunch(conditions=['cond1'], onsets=[[2, 50, 100, 180]],
↳durations=[[1]])
>>> evs_run3 = Bunch(conditions=['cond1'], onsets=[[30, 40, 100, 150]],
↳durations=[[1]])
>>> s.inputs.subject_info = [evs_run2, evs_run3]
```

Inputs:

```
[Mandatory]
time_acquisition: (a float)
    Time in seconds to acquire a single image volume
subject_info: (a list of items which are a Bunch or None)
    Bunch or List(Bunch) subject-specific condition information. see
    :ref:`SpecifyModel` or SpecifyModel.__doc__ for details
mutually_exclusive: subject_info, event_files, bids_event_file
event_files: (a list of items which are a list of items which are a
    pathlike object or string representing an existing file)
    List of event description files 1, 2 or 3 column format
    corresponding to onsets, durations and amplitudes
    mutually_exclusive: subject_info, event_files, bids_event_file
bids_event_file: (a list of items which are a pathlike object or
    string representing an existing file)
    TSV event file containing common BIDS fields: `onset`, `duration`,
    and categorization and amplitude columns
    mutually_exclusive: subject_info, event_files, bids_event_file
functional_runs: (a list of items which are a list of items which are
    a pathlike object or string representing an existing file or a
    pathlike object or string representing an existing file)
    Data files for model. List of 4D files or list of list of 3D files
    per session
input_units: ('secs' or 'scans')
    Units of event onsets and durations (secs or scans). Output units
    are always in secs
high_pass_filter_cutoff: (a float)
    High-pass filter cutoff in secs
time_repetition: (a float)
    Time between the start of one volume to the start of the next image
    volume.

[Optional]
volumes_in_cluster: (a long integer >= 1, nipy default value: 1)
    Number of scan volumes in a cluster
```

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```

model_hrf: (a boolean)
    Model sparse events with hrf
stimuli_as_impulses: (a boolean, nipyne default value: True)
    Treat each stimulus to be impulse-like
use_temporal_deriv: (a boolean)
    Create a temporal derivative in addition to regular regressor
    requires: model_hrf
scale_regressors: (a boolean, nipyne default value: True)
    Scale regressors by the peak
scan_onset: (a float, nipyne default value: 0.0)
    Start of scanning relative to onset of run in secs
save_plot: (a boolean)
    Save plot of sparse design calculation (requires matplotlib)
bids_condition_column: (a unicode string, nipyne default value:
    trial_type)
    Column of the file passed to `bids_event_file` to the unique values
    of which events will be assigned to regressors
bids_amplitude_column: (a unicode string)
    Column of the file passed to `bids_event_file` according to which to
    assign amplitudes to events
realignment_parameters: (a list of items which are a pathlike object
    or string representing an existing file)
    Realignment parameters returned by motion correction algorithm
parameter_source: ('SPM' or 'FSL' or 'AFNI' or 'FSFAST' or 'NIPY',
    nipyne default value: SPM)
    Source of motion parameters
outlier_files: (a list of items which are a pathlike object or string
    representing an existing file)
    Files containing scan outlier indices that should be tossed

```

Outputs:

```

sparse_png_file: (a pathlike object or string representing a file)
    PNG file showing sparse design
sparse_svg_file: (a pathlike object or string representing a file)
    SVG file showing sparse design
session_info: (any value)
    Session info for level1 designs

```

48.4 bids_gen_info()

[Link to code](#)

Generate subject_info structure from a list of BIDS .tsv event files.

48.4.1 Parameters

bids_event_files [list of str] Filenames of BIDS .tsv event files containing columns including: 'onset', 'duration', and 'trial_type' or the *condition_column* value.**condition_column** [str] Column of files in *bids_event_files* based on the values of which events will be sorted into different regressors**amplitude_column** [str] Column of files in *bids_event_files* based on the values of which to apply amplitudes to events. If unspecified, all events will be represented with an amplitude of 1.

48.4.2 Returns

list of Bunch

48.5 gcd()

[Link to code](#)

Returns the greatest common divisor of two integers
uses Euclid's algorithm

```
>>> gcd(4, 5)
~
>>> gcd(4, 8)
~
>>> gcd(22, 55)
~~
```

48.6 gen_info()

[Link to code](#)

Generate subject_info structure from a list of event files

48.7 orth()

[Link to code](#)

Orthogonalize y_in with respect to x_in.

```
>>> orth_expected = np.array([1.7142857142857144, 0.42857142857142883,
↪ -0.85714285714285676])
>>> err = np.abs(np.array(orth([1, 2, 3],[4, 5, 6]) - orth_expected))
>>> all(err < np.finfo(float).eps)
True
```

48.8 scale_timings()

[Link to code](#)

Scales timings given input and output units (scans/secs)

48.8.1 Parameters

timelist: list of times to scale input_units: 'secs' or 'scans' output_units: Ibid. time_repetition: float in seconds

48.9 spm_hrf()

[Link to code](#)

python implementation of spm_hrf

see spm_hrf for implementation details

% RT - scan repeat time % p - parameters of the response function (two gamma % functions) % defaults (seconds) % p(0) - delay of response (relative to onset) 6 % p(1) - delay of undershoot (relative to onset) 16 % p(2) - dispersion of response 1 % p(3) - dispersion of undershoot 1 % p(4) - ratio of response to undershoot 6 % p(5) - onset (seconds) 0 % p(6) - length of kernel (seconds) 32 ~ % hrf - hemodynamic response function % p - parameters of the response function
the following code using scipy.stats.distributions.gamma doesn't return the same result as the spm_Gpdf function

```
hrf = gamma.pdf(u, p[0]/p[2], scale=dt/p[2]) -  
      gamma.pdf(u, p[1]/p[3], scale=dt/p[3])/p[4]
```

```
>>> print(spm_hrf(2))  
[ 0.00000000e+00  8.65660810e-02  3.74888236e-01  3.84923382e-01  
 2.16117316e-01  7.68695653e-02  1.62017720e-03 -3.06078117e-02  
-3.73060781e-02 -3.08373716e-02 -2.05161334e-02 -1.16441637e-02  
-5.82063147e-03 -2.61854250e-03 -1.07732374e-03 -4.10443522e-04  
-1.46257507e-04]
```

49.1 ArtifactDetect

[Link to code](#)

Detects outliers in a functional imaging series

Uses intensity and motion parameters to infer outliers. If *use_norm* is True, it computes the movement of the center of each face a cuboid centered around the head and returns the maximal movement across the centers. If you wish to use individual thresholds instead, import *Undefined* from *nipype.interfaces.base* and set *...inputs.use_norm = Undefined*

49.1.1 Examples

```
>>> ad = ArtifactDetect()
>>> ad.inputs.realigned_files = 'functional.nii'
>>> ad.inputs.realignment_parameters = 'functional.par'
>>> ad.inputs.parameter_source = 'FSL'
>>> ad.inputs.norm_threshold = 1
>>> ad.inputs.use_differences = [True, False]
>>> ad.inputs.zintensity_threshold = 3
>>> ad.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
realigned_files: (a list of items which are a pathlike object or
                  string representing an existing file)
                  Names of realigned functional data files
realignment_parameters: (a list of items which are a pathlike object
                         or string representing an existing file)
                         Names of realignment parameters corresponding to the functional data
                         files
parameter_source: ('SPM' or 'FSL' or 'AFNI' or 'NiPy' or 'FSFAST')
                  Source of movement parameters
norm_threshold: (a float)
                Threshold to use to detect motion-related outliers when composite
                motion is being used
```

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```

        mutually_exclusive: rotation_threshold, translation_threshold
rotation_threshold: (a float)
    Threshold (in radians) to use to detect rotation-related outliers
        mutually_exclusive: norm_threshold
translation_threshold: (a float)
    Threshold (in mm) to use to detect translation-related outliers
        mutually_exclusive: norm_threshold
zintensity_threshold: (a float)
    Intensity Z-threshold use to detection images that deviate from the
    mean
mask_type: ('spm_global' or 'file' or 'thresh')
    Type of mask that should be used to mask the functional data.
    *spm_global* uses an spm_global like calculation to determine the
    brain mask. *file* specifies a brain mask file (should be an image
    file consisting of 0s and 1s). *thresh* specifies a threshold to
    use. By default all voxels are used, unless one of these mask types
    are defined

[Optional]
use_differences: (a list of items which are a bool or None, nipy
    default value: [True, False])
    Use differences between successive motion (first element) and
    intensity parameter (second element) estimates in order to determine
    outliers. (default is [True, False])
use_norm: (a boolean, nipy default value: True)
    Uses a composite of the motion parameters in order to determine
    outliers.
    requires: norm_threshold
mask_file: (a pathlike object or string representing an existing
    file)
    Mask file to be used if mask_type is 'file'.
mask_threshold: (a float)
    Mask threshold to be used if mask_type is 'thresh'.
intersect_mask: (a boolean, nipy default value: True)
    Intersect the masks when computed from spm_global.
save_plot: (a boolean, nipy default value: True)
    save plots containing outliers
plot_type: ('png' or 'svg' or 'eps' or 'pdf', nipy default value:
    png)
    file type of the outlier plot
bound_by_brainmask: (a boolean, nipy default value: False)
    use the brain mask to determine bounding box for composite norm
    (works for SPM and Nipy - currently inaccurate for FSL, AFNI)
global_threshold: (a float, nipy default value: 8.0)
    use this threshold when mask type equal's spm_global

```

Outputs:

```

outlier_files: (a list of items which are a pathlike object or string
    representing an existing file)
    One file for each functional run containing a list of 0-based
    indices corresponding to outlier volumes
intensity_files: (a list of items which are a pathlike object or
    string representing an existing file)
    One file for each functional run containing the global intensity
    values determined from the brainmask
norm_files: (a list of items which are a pathlike object or string

```

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```

        representing a file)
        One file for each functional run containing the composite norm
statistic_files: (a list of items which are a pathlike object or
        string representing an existing file)
        One file for each functional run containing information about the
        different types of artifacts and if design info is provided then
        details of stimulus correlated motion and a listing or artifacts by
        event type.
plot_files: (a list of items which are a pathlike object or string
        representing a file)
        One image file for each functional run containing the detected
        outliers
mask_files: (a list of items which are a pathlike object or string
        representing a file)
        One image file for each functional run containing the mask used for
global signal calculation
displacement_files: (a list of items which are a pathlike object or
        string representing a file)
        One image file for each functional run containing the voxel
        displacement timeseries

```

49.2 StimulusCorrelation

[Link to code](#)

Determines if stimuli are correlated with motion or intensity parameters.

Currently this class supports an SPM generated design matrix and requires intensity parameters. This implies that one must run *ArtifactDetect* and *Level1Design* prior to running this or provide an SPM.mat file and intensity parameters through some other means.

49.2.1 Examples

```

>>> sc = StimulusCorrelation()
>>> sc.inputs.realignment_parameters = 'functional.par'
>>> sc.inputs.intensity_values = 'functional.rms'
>>> sc.inputs.spm_mat_file = 'SPM.mat'
>>> sc.inputs.concatenated_design = False
>>> sc.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
realignment_parameters: (a list of items which are a pathlike object
        or string representing an existing file)
        Names of realignment parameters corresponding to the functional data
        files
intensity_values: (a list of items which are a pathlike object or
        string representing an existing file)
        Name of file containing intensity values
spm_mat_file: (a pathlike object or string representing an existing
        file)
        SPM mat file (use pre-estimate SPM.mat file)
concatenated_design: (a boolean)
        state if the design matrix contains concatenated sessions

```

Outputs:

```
stimcorr_files: (a list of items which are a pathlike object or  
                 string representing an existing file)  
                 List of files containing correlation values
```

50.1 ActivationCount

[Link to code](#)

Calculate a simple Activation Count Maps

Adapted from: https://github.com/poldracklab/CNP_task_analysis/blob/61c27f5992db9d8800884f8ffceb73e6957db8af/CNP_2n

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
           representing an existing file)
           input file, generally a list of z-stat maps
threshold: (a float)
            binarization threshold. E.g. a threshold of 1.65 corresponds to a
            two-sided Z-test of  $p < .10$ 
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
           output activation count map
acm_pos: (a pathlike object or string representing an existing file)
          positive activation count map
acm_neg: (a pathlike object or string representing an existing file)
          negative activation count map
```


51.1 interfaces.afni.base

51.1.1 AFNI Python Command

[Link to code](#)

A subtype of AFNI command line for Python scripts.

Inputs:

```
[Optional]
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
out_file: (a pathlike object or string representing a file)
    output image file name
    argument: ``-prefix %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

None

References:

None None

51.2 interfaces.afni.model

51.2.1 Deconvolve

[Link to code](#)

Wraps the executable command 3dDeconvolve.

Performs OLS regression given a 4D neuroimage file and stimulus timings

For complete details, see the [3dDeconvolve Documentation](#).

Examples

```
>>> from nipy.interfaces import afni
>>> deconvolve = afni.Deconvolve()
>>> deconvolve.inputs.in_files = ['functional.nii', 'functional2.nii']
>>> deconvolve.inputs.out_file = 'output.nii'
>>> deconvolve.inputs.x1D = 'output.1D'
>>> stim_times = [(1, 'timeseries.txt', 'SPMG1(4)')]
>>> deconvolve.inputs.stim_times = stim_times
>>> deconvolve.inputs.stim_label = [(1, 'Houses')]
>>> deconvolve.inputs.glt_sym = ['SYM: +Houses']
>>> deconvolve.inputs.glt_label = [(1, 'Houses')]
>>> deconvolve.cmdline
"3dDeconvolve -input functional.nii functional2.nii -bucket output.nii -x1D_
↪output.1D -num_stimts 1 -stim_times 1 timeseries.txt 'SPMG1(4)' -stim_label 1_
↪Houses -num_glt 1 -glt_sym 'SYM: +Houses' -glt_label 1 Houses"
>>> res = deconvolve.run() # doctest: +SKIP
```

Inputs:

```
[Optional]
in_files: (a list of items which are a pathlike object or string
           representing an existing file)
           filenames of 3D+time input datasets. More than one filename can be
           given and the datasets will be auto-catenated in time. You can input
           a 1D time series file here, but the time axis should run along the
           ROW direction, not the COLUMN direction as in the 'input1D' option.
           argument: ``-input %s``, position: 1
sat: (a boolean)
      check the dataset time series for initial saturation transients,
      which should normally have been excised before data analysis.
      argument: ``-sat``
      mutually_exclusive: trans
trans: (a boolean)
      check the dataset time series for initial saturation transients,
      which should normally have been excised before data analysis.
      argument: ``-trans``
      mutually_exclusive: sat
noblock: (a boolean)
          normally, if you input multiple datasets with 'input', then the
          separate datasets are taken to be separate image runs that get
          separate baseline models. Use this options if you want to have the
          program consider these to be all one big run.* If any of the input
          dataset has only 1 sub-brick, then this option is automatically
          invoked!* If the auto-catenation feature isn't used, then this
          option has no effect, no how, no way.
          argument: ``-noblock``
force_TR: (a float)
```

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```

        use this value instead of the TR in the 'input' dataset. (It's
        better to fix the input using Refit.)
        argument: ``-force_TR %f``, position: 0
input1D: (a pathlike object or string representing an existing file)
        filename of single (fMRI) .1D time series where time runs down the
        column.
        argument: ``-input1D %s``
TR_1D: (a float)
        TR to use with 'input1D'. This option has no effect if you do not
        also use 'input1D'.
        argument: ``-TR_1D %f``
legendre: (a boolean)
        use Legendre polynomials for null hypothesis (baseline model)
        argument: ``-legendre``
nolegendre: (a boolean)
        use power polynomials for null hypotheses. Don't do this unless you
        are crazy!
        argument: ``-nolegendre``
nodmbase: (a boolean)
        don't de-mean baseline time series
        argument: ``-nodmbase``
dmbase: (a boolean)
        de-mean baseline time series (default if 'polort' >= 0)
        argument: ``-dmbase``
svd: (a boolean)
        use SVD instead of Gaussian elimination (default)
        argument: ``-svd``
nosvd: (a boolean)
        use Gaussian elimination instead of SVD
        argument: ``-nosvd``
rmsmin: (a float)
        minimum rms error to reject reduced model (default = 0; don't use
        this option normally!)
        argument: ``-rmsmin %f``
nocond: (a boolean)
        DON'T calculate matrix condition number
        argument: ``-nocond``
singvals: (a boolean)
        print out the matrix singular values
        argument: ``-singvals``
goforit: (an integer (int or long))
        use this to proceed even if the matrix has bad problems (e.g.,
        duplicate columns, large condition number, etc.).
        argument: ``-GOFORIT %i``
allzero_OK: (a boolean)
        don't consider all zero matrix columns to be the type of error that
        'gotforit' is needed to ignore.
        argument: ``-allzero_OK``
dname: (a tuple of the form: (a unicode string, a unicode string))
        set environmental variable to provided value
        argument: ``-D%s=%s``
mask: (a pathlike object or string representing an existing file)
        filename of 3D mask dataset; only data time series from within the
        mask will be analyzed; results for voxels outside the mask will be
        set to zero.
        argument: ``-mask %s``
automask: (a boolean)

```

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```

    build a mask automatically from input data (will be slow for long
    time series datasets)
    argument: ``-automask``
STATmask: (a pathlike object or string representing an existing file)
    build a mask from provided file, and use this mask for the purpose
    of reporting truncation-to float issues AND for computing the FDR
    curves. The actual results ARE not masked with this option (only
    with 'mask' or 'automask' options).
    argument: ``-STATmask %s``
censor: (a pathlike object or string representing an existing file)
    filename of censor .1D time series. This is a file of 1s and 0s,
    indicating which time points are to be included (1) and which are to
    be excluded (0).
    argument: ``-censor %s``
polort: (an integer (int or long))
    degree of polynomial corresponding to the null hypothesis [default:
    1]
    argument: ``-polort %d``
ortvec: (a tuple of the form: (a pathlike object or string
    representing an existing file, a unicode string))
    this option lets you input a rectangular array of 1 or more baseline
    vectors from a file. This method is a fast way to include a lot of
    baseline regressors in one step.
    argument: ``-ortvec %s %s``
x1D: (a pathlike object or string representing a file)
    specify name for saved X matrix
    argument: ``-x1D %s``
x1D_stop: (a boolean)
    stop running after writing .xmat.1D file
    argument: ``-x1D_stop``
cbucket: (a unicode string)
    Name for dataset in which to save the regression coefficients (no
    statistics). This dataset will be used in a -xrestore run [not yet
    implemented] instead of the bucket dataset, if possible.
    argument: ``-cbucket %s``
out_file: (a pathlike object or string representing a file)
    output statistics file
    argument: ``-bucket %s``
num_threads: (an integer (int or long))
    run the program with provided number of sub-processes
    argument: ``-jobs %d``
fout: (a boolean)
    output F-statistic for each stimulus
    argument: ``-fout``
rout: (a boolean)
    output the R^2 statistic for each stimulus
    argument: ``-rout``
tout: (a boolean)
    output the T-statistic for each stimulus
    argument: ``-tout``
vout: (a boolean)
    output the sample variance (MSE) for each stimulus
    argument: ``-vout``
nofdr: (a boolean)
    Don't compute the statistic-vs-FDR curves for the bucket dataset.
    argument: ``-noFDR``
global_times: (a boolean)

```

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```

    use global timing for stimulus timing files
    argument: ``-global_times``
    mutually_exclusive: local_times
local_times: (a boolean)
    use local timing for stimulus timing files
    argument: ``-local_times``
    mutually_exclusive: global_times
num_stimts: (an integer (int or long))
    number of stimulus timing files
    argument: ``-num_stimts %d``, position: -6
stim_times: (a list of items which are a tuple of the form: (an
    integer (int or long), a pathlike object or string representing an
    existing file, a unicode string))
    generate a response model from a set of stimulus times given in
    file.
    argument: ``-stim_times %d %s '%s'...``, position: -5
stim_label: (a list of items which are a tuple of the form: (an
    integer (int or long), a unicode string))
    label for kth input stimulus (e.g., Label1)
    argument: ``-stim_label %d %s...``, position: -4
    requires: stim_times
stim_times_subtract: (a float)
    this option means to subtract specified seconds from each time
    encountered in any 'stim_times' option. The purpose of this option
    is to make it simple to adjust timing files for the removal of
    images from the start of each imaging run.
    argument: ``-stim_times_subtract %f``
num_glt: (an integer (int or long))
    number of general linear tests (i.e., contrasts)
    argument: ``-num_glt %d``, position: -3
gltsym: (a list of items which are a unicode string)
    general linear tests (i.e., contrasts) using symbolic conventions
    (e.g., '+Label1 -Label2')
    argument: ``-gltsym 'SYM: %s'...``, position: -2
glt_label: (a list of items which are a tuple of the form: (an
    integer (int or long), a unicode string))
    general linear test (i.e., contrast) labels
    argument: ``-glt_label %d %s...``, position: -1
    requires: gltsym
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output statistics file
reml_script: (a pathlike object or string representing an existing
    file)
    automatical generated script to run 3dREMLfit
x1D: (a pathlike object or string representing an existing file)

```

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```

    save out X matrix
cbucket: (a pathlike object or string representing a file)
    output regression coefficients file (if generated)

```

References:

None None

51.2.2 Remlfit[Link to code](#)

Wraps the executable command 3dREMLfit.

Performs Generalized least squares time series fit with Restricted Maximum Likelihood (REML) estimation of the temporal auto-correlation structure.

For complete details, see the [3dREMLfit Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> remlfit = afni.Remlfit()
>>> remlfit.inputs.in_files = ['functional.nii', 'functional2.nii']
>>> remlfit.inputs.out_file = 'output.nii'
>>> remlfit.inputs.matrix = 'output.1D'
>>> remlfit.inputs.gltsym = [('SYM: +Lab1 -Lab2', 'TestSYM'), ('timeseries.txt',
↪ 'TestFile')]
>>> remlfit.cmdline
'3dREMLfit -gltsym "SYM: +Lab1 -Lab2" TestSYM -gltsym "timeseries.txt" TestFile -
↪input "functional.nii functional2.nii" -matrix output.1D -Rbuck output.nii'
>>> res = remlfit.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string
    representing an existing file)
    Read time series dataset
    argument: ``-input "%s"``
matrix: (a pathlike object or string representing a file)
    the design matrix file, which should have been output from
    Deconvolve via the 'x1D' option
    argument: ``-matrix %s``

[Optional]
polort: (an integer (int or long))
    if no 'matrix' option is given, AND no 'matim' option, create a
    matrix with Legendre polynomial regressors up to the specified order.
    The default value is 0, which produces a matrix with a single column
    of all ones
    argument: ``-polort %d``
mutually_exclusive: matrix
matim: (a pathlike object or string representing a file)
    read a standard file as the matrix. You can use only Col as a name
    in GLTs with these nonstandard matrix input methods, since the other
    names come from the 'matrix' file. These mutually exclusive options
    are ignored if 'matrix' is used.

```

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```

    argument: ``-matim %s``
    mutually_exclusive: matrix
mask: (a pathlike object or string representing an existing file)
    filename of 3D mask dataset; only data time series from within the
    mask will be analyzed; results for voxels outside the mask will be
    set to zero.
    argument: ``-mask %s``
automask: (a boolean, nipy default value: False)
    build a mask automatically from input data (will be slow for long
    time series datasets)
    argument: ``-automask``
STATmask: (a pathlike object or string representing an existing file)
    filename of 3D mask dataset to be used for the purpose of reporting
    truncation-to float issues AND for computing the FDR curves. The
    actual results ARE not masked with this option (only with 'mask' or
    'automask' options).
    argument: ``-STATmask %s``
addbase: (a list of items which are a pathlike object or string
    representing an existing file)
    file(s) to add baseline model columns to the matrix with this
    option. Each column in the specified file(s) will be appended to the
    matrix. File(s) must have at least as many rows as the matrix does.
    argument: ``-addbase %s``
slibase: (a list of items which are a pathlike object or string
    representing an existing file)
    similar to 'addbase' in concept, BUT each specified file must have
    an integer multiple of the number of slices in the input dataset(s);
    then, separate regression matrices are generated for each slice,
    with the first column of the file appended to the matrix for the
    first slice of the dataset, the second column of the file appended
    to the matrix for the first slice of the dataset, and so on.
    Intended to help model physiological noise in FMRI, or other effects
    you want to regress out that might change significantly in the
    inter-slice time intervals. This will slow the program down, and
    make it use a lot more memory (to hold all the matrix stuff).
    argument: ``-slibase %s``
slibase_sm: (a list of items which are a pathlike object or string
    representing an existing file)
    similar to 'slibase', BUT each file must be in slice major order
    (i.e. all slice0 columns come first, then all slice1 columns, etc).
    argument: ``-slibase_sm %s``
usetemp: (a boolean)
    write intermediate stuff to disk, to economize on RAM. Using this
    option might be necessary to run with 'slibase' and with 'Grid'
    values above the default, since the program has to store a large
    number of matrices for such a problem: two for every slice and for
    every (a,b) pair in the ARMA parameter grid. Temporary files are
    written to the directory given in environment variable TMPDIR, or in
    /tmp, or in ./ (preference is in that order)
    argument: ``-usetemp``
nodmbase: (a boolean)
    by default, baseline columns added to the matrix via 'addbase' or
    'slibase' or 'dsort' will each have their mean removed (as is done
    in Deconvolve); this option turns this centering off
    argument: ``-nodmbase``
    requires: addbase, dsort
dsort: (a pathlike object or string representing an existing file)

```

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```

    4D dataset to be used as voxelwise baseline regressor
    argument: ``-dsort %s``
dsort_nods: (a boolean)
    if 'dsort' option is used, this command will output additional
    results files excluding the 'dsort' file
    argument: ``-dsort_nods``
    requires: dsort
fout: (a boolean)
    output F-statistic for each stimulus
    argument: ``-fout``
rout: (a boolean)
    output the R^2 statistic for each stimulus
    argument: ``-rout``
tout: (a boolean)
    output the T-statistic for each stimulus; if you use 'out_file' and
    do not give any of 'fout', 'tout', or 'rout', then the program
    assumes 'fout' is activated.
    argument: ``-tout``
nofdr: (a boolean)
    do NOT add FDR curve data to bucket datasets; FDR curves can take a
    long time if 'tout' is used
    argument: ``-noFDR``
nobout: (a boolean)
    do NOT add baseline (null hypothesis) regressor betas to the
    'rbeta_file' and/or 'obeta_file' output datasets.
    argument: ``-nobout``
gltsym: (a list of items which are a tuple of the form: (a pathlike
    object or string representing an existing file, a unicode string)
    or a tuple of the form: (a unicode string, a unicode string))
    read a symbolic GLT from input file and associate it with a label.
    As in Deconvolve, you can also use the 'SYM:' method to provide the
    definition of the GLT directly as a string (e.g., with 'SYM: +Label1
    -Label2'). Unlike Deconvolve, you MUST specify 'SYM: ' if providing
    the GLT directly as a string instead of from a file
    argument: ``-gltsym "%s" %s...``
out_file: (a pathlike object or string representing a file)
    output dataset for beta + statistics from the REML estimation; also
    contains the results of any GLT analysis requested in the Deconvolve
    setup, similar to the 'bucket' output from Deconvolve. This dataset
    does NOT get the betas (or statistics) of those regressors marked as
    'baseline' in the matrix file.
    argument: ``-Rbuck %s``
var_file: (a pathlike object or string representing a file)
    output dataset for REML variance parameters
    argument: ``-Rvar %s``
rbeta_file: (a pathlike object or string representing a file)
    output dataset for beta weights from the REML estimation, similar to
    the 'cbucket' output from Deconvolve. This dataset will contain all
    the beta weights, for baseline and stimulus regressors alike, unless
    the '-nobout' option is given -- in that case, this dataset will
    only get the betas for the stimulus regressors.
    argument: ``-Rbeta %s``
glt_file: (a pathlike object or string representing a file)
    output dataset for beta + statistics from the REML estimation, but
    ONLY for the GLTs added on the REMLfit command line itself via
    'gltsym'; GLTs from Deconvolve's command line will NOT be included.
    argument: ``-Rglt %s``

```

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```

fitts_file: (a pathlike object or string representing a file)
    output dataset for REML fitted model
    argument: ``-Rfitts %s``
errts_file: (a pathlike object or string representing a file)
    output dataset for REML residuals = data - fitted model
    argument: ``-Rerrts %s``
wherr_file: (a pathlike object or string representing a file)
    dataset for REML residual, whitened using the estimated ARMA(1,1)
    correlation matrix of the noise
    argument: ``-Rwherr %s``
quiet: (a boolean)
    turn off most progress messages
    argument: ``-quiet``
verb: (a boolean)
    turns on more progress messages, including memory usage progress
    reports at various stages
    argument: ``-verb``
ovar: (a pathlike object or string representing a file)
    dataset for OLSQ st.dev. parameter (kind of boring)
    argument: ``-Ovar %s``
obeta: (a pathlike object or string representing a file)
    dataset for beta weights from the OLSQ estimation
    argument: ``-Obeta %s``
obuck: (a pathlike object or string representing a file)
    dataset for beta + statistics from the OLSQ estimation
    argument: ``-Obuck %s``
oglt: (a pathlike object or string representing a file)
    dataset for beta + statistics from 'gltsym' options
    argument: ``-Oglt %s``
ofitts: (a pathlike object or string representing a file)
    dataset for OLSQ fitted model
    argument: ``-Ofitts %s``
oerrts: (a pathlike object or string representing a file)
    dataset for OLSQ residuals (data - fitted model)
    argument: ``-Oerrts %s``
num_threads: (an integer (int or long), nipype default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    dataset for beta + statistics from the REML estimation (if generated)
var_file: (a pathlike object or string representing a file)
    dataset for REML variance parameters (if generated)
rbeta_file: (a pathlike object or string representing a file)
    output dataset for beta weights from the REML estimation (if
    generated)
glt_file: (a pathlike object or string representing a file)

```

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```

        output dataset for beta + statistics from the REML estimation, but
        ONLY for the GLTs added on the REMLfit command line itself via
        'gltsym' (if generated)
fitts_file: (a pathlike object or string representing a file)
        ouput dataset for REML fitted model (if generated)
errts_file: (a pathlike object or string representing a file)
        output dataset for REML residuals = data - fitted model (if
        generated)
wherr_file: (a pathlike object or string representing a file)
        dataset for REML residual, whitened using the estimated ARMA(1,1)
        correlation matrix of the noise (if generated)
ovar: (a pathlike object or string representing a file)
        dataset for OLSQ st.dev. parameter (if generated)
obeta: (a pathlike object or string representing a file)
        dataset for beta weights from the OLSQ estimation (if generated)
obuck: (a pathlike object or string representing a file)
        dataset for beta + statistics from the OLSQ estimation (if
        generated)
oglt: (a pathlike object or string representing a file)
        dataset for beta + statistics from 'gltsym' options (if generated)
ofitts: (a pathlike object or string representing a file)
        dataset for OLSQ fitted model (if generated)
oerrts: (a pathlike object or string representing a file)
        dataset for OLSQ residuals = data - fitted model (if generated)

```

References:

None None

51.2.3 Synthesize

[Link to code](#)

Wraps the executable command 3dSynthesize.

Reads a ‘-cbucket’ dataset and a ‘.xmat.1D’ matrix from 3dDeconvolve, and synthesizes a fit dataset using user-selected sub-bricks and matrix columns.For complete details, see the [3dSynthesize Documentation](#).

Examples

```

>>> from nipy.interfaces import afni
>>> synthesize = afni.Synthesize()
>>> synthesize.inputs.cbucket = 'functional.nii'
>>> synthesize.inputs.matrix = 'output.1D'
>>> synthesize.inputs.select = ['baseline']
>>> synthesize.cmdline
'3dSynthesize -cbucket functional.nii -matrix output.1D -select baseline'
>>> syn = synthesize.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
cbucket: (a pathlike object or string representing a file)
        Read the dataset output from 3dDeconvolve via the '-cbucket' option.
        argument: ``-cbucket %s``
matrix: (a pathlike object or string representing a file)

```

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```

    Read the matrix output from 3dDeconvolve via the '-x1D' option.
    argument: ``-matrix %s``
select: (a list of items which are a unicode string)
    A list of selected columns from the matrix (and the corresponding
    coefficient sub-bricks from the cbucket). Valid types include
    'baseline', 'polort', 'allfunc', 'allstim', 'all', Can also provide
    'something' where something matches a stim_label from 3dDeconvolve,
    and 'digits' where digits are the numbers of the select matrix
    columns by numbers (starting at 0), or number ranges of the form
    '3..7' and '3-7'.
    argument: ``-select %s``

[Optional]
out_file: (a pathlike object or string representing a file)
    output dataset prefix name (default 'syn')
    argument: ``-prefix %s``
dry_run: (a boolean)
    Don't compute the output, just check the inputs.
    argument: ``-dry``
TR: (a float)
    TR to set in the output. The default value of TR is read from the
    header of the matrix file.
    argument: ``-TR %f``
cenfill: ('zero' or 'nbhr' or 'none')
    Determines how censored time points from the 3dDeconvolve run will
    be filled. Valid types are 'zero', 'nbhr' and 'none'.
    argument: ``-cenfill %s``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.3 interfaces.afni.preprocess

51.3.1 AlignEpiAnatPy

[Link to code](#)

Wraps the executable command align_epi_anat.py.

Align EPI to anatomical datasets or vice versa This Python script computes the alignment between two datasets, typically an EPI and an anatomical structural dataset, and applies the resulting transformation to one or the other

to bring them into alignment.

This script computes the transforms needed to align EPI and anatomical datasets using a cost function designed for this purpose. The script combines multiple transformations, thereby minimizing the amount of interpolation applied to the data.

Basic Usage: `align_epi_anat.py -anat anat+orig -epi epi+orig -epi_base 5`

The user must provide EPI and anatomical datasets and specify the EPI sub-brick to use as a base in the alignment.

Internally, the script always aligns the anatomical to the EPI dataset, and the resulting transformation is saved to a 1D file. As a user option, the inverse of this transformation may be applied to the EPI dataset in order to align it to the anatomical data instead.

This program generates several kinds of output in the form of datasets and transformation matrices which can be applied to other datasets if needed. Time-series volume registration, oblique data transformations and Talairach (standard template) transformations will be combined as needed and requested (with options to turn on and off each of the steps) in order to create the aligned datasets.

For complete details, see the `align_epi_anat.py` Documentation.

Examples

```
>>> from nipy.interfaces import afni
>>> al_ea = afni.AlignEpiAnatPy()
>>> al_ea.inputs.anat = "structural.nii"
>>> al_ea.inputs.in_file = "functional.nii"
>>> al_ea.inputs.epi_base = 0
>>> al_ea.inputs.epi_strip = '3dAutomask'
>>> al_ea.inputs.volreg = 'off'
>>> al_ea.inputs.tshift = 'off'
>>> al_ea.inputs.save_skullstrip = True
>>> al_ea.cmdline # doctest: +ELLIPSIS
'python2 ...align_epi_anat.py -anat structural.nii -epi_base 0 -epi_strip_
↪3dAutomask -epi functional.nii -save_skullstrip -suffix _al -tshift off -volreg_
↪off'
>>> res = allineate.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        EPI dataset to align
        argument: ``-epi %s``
anat: (a pathlike object or string representing an existing file)
      name of structural dataset
      argument: ``-anat %s``
epi_base: (a long integer >= 0 or 'mean' or 'median' or 'max')
          the epi base used in alignment should be one of
          (0/mean/median/max/subbrick#)
          argument: ``-epi_base %s``

[Optional]
anat2epi: (a boolean)
          align anatomical to EPI dataset (default)
          argument: ``-anat2epi``
epi2anat: (a boolean)
          align EPI to anatomical dataset
          argument: ``-epi2anat``
save_skullstrip: (a boolean)
                 save skull-stripped (not aligned)
```

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```

        argument: ``-save_skullstrip``
suffix: (a unicode string, nipy default value: _al)
        append suffix to the original anat/epi dataset to use in the
        resulting dataset names (default is "_al")
        argument: ``-suffix %s``
epi_strip: ('3dSkullStrip' or '3dAutomask' or 'None')
        method to mask brain in EPI data should be one
        of [3dSkullStrip]/3dAutomask/None)
        argument: ``-epi_strip %s``
volreg: ('on' or 'off', nipy default value: on)
        do volume registration on EPI dataset before alignment should be 'on'
        or 'off', defaults to 'on'
        argument: ``-volreg %s``
tshift: ('on' or 'off', nipy default value: on)
        do time shifting of EPI dataset before alignment should be 'on' or
        'off', defaults to 'on'
        argument: ``-tshift %s``
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
        AFNI output filetype
py27_path: (a pathlike object or string representing an existing file
        or 'python2', nipy default value: python2)
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

anat_al_orig: (a pathlike object or string representing a file)
        A version of the anatomy that is aligned to the EPI
epi_al_orig: (a pathlike object or string representing a file)
        A version of the EPI dataset aligned to the anatomy
epi_tlrc_al: (a pathlike object or string representing a file)
        A version of the EPI dataset aligned to a standard template
anat_al_mat: (a pathlike object or string representing a file)
        matrix to align anatomy to the EPI
epi_al_mat: (a pathlike object or string representing a file)
        matrix to align EPI to anatomy
epi_vr_al_mat: (a pathlike object or string representing a file)
        matrix to volume register EPI
epi_reg_al_mat: (a pathlike object or string representing a file)
        matrix to volume register and align epi to anatomy
epi_al_tlrc_mat: (a pathlike object or string representing a file)
        matrix to volume register and align epi to anatomy and put into
        standard space
epi_vr_motion: (a pathlike object or string representing a file)
        motion parameters from EPI time-series registration (tsh included in
        name if slicetiming correction is also included).
skullstrip: (a pathlike object or string representing a file)
        skull-stripped (not aligned) volume

```

References:

None None

51.3.2 Allineate

[Link to code](#)

Wraps the executable command 3dAllineate.

Program to align one dataset (the ‘source’) to a base dataset

For complete details, see the [3dAllineate Documenta  on](#).

Examples

```
>>> from nipy.interfaces import afni
>>> allineate = afni.Allineate()
>>> allineate.inputs.in_file = 'functional.nii'
>>> allineate.inputs.out_file = 'functional_allineate.nii'
>>> allineate.inputs.in_matrix = 'cmatrix.mat'
>>> allineate.cmdline
'3dAllineate -source functional.nii -prefix functional_allineate.nii -lDmatrix_
↪apply cmatrix.mat'
>>> res = allineate.run() # doctest: +SKIP
```

```
>>> allineate = afni.Allineate()
>>> allineate.inputs.in_file = 'functional.nii'
>>> allineate.inputs.reference = 'structural.nii'
>>> allineate.inputs.allcostx = 'out.allcostX.txt'
>>> allineate.cmdline
'3dAllineate -source functional.nii -base structural.nii -allcostx |& tee out.
↪allcostX.txt'
>>> res = allineate.run() # doctest: +SKIP
```

```
>>> allineate = afni.Allineate()
>>> allineate.inputs.in_file = 'functional.nii'
>>> allineate.inputs.reference = 'structural.nii'
>>> allineate.inputs.nwarp_fixmot = ['X', 'Y']
>>> allineate.cmdline
'3dAllineate -source functional.nii -nwarp_fixmotX -nwarp_fixmotY -prefix_
↪functional_allineate -base structural.nii'
>>> res = allineate.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dAllineate
         argument: ``-source %s``

[Optional]
reference: (a pathlike object or string representing an existing
           file)
           file to be used as reference, the first volume will be used if not
           given the reference will be the first volume of in_file.
           argument: ``-base %s``
out_file: (a pathlike object or string representing a file)
           output file from 3dAllineate
           argument: ``-prefix %s``
           mutually_exclusive: allcostx
out_param_file: (a pathlike object or string representing a file)
                 Save the warp parameters in ASCII (.1D) format.
                 argument: ``-lDparam_save %s``
```

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```

    mutually_exclusive: in_param_file, allcostx
in_param_file: (a pathlike object or string representing an existing
    file)
    Read warp parameters from file and apply them to the source dataset,
    and produce a new dataset
    argument: ``-lDparam_apply %s``
    mutually_exclusive: out_param_file
out_matrix: (a pathlike object or string representing a file)
    Save the transformation matrix for each volume.
    argument: ``-lDmatrix_save %s``
    mutually_exclusive: in_matrix, allcostx
in_matrix: (a pathlike object or string representing a file)
    matrix to align input file
    argument: ``-lDmatrix_apply %s``, position: -3
    mutually_exclusive: out_matrix
overwrite: (a boolean)
    overwrite output file if it already exists
    argument: ``-overwrite``
allcostx: (a pathlike object or string representing a file)
    Compute and print ALL available cost functionals for the un-warped
    inputs AND THEN QUIT. If you use this option none of the other
    expected outputs will be produced
    argument: ``-allcostx |& tee %s``, position: -1
    mutually_exclusive: out_file, out_matrix, out_param_file,
        out_weight_file
cost: ('leastsq' or 'ls' or 'mutualinfo' or 'mi' or 'corratio_mul' or
    'crM' or 'norm_mutualinfo' or 'nmi' or 'hellinger' or 'hel' or
    'corratio_add' or 'crA' or 'corratio_uns' or 'crU')
    Defines the 'cost' function that defines the matching between the
    source and the base
    argument: ``-cost %s``
interpolation: ('nearestneighbour' or 'linear' or 'cubic' or
    'quintic')
    Defines interpolation method to use during matching
    argument: ``-interp %s``
final_interpolation: ('nearestneighbour' or 'linear' or 'cubic' or
    'quintic' or 'wsinc5')
    Defines interpolation method used to create the output dataset
    argument: ``-final %s``
nmatch: (an integer (int or long))
    Use at most n scattered points to match the datasets.
    argument: ``-nmatch %d``
no_pad: (a boolean)
    Do not use zero-padding on the base image.
    argument: ``-nopad``
zclip: (a boolean)
    Replace negative values in the input datasets (source & base) with
    zero.
    argument: ``-zclip``
convergence: (a float)
    Convergence test in millimeters (default 0.05mm).
    argument: ``-conv %f``
usetemp: (a boolean)
    temporary file use
    argument: ``-usetemp``
check: (a list of items which are 'leastsq' or 'ls' or 'mutualinfo'
    or 'mi' or 'corratio_mul' or 'crM' or 'norm_mutualinfo' or 'nmi'

```

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```

    or 'hellinger' or 'hel' or 'corratio_add' or 'crA' or
    'corratio_uns' or 'crU')
    After cost functional optimization is done, start at the final
    parameters and RE-optimize using this new cost functions. If the
    results are too different, a warning message will be printed.
    However, the final parameters from the original optimization will be
    used to create the output dataset.
    argument: ``-check %s``
one_pass: (a boolean)
    Use only the refining pass -- do not try a coarse resolution pass
    first. Useful if you know that only small amounts of image alignment
    are needed.
    argument: ``-onepass``
two_pass: (a boolean)
    Use a two pass alignment strategy for all volumes, searching for a
    large rotation+shift and then refining the alignment.
    argument: ``-twopass``
two_blur: (a float)
    Set the blurring radius for the first pass in mm.
    argument: ``-twoblur %f``
two_first: (a boolean)
    Use -twopass on the first image to be registered, and then on all
    subsequent images from the source dataset, use results from the
    first image's coarse pass to start the fine pass.
    argument: ``-twofirst``
two_best: (an integer (int or long))
    In the coarse pass, use the best 'bb' set of initialpoints to search
    for the starting point for the finepass. If bb==0, then no search is
    made for the beststarting point, and the identity transformation
    isused as the starting point. [Default=5; min=0 max=11]
    argument: ``-twobest %d``
fine_blur: (a float)
    Set the blurring radius to use in the fine resolution pass to 'x'
    mm. A small amount (1-2 mm?) of blurring at the fine step may help
    with convergence, if there is some problem, especially if the base
    volume is very noisy. [Default == 0 mm = no blurring at the final
    alignment pass]
    argument: ``-fineblur %f``
center_of_mass: (a unicode string)
    Use the center-of-mass calculation to bracket the shifts.
    argument: ``-cmass%s``
autoweight: (a unicode string)
    Compute a weight function using the 3dAutomask algorithm plus some
    blurring of the base image.
    argument: ``-autoweight%s``
automask: (an integer (int or long))
    Compute a mask function, set a value for dilation or 0.
    argument: ``-automask+%d``
autobox: (a boolean)
    Expand the -automask function to enclose a rectangular box that
    holds the irregular mask.
    argument: ``-autobox``
nomask: (a boolean)
    Don't compute the autoweight/mask; if -weight is not also used, then
    every voxel will be counted equally.
    argument: ``-nomask``
weight_file: (a pathlike object or string representing an existing

```

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    file)
    Set the weighting for each voxel in the base dataset; larger weights
    mean that voxel count more in the cost function. Must be defined on
    the same grid as the base dataset
    argument: ``-weight %s``
weight: (a pathlike object or string representing an existing file or
        a float)
    Set the weighting for each voxel in the base dataset; larger weights
    mean that voxel count more in the cost function. If an image file is
    given, the volume must be defined on the same grid as the base
    dataset
    argument: ``-weight %s``
out_weight_file: (a pathlike object or string representing a file)
    Write the weight volume to disk as a dataset
    argument: ``-wtprefix %s``
    mutually_exclusive: allcostx
source_mask: (a pathlike object or string representing an existing
             file)
    mask the input dataset
    argument: ``-source_mask %s``
source_automask: (an integer (int or long))
    Automatically mask the source dataset with dilation or 0.
    argument: ``-source_automask+%d``
warp_type: ('shift_only' or 'shift_rotate' or 'shift_rotate_scale' or
            'affine_general')
    Set the warp type.
    argument: ``-warp %s``
warpfreeze: (a boolean)
    Freeze the non-rigid body parameters after first volume.
    argument: ``-warpfreeze``
replacebase: (a boolean)
    If the source has more than one volume, then after the first volume
    is aligned to the base.
    argument: ``-replacebase``
replacemeth: ('leastsq' or 'ls' or 'mutualinfo' or 'mi' or
              'corratio_mul' or 'crM' or 'norm_mutualinfo' or 'nmi' or
              'hellinger' or 'hel' or 'corratio_add' or 'crA' or 'corratio_uns'
              or 'crU')
    After first volume is aligned, switch method for later volumes. For
    use with '-replacebase'.
    argument: ``-replacemeth %s``
epi: (a boolean)
    Treat the source dataset as being composed of warped EPI slices, and
    the base as comprising anatomically 'true' images. Only phase-
    encoding direction image shearing and scaling will be allowed with
    this option.
    argument: ``-EPI``
maxrot: (a float)
    Maximum allowed rotation in degrees.
    argument: ``-maxrot %f``
maxshf: (a float)
    Maximum allowed shift in mm.
    argument: ``-maxshf %f``
maxscl: (a float)
    Maximum allowed scaling factor.
    argument: ``-maxscl %f``
maxshr: (a float)

```

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Maximum allowed shearing factor.
argument: ``-maxshr %f``
master: (a pathlike object or string representing an existing file)
Write the output dataset on the same grid as this file.
argument: ``-master %s``
newgrid: (a float)
Write the output dataset using isotropic grid spacing in mm.
argument: ``-newgrid %f``
nwarp: ('bilinear' or 'cubic' or 'quintic' or 'heptic' or 'nonic' or
'poly3' or 'poly5' or 'poly7' or 'poly9')
Experimental nonlinear warping: bilinear or legendre poly.
argument: ``-nwarp %s``
nwarp_fixmot: (a list of items which are 'X' or 'Y' or 'Z' or 'I' or
'J' or 'K')
To fix motion along directions.
argument: ``-nwarp_fixmot%s...``
nwarp_fixdep: (a list of items which are 'X' or 'Y' or 'Z' or 'I' or
'J' or 'K')
To fix non-linear warp dependency along directions.
argument: ``-nwarp_fixdep%s...``
verbose: (a boolean)
Print out verbose progress reports.
argument: ``-verb``
quiet: (a boolean)
Don't print out verbose progress reports.
argument: ``-quiet``
num_threads: (an integer (int or long), nipy default value: 1)
set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
AFNI output filetype
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
output image file name
out_matrix: (a pathlike object or string representing an existing
file)
matrix to align input file
out_param_file: (a pathlike object or string representing an existing
file)
warp parameters
out_weight_file: (a pathlike object or string representing an
existing file)
weight volume
allcostx: (a pathlike object or string representing a file)
Compute and print ALL available cost functionals for the un-warped
inputs

```

References:

None None

51.3.3 AutoTLRC

[Link to code](#)

Wraps the executable command `@auto_tlrc`.

A minimal wrapper for the AutoTLRC script. The only option currently supported is `no_ss`. For complete details, see the [3dQwarp Documenta­tion](#).

Examples

```
>>> from nipy.interfaces import afni
>>> autoTLRC = afni.AutoTLRC()
>>> autoTLRC.inputs.in_file = 'structural.nii'
>>> autoTLRC.inputs.no_ss = True
>>> autoTLRC.inputs.base = "TT_N27+tlrc"
>>> autoTLRC.cmdline
'@auto_tlrc -base TT_N27+tlrc -input structural.nii -no_ss'
>>> res = autoTLRC.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Original anatomical volume (+orig). The skull is removed by this
    script unless instructed otherwise (-no_ss).
    argument: ``-input %s``
base: (a unicode string)
    Reference anatomical volume. Usually this volume is in some standard
    space like TLRC or MNI space and with afni dataset view of (+tlrc).
    Preferably, this reference volume should have had the skull removed
    but that is not mandatory. AFNI's distribution contains several
    templates. For a longer list, use "whereami
    -show_templates"TT_N27+tlrc --> Single subject, skull stripped
    volume. This volume is also known as N27_SurfVol_NoSkull+tlrc
    elsewhere in AFNI and SUMA land. (www.loni.ucla.edu,
    www.bic.mni.mcgill.ca) This template has a full set of FreeSurfer
    (surfer.nmr.mgh.harvard.edu) surface models that can be used in
    SUMA. For details, see Talairach-related link:
    https://afni.nimh.nih.gov/afni/sumaTT_icbm452+tlrc --> Average
    volume of 452 normal brains. Skull Stripped.
    (www.loni.ucla.edu)TT_avg152T1+tlrc --> Average volume of 152 normal
    brains. Skull Stripped. (www.bic.mni.mcgill.ca)TT_EPI+tlrc --> EPI
    template from spm2, masked as TT_avg152T1 TT_avg152 and TT_EPI
    volume sources are from SPM's distribution.
    (www.fil.ion.ucl.ac.uk/spm/) If you do not specify a path for the
    template, the script will attempt to locate the template AFNI's
    binaries directory. NOTE: These datasets have been slightly modified
    from their original size to match the standard TLRC dimensions (Jean
    Talairach and Pierre Tournoux Co-Planar Stereotaxic Atlas of the
    Human Brain Thieme Medical Publishers, New York, 1988). That was
    done for internal consistency in AFNI. You may use the original form
    of these volumes if you choose but your TLRC coordinates will not be
    consistent with AFNI's TLRC database (San Antonio Talairach Daemon
    database), for example.
    argument: ``-base %s``

[Optional]
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
```

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```

no_ss: (a boolean)
    Do not strip skull of input data set(because skull has already been
    removedor because template still has the skull)NOTE: The -no_ss
    option is not all that optional. Here is a table of when you should
    and should not use -no_ss Template Template WITH skull WITHOUT skull
    Dset. WITH skull -no_ss xxx WITHOUT skull No Cigar -no_ss Template
    means: Your template of choice Dset. means: Your anatomical dataset
    -no_ss means: Skull stripping should not be attempted on Dset xxx
    means: Don't put anything, the script will strip Dset No Cigar
    means: Don't try that combination, it makes no sense.
    argument: ``-no_ss``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.3.4 AutoTcorrelate[Link to code](#)

Wraps the executable command 3dAutoTcorrelate.

Computes the correlation coefficient between the time series of each pair of voxels in the input dataset, and stores the output into a new anatomical bucket dataset [scaled to shorts to save memory space].

For complete details, see the [3dAutoTcorrelate Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> corr = afni.AutoTcorrelate()
>>> corr.inputs.in_file = 'functional.nii'
>>> corr.inputs.polort = -1
>>> corr.inputs.eta2 = True
>>> corr.inputs.mask = 'mask.nii'
>>> corr.inputs.mask_only_targets = True
>>> corr.cmdline # doctest: +ELLIPSIS
'3dAutoTcorrelate -eta2 -mask mask.nii -mask_only_targets -prefix functional_
  ↳similarity_matrix.1D -polort -1 functional.nii'
>>> res = corr.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    timeseries x space (volume or surface) file
    argument: ``%s``, position: -1

```

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```
[Optional]
polort: (an integer (int or long))
    Remove polynomial trend of order m or -1 for no detrending
    argument: ``-polort %d``
eta2: (a boolean)
    eta^2 similarity
    argument: ``-eta2``
mask: (a pathlike object or string representing an existing file)
    mask of voxels
    argument: ``-mask %s``
mask_only_targets: (a boolean)
    use mask only on targets voxels
    argument: ``-mask_only_targets``
    mutually_exclusive: mask_source
mask_source: (a pathlike object or string representing an existing
    file)
    mask for source voxels
    argument: ``-mask_source %s``
    mutually_exclusive: mask_only_targets
out_file: (a pathlike object or string representing a file)
    output image file name
    argument: ``-prefix %s``
num_threads: (an integer (int or long), nipyne default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
    output file
```

References:

None None

51.3.5 Automask

[Link to code](#)

Wraps the executable command 3dAutomask.

Create a brain-only mask of the image using AFNI 3dAutomask command

For complete details, see the [3dAutomask Documentation](#).

Examples

```
>>> from nipyne.interfaces import afni
>>> automask = afni.Automask()
```

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```
>>> automask.inputs.in_file = 'functional.nii'
>>> automask.inputs.dilate = 1
>>> automask.inputs.outputtype = 'NIFTI'
>>> automask.cmdline # doctest: +ELLIPSIS
'3dAutomask -apply_prefix functional_masked.nii -dilate 1 -prefix functional_mask.
↪nii functional.nii'
>>> res = automask.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dAutomask
         argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
         output image file name
         argument: ``-prefix %s``
brain_file: (a pathlike object or string representing a file)
         output file from 3dAutomask
         argument: ``-apply_prefix %s``
clfrac: (a float)
         sets the clip level fraction (must be 0.1-0.9). A small value will
         tend to make the mask larger [default = 0.5].
         argument: ``-clfrac %s``
dilate: (an integer (int or long))
         dilate the mask outwards
         argument: ``-dilate %s``
erode: (an integer (int or long))
         erode the mask inwards
         argument: ``-erode %s``
num_threads: (an integer (int or long), nipy default value: 1)
         set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
         AFNI output filetype
args: (a unicode string)
         Additional parameters to the command
         argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
         mask file
brain_file: (a pathlike object or string representing an existing
         file)
         brain file (skull stripped)
```

References:

None None

51.3.6 Bandpass

[Link to code](#)

Wraps the executable command 3dBandpass.

Program to lowpass and/or highpass each voxel time series in a dataset, offering more/different options than Fourier

For complete details, see the [3dBandpass Documenta  on](#).

Examples

```
>>> from nipy.interfaces import afni
>>> from nipy.testing import example_data
>>> bandpass = afni.Bandpass()
>>> bandpass.inputs.in_file = 'functional.nii'
>>> bandpass.inputs.highpass = 0.005
>>> bandpass.inputs.lowpass = 0.1
>>> bandpass.cmdline
'3dBandpass -prefix functional_bp 0.005000 0.100000 functional.nii'
>>> res = bandpass.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dBandpass
         argument: ``%s``, position: -1
lowpass: (a float)
         lowpass
         argument: ``%f``, position: -2
highpass: (a float)
         highpass
         argument: ``%f``, position: -3

[Optional]
out_file: (a pathlike object or string representing a file)
         output file from 3dBandpass
         argument: ``-prefix %s``, position: 1
mask: (a pathlike object or string representing an existing file)
      mask file
      argument: ``-mask %s``, position: 2
despike: (a boolean)
         Despike each time series before other processing. Hopefully, you
         don't actually need to do this, which is why it is optional.
         argument: ``-despike``
orthogonalize_file: (a list of items which are a pathlike object or
                    string representing an existing file)
                    Also orthogonalize input to columns in f.1D. Multiple '-ort' options
                    are allowed.
                    argument: ``-ort %s``
orthogonalize_dset: (a pathlike object or string representing an
                    existing file)
                    Orthogonalize each voxel to the corresponding voxel time series in
                    dataset 'fset', which must have the same spatial and temporal grid
                    structure as the main input dataset. At present, only one '-dsort'
                    option is allowed.
                    argument: ``-dsort %s``
no_detrend: (a boolean)
            Skip the quadratic detrending of the input that occurs before the
```

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```

        FFT-based bandpassing. You would only want to do this if the dataset
        had been detrended already in some other program.
        argument: ``-nodetrend``
tr: (a float)
    Set time step (TR) in sec [default=from dataset header].
    argument: ``-dt %f``
nfft: (an integer (int or long))
    Set the FFT length [must be a legal value].
    argument: ``-nfft %d``
normalize: (a boolean)
    Make all output time series have L2 norm = 1 (i.e., sum of squares =
    1).
    argument: ``-norm``
automask: (a boolean)
    Create a mask from the input dataset.
    argument: ``-automask``
blur: (a float)
    Blur (inside the mask only) with a filter width (FWHM) of 'fff'
    millimeters.
    argument: ``-blur %f``
localPV: (a float)
    Replace each vector by the local Principal Vector (AKA first
    singular vector) from a neighborhood of radius 'rrr' millimeters.
    Note that the PV time series is L2 normalized. This option is mostly
    for Bob Cox to have fun with.
    argument: ``-localPV %f``
notrans: (a boolean)
    Don't check for initial positive transients in the data. The test is
    a little slow, so skipping it is OK, if you KNOW the data time
    series are transient-free.
    argument: ``-notrans``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.3.7 BlurInMask[Link to code](#)

Wraps the executable command 3dBlurInMask.

Blurs a dataset spatially inside a mask. That's all. Experimental.

For complete details, see the [3dBlurInMask Documentation](#).

Examples

```
>>> from nipy.interfaces import afni
>>> bim = afni.BlurInMask()
>>> bim.inputs.in_file = 'functional.nii'
>>> bim.inputs.mask = 'mask.nii'
>>> bim.inputs.fwhm = 5.0
>>> bim.cmdline # doctest: +ELLIPSIS
'3dBlurInMask -input functional.nii -FWHM 5.000000 -mask mask.nii -prefix_
↳functional_blur'
>>> res = bim.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dSkullStrip
         argument: ``-input %s``, position: 1
fwhm: (a float)
      fwhm kernel size
      argument: ``-FWHM %f``

[Optional]
out_file: (a pathlike object or string representing a file)
          output to the file
          argument: ``-prefix %s``, position: -1
mask: (a pathlike object or string representing a file)
      Mask dataset, if desired. Blurring will occur only within the mask.
      Voxels NOT in the mask will be set to zero in the output.
      argument: ``-mask %s``
multimask: (a pathlike object or string representing a file)
          Multi-mask dataset -- each distinct nonzero value in dataset will be
          treated as a separate mask for blurring purposes.
          argument: ``-Mmask %s``
automask: (a boolean)
          Create an automask from the input dataset.
          argument: ``-automask``
preserve: (a boolean)
          Normally, voxels not in the mask will be set to zero in the output.
          If you want the original values in the dataset to be preserved in
          the output, use this option.
          argument: ``-preserve``
float_out: (a boolean)
          Save dataset as floats, no matter what the input data type is.
          argument: ``-float``
options: (a unicode string)
          options
          argument: ``%s``, position: 2
num_threads: (an integer (int or long), nipy default value: 1)
             set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
```

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```

of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          output file

```

References:

None None

51.3.8 BlurToFWHM[Link to code](#)

Wraps the executable command 3dBlurToFWHM.

Blurs a ‘master’ dataset until it reaches a specified FWHM smoothness (approximately).

For complete details, see the [3dBlurToFWHM Documentation](#)**Examples**

```

>>> from nipy.interfaces import afni
>>> blur = afni.preprocess.BlurToFWHM()
>>> blur.inputs.in_file = 'epi.nii'
>>> blur.inputs.fwhm = 2.5
>>> blur.cmdline # doctest: +ELLIPSIS
'3dBlurToFWHM -FWHM 2.500000 -input epi.nii -prefix epi_afni'
>>> res = blur.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         The dataset that will be smoothed
         argument: ``-input %s``

[Optional]
automask: (a boolean)
          Create an automask from the input dataset.
          argument: ``-automask``

fwhm: (a float)
      Blur until the 3D FWHM reaches this value (in mm)
      argument: ``-FWHM %f``

fwhmxy: (a float)
      Blur until the 2D (x,y)-plane FWHM reaches this value (in mm)
      argument: ``-FWHMxy %f``

blurmaster: (a pathlike object or string representing an existing
            file)
            The dataset whose smoothness controls the process.
            argument: ``-blurmaster %s``

mask: (a pathlike object or string representing an existing file)
      Mask dataset, if desired. Voxels NOT in mask will be set to zero in
      output.
      argument: ``-mask %s``

num_threads: (an integer (int or long), nipy default value: 1)

```

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```

        set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
        AFNI output filetype
out_file: (a pathlike object or string representing a file)
        output image file name
        argument: ``-prefix %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        output file

```

References:

None None

51.3.9 ClipLevel[Link to code](#)

Wraps the executable command 3dClipLevel.

Estimates the value at which to clip the anatomical dataset so that background regions are set to zero.For complete details, see the [3dClipLevel Documentation](#).**Examples**

```

>>> from nipy.interfaces.afni import preprocess
>>> cliplevel = preprocess.ClipLevel()
>>> cliplevel.inputs.in_file = 'anatomical.nii'
>>> cliplevel.cmdline
'3dClipLevel anatomical.nii'
>>> res = cliplevel.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input file to 3dClipLevel
        argument: ``%s``, position: -1

[Optional]
mfrac: (a float)
        Use the number ff instead of 0.50 in the algorithm
        argument: ``-mfrac %s``, position: 2
doall: (a boolean)
        Apply the algorithm to each sub-brick separately.
        argument: ``-doall``, position: 3
        mutually_exclusive: g, r, a, d
grad: (a pathlike object or string representing a file)
        Also compute a 'gradual' clip level as a function of voxel position,

```

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```

    and output that to a dataset.
    argument: ``-grad %s``, position: 3
    mutually_exclusive: d, o, a, l, l
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

clip_val: (a float)
    output

```

51.3.10 DegreeCentrality

[Link to code](#)

Wraps the executable command 3dDegreeCentrality.

Performs degree centrality on a dataset using a given maskfile via 3dDegreeCentrality

For complete details, see the [3dDegreeCentrality Documenta  on](#).

Examples

```

>>> from nipy.interfaces import afni
>>> degree = afni.DegreeCentrality()
>>> degree.inputs.in_file = 'functional.nii'
>>> degree.inputs.mask = 'mask.nii'
>>> degree.inputs.sparsity = 1 # keep the top one percent of connections
>>> degree.inputs.out_file = 'out.nii'
>>> degree.cmdline
'3dDegreeCentrality -mask mask.nii -prefix out.nii -sparsity 1.000000 functional.
↪nii'
>>> res = degree.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    input file to 3dDegreeCentrality
    argument: ``%s``, position: -1

[Optional]
sparsity: (a float)
    only take the top percent of connections
    argument: ``-sparsity %f``
oned_file: (a unicode string)
    output filepath to text dump of correlation matrix
    argument: ``-out1D %s``
mask: (a pathlike object or string representing an existing file)
    mask file to mask input data
    argument: ``-mask %s``
thresh: (a float)
    threshold to exclude connections where corr <= thresh
    argument: ``-thresh %f``

```

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```

polort: (an integer (int or long))
        argument: ``-polort %d``
autoclip: (a boolean)
        Clip off low-intensity regions in the dataset
        argument: ``-autoclip``
automask: (a boolean)
        Mask the dataset to target brain-only voxels
        argument: ``-automask``
num_threads: (an integer (int or long), nipy default value: 1)
        set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
        AFNI output filetype
out_file: (a pathlike object or string representing a file)
        output image file name
        argument: ``-prefix %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

oned_file: (a pathlike object or string representing a file)
        The text output of the similarity matrix computed after thresholding
        with one-dimensional and ijk voxel indices, correlations, image
        extents, and affine matrix.
out_file: (a pathlike object or string representing an existing file)
        output file

```

References:

None None

51.3.11 Despike[Link to code](#)

Wraps the executable command 3dDespike.

Removes ‘spikes’ from the 3D+time input dataset

For complete details, see the [3dDespike Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> despike = afni.Despike()
>>> despike.inputs.in_file = 'functional.nii'
>>> despike.cmdline
'3dDespike -prefix functional_despike functional.nii'
>>> res = despike.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)

```

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```

        input file to 3dDespike
        argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
        output image file name
        argument: ``-prefix %s``
num_threads: (an integer (int or long), nipy default value: 1)
        set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
        AFNI output filetype
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        output file

```

References:

None None

51.3.12 Detrend[Link to code](#)

Wraps the executable command 3dDetrend.

This program removes components from voxel time series using linear least squares

For complete details, see the [3dDetrend Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> detrend = afni.Detrend()
>>> detrend.inputs.in_file = 'functional.nii'
>>> detrend.inputs.args = '-polort 2'
>>> detrend.inputs.outputtype = 'AFNI'
>>> detrend.cmdline
'3dDetrend -polort 2 -prefix functional_detrend functional.nii'
>>> res = detrend.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input file to 3dDetrend
        argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
        output image file name

```

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```

    argument: ``-prefix %s``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.3.13 ECM[Link to code](#)

Wraps the executable command 3dECM.

Performs degree centrality on a dataset using a given maskfile via the 3dECM command

For complete details, see the [3dECM Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> ecm = afni.ECM()
>>> ecm.inputs.in_file = 'functional.nii'
>>> ecm.inputs.mask = 'mask.nii'
>>> ecm.inputs.sparsity = 0.1 # keep top 0.1% of connections
>>> ecm.inputs.out_file = 'out.nii'
>>> ecm.cmdline
'3dECM -mask mask.nii -prefix out.nii -sparsity 0.100000 functional.nii'
>>> res = ecm.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    input file to 3dECM
    argument: ``%s``, position: -1

[Optional]
sparsity: (a float)
    only take the top percent of connections
    argument: ``-sparsity %f``
full: (a boolean)
    Full power method; enables thresholding; automatically selected if
    -thresh or -sparsity are set
    argument: ``-full``

```

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```

fecm: (a boolean)
    Fast centrality method; substantial speed increase but cannot
    accomodate thresholding; automatically selected if -thresh or
    -sparsity are not set
    argument: ``-fecm``
shift: (a float)
    shift correlation coefficients in similarity matrix to enforce non-
    negativity, s >= 0.0; default = 0.0 for -full, 1.0 for -fecm
    argument: ``-shift %f``
scale: (a float)
    scale correlation coefficients in similarity matrix to after
    shifting, x >= 0.0; default = 1.0 for -full, 0.5 for -fecm
    argument: ``-scale %f``
eps: (a float)
    sets the stopping criterion for the power iteration;  $12|v_{old} - v_{new}| < eps * |v_{old}|$ ; default = 0.001
    argument: ``-eps %f``
max_iter: (an integer (int or long))
    sets the maximum number of iterations to use in the power iteration;
    default = 1000
    argument: ``-max_iter %d``
memory: (a float)
    Limit memory consumption on system by setting the amount of GB to
    limit the algorithm to; default = 2GB
    argument: ``-memory %f``
mask: (a pathlike object or string representing an existing file)
    mask file to mask input data
    argument: ``-mask %s``
thresh: (a float)
    threshold to exclude connections where corr <= thresh
    argument: ``-thresh %f``
polort: (an integer (int or long))
    argument: ``-polort %d``
autoclip: (a boolean)
    Clip off low-intensity regions in the dataset
    argument: ``-autoclip``
automask: (a boolean)
    Mask the dataset to target brain-only voxels
    argument: ``-automask``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
out_file: (a pathlike object or string representing a file)
    output image file name
    argument: ``-prefix %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)

```

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output file

References:

None None

51.3.14 Fim[Link to code](#)

Wraps the executable command 3dfim+.

Program to calculate the cross-correlation of an ideal reference waveform with the measured FMRI time series for each voxel.

For complete details, see the [3dfim+ Documenta**tion**](#).**Examples**

```
>>> from nipy.interfaces import afni
>>> fim = afni.Fim()
>>> fim.inputs.in_file = 'functional.nii'
>>> fim.inputs.ideal_file= 'seed.1D'
>>> fim.inputs.out_file = 'functional_corr.nii'
>>> fim.inputs.out = 'Correlation'
>>> fim.inputs.fim_thr = 0.0009
>>> fim.cmdline
'3dfim+ -input functional.nii -ideal_file seed.1D -fim_thr 0.000900 -out_
↪Correlation -bucket functional_corr.nii'
>>> res = fim.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dfim+
         argument: ``-input %s``, position: 1
ideal_file: (a pathlike object or string representing an existing
            file)
            ideal time series file name
            argument: ``-ideal_file %s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
          output image file name
          argument: ``-bucket %s``
fim_thr: (a float)
         fim internal mask threshold value
         argument: ``-fim_thr %f``, position: 3
out: (a unicode string)
     Flag to output the specified parameter
     argument: ``-out %s``, position: 4
num_threads: (an integer (int or long), nipy default value: 1)
             set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
      Additional parameters to the command
```

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```

    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          output file

```

References:

None None

51.3.15 Fourier[Link to code](#)

Wraps the executable command 3dFourier.

Program to lowpass and/or highpass each voxel time series in a dataset, via the FFT

For complete details, see the [3dFourier Documenta**tion**](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> fourier = afni.Fourier()
>>> fourier.inputs.in_file = 'functional.nii'
>>> fourier.inputs.retrend = True
>>> fourier.inputs.highpass = 0.005
>>> fourier.inputs.lowpass = 0.1
>>> fourier.cmdline
'3dFourier -highpass 0.005000 -lowpass 0.100000 -prefix functional_fourier -
↳retrend functional.nii'
>>> res = fourier.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dFourier
         argument: ``%s``, position: -1
lowpass: (a float)
         lowpass
         argument: ``-lowpass %f``
highpass: (a float)
         highpass
         argument: ``-highpass %f``

[Optional]
out_file: (a pathlike object or string representing a file)
         output image file name
         argument: ``-prefix %s``
retrend: (a boolean)
         Any mean and linear trend are removed before filtering. This will
         restore the trend after filtering.
         argument: ``-retrend``

```

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```

num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.3.16 Hist[Link to code](#)

Wraps the executable command 3dHist.

Computes average of all voxels in the input dataset which satisfy the criterion in the options list

For complete details, see the [3dHist Documenta**tion**](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> hist = afni.Hist()
>>> hist.inputs.in_file = 'functional.nii'
>>> hist.cmdline
'3dHist -input functional.nii -prefix functional_hist'
>>> res = hist.run()  # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    input file to 3dHist
    argument: ``-input %s``, position: 1

[Optional]
out_file: (a pathlike object or string representing a file)
    Write histogram to nlm file with this prefix
    argument: ``-prefix %s``
showhist: (a boolean, nipy default value: False)
    write a text visual histogram
    argument: ``-showhist``
out_show: (a pathlike object or string representing a file)
    output image file name
    argument: ``> %s``, position: -1
mask: (a pathlike object or string representing an existing file)
    matrix to align input file

```

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```

        argument: ``-mask %s``
nbin: (an integer (int or long))
        number of bins
        argument: ``-nbin %d``
max_value: (a float)
        maximum intensity value
        argument: ``-max %f``
min_value: (a float)
        minimum intensity value
        argument: ``-min %f``
bin_width: (a float)
        bin width
        argument: ``-binwidth %f``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        output file
out_show: (a pathlike object or string representing a file)
        output visual histogram

```

51.3.17 LFCD[Link to code](#)

Wraps the executable command 3dLFCD.

Performs degree centrality on a dataset using a given maskfile via the 3dLFCD command

For complete details, see the [3dLFCD Documenta  on](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> lfcd = afni.LFCD()
>>> lfcd.inputs.in_file = 'functional.nii'
>>> lfcd.inputs.mask = 'mask.nii'
>>> lfcd.inputs.thresh = 0.8 # keep all connections with corr >= 0.8
>>> lfcd.inputs.out_file = 'out.nii'
>>> lfcd.cmdline
'3dLFCD -mask mask.nii -prefix out.nii -thresh 0.800000 functional.nii'
>>> res = lfcd.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input file to 3dLFCD
        argument: ``%s``, position: -1

[Optional]
mask: (a pathlike object or string representing an existing file)

```

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```

        mask file to mask input data
        argument: ``-mask %s``
thresh: (a float)
        threshold to exclude connections where corr <= thresh
        argument: ``-thresh %f``
polort: (an integer (int or long))
        argument: ``-polort %d``
autoclip: (a boolean)
        Clip off low-intensity regions in the dataset
        argument: ``-autoclip``
automask: (a boolean)
        Mask the dataset to target brain-only voxels
        argument: ``-automask``
num_threads: (an integer (int or long), nipy default value: 1)
        set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
        AFNI output filetype
out_file: (a pathlike object or string representing a file)
        output image file name
        argument: ``-prefix %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        output file

```

References:

None None

51.3.18 Maskave[Link to code](#)

Wraps the executable command 3dmaskave.

Computes average of all voxels in the input dataset which satisfy the criterion in the options list

For complete details, see the [3dmaskave Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> maskave = afni.Maskave()
>>> maskave.inputs.in_file = 'functional.nii'
>>> maskave.inputs.mask= 'seed_mask.nii'
>>> maskave.inputs.quiet= True
>>> maskave.cmdline # doctest: +ELLIPSIS
'3dmaskave -mask seed_mask.nii -quiet functional.nii > functional_maskave.1D'
>>> res = maskave.run() # doctest: +SKIP

```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input file to 3dmaskave
        argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
        output image file name
        argument: ``> %s``, position: -1
mask: (a pathlike object or string representing an existing file)
        matrix to align input file
        argument: ``-mask %s``, position: 1
quiet: (a boolean)
        matrix to align input file
        argument: ``-quiet``, position: 2
num_threads: (an integer (int or long), nipyne default value: 1)
        set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
        AFNI output filetype
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipyne default value: {})
        Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
        output file
```

References:

None None

51.3.19 Means

[Link to code](#)

Wraps the executable command 3dMean.

Takes the voxel-by-voxel mean of all input datasets using 3dMean

For complete details, see the [3dMean Documentation](#).

Examples

```
>>> from nipyne.interfaces import afni
>>> means = afni.Mean()
>>> means.inputs.in_file_a = 'im1.nii'
>>> means.inputs.in_file_b = 'im2.nii'
>>> means.inputs.out_file = 'output.nii'
>>> means.cmdline
'3dMean -prefix output.nii im1.nii im2.nii'
>>> res = means.run() # doctest: +SKIP
```

```
>>> from nipyne.interfaces import afni
>>> means = afni.Mean()
```

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```

>>> means.inputs.in_file_a = 'iml.nii'
>>> means.inputs.out_file = 'output.nii'
>>> means.inputs.datum = 'short'
>>> means.cmdline
'3dMean -datum short -prefix output.nii iml.nii'
>>> res = means.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file_a: (a pathlike object or string representing an existing
            file)
            input file to 3dMean
            argument: ``%s``, position: -2

[Optional]
in_file_b: (a pathlike object or string representing an existing
            file)
            another input file to 3dMean
            argument: ``%s``, position: -1
datum: (a unicode string)
        Sets the data type of the output dataset
        argument: ``-datum %s``
out_file: (a pathlike object or string representing a file)
            output image file name
            argument: ``-prefix %s``
scale: (a unicode string)
        scaling of output
        argument: ``-%sscale``
non_zero: (a boolean)
            use only non-zero values
            argument: ``-non_zero``
std_dev: (a boolean)
            calculate std dev
            argument: ``-stdev``
sqr: (a boolean)
        mean square instead of value
        argument: ``-sqr``
summ: (a boolean)
        take sum, (not average)
        argument: ``-sum``
count: (a boolean)
        compute count of non-zero voxels
        argument: ``-count``
mask_inter: (a boolean)
            create intersection mask
            argument: ``-mask_inter``
mask_union: (a boolean)
            create union mask
            argument: ``-mask_union``
num_threads: (an integer (int or long), nipy default value: 1)
            set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``

```

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```
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
output file
```

References:

None None

51.3.20 OutlierCount[Link to code](#)

Wraps the executable command 3dToutcount.

Calculates number of ‘outliers’ at each time point of a 3D+time dataset.

For complete details, see the [3dToutcount Documenta**tion**](#)**Examples**

```
>>> from nipy.interfaces import afni
>>> toutcount = afni.OutlierCount()
>>> toutcount.inputs.in_file = 'functional.nii'
>>> toutcount.cmdline # doctest: +ELLIPSIS
'3dToutcount -qthr 0.00100 functional.nii'
>>> res = toutcount.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
input dataset
argument: ``%s``, position: -2

[Optional]
mask: (a pathlike object or string representing an existing file)
only count voxels within the given mask
argument: ``-mask %s``
mutually_exclusive: autoclip, automask
qthr: (0.0 <= a floating point number <= 1.0, nipy default value:
      0.001)
      indicate a value for q to compute alpha
      argument: ``-qthr %.5f``
autoclip: (a boolean, nipy default value: False)
clip off small voxels
argument: ``-autoclip``
mutually_exclusive: mask
automask: (a boolean, nipy default value: False)
clip off small voxels
argument: ``-automask``
mutually_exclusive: mask
fraction: (a boolean, nipy default value: False)
write out the fraction of masked voxels which are outliers at each
```

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```

        timepoint
        argument: ``-fraction``
interval: (a boolean, nipy default value: False)
        write out the median + 3.5 MAD of outlier count with each timepoint
        argument: ``-range``
save_outliers: (a boolean, nipy default value: False)
        enables out_file option
outliers_file: (a pathlike object or string representing a file)
        output image file name
        argument: ``-save %s``
polort: (an integer (int or long))
        detrend each voxel timeseries with polynomials
        argument: ``-polort %d``
legendre: (a boolean, nipy default value: False)
        use Legendre polynomials
        argument: ``-legendre``
out_file: (a pathlike object or string representing a file)
        capture standard output
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_outliers: (a pathlike object or string representing an existing
        file)
        output image file name
out_file: (a pathlike object or string representing a file)
        capture standard output

```

51.3.21 QualityIndex[Link to code](#)

Wraps the executable command 3dTqual.

Computes a 'quality index' for each sub-brick in a 3D+time dataset. The output is a 1D time series with the index for each sub-brick. The results are written to stdout.

For complete details, see the [3dTqual Documentation](#)

Examples

```

>>> from nipy.interfaces import afni
>>> tqual = afni.QualityIndex()
>>> tqual.inputs.in_file = 'functional.nii'
>>> tqual.cmdline # doctest: +ELLIPSIS
'3dTqual functional.nii > functional_tqual'
>>> res = tqual.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input dataset

```

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```

        argument: ``%s``, position: -2

[Optional]
mask: (a pathlike object or string representing an existing file)
    compute correlation only across masked voxels
    argument: ``-mask %s``
    mutually_exclusive: autoclip, automask
spearman: (a boolean, nipy default value: False)
    Quality index is 1 minus the Spearman (rank) correlation coefficient
    of each sub-brick with the median sub-brick. (default).
    argument: ``-spearman``
quadrant: (a boolean, nipy default value: False)
    Similar to -spearman, but using 1 minus the quadrant correlation
    coefficient as the quality index.
    argument: ``-quadrant``
autoclip: (a boolean, nipy default value: False)
    clip off small voxels
    argument: ``-autoclip``
    mutually_exclusive: mask
automask: (a boolean, nipy default value: False)
    clip off small voxels
    argument: ``-automask``
    mutually_exclusive: mask
clip: (a float)
    clip off values below
    argument: ``-clip %f``
interval: (a boolean, nipy default value: False)
    write out the median + 3.5 MAD of outlier count with each timepoint
    argument: ``-range``
out_file: (a pathlike object or string representing a file)
    capture standard output
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    file containing the captured standard output

```

51.3.22 Qwarp[Link to code](#)

Wraps the executable command 3dQwarp.

A version of 3dQwarp Allineate your images prior to passing them to this workflow.

For complete details, see the [3dQwarp Documentation](#).**Examples**

```
>>> from nipyne.interfaces import afni
>>> qwarp = afni.Qwarp()
>>> qwarp.inputs.in_file = 'sub-01_dir-LR_epi.nii.gz'
>>> qwarp.inputs.nopadWARP = True
>>> qwarp.inputs.base_file = 'sub-01_dir-RL_epi.nii.gz'
>>> qwarp.inputs.plusminus = True
>>> qwarp.cmdline
'3dQwarp -base sub-01_dir-RL_epi.nii.gz -source sub-01_dir-LR_epi.nii.gz -
↳nopadWARP -prefix ppp_sub-01_dir-LR_epi -plusminus'
>>> res = qwarp.run() # doctest: +SKIP
```

```
>>> from nipyne.interfaces import afni
>>> qwarp = afni.Qwarp()
>>> qwarp.inputs.in_file = 'structural.nii'
>>> qwarp.inputs.base_file = 'mni.nii'
>>> qwarp.inputs.resample = True
>>> qwarp.cmdline
'3dQwarp -base mni.nii -source structural.nii -prefix ppp_structural -resample'
>>> res = qwarp.run() # doctest: +SKIP
```

```
>>> from nipyne.interfaces import afni
>>> qwarp = afni.Qwarp()
>>> qwarp.inputs.in_file = 'structural.nii'
>>> qwarp.inputs.base_file = 'epi.nii'
>>> qwarp.inputs.out_file = 'anatSSQ.nii.gz'
>>> qwarp.inputs.resample = True
>>> qwarp.inputs.lpc = True
>>> qwarp.inputs.verb = True
>>> qwarp.inputs.iwarp = True
>>> qwarp.inputs.blur = [0,3]
>>> qwarp.cmdline
'3dQwarp -base epi.nii -blur 0.0 3.0 -source structural.nii -iwarp -prefix_
↳anatSSQ.nii.gz -resample -verb -lpc'
>>> res = qwarp.run() # doctest: +SKIP
```

```
>>> from nipyne.interfaces import afni
>>> qwarp = afni.Qwarp()
>>> qwarp.inputs.in_file = 'structural.nii'
>>> qwarp.inputs.base_file = 'mni.nii'
>>> qwarp.inputs.duplo = True
>>> qwarp.inputs.blur = [0,3]
>>> qwarp.cmdline
'3dQwarp -base mni.nii -blur 0.0 3.0 -duplo -source structural.nii -prefix ppp_
↳structural'
>>> res = qwarp.run() # doctest: +SKIP
```

```
>>> from nipyne.interfaces import afni
>>> qwarp = afni.Qwarp()
>>> qwarp.inputs.in_file = 'structural.nii'
>>> qwarp.inputs.base_file = 'mni.nii'
>>> qwarp.inputs.duplo = True
>>> qwarp.inputs.minpatch = 25
>>> qwarp.inputs.blur = [0,3]
>>> qwarp.inputs.out_file = 'Q25'
>>> qwarp.cmdline
'3dQwarp -base mni.nii -blur 0.0 3.0 -duplo -source structural.nii -minpatch 25 -
↳prefix Q25'
```

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```

>>> res = qwarp.run() # doctest: +SKIP
>>> qwarp2 = afni.Qwarp()
>>> qwarp2.inputs.in_file = 'structural.nii'
>>> qwarp2.inputs.base_file = 'mni.nii'
>>> qwarp2.inputs.blur = [0,2]
>>> qwarp2.inputs.out_file = 'Q11'
>>> qwarp2.inputs.inilev = 7
>>> qwarp2.inputs.iniwarp = ['Q25_warp+tlrc.HEAD']
>>> qwarp2.cmdline
'3dQwarp -base mni.nii -blur 0.0 2.0 -source structural.nii -inilev 7 -iniwarp_
↳Q25_warp+tlrc.HEAD -prefix Q11'
>>> res2 = qwarp2.run() # doctest: +SKIP
>>> res2 = qwarp2.run() # doctest: +SKIP
>>> qwarp3 = afni.Qwarp()
>>> qwarp3.inputs.in_file = 'structural.nii'
>>> qwarp3.inputs.base_file = 'mni.nii'
>>> qwarp3.inputs.allineate = True
>>> qwarp3.inputs.allineate_opts = '-cose lpa -verb'
>>> qwarp3.cmdline
"3dQwarp -allineate -allineate_opts '-cose lpa -verb' -base mni.nii -source_
↳structural.nii -prefix ppp_structural"
>>> res3 = qwarp3.run() # doctest: +SKIP

```

Inputs:

[Mandatory]

in_file: (a pathlike object or string representing an existing file)
 Source image (opposite phase encoding direction than base image).
 argument: ``-source %s``

base_file: (a pathlike object or string representing an existing file)
 Base image (opposite phase encoding direction than source image).
 argument: ``-base %s``

[Optional]

out_file: (a pathlike object or string representing a file)
 Sets the prefix/suffix for the output datasets.

- * The source dataset is warped to match the base and gets prefix 'ppp'. (Except if '-plusminus' is used)
- * The final interpolation to this output dataset is done using the 'wsinc5' method. See the output of 3dAllineate -HELP (in the "Modifying '-final wsinc5'" section) for the lengthy technical details.
- * The 3D warp used is saved in a dataset with prefix 'ppp_WARP' -- this dataset can be used with 3dNwarpApply and 3dNwarpCat, for example.
- * To be clear, this is the warp from source dataset coordinates to base dataset coordinates, where the values at each base grid point are the xyz displacements needed to move that grid point's xyz values to the corresponding xyz values in the source dataset:

$$\text{base}(x,y,z) + \text{WARP}(x,y,z) \text{ matches source}(x,y,z)$$
 Another way to think of this warp is that it 'pulls' values back from source space to base space.
- * 3dNwarpApply would use 'ppp_WARP' to transform datasets aligned with the source dataset to be aligned with the

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base dataset.
** If you do NOT want this warp saved, use the option '-nowarp'.
-->> (However, this warp is usually the most valuable possible
output!)
* If you want to calculate and save the inverse 3D warp,
use the option '-iwarp'. This inverse warp will then be
saved in a dataset with prefix 'ppp_WARPINV'.
* This inverse warp could be used to transform data from base
space to source space, if you need to do such an operation.
* You can easily compute the inverse later, say by a command like
  3dNwarpCat -prefix Z_WARPINV 'INV(Z_WARP+tlrc)'
or the inverse can be computed as needed in 3dNwarpApply, like
  3dNwarpApply -nwarp 'INV(Z_WARP+tlrc)' -source Dataset.nii ...
argument: ``-prefix %s``

resample: (a boolean)
This option simply resamples the source dataset to match thebase
dataset grid. You can use this if the two datasetsoverlap well (as
seen in the AFNI GUI), but are not on thesame 3D grid.* If they
don't overlap well, allineate them first* The reampling here is done
with the'wsinc5' method, which has very little blurring artifact.*
If the base and source datasets ARE on the same 3D grid,then the
-resample option will be ignored.* You CAN use -resample with these
3dQwarp options:-plusminus -inilev -iniwarp -duplo
argument: ``-resample``

allineate: (a boolean)
This option will make 3dQwarp run 3dAllineate first, to align the
source dataset to the base with an affine transformation. It will
then use that alignment as a starting point for the nonlinear
warping.
argument: ``-allineate``

allineate_opts: (a unicode string)
add extra options to the 3dAllineate command to be run by 3dQwarp.
argument: ``-allineate_opts %s``
requires: allineate

nowarp: (a boolean)
Do not save the _WARP file.
argument: ``-nowarp``

iwarp: (a boolean)
Do compute and save the _WARPINV file.
argument: ``-iwarp``
mutually_exclusive: plusminus

pear: (a boolean)
Use strict Pearson correlation for matching.* Not usually
recommended, since the 'clipped Pearson' methodused by default will
reduce the impact of outlier values.
argument: ``-pear``

noneg: (a boolean)
Replace negative values in either input volume with 0.* If there ARE
negative input values, and you do NOT use -noneg,then strict Pearson
correlation will be used, since the 'clipped'method only is
implemented for non-negative volumes.* '-noneg' is not the default,
since there might be situations whereyou want to align datasets with
positive and negative values mixed.* But, in many cases, the
negative values in a dataset are just theresult of interpolation
artifacts (or other peculiarities), and sothey should be ignored.
That is what '-noneg' is for.
argument: ``-noneg``

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nopenalty: (a boolean)
    Replace negative values in either input volume with 0.* If there ARE
    negative input values, and you do NOT use -noneg, then strict Pearson
    correlation will be used, since the 'clipped' method only is
    implemented for non-negative volumes.* '-noneg' is not the default,
    since there might be situations where you want to align datasets with
    positive and negative values mixed.* But, in many cases, the
    negative values in a dataset are just the result of interpolation
    artifacts (or other peculiarities), and so they should be ignored.
    That is what '-noneg' is for.
    argument: ``-nopenalty``

penfac: (a float)
    Use this value to weight the penalty. The default value is 1. Larger
    values mean the penalty counts more, reducing grid
    distortions, insha'Allah; '-nopenalty' is the same as '-penfac 0'.
    --> [23 Sep 2013] -- Zhark increased the default value of the
    penalty by a factor of 5, and also made it get progressively larger
    with each level of refinement. Thus, warping results will vary from
    earlier instances of 3dQwarp.* The progressive increase in the
    penalty at higher levels means that the 'cost function' can actually
    look like the alignment is getting worse when the levels change.*
    IF you wish to turn off this progression, for whatever reason (e.g.,
    to keep compatibility with older results), use the option
    '-penold'. To be completely compatible with the older 3dQwarp, you'll
    also have to use '-penfac 0.2'.
    argument: ``-penfac %f``

noweight: (a boolean)
    If you want a binary weight (the old default), use this option. That
    is, each voxel in the base volume automask will be weighted the same
    in the computation of the cost functional.
    argument: ``-noweight``

weight: (a pathlike object or string representing an existing file)
    Instead of computing the weight from the base dataset, directly input
    the weight volume from dataset 'www'.* Useful if you know what over
    parts of the base image you want to emphasize or de-emphasize the
    matching functional.
    argument: ``-weight %s``

wball: (a list of from 5 to 5 items which are an integer (int or
    long))
    -wball x y z r f Enhance automatic weight from '-useweight' by a
    factor of 1+f*Gaussian(FWHM=r) centered in the base image at DICOM
    coordinates (x,y,z) and with radius 'r'. The goal of this option is
    to try and make the alignment better in a specific part of the
    brain.* Example: -wball 0 14 6 30 40 to emphasize the thalamic area
    (in MNI/Talairach space).* The 'r' parameter must be positive!* The
    'f' parameter must be between 1 and 100 (inclusive).* '-wball' does
    nothing if you input your own weight with the '-weight' option.*
    '-wball' does change the binary weight created by the '-noweight'
    option.* You can only use '-wball' once in a run of 3dQwarp.*** The
    effect of '-wball' is not dramatic. The example above makes the
    average brain image across a collection of subjects a little sharper
    in the thalamic area, which might have some small value. If you care
    enough about alignment to use '-wball', then you should examine
    the results from 3dQwarp for each subject, to see if the alignments
    are good enough for your purposes.
    argument: ``-wball %s``

wmask: (a tuple of the form: (a pathlike object or string

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    representing an existing file, a float))
    -wmask ws fSimilar to '-wball', but here, you provide a dataset
    'ws' that indicates where to increase the weight.* The 'ws' dataset
    must be on the same 3D grid as the base dataset.* 'ws' is treated as
    a mask -- it only matters where it is nonzero -- otherwise, the
    values inside are not used.* After 'ws' comes the factor 'f' by
    which to increase the automatically computed weight. Where 'ws' is
    nonzero, the weighting will be multiplied by (1+f).* As with
    '-wball', the factor 'f' should be between 1 and 100.* You cannot
    use '-wball' and '-wmask' together!
    argument: ``-wpass %s %f``
out_weight_file: (a pathlike object or string representing a file)
    Write the weight volume to disk as a dataset
    argument: ``-wt prefix %s``
blur: (a list of from 1 to 2 items which are a float)
    Gaussian blur the input images by 'bb' (FWHM) voxels before doing the
    alignment (the output dataset will not be blurred). The default is
    2.345 (for no good reason).* Optionally, you can provide 2 values
    for 'bb', and then the first one is applied to the base volume, the
    second to the source volume.--> e.g., '-blur 0 3' to skip blurring
    the base image (if the base is a blurry template, for example).* A
    negative blur radius means to use 3D median filtering, rather than
    Gaussian blurring. This type of filtering will better preserve edges,
    which can be important in alignment.* If the base is a template
    volume that is already blurry, you probably don't want to blur it
    again, but blurring the source volume a little is probably a good
    idea, to help the program avoid trying to match tiny features.* Note
    that -duplo will blur the volumes some extra amount for the initial
    small-scale warping, to make that phase of the program converge more
    rapidly.
    argument: ``-blur %s``
pblur: (a list of from 1 to 2 items which are a float)
    Use progressive blurring; that is, for larger patch sizes, the amount
    of blurring is larger. The general idea is to avoid trying to match
    finer details when the patch size and incremental warps are coarse.
    When '-blur' is used as well, it sets a minimum amount of blurring
    that will be used. [06 Aug 2014 -- '-pblur' may become the default
    someday].* You can optionally give the fraction of the patch size
    that is used for the progressive blur by providing a value between 0
    and 0.25 after '-pblur'. If you provide TWO values, then the first
    fraction is used for progressively blurring the base image and the
    second for the source image. The default parameters when just
    '-pblur' is given is the same as giving the options as '-pblur 0.09
    0.09'.* '-pblur' is useful when trying to match 2 volumes with
    high amounts of detail; e.g., warping one subject's brain image
    to match another's, or trying to warp to match a detailed template.*
    Note that using negative values with '-blur' means that
    the progressive blurring will be done with median filters, rather than
    Gaussian linear blurring.-->*** The combination of the -allineate
    and -pblur options will make the results of using 3dQwarp to align to
    a template somewhat less sensitive to initial head position and
    scaling.
    argument: ``-pblur %s``
emask: (a pathlike object or string representing an existing file)
    Here, 'ee' is a dataset to specify a mask of voxels to EXCLUDE from
    the analysis -- all voxels in 'ee' that are NONZERO will not be used
    in the alignment.* The base image always automasked -- the emask

```

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    isextra, to indicate voxels you definitely DON'T want included in the
    matching process, even if they are inside the brain.
    argument: ``-emask %s``
noXdis: (a boolean)
    Warp will not displace in x direction
    argument: ``-noXdis``
noYdis: (a boolean)
    Warp will not displace in y direction
    argument: ``-noYdis``
noZdis: (a boolean)
    Warp will not displace in z direction
    argument: ``-noZdis``
iniwarp: (a list of items which are a pathlike object or string
    representing an existing file)
    A dataset with an initial nonlinear warp to use.* If this option is
    not used, the initial warp is the identity.* You can specify a
    catenation of warps (in quotes) here, as in program 3dNwarpApply.* As
    a special case, if you just input an affine matrix in a .1D file,
    that will work also -- it is treated as giving the initial warp via
    the string "IDENT(base_dataset) matrix_file.aff12.1D".* You CANNOT
    use this option with -duplo !!* -iniwarp is usually used with
    -inilev to re-start 3dQwarp from a previous stopping point.
    argument: ``-iniwarp %s``
    mutually_exclusive: duplo
inilev: (an integer (int or long))
    The initial refinement 'level' at which to start.* Usually used with
    -iniwarp; CANNOT be used with -duplo.* The combination of -inilev
    and -iniwarp lets you take the results of a previous 3dQwarp run and
    refine them further: Note that the source dataset in the second run
    is the SAME as in the first run. If you don't see why this is
    necessary, then you probably need to seek help from an AFNI guru.
    argument: ``-inilev %d``
    mutually_exclusive: duplo
minpatch: (an integer (int or long))
    * The value of mm should be an odd integer.* The default value of mm
    is 25.* For more accurate results than mm=25, try 19 or 13.* The
    smallest allowed patch size is 5.* You may want to stop at a larger
    patch size (say 7 or 9) and use the -Qfinal option to run that final
    level with quintic warps, which might run faster and provide the same
    degree of warp detail.* Trying to make two different brain volumes
    match in fine detail is usually a waste of time, especially in
    humans. There is too much variability in anatomy to match gyri to
    gyri accurately. For this reason, the default minimum patch size is
    25 voxels. Using a smaller '-minpatch' might try to force the warp
    to match features that do not match, and the result can be
    useless image distortions -- another reason to LOOK AT THE RESULTS.
    argument: ``-minpatch %d``
maxlev: (an integer (int or long))
    The initial refinement 'level' at which to start.* Usually used with
    -iniwarp; CANNOT be used with -duplo.* The combination of -inilev
    and -iniwarp lets you take the results of a previous 3dQwarp run and
    refine them further: Note that the source dataset in the second run
    is the SAME as in the first run. If you don't see why this is
    necessary, then you probably need to seek help from an AFNI guru.
    argument: ``-maxlev %d``, position: -1
    mutually_exclusive: duplo
gridlist: (a pathlike object or string representing an existing file)

```

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This option provides an alternate way to specify the patchgrid sizes used in the warp optimization process. 'gl' is a 1D file with a list of patches to use -- in most cases, you will want to use it in the following form: `-gridlist '1D: 0 151 101 75 51'`* Here, a 0 patch size means the global domain. Patch sizes otherwise should be odd integers ≥ 5 .* If you use the '0' patch size again after the first position, you will actually get an iteration at the size of the default patch level 1, where the patch sizes are 75% of the volume dimension. There is no way to force the program to literally repeat the sui generis step of `lev=0`.* You cannot use `-gridlist` with `-duplo` or `-plusminus`!

argument: `--gridlist %s``
mutually_exclusive: `duplo, plusminus`

allsave: (a boolean)
This option lets you save the output warps from each level of the refinement process. Mostly used for experimenting.* Cannot be used with `-nopadWARP`, `-duplo`, or `-plusminus`.* Will only save all the outputs if the program terminates normally -- if it crashes, or freezes, then all these warps are lost.
argument: `--allsave``
mutually_exclusive: `nopadWARP, duplo, plusminus`

duplo: (a boolean)
Start off with 1/2 scale versions of the volumes, for getting a speedy coarse first alignment.* Then scales back up to register the full volumes. The goal is greater speed, and it seems to help this positively piggish program to be more expeditious.* However, accuracy is somewhat lower with `'-duplo'`, for reasons that currently elude Zhark; for this reason, the Emperor does not usually use `'-duplo'`.
argument: `--duplo``
mutually_exclusive: `gridlist, maxlev, inilev, iniwarp, plusminus, allsave`

workhard: (a boolean)
Iterate more times, which can help when the volumes are hard to align at all, or when you hope to get a more precise alignment.* Slows the program down (possibly a lot), of course.* When you combine `'-workhard'` with `'-duplo'`, only the full size volumes get the extra iterations.* For finer control over which refinement levels work hard, you can use this option in the form (for example) `-workhard:4:7` which implies the extra iterations will be done at levels 4, 5, 6, and 7, but not otherwise.* You can also use `'-superhard'` to iterate even more, but this extra option will REALLY slow things down.-->* Under most circumstances, you should not need to use either `-workhard` or `-superhard`.-->* The fastest way to register to a template image is via the `-duplo` option, and without the `-workhard` or `-superhard` options.-->* If you use this option in the form `'-Workhard'` (first letter in upper case), then the second iteration at each level is done with quintic polynomial warps.
argument: `--workhard``
mutually_exclusive: `boxopt, ballopt`

Qfinal: (a boolean)
At the finest patch size (the final level), use Hermite quintic polynomials for the warp instead of cubic polynomials.* In a 3D 'patch', there are $2 \times 2 \times 2 = 8$ cubic polynomial basis function parameters over which to optimize (2 polynomials dependent on each of the x, y, z directions, and 3 different directions of displacement).* There are $3 \times 3 \times 3 = 27$ quintic polynomial parameters per patch.* With

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-Qfinal, the final level will have more detail in the allowed warps,
at the cost of yet more CPU time.* However, no patch below 7x7x7 in
size will be done with quintic polynomials.* This option is also not
usually needed, and is experimental.
argument: ``-Qfinal``

Qonly: (a boolean)
Use Hermite quintic polynomials at all levels.* Very slow (about 4
times longer). Also experimental.* Will produce a (discrete
representation of a) C2 warp.
argument: ``-Qonly``

plusminus: (a boolean)
Normally, the warp displacements  $\text{dis}(x)$  are defined to match  $\text{base}(x)$ 
to  $\text{source}(x + \text{dis}(x))$ . With this option, the match is between
 $\text{base}(x - \text{dis}(x))$  and  $\text{source}(x + \text{dis}(x))$  -- the two images 'meet in the
middle'.* One goal is to mimic the warping done to MRI EPI data
by field inhomogeneities, when registering between a 'blip up' and a
'blip down' down volume, which will have opposed distortions.*
Define  $\text{Wp}(x) = x + \text{dis}(x)$  and  $\text{Wm}(x) = x - \text{dis}(x)$ . Then since  $\text{base}(\text{Wm}(x))$ 
matches  $\text{source}(\text{Wp}(x))$ , by substituting  $\text{INV}(\text{Wm}(x))$  wherever we see  $x$ ,
we have  $\text{base}(x)$  matches  $\text{source}(\text{Wp}(\text{INV}(\text{Wm}(x))))$ ; that is, the warp
 $V(x)$  that one would get from the 'usual' way of running 3dQwarp is
 $V(x) = \text{Wp}(\text{INV}(\text{Wm}(x)))$ .* Conversely, we can calculate  $\text{Wp}(x)$  in terms
of  $V(x)$  as follows: If  $V(x) = x + \text{dv}(x)$ , define  $\text{Vh}(x) = x +$ 
 $\text{dv}(x)/2$ ; then  $\text{Wp}(x) = V(\text{INV}(\text{Vh}(x)))$ .* With the above formulas, it is
possible to compute  $\text{Wp}(x)$  from  $V(x)$  and vice-versa, using program
3dNwarpCalc. The requisite commands are left as an exercise for the
aspiring AFNI Jedi Master.* You can use the semi-secret '-pmBASE'
option to get the  $V(x)$  warp and the source dataset warped to base
space, in addition to the  $\text{Wp}(x)$  '_PLUS' and  $\text{Wm}(x)$  '_MINUS'
warps.-->* Alas: -plusminus does not work with -duplo or -allineate
:-( * However, you can use -iniwarp with -plusminus :)-->* The
outputs have _PLUS (from the source dataset) and _MINUS (from the
base dataset) in their filenames, in addition to the prefix. The
-iwarp option, if present, will be ignored.
argument: ``-plusminus``

mutually_exclusive: duplo, allsave, iwarp

nopad: (a boolean)
Do NOT use zero-padding on the 3D base and source images. [Default ==
zero-pad, if needed]* The underlying model for deformations goes to
zero at the edge of the volume being warped. However, if there
is significant data near an edge of the volume, then it won't get
displaced much, and so the results might not be good.* Zero padding
is designed as a way to work around this potential problem. You
should NOT need the '-nopad' option for any reason that Zhark can
think of, but it is here to be symmetrical with 3dAllineate.* Note
that the output (warped from source) dataset will be on the base
dataset grid whether or not zero-padding is allowed. However, unless
you use the following option, allowing zero-padding (i.e., the
default operation) will make the output WARP dataset(s) be on a
larger grid (also see '-expad' below).
argument: ``-nopad``

nopadWARP: (a boolean)
If for some reason you require the warp volume to match the base
volume, then use this option to have the output WARP dataset(s)
truncated.
argument: ``-nopadWARP``

mutually_exclusive: allsave, expad

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expad: (an integer (int or long))
    This option instructs the program to pad the warp by an extra 'EE'
    voxels (and then 3dQwarp starts optimizing it). * This option is
    seldom needed, but can be useful if you might later catenate the
    nonlinear warp -- via 3dNwarpCat -- with an affine transformation
    that contains a large shift. Under that circumstance, the nonlinear
    warp might be shifted partially outside its original grid, so
    expanding that grid can avoid this problem. * Note that this option
    performs turns off '-nopadWARP'.
    argument: ``-expad %d``
    mutually_exclusive: nopadWARP

ballopt: (a boolean)
    Normally, the incremental warp parameters are optimized inside a
    rectangular 'box' (24 dimensional for cubic patches, 81 for quintic
    patches), whose limits define the amount of distortion allowed at
    each step. Using '-ballopt' switches these limits to be applied to a
    'ball' (interior of a hypersphere), which can allow for larger
    incremental displacements. Use this option if you think things need
    to be able to move farther.
    argument: ``-ballopt``
    mutually_exclusive: workhard, boxopt

boxopt: (a boolean)
    Use the 'box' optimization limits instead of the 'ball' [this is the
    default at present]. * Note that if '-workhard' is used, then ball
    and box optimization are alternated in the different iterations at
    each level, so these two options have no effect in that case.
    argument: ``-boxopt``
    mutually_exclusive: workhard, ballopt

verb: (a boolean)
    more detailed description of the process
    argument: ``-verb``
    mutually_exclusive: quiet

quiet: (a boolean)
    Cut out most of the fun fun fun progress messages :-(
    argument: ``-quiet``
    mutually_exclusive: verb

overwrite: (a boolean)
    Overwrite outputs
    argument: ``-overwrite``

lpc: (a boolean)
    Local Pearson minimization (i.e., EPI-T1 registration) This option
    has not been extensively tested. If you use '-lpc', then '-maxlev 0' is
    automatically set. If you want to go to more refined levels, you can
    set '-maxlev'. This should be set up to have lpc as the second to last
    argument and maxlev as the second to last argument, as needed by
    AFNI. Using maxlev > 1 is not recommended for EPI-T1 alignment.
    argument: ``-lpc``, position: -2
    mutually_exclusive: nmi, mi, hel, lpa, pear

lpa: (a boolean)
    Local Pearson maximization This option has not been extensively tested
    argument: ``-lpa``
    mutually_exclusive: nmi, mi, lpc, hel, pear

hel: (a boolean)
    Hellinger distance: a matching function for the adventurous This
    option has NOT been extensively tested for usefulness and should be
    considered experimental at this infundibulum.
    argument: ``-hel``

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    mutually_exclusive: nmi, mi, lpc, lpa, pear
mi: (a boolean)
    Mutual Information: a matching function for the adventurousThis
    option has NOT be extensively tested for usefullnessand should be
    considered experimental at this infundibulum.
    argument: ``-mi``
    mutually_exclusive: mi, hel, lpc, lpa, pear
nmi: (a boolean)
    Normalized Mutual Information: a matching function for the
    adventurousThis option has NOT be extensively tested for
    usefullnessand should be considered experimental at this
    infundibulum.
    argument: ``-nmi``
    mutually_exclusive: nmi, hel, lpc, lpa, pear
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

warped_source: (a pathlike object or string representing a file)
    Warped source file. If plusminus is used, this is the
    undistortedsource file.
warped_base: (a pathlike object or string representing a file)
    Undistorted base file.
source_warp: (a pathlike object or string representing a file)
    Displacement in mm for the source image.If plusminus is used this is
    the field suceptibility correctionwarp (in 'mm') for source image.
base_warp: (a pathlike object or string representing a file)
    Displacement in mm for the base image.If plus minus is used, this is
    the field suceptibility correctionwarp (in 'mm') for base image.
    This is only output if plusminusor iwarp options are passed
weights: (a pathlike object or string representing a file)
    Auto-computed weight volume.

```

References:

None None

51.3.23 QwarpPlusMinus[Link to code](#)

Wraps the executable command 3dQwarp.

A version of 3dQwarp for performing field susceptibility correction using two images with opposing phase encoding directions.

For complete details, see the [3dQwarp Documentation](#).

Examples

```
>>> from nipyne.interfaces import afni
>>> qwarp = afni.QwarpPlusMinus()
>>> qwarp.inputs.in_file = 'sub-01_dir-LR_epi.nii.gz'
>>> qwarp.inputs.nopadWARP = True
>>> qwarp.inputs.base_file = 'sub-01_dir-RL_epi.nii.gz'
>>> qwarp.cmdline
'3dQwarp -prefix Qwarp.nii.gz -plusminus -base sub-01_dir-RL_epi.nii.gz -
↳source sub-01_dir-LR_epi.nii.gz -nopadWARP'
>>> res = warp.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        Source image (opposite phase encoding direction than base image).
        argument: ``-source %s``
base_file: (a pathlike object or string representing an existing
            file)
        Base image (opposite phase encoding direction than source image).
        argument: ``-base %s``

[Optional]
source_file: (a pathlike object or string representing an existing
            file)
        Source image (opposite phase encoding direction than base image)
        argument: ``-source %s``
out_file: (a pathlike object or string representing a file, nipyne
          default value: Qwarp.nii.gz)
        Output file
        argument: ``-prefix %s``, position: 0
plusminus: (a boolean, nipyne default value: True)
        Normally, the warp displacements dis(x) are defined to match base(x)
        to source(x+dis(x)). With this option, the match is between
        base(x-dis(x)) and source(x+dis(x)) -- the two images 'meet in the
        middle'. For more info, view Qwarp` interface
        argument: ``-plusminus``, position: 1
        mutually_exclusive: duplo, allsave, iwarp
resample: (a boolean)
        This option simply resamples the source dataset to match the base
        dataset grid. You can use this if the two datasets overlap well (as
        seen in the AFNI GUI), but are not on the same 3D grid.* If they
        don't overlap well, allineate them first* The resampling here is done
        with the 'wsinc5' method, which has very little blurring artifact.*
        If the base and source datasets ARE on the same 3D grid, then the
        -resample option will be ignored.* You CAN use -resample with these
        3dQwarp options: -plusminus -inilev -iniwarp -duplo
        argument: ``-resample``
allineate: (a boolean)
        This option will make 3dQwarp run 3dAllineate first, to align the
        source dataset to the base with an affine transformation. It will
        then use that alignment as a starting point for the nonlinear
        warping.
        argument: ``-allineate``
allineate_opts: (a unicode string)
        add extra options to the 3dAllineate command to be run by 3dQwarp.
        argument: ``-allineate_opts %s``
```

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```

requires: allineate
nowarp: (a boolean)
    Do not save the _WARP file.
    argument: ``-nowarp``
iwarp: (a boolean)
    Do compute and save the _WARPINV file.
    argument: ``-iwarp``
    mutually_exclusive: plusminus
pear: (a boolean)
    Use strict Pearson correlation for matching.* Not usually
    recommended, since the 'clipped Pearson' method used by default will
    reduce the impact of outlier values.
    argument: ``-pear``
noneg: (a boolean)
    Replace negative values in either input volume with 0.* If there ARE
    negative input values, and you do NOT use -noneg, then strict Pearson
    correlation will be used, since the 'clipped' method only is
    implemented for non-negative volumes.* '-noneg' is not the default,
    since there might be situations where you want to align datasets with
    positive and negative values mixed.* But, in many cases, the
    negative values in a dataset are just the result of interpolation
    artifacts (or other peculiarities), and so they should be ignored.
    That is what '-noneg' is for.
    argument: ``-noneg``
nopenalty: (a boolean)
    Replace negative values in either input volume with 0.* If there ARE
    negative input values, and you do NOT use -noneg, then strict Pearson
    correlation will be used, since the 'clipped' method only is
    implemented for non-negative volumes.* '-noneg' is not the default,
    since there might be situations where you want to align datasets with
    positive and negative values mixed.* But, in many cases, the
    negative values in a dataset are just the result of interpolation
    artifacts (or other peculiarities), and so they should be ignored.
    That is what '-noneg' is for.
    argument: ``-nopenalty``
penfac: (a float)
    Use this value to weight the penalty. The default value is 1. Larger
    values mean the penalty counts more, reducing grid
    distortions, insha'Allah; '-nopenalty' is the same as '-penfac 0'.
    -->* [23 Sep 2013] -- Zhark increased the default value of the
    penalty by a factor of 5, and also made it get progressively larger
    with each level of refinement. Thus, warping results will vary from
    earlier instances of 3dQwarp. * The progressive increase in the
    penalty at higher levels means that the 'cost function' can actually
    look like the alignment is getting worse when the levels change. *
    IF you wish to turn off this progression, for whatever reason (e.g.,
    to keep compatibility with older results), use the option
    '-penold'. To be completely compatible with the older 3dQwarp, you'll
    also have to use '-penfac 0.2'.
    argument: ``-penfac %f``
noweight: (a boolean)
    If you want a binary weight (the old default), use this option. That
    is, each voxel in the base volume automask will be weighted the same
    in the computation of the cost functional.
    argument: ``-noweight``
weight: (a pathlike object or string representing an existing file)
    Instead of computing the weight from the base dataset, directly input

```

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```

the weight volume from dataset 'www'.* Useful if you know what over
parts of the base image you want to emphasize or de-emphasize the
matching functional.
argument: ``-weight %s``

wball: (a list of from 5 to 5 items which are an integer (int or
long))
-wball x y z r fEnhance automatic weight from '-useweight' by a
factor of 1+f*Gaussian(FWHM=r) centered in the base image at DICOM
coordinates (x,y,z) and with radius 'r'. The goal of this option is
to try and make the alignment better in a specific part of the
brain.* Example: -wball 0 14 6 30 40 to emphasize the thalamic area
(in MNI/Talairach space).* The 'r' parameter must be positive!* The
'f' parameter must be between 1 and 100 (inclusive).* '-wball' does
nothing if you input your own weight with the '-weight' option.*
'-wball' does change the binary weight created by the '-noweight'
option.* You can only use '-wball' once in a run of 3dQwarp.*** The
effect of '-wball' is not dramatic. The example above makes the
average brain image across a collection of subjects a little sharper
in the thalamic area, which might have some small value. If you care
enough about alignment to use '-wball', then you should examine
the results from 3dQwarp for each subject, to see if the alignments
are good enough for your purposes.
argument: ``-wball %s``

wmask: (a tuple of the form: (a pathlike object or string
representing an existing file, a float))
-wmask ws fSimilar to '-wball', but here, you provide a dataset
'ws' that indicates where to increase the weight.* The 'ws' dataset
must be on the same 3D grid as the base dataset.* 'ws' is treated as
a mask -- it only matters where it is nonzero -- otherwise, the
values inside are not used.* After 'ws' comes the factor 'f' by
which to increase the automatically computed weight. Where 'ws' is
nonzero, the weighting will be multiplied by (1+f).* As with
'-wball', the factor 'f' should be between 1 and 100.* You cannot
use '-wball' and '-wmask' together!
argument: ``-wpass %s %f``

out_weight_file: (a pathlike object or string representing a file)
Write the weight volume to disk as a dataset
argument: ``-wtprefix %s``

blur: (a list of from 1 to 2 items which are a float)
Gaussian blur the input images by 'bb' (FWHM) voxels before doing the
alignment (the output dataset will not be blurred). The default is
2.345 (for no good reason).* Optionally, you can provide 2 values
for 'bb', and then the first one is applied to the base volume, the
second to the source volume.-->>* e.g., '-blur 0 3' to skip blurring
the base image (if the base is a blurry template, for example).* A
negative blur radius means to use 3D median filtering, rather than
Gaussian blurring. This type of filtering will better preserve edges,
which can be important in alignment.* If the base is a template
volume that is already blurry, you probably don't want to blur it
again, but blurring the source volume a little is probably a good
idea, to help the program avoid trying to match tiny features.* Note
that -duplo will blur the volumes some extra amount for the initial
small-scale warping, to make that phase of the program converge more
rapidly.
argument: ``-blur %s``

pblur: (a list of from 1 to 2 items which are a float)
Use progressive blurring; that is, for larger patch sizes, the amount

```

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of blurring is larger. The general idea is to avoid trying to match finer details when the patch size and incremental warps are coarse. When '-blur' is used as well, it sets a minimum amount of blurring that will be used. [06 Aug 2014 -- '-pblur' may become the default someday].* You can optionally give the fraction of the patch size that is used for the progressive blur by providing a value between 0 and 0.25 after '-pblur'. If you provide TWO values, the first fraction is used for progressively blurring the base image and the second for the source image. The default parameters when just '-pblur' is given is the same as giving the options as '-pblur 0.09 0.09'.* '-pblur' is useful when trying to match 2 volumes with high amounts of detail; e.g, warping one subject's brain image to match another's, or trying to warp to match a detailed template.* Note that using negative values with '-blur' means that the progressive blurring will be done with median filters, rather than Gaussian linear blurring.-->>*** The combination of the -allineate and -pblur options will make the results of using 3dQwarp to align to a template somewhat less sensitive to initial head position and scaling.

argument: ``-pblur %s``

emask: (a pathlike object or string representing an existing file)
Here, 'ee' is a dataset to specify a mask of voxels to EXCLUDE from the analysis -- all voxels in 'ee' that are NONZERO will not be used in the alignment.* The base image always automasked -- the emask is extra, to indicate voxels you definitely DON'T want included in the matching process, even if they are inside the brain.

argument: ``-emask %s``

noXdis: (a boolean)
Warp will not displace in x direction
argument: ``-noXdis``

noYdis: (a boolean)
Warp will not displace in y direction
argument: ``-noYdis``

noZdis: (a boolean)
Warp will not displace in z direction
argument: ``-noZdis``

iniwarp: (a list of items which are a pathlike object or string representing an existing file)
A dataset with an initial nonlinear warp to use.* If this option is not used, the initial warp is the identity.* You can specify a catenation of warps (in quotes) here, as in program 3dNwarpApply.* As a special case, if you just input an affine matrix in a .1D file, that will work also -- it is treated as giving the initial warp via the string "IDENT(base_dataset) matrix_file.aff12.1D".* You CANNOT use this option with -duplo !!* -iniwarp is usually used with -inilev to re-start 3dQwarp from a previous stopping point.

argument: ``-iniwarp %s``
mutually_exclusive: duplo

inilev: (an integer (int or long))
The initial refinement 'level' at which to start.* Usually used with -iniwarp; CANNOT be used with -duplo.* The combination of -inilev and -iniwarp lets you take the results of a previous 3dQwarp run and refine them further: Note that the source dataset in the second run is the SAME as in the first run. If you don't see why this is necessary, then you probably need to seek help from an AFNI guru.

argument: ``-inilev %d``
mutually_exclusive: duplo

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minpatch: (an integer (int or long))
    * The value of mm should be an odd integer.* The default value of mm
    is 25.* For more accurate results than mm=25, try 19 or 13.* The
    smallest allowed patch size is 5.* You may want stop at a larger
    patch size (say 7 or 9) and use the -Qfinal option to run that final
    level with quintic warps, which might run faster and provide the same
    degree of warp detail.* Trying to make two different brain volumes
    match in fine detail is usually a waste of time, especially in
    humans. There is too much variability in anatomy to match gyri to
    gyri accurately. For this reason, the default minimum patch size is
    25 voxels. Using a smaller '-minpatch' might try to force the warp
    to match features that do not match, and the result can be
    useless image distortions -- another reason to LOOK AT THE RESULTS.
    argument: ``-minpatch %d``

maxlev: (an integer (int or long))
    The initial refinement 'level' at which to start.* Usually used with
    -iniwarp; CANNOT be used with -duplo.* The combination of -inilev
    and -iniwarp lets you take the results of a previous 3dQwarp run and
    refine them further: Note that the source dataset in the second run
    is the SAME as in the first run. If you don't see why this is
    necessary, then you probably need to seek help from an AFNI guru.
    argument: ``-maxlev %d``, position: -1
    mutually_exclusive: duplo

gridlist: (a pathlike object or string representing an existing file)
    This option provides an alternate way to specify the patchgrid sizes
    used in the warp optimization process. 'gl' is a 1D file with a list
    of patches to use -- in most cases, you will want to use it in the
    following form: -gridlist '1D: 0 151 101 75 51'* Here, a 0 patch size
    means the global domain. Patch sizes otherwise should be odd integers
    >= 5.* If you use the '0' patch size again after the first
    position, you will actually get an iteration at the size of
    the default patch level 1, where the patch sizes are 75% of the volume
    dimension. There is no way to force the program to literally repeat
    the same step of lev=0.* You cannot use -gridlist with -duplo
    or -plusminus!
    argument: ``-gridlist %s``
    mutually_exclusive: duplo, plusminus

allsave: (a boolean)
    This option lets you save the output warps from each level of the
    refinement process. Mostly used for experimenting.* Cannot be used
    with -nopadWARP, -duplo, or -plusminus.* Will only save all the
    outputs if the program terminates normally -- if it crashes, or
    freezes, then all these warps are lost.
    argument: ``-allsave``
    mutually_exclusive: nopadWARP, duplo, plusminus

duplo: (a boolean)
    Start off with 1/2 scale versions of the volumes, for getting a
    speedy coarse first alignment.* Then scale back up to register the
    full volumes. The goal is greater speed, and it seems to help
    this positively piggy program to be more expeditious.* However,
    accuracy is somewhat lower with '-duplo', for reasons that currently
    elude Zhark; for this reason, the Emperor does not usually use
    '-duplo'.
    argument: ``-duplo``
    mutually_exclusive: gridlist, maxlev, inilev, iniwarp, plusminus,
    allsave

workhard: (a boolean)

```

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Iterate more times, which can help when the volumes are hard to align
at all, or when you hope to get a more precise alignment.* Slows the
program down (possibly a lot), of course.* When you combine
'-workhard' with '-duplo', only the full size volumes get the extra
iterations.* For finer control over which refinement levels work
hard, you can use this option in the form (for example)
-workhard:4:7 which implies the extra iterations will be done at
levels 4, 5, 6, and 7, but not otherwise.* You can also use
'-superhard' to iterate even more, but this extra option will REALLY
slow things down.-->*> Under most circumstances, you should not need
to use either -workhard or -superhard.-->*> The fastest way to
register to a template image is via the -duplo option, and without
the -workhard or -superhard options.-->*> If you use this option in
the form '-Workhard' (first letter in upper case), then the second
iteration at each level is done with quintic polynomial warps.
argument: ``-workhard``
mutually_exclusive: boxopt, ballopt

Qfinal: (a boolean)
At the finest patch size (the final level), use Hermite quintic
polynomials for the warp instead of cubic polynomials.* In a 3D
'patch', there are 2x2x2x3=24 cubic polynomial basis function
parameters over which to optimize (2 polynomials dependent on each of
the x,y,z directions, and 3 different directions of displacement).*
There are 3x3x3x3=81 quintic polynomial parameters per patch.* With
-Qfinal, the final level will have more detail in the allowed warps,
at the cost of yet more CPU time.* However, no patch below 7x7x7 in
size will be done with quintic polynomials.* This option is also not
usually needed, and is experimental.
argument: ``-Qfinal``

Qonly: (a boolean)
Use Hermite quintic polynomials at all levels.* Very slow (about 4
times longer). Also experimental.* Will produce a (discrete
representation of a) C2 warp.
argument: ``-Qonly``

nopad: (a boolean)
Do NOT use zero-padding on the 3D base and source images.[Default ==
zero-pad, if needed]* The underlying model for deformations goes to
zero at the edge of the volume being warped. However, if there
is significant data near an edge of the volume, then it won't get
displaced much, and so the results might not be good.* Zero padding
is designed as a way to work around this potential problem. You
should NOT need the '-nopad' option for any reason that Zhark can
think of, but it is here to be symmetrical with 3dAllineate.* Note
that the output (warped from source) dataset will be on the base
dataset grid whether or not zero-padding is allowed. However, unless
you use the following option, allowing zero-padding (i.e., the
default operation) will make the output WARP dataset(s) be on a
larger grid (also see '-expad' below).
argument: ``-nopad``

nopadWARP: (a boolean)
If for some reason you require the warp volume to match the base
volume, then use this option to have the output WARP dataset(s)
truncated.
argument: ``-nopadWARP``
mutually_exclusive: allsave, expad

expad: (an integer (int or long))
This option instructs the program to pad the warp by an extra 'EE'

```

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voxels (and then 3dQwarp starts optimizing it). * This option is
seldom needed, but can be useful if you might later catenate the
nonlinear warp -- via 3dNwarpCat -- with an affine transformation
that contains a large shift. Under that circumstance, the nonlinear
warp might be shifted partially outside its original grid, so
expanding that grid can avoid this problem. * Note that this option
perforce turns off '-nopadWARP'.
argument: ``-expad %d``
mutually_exclusive: nopadWARP
ballopt: (a boolean)
    Normally, the incremental warp parameters are optimized inside a
    rectangular 'box' (24 dimensional for cubic patches, 81 for quintic
    patches), whose limits define the amount of distortion allowed at
    each step. Using '-ballopt' switches these limits to be applied to a
    'ball' (interior of a hypersphere), which can allow for larger
    incremental displacements. Use this option if you think things need
    to be able to move farther.
    argument: ``-ballopt``
    mutually_exclusive: workhard, boxopt
baxopt: (a boolean)
    Use the 'box' optimization limits instead of the 'ball' [this is the
    default at present]. * Note that if '-workhard' is used, then ball
    and box optimization are alternated in the different iterations at
    each level, so these two options have no effect in that case.
    argument: ``-boxopt``
    mutually_exclusive: workhard, ballopt
verb: (a boolean)
    more detailed description of the process
    argument: ``-verb``
    mutually_exclusive: quiet
quiet: (a boolean)
    Cut out most of the fun fun fun progress messages :-(
    argument: ``-quiet``
    mutually_exclusive: verb
overwrite: (a boolean)
    Overwrite outputs
    argument: ``-overwrite``
lpc: (a boolean)
    Local Pearson minimization (i.e., EPI-T1 registration) This option
    has not been extensively tested. If you use '-lpc', then '-maxlev 0' is
    automatically set. If you want to go to more refined levels, you can
    set '-maxlev'. This should be set up to have lpc as the second to last
    argument and maxlev as the second to last argument, as needed by
    AFNI. Using maxlev > 1 is not recommended for EPI-T1 alignment.
    argument: ``-lpc``, position: -2
    mutually_exclusive: nmi, mi, hel, lpa, pear
lpa: (a boolean)
    Local Pearson maximization This option has not been extensively tested
    argument: ``-lpa``
    mutually_exclusive: nmi, mi, lpc, hel, pear
hel: (a boolean)
    Hellinger distance: a matching function for the adventurous This
    option has NOT been extensively tested for usefulness and should be
    considered experimental at this infundibulum.
    argument: ``-hel``
    mutually_exclusive: nmi, mi, lpc, lpa, pear
mi: (a boolean)

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    Mutual Information: a matching function for the adventurousThis
    option has NOT be extensively tested for usefullnessand should be
    considered experimental at this infundibulum.
    argument: ``-mi``
    mutually_exclusive: mi, hel, lpc, lpa, pear
nmi: (a boolean)
    Normalized Mutual Information: a matching function for the
    adventurousThis option has NOT be extensively tested for
    usefullnessand should be considered experimental at this
    infundibulum.
    argument: ``-nmi``
    mutually_exclusive: nmi, hel, lpc, lpa, pear
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

warped_source: (a pathlike object or string representing a file)
    Warped source file. If plusminus is used, this is the
    undistortedsource file.
warped_base: (a pathlike object or string representing a file)
    Undistorted base file.
source_warp: (a pathlike object or string representing a file)
    Displacement in mm for the source image.If plusminus is used this is
    the field suceptibility correctionwarp (in 'mm') for source image.
base_warp: (a pathlike object or string representing a file)
    Displacement in mm for the base image.If plus minus is used, this is
    the field suceptibility correctionwarp (in 'mm') for base image.
    This is only output if plusminusor iwarp options are passed
weights: (a pathlike object or string representing a file)
    Auto-computed weight volume.

```

References:

None None

51.3.24 ROIStats[Link to code](#)

Wraps the executable command 3dROIstats.

Display statistics over masked regions

For complete details, see the [3dROIstats Documentation](#)**Examples**


```

>>> from nipy.interfaces import afni
>>> roistats = afni.ROIStats()
>>> roistats.inputs.in_file = 'functional.nii'
>>> roistats.inputs.mask_file = 'skeleton_mask.nii.gz'
>>> roistats.inputs.stat = ['mean', 'median', 'voxels']
>>> roistats.inputs.nomeanout = True
>>> roistats.cmdline
'3dROIStats -mask skeleton_mask.nii.gz -nomeanout -nzmean -nzmedian -nzvoxels_
↳functional.nii > functional_roistat.1D'
>>> res = roistats.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input dataset
         argument: ``%s``, position: -2

[Optional]
mask: (a pathlike object or string representing an existing file)
      input mask
      argument: ``-mask %s``, position: 3
mask_file: (a pathlike object or string representing an existing
            file)
            input mask
            argument: ``-mask %s``
mask_f2short: (a boolean)
              Tells the program to convert a float mask to short integers, by
              simple rounding.
              argument: ``-mask_f2short``
num_roi: (an integer (int or long))
          Forces the assumption that the mask dataset's ROIs are denoted by 1
          to n inclusive. Normally, the program figures out the ROIs on its
          own. This option is useful if a) you are certain that the mask
          dataset has no values outside the range [0 n], b) there may be some
          ROIs missing between [1 n] in the mask data-set and c) you want
          those columns in the output any-way so the output lines up with the
          output from other invocations of 3dROIStats.
          argument: ``-numroi %s``
zerofill: (a unicode string)
          For ROI labels not found, use the provided string instead of a '0'
          in the output file. Only active if `num_roi` is enabled.
          argument: ``-zerofill %s``
          requires: num_roi
roisel: (a pathlike object or string representing an existing file)
        Only considers ROIs denoted by values found in the specified file.
        Note that the order of the ROIs as specified in the file is not
        preserved. So an SEL.1D of '2 8 20' produces the same output as '8
        20 2'
        argument: ``-roisel %s``
debug: (a boolean)
       print debug information
       argument: ``-debug``
quiet: (a boolean)
       execute quietly
       argument: ``-quiet``
nomeanout: (a boolean)
           Do not include the (zero-inclusive) mean among computed stats

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        argument: ``-nomeanout``
nobriklab: (a boolean)
    Do not print the sub-brick label next to its index
    argument: ``-nobriklab``
format1D: (a boolean)
    Output results in a 1D format that includes commented labels
    argument: ``-1Dformat``
    mutually_exclusive: format1DR
format1DR: (a boolean)
    Output results in a 1D format that includes uncommented labels. May
    not work optimally with typical 1D functions, but is useful for R
    functions.
    argument: ``-1DRformat``
    mutually_exclusive: format1D
stat: (a list of items which are 'mean' or 'sum' or 'voxels' or
      'minmax' or 'sigma' or 'median' or 'mode' or 'summary' or
      'zerominmax' or 'zerosigma' or 'zeromedian' or 'zeromode')
    statistics to compute. Options include: * mean = Compute the mean
    using only non_zero voxels. Implies the opposite for the mean
    computed by default.
    * median = Compute the median of nonzero voxels
    * mode = Compute the mode of nonzero voxels. (integral valued sets
    only)
    * minmax = Compute the min/max of nonzero voxels
    * sum = Compute the sum using only nonzero voxels.
    * voxels = Compute the number of nonzero voxels
    * sigma = Compute the standard deviation of nonzero voxels
    Statistics that include zero-valued voxels:
    * zerominmax = Compute the min/max of all voxels.
    * zerosigma = Compute the standard deviation of all voxels.
    * zeromedian = Compute the median of all voxels.
    * zeromode = Compute the mode of all voxels.
    * summary = Only output a summary line with the grand mean across
    all briks in the input dataset. This option cannot be used with
    nomeanout.
    More that one option can be specified.
    argument: ``%s...``
out_file: (a pathlike object or string representing a file)
    output file
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output tab-separated values file

```

51.3.25 Retroicor[Link to code](#)

Wraps the executable command 3dretroicor.

Performs Retrospective Image Correction for physiological motion effects, using a slightly modified version of the RETROICOR algorithm

The durations of the physiological inputs are assumed to equal the duration of the dataset. Any constant sampling rate may be used, but 40 Hz seems to be acceptable. This program's cardiac peak detection algorithm is rather simplistic, so you might try using the scanner's cardiac gating output (transform it to a spike wave if necessary). This program uses slice timing information embedded in the dataset to estimate the proper cardiac/respiratory phase for each slice. It makes sense to run this program before any program that may destroy the slice timings (e.g. 3dvolreg for motion correction).

For complete details, see the [3dretroicor Documenta**tion**](#).

Examples

```
>>> from nipy.interfaces import afni
>>> ret = afni.Retroicor()
>>> ret.inputs.in_file = 'functional.nii'
>>> ret.inputs.card = 'mask.1D'
>>> ret.inputs.resp = 'resp.1D'
>>> ret.inputs.outputtype = 'NIFTI'
>>> ret.cmdline
'3dretroicor -prefix functional_retroicor.nii -resp resp.1D -card mask.1D_
↳functional.nii'
>>> res = ret.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dretroicor
         argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
         output image file name
         argument: ``-prefix %s``, position: 1
card: (a pathlike object or string representing an existing file)
      1D cardiac data file for cardiac correction
      argument: ``-card %s``, position: -2
resp: (a pathlike object or string representing an existing file)
      1D respiratory waveform data for correction
      argument: ``-resp %s``, position: -3
threshold: (an integer (int or long))
           Threshold for detection of R-wave peaks in input (Make sure it is
           above the background noise level, Try 3/4 or 4/5 times range plus
           minimum)
           argument: ``-threshold %d``, position: -4
order: (an integer (int or long))
       The order of the correction (2 is typical)
       argument: ``-order %s``, position: -5
cardphase: (a pathlike object or string representing a file)
           Filename for 1D cardiac phase output
           argument: ``-cardphase %s``, position: -6
respphase: (a pathlike object or string representing a file)
           Filename for 1D resp phase output
           argument: ``-respphase %s``, position: -7
num_threads: (an integer (int or long), nipy default value: 1)
            set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
```

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```

    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.3.26 Seg[Link to code](#)

Wraps the executable command 3dSeg.

3dSeg segments brain volumes into tissue classes. The program allows for adding a variety of global and voxelwise priors. However for the moment, only mixing fractions and MRF are documented.

For complete details, see the [3dSeg Documentation](#).

Examples

```

>>> from nipy.interfaces.afni import preprocess
>>> seg = preprocess.Seg()
>>> seg.inputs.in_file = 'structural.nii'
>>> seg.inputs.mask = 'AUTO'
>>> seg.cmdline
'3dSeg -mask AUTO -anat structural.nii'
>>> res = seg.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    ANAT is the volume to segment
    argument: ``-anat %s``, position: -1
mask: ('AUTO' or a pathlike object or string representing an existing
    file)
    only non-zero voxels in mask are analyzed. mask can either be a
    dataset or the string "AUTO" which would use AFNI's automask
    function to create the mask.
    argument: ``-mask %s``, position: -2

[Optional]
blur_meth: ('BFT' or 'BIM')
    set the blurring method for bias field estimation
    argument: ``-blur_meth %s``
bias_fwhm: (a float)
    The amount of blurring used when estimating the field bias with the
    Wells method

```

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```

        argument: ``-bias_fwhm %f``
classes: (a unicode string)
        CLASS_STRING is a semicolon delimited string of class labels
        argument: ``-classes %s``
bmrfr: (a float)
        Weighting factor controlling spatial homogeneity of the
        classifications
        argument: ``-bmrfr %f``
bias_classes: (a unicode string)
        A semicolon delimited string of classes that contribute to the
        estimation of the bias field
        argument: ``-bias_classes %s``
prefix: (a unicode string)
        the prefix for the output folder containing all output volumes
        argument: ``-prefix %s``
mixfrac: (a unicode string)
        MIXFRAC sets up the volume-wide (within mask) tissue fractions while
        initializing the segmentation (see IGNORE for exception)
        argument: ``-mixfrac %s``
mixfloor: (a float)
        Set the minimum value for any class's mixing fraction
        argument: ``-mixfloor %f``
main_N: (an integer (int or long))
        Number of iterations to perform.
        argument: ``-main_N %d``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        output file

```

51.3.27 SkullStrip[Link to code](#)

Wraps the executable command 3dSkullStrip.

A program to extract the brain from surrounding tissue from MRI T1-weighted images. TODO Add optional arguments.

For complete details, see the [3dSkullStrip Documentation](#).

Examples

```

>>> from nipy.interfaces import afni
>>> skullstrip = afni.SkullStrip()
>>> skullstrip.inputs.in_file = 'functional.nii'
>>> skullstrip.inputs.args = '-o_ply'
>>> skullstrip.cmdline
'3dSkullStrip -input functional.nii -o_ply -prefix functional_skullstrip'
>>> res = skullstrip.run() # doctest: +SKIP

```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input file to 3dSkullStrip
        argument: ``-input %s``, position: 1

[Optional]
out_file: (a pathlike object or string representing a file)
        output image file name
        argument: ``-prefix %s``
num_threads: (an integer (int or long), nipy default value: 1)
        set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
        AFNI output filetype
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
        output file
```

References:

None None

51.3.28 TCorr1D

[Link to code](#)

Wraps the executable command 3dTcorr1D.

Computes the correlation coefficient between each voxel time series in the input 3D+time dataset.

For complete details, see the [3dTcorr1D Documentation](#).

```
>>> from nipy.interfaces import afni
>>> tcorr1D = afni.TCorr1D()
>>> tcorr1D.inputs.xset= 'u_rclsl_Template.nii'
>>> tcorr1D.inputs.y_1d = 'seed.1D'
>>> tcorr1D.cmdline
'3dTcorr1D -prefix u_rclsl_Template_correlation.nii.gz u_rclsl_Template.nii
↳seed.1D'
>>> res = tcorr1D.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
xset: (a pathlike object or string representing an existing file)
        3d+time dataset input
        argument: `` %s``, position: -2
y_1d: (a pathlike object or string representing an existing file)
        1D time series file input
        argument: `` %s``, position: -1

[Optional]
```

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```

out_file: (a pathlike object or string representing a file)
    output filename prefix
    argument: ``-prefix %s``
pearson: (a boolean)
    Correlation is the normal Pearson correlation coefficient
    argument: ``-pearson``, position: 1
    mutually_exclusive: spearman, quadrant, ktaub
spearman: (a boolean)
    Correlation is the Spearman (rank) correlation coefficient
    argument: ``-spearman``, position: 1
    mutually_exclusive: pearson, quadrant, ktaub
quadrant: (a boolean)
    Correlation is the quadrant correlation coefficient
    argument: ``-quadrant``, position: 1
    mutually_exclusive: pearson, spearman, ktaub
ktaub: (a boolean)
    Correlation is the Kendall's tau_b correlation coefficient
    argument: ``-ktaub``, position: 1
    mutually_exclusive: pearson, spearman, quadrant
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file containing correlations

```

References:

None None

51.3.29 TCorrMap[Link to code](#)

Wraps the executable command 3dTcorrMap.

For each voxel time series, computes the correlation between it and all other voxels, and combines this set of values into the output dataset(s) in some way.

For complete details, see the [3dTcorrMap Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> tcm = afni.TCorrMap()
>>> tcm.inputs.in_file = 'functional.nii'
>>> tcm.inputs.mask = 'mask.nii'
>>> tcm.mean_file = 'functional_meancorr.nii'

```

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```
>>> tcm.cmdline # doctest: +SKIP
'3dTcorrMap -input functional.nii -mask mask.nii -Mean functional_meancorr.nii'
>>> res = tcm.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         argument: ``-input %s``

[Optional]
seeds: (a pathlike object or string representing an existing file)
       argument: ``-seed %s``
       mutually_exclusive: s, e, e, d, s, _, w, i, d, t, h
mask: (a pathlike object or string representing an existing file)
      argument: ``-mask %s``
automask: (a boolean)
          argument: ``-automask``
polort: (an integer (int or long))
        argument: ``-polort %d``
bandpass: (a tuple of the form: (a float, a float))
          argument: ``-bpass %f %f``
regress_out_timeseries: (a pathlike object or string representing an
                        existing file)
                        argument: ``-ort %s``
blur_fwhm: (a float)
           argument: ``-Gblur %f``
seeds_width: (a float)
             argument: ``-Mseed %f``
             mutually_exclusive: s, e, e, d, s
mean_file: (a pathlike object or string representing a file)
           argument: ``-Mean %s``
zmean: (a pathlike object or string representing a file)
       argument: ``-Zmean %s``
qmean: (a pathlike object or string representing a file)
       argument: ``-Qmean %s``
pmean: (a pathlike object or string representing a file)
       argument: ``-Pmean %s``
thresholds: (a list of items which are an integer (int or long))
absolute_threshold: (a pathlike object or string representing a file)
                   argument: ``-Thresh %f %s``
                   mutually_exclusive: absolute_threshold, var_absolute_threshold,
                   var_absolute_threshold_normalize
var_absolute_threshold: (a pathlike object or string representing a
                        file)
                        argument: ``-VarThresh %f %f %f %s``
                        mutually_exclusive: absolute_threshold, var_absolute_threshold,
                        var_absolute_threshold_normalize
var_absolute_threshold_normalize: (a pathlike object or string
                                representing a file)
                                argument: ``-VarThreshN %f %f %f %s``
                                mutually_exclusive: absolute_threshold, var_absolute_threshold,
                                var_absolute_threshold_normalize
correlation_maps: (a pathlike object or string representing a file)
                  argument: ``-CorrMap %s``
correlation_maps_masked: (a pathlike object or string representing a
                        file)
```

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```

        argument: ``-CorrMask %s``
expr: (a unicode string)
average_expr: (a pathlike object or string representing a file)
        argument: ``-Aexpr %s %s``
        mutually_exclusive: average_expr, average_expr_nonzero, sum_expr
average_expr_nonzero: (a pathlike object or string representing a
        file)
        argument: ``-Cexpr %s %s``
        mutually_exclusive: average_expr, average_expr_nonzero, sum_expr
sum_expr: (a pathlike object or string representing a file)
        argument: ``-Sexpr %s %s``
        mutually_exclusive: average_expr, average_expr_nonzero, sum_expr
histogram_bin_numbers: (an integer (int or long))
histogram: (a pathlike object or string representing a file)
        argument: ``-Hist %d %s``
num_threads: (an integer (int or long), nipy default value: 1)
        set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
        AFNI output filetype
out_file: (a pathlike object or string representing a file)
        output image file name
        argument: ``-prefix %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

mean_file: (a pathlike object or string representing a file)
zmean: (a pathlike object or string representing a file)
qmean: (a pathlike object or string representing a file)
pmean: (a pathlike object or string representing a file)
absolute_threshold: (a pathlike object or string representing a file)
var_absolute_threshold: (a pathlike object or string representing a
        file)
var_absolute_threshold_normalize: (a pathlike object or string
        representing a file)
correlation_maps: (a pathlike object or string representing a file)
correlation_maps_masked: (a pathlike object or string representing a
        file)
average_expr: (a pathlike object or string representing a file)
average_expr_nonzero: (a pathlike object or string representing a
        file)
sum_expr: (a pathlike object or string representing a file)
histogram: (a pathlike object or string representing a file)

```

References:

None None

51.3.30 TCorrelate[Link to code](#)

Wraps the executable command 3dTcorrelate.

Computes the correlation coefficient between corresponding voxel time series in two input 3D+time datasets 'xset' and 'yset'

For complete details, see the [3dTcorrelate Documentation](#).

Examples

```
>>> from nipy.interfaces import afni
>>> tcorrelate = afni.TCorrelate()
>>> tcorrelate.inputs.xset= 'u_rcls1_Template.nii'
>>> tcorrelate.inputs.yset = 'u_rcls2_Template.nii'
>>> tcorrelate.inputs.out_file = 'functional_tcorrelate.nii.gz'
>>> tcorrelate.inputs.polort = -1
>>> tcorrelate.inputs.pearson = True
>>> tcorrelate.cmdline
'3dTcorrelate -prefix functional_tcorrelate.nii.gz -pearson -polort -1 u_rcls1_
↪Template.nii u_rcls2_Template.nii'
>>> res = tcorrelate.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
xset: (a pathlike object or string representing an existing file)
      input xset
      argument: ``%s``, position: -2
yset: (a pathlike object or string representing an existing file)
      input yset
      argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
          output image file name
          argument: ``-prefix %s``
pearson: (a boolean)
          Correlation is the normal Pearson correlation coefficient
          argument: ``-pearson``
polort: (an integer (int or long))
          Remove polynomial trend of order m
          argument: ``-polort %d``
num_threads: (an integer (int or long), nipy default value: 1)
              set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
             AFNI output filetype
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          output file
```

References:

None None

51.3.31 TNorm[Link to code](#)

Wraps the executable command 3dTnorm.

Shifts voxel time series from input so that separate slices are aligned to the same temporal origin.

For complete details, see the [3dTnorm Documentation](#).**Examples**

```
>>> from nipy.interfaces import afni
>>> tnorm = afni.TNorm()
>>> tnorm.inputs.in_file = 'functional.nii'
>>> tnorm.inputs.norm2 = True
>>> tnorm.inputs.out_file = 'rm.errts.unit errts+tlrc'
>>> tnorm.cmdline
'3dTnorm -norm2 -prefix rm.errts.unit errts+tlrc functional.nii'
>>> res = tshift.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dTNorm
         argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
          output image file name
          argument: ``-prefix %s``
norm2: (a boolean)
        L2 normalize (sum of squares = 1) [DEFAULT]
        argument: ``-norm2``
normR: (a boolean)
        normalize so sum of squares = number of time points * e.g., so RMS =
        1.
        argument: ``-normR``
norm1: (a boolean)
        L1 normalize (sum of absolute values = 1)
        argument: ``-norm1``
normx: (a boolean)
        Scale so max absolute value = 1 (L_infinity norm)
        argument: ``-normx``
polort: (an integer (int or long))
        Detrend with polynomials of order p before normalizing
        [DEFAULT = don't do this]
        * Use '-polort 0' to remove the mean, for example
        argument: ``-polort %s``
L1fit: (a boolean)
        Detrend with L1 regression (L2 is the default)
        * This option is here just for the hell of it
        argument: ``-L1fit``
num_threads: (an integer (int or long), nipy default value: 1)
              set number of threads
```

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```

outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          output file

```

References:

None None

51.3.32 TProject[Link to code](#)

Wraps the executable command 3dTproject.

This program projects (detrends) out various ‘nuisance’ time series from each voxel in the input dataset. Note that all the projections are done via linear regression, including the frequency-based options such as ‘-passband’. In this way, you can bandpass time-censored data, and at the same time, remove other time series of no interest (e.g., physiological estimates, motion parameters). Shifts voxel time series from input so that separate slices are aligned to the same temporal origin.

For complete details, see the [3dTproject Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> tproject = afni.TProject()
>>> tproject.inputs.in_file = 'functional.nii'
>>> tproject.inputs.bandpass = (0.00667, 99999)
>>> tproject.inputs.polort = 3
>>> tproject.inputs.automask = True
>>> tproject.inputs.out_file = 'projected.nii.gz'
>>> tproject.cmdline
'3dTproject -input functional.nii -automask -bandpass 0.00667 99999 -polort 3 -
↳prefix projected.nii.gz'
>>> res = tproject.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dTproject
         argument: ``-input %s``, position: 1

[Optional]
out_file: (a pathlike object or string representing a file)
          output image file name
          argument: ``-prefix %s``, position: -1

```

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```

censor: (a pathlike object or string representing an existing file)
filename of censor .1D time series
* This is a file of 1s and 0s, indicating which
time points are to be included (1) and which are
to be excluded (0).
argument: ``-censor %s``

censortr: (a list of items which are a unicode string)
list of strings that specify time indexes
to be removed from the analysis. Each string is
of one of the following forms:
37 => remove global time index #37
2:37 => remove time index #37 in run #2
37..47 => remove global time indexes #37-47
37-47 => same as above
2:37..47 => remove time indexes #37-47 in run #2
*:0-2 => remove time indexes #0-2 in all runs
+Time indexes within each run start at 0.
+Run indexes start at 1 (just be to confusing).
+N.B.: 2:37,47 means index #37 in run #2 and
global time index 47; it does NOT mean
index #37 in run #2 AND index #47 in run #2.
argument: ``-CENSORTR %s``

cenmode: ('KILL' or 'ZERO' or 'NTRP')
specifies how censored time points are treated in
the output dataset:
+ mode = ZERO ==> put zero values in their place
==> output dataset is same length as input
+ mode = KILL ==> remove those time points
==> output dataset is shorter than input
+ mode = NTRP ==> censored values are replaced by interpolated
neighboring (in time) non-censored values,
BEFORE any projections, and then the
analysis proceeds without actual removal
of any time points -- this feature is to
keep the Spanish Inquisition happy.
* The default mode is KILL !!!
argument: ``-cenmode %s``

concat: (a pathlike object or string representing an existing file)
The catenation file, as in 3dDeconvolve, containing the
TR indexes of the start points for each contiguous run
within the input dataset (the first entry should be 0).
++ Also as in 3dDeconvolve, if the input dataset is
automatically catenated from a collection of datasets,
then the run start indexes are determined directly,
and '-concat' is not needed (and will be ignored).
++ Each run must have at least 9 time points AFTER
censoring, or the program will not work!
++ The only use made of this input is in setting up
the bandpass/stopband regressors.
++ '-ort' and '-dsort' regressors run through all time
points, as read in. If you want separate projections
in each run, then you must either break these ort files
into appropriate components, OR you must run 3dTproject
for each run separately, using the appropriate pieces
from the ort files via the '{...}' selector for the
1D files and the '[...]' selector for the datasets.
argument: ``-concat %s``

```

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```

noblock: (a boolean)
    Also as in 3dDeconvolve, if you want the program to treat
    an auto-catenated dataset as one long run, use this option.
    ++ However, '-noblock' will not affect catenation if you use
    the '-concat' option.
    argument: ``-noblock``

ort: (a pathlike object or string representing an existing file)
    Remove each column in file
    ++ Each column will have its mean removed.
    argument: ``-ort %s``

polort: (an integer (int or long))
    Remove polynomials up to and including degree pp.
    ++ Default value is 2.
    ++ It makes no sense to use a value of pp greater than
    2, if you are bandpassing out the lower frequencies!
    ++ For catenated datasets, each run gets a separate set
    set of pp+1 Legendre polynomial regressors.
    ++ Use of -polort -1 is not advised (if data mean != 0),
    even if -ort contains constant terms, as all means are
    removed.
    argument: ``-polort %d``

dsort: (a list of items which are a pathlike object or string
    representing an existing file)
    Remove the 3D+time time series in dataset fset.
    ++ That is, 'fset' contains a different nuisance time
    series for each voxel (e.g., from AnatomicOR).
    ++ Multiple -dsort options are allowed.
    argument: ``-dsort %s...``

bandpass: (a tuple of the form: (a float, a float))
    Remove all frequencies EXCEPT those in the range
    argument: ``-bandpass %g %g``

stopband: (a tuple of the form: (a float, a float))
    Remove all frequencies in the range
    argument: ``-stopband %g %g``

TR: (a float)
    Use time step dd for the frequency calculations,
    rather than the value stored in the dataset header.
    argument: ``-TR %g``

mask: (a pathlike object or string representing an existing file)
    Only operate on voxels nonzero in the mset dataset.
    ++ Voxels outside the mask will be filled with zeros.
    ++ If no masking option is given, then all voxels
    will be processed.
    argument: ``-mask %s``

automask: (a boolean)
    Generate a mask automatically
    argument: ``-automask``
    mutually_exclusive: mask

blur: (a float)
    Blur (inside the mask only) with a filter that has
    width (FWHM) of fff millimeters.
    ++ Spatial blurring (if done) is after the time
    series filtering.
    argument: ``-blur %g``

norm: (a boolean)
    Normalize each output time series to have sum of
    squares = 1. This is the LAST operation.

```

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```

        argument: ``-norm``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.3.33 TShift[Link to code](#)

Wraps the executable command 3dTshift.

Shifts voxel time series from input so that separate slices are aligned to the same temporal origin.

For complete details, see the [3dTshift Documentation](#).**Examples**Slice timing details may be specified explicitly via the `slice_timing` input:

```

>>> from nipy.interfaces import afni
>>> TR = 2.5
>>> tshift = afni.TShift()
>>> tshift.inputs.in_file = 'functional.nii'
>>> tshift.inputs.tzero = 0.0
>>> tshift.inputs.tr = '%.1fs' % TR
>>> tshift.inputs.slice_timing = list(np.arange(40) / TR)
>>> tshift.cmdline
'3dTshift -prefix functional_tshift -tpattern @slice_timing.1D -TR 2.5s -tzero 0.
↪0 functional.nii'

```

When the `slice_timing` input is used, the `timing_file` output is populated, in this case with the generated file.

```

>>> tshift._list_outputs()['timing_file'] # doctest: +ELLIPSIS
'.../slice_timing.1D'

```

```

>>> np.loadtxt(tshift._list_outputs()['timing_file']).tolist()[5]
[0.0, 0.4, 0.8, 1.2, 1.6]

```

If `slice_encoding_direction` is set to 'k-', the slice timing is reversed:

```

>>> tshift.inputs.slice_encoding_direction = 'k-'
>>> tshift.cmdline

```

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```
'3dTshift -prefix functional_tshift -tpattern @slice_timing.1D -TR 2.5s -tzero 0.
↳0 functional.nii'
>>> np.loadtxt(tshift._list_outputs()['timing_file']).tolist()[5]
[15.6, 15.2, 14.8, 14.4, 14.0]
```

This method creates a `slice_timing.1D` file to be passed to `3dTshift`. A pre-existing slice-timing file may be used in the same way:

```
>>> tshift = afni.TShift()
>>> tshift.inputs.in_file = 'functional.nii'
>>> tshift.inputs.tzero = 0.0
>>> tshift.inputs.tr = '%.1fs' % TR
>>> tshift.inputs.slice_timing = 'slice_timing.1D'
>>> tshift.cmdline
'3dTshift -prefix functional_tshift -tpattern @slice_timing.1D -TR 2.5s -tzero 0.
↳0 functional.nii'
```

When a pre-existing file is provided, `timing_file` is simply passed through.

```
>>> tshift._list_outputs()['timing_file'] # doctest: +ELLIPSIS
'.../slice_timing.1D'
```

Alternatively, pre-specified slice timing patterns may be specified with the `tpattern` input. For example, to specify an alternating, ascending slice timing pattern:

```
>>> tshift = afni.TShift()
>>> tshift.inputs.in_file = 'functional.nii'
>>> tshift.inputs.tzero = 0.0
>>> tshift.inputs.tr = '%.1fs' % TR
>>> tshift.inputs.tpattern = 'alt+z'
>>> tshift.cmdline
'3dTshift -prefix functional_tshift -tpattern alt+z -TR 2.5s -tzero 0.0_
↳functional.nii'
```

For backwards compatibility, `tpattern` may also take filenames prefixed with `@`. However, in this case, filenames are not validated, so this usage will be deprecated in future versions of Nipy.

```
>>> tshift = afni.TShift()
>>> tshift.inputs.in_file = 'functional.nii'
>>> tshift.inputs.tzero = 0.0
>>> tshift.inputs.tr = '%.1fs' % TR
>>> tshift.inputs.tpattern = '@slice_timing.1D'
>>> tshift.cmdline
'3dTshift -prefix functional_tshift -tpattern @slice_timing.1D -TR 2.5s -tzero 0.
↳0 functional.nii'
```

In these cases, `timing_file` is undefined.

```
>>> tshift._list_outputs()['timing_file'] # doctest: +ELLIPSIS
<undefined>
```

In any configuration, the interface may be run as usual:

```
>>> res = tshift.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dTshift
```

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```

    argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
    output image file name
    argument: ``-prefix %s``
tr: (a unicode string)
    manually set the TR. You can attach suffix "s" for seconds or "ms"
    for milliseconds.
    argument: ``-TR %s``
tzero: (a float)
    align each slice to given time offset
    argument: ``-tzero %s``
    mutually_exclusive: tslice
tslice: (an integer (int or long))
    align each slice to time offset of given slice
    argument: ``-slice %s``
    mutually_exclusive: tzero
ignore: (an integer (int or long))
    ignore the first set of points specified
    argument: ``-ignore %s``
interp: ('Fourier' or 'linear' or 'cubic' or 'quintic' or 'heptic')
    different interpolation methods (see 3dTshift for details) default =
    Fourier
    argument: ``-%s``
tpattern: ('alt+z' or 'altplus' or 'alt+z2' or 'alt-z' or 'altminus'
    or 'alt-z2' or 'seq+z' or 'seqplus' or 'seq-z' or 'seqminus' or a
    unicode string)
    use specified slice time pattern rather than one in header
    argument: ``-tpattern %s``
    mutually_exclusive: slice_timing
slice_timing: (a pathlike object or string representing an existing
    file or a list of items which are a float)
    time offsets from the volume acquisition onset for each slice
    argument: ``-tpattern @%s``
    mutually_exclusive: tpattern
slice_encoding_direction: ('k' or 'k-', nipy default value: k)
    Direction in which slice_timing is specified (default: k). If
    negative, slice_timing is defined in reverse order, that is, the
    first entry corresponds to the slice with the largest index, and the
    final entry corresponds to slice index zero. Only in effect when
    slice_timing is passed as list, not when it is passed as file.
rlt: (a boolean)
    Before shifting, remove the mean and linear trend
    argument: ``-rlt``
rltplus: (a boolean)
    Before shifting, remove the mean and linear trend and later put back
    the mean
    argument: ``-rlt+``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value

```

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```

of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

timing_file: (a pathlike object or string representing a file)
             AFNI formatted timing file, if ``slice_timing`` is a list
out_file:   (a pathlike object or string representing an existing file)
             output file

```

References:

None None

51.3.34 TSmooth[Link to code](#)

Wraps the executable command 3dTsmooth.

Smooths each voxel time series in a 3D+time dataset and produces as output a new 3D+time dataset (e.g., lowpass filter in time).

For complete details, see the [3dTsmooth Documenta  on](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> from nipy.testing import example_data
>>> smooth = afni.TSmooth()
>>> smooth.inputs.in_file = 'functional.nii'
>>> smooth.inputs.adaptive = 5
>>> smooth.cmdline
'3dTsmooth -adaptive 5 -prefix functional_smooth functional.nii'
>>> res = smooth.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
          input file to 3dTSmooth
          argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
          output file from 3dTSmooth
          argument: ``-prefix %s``
datum:   (a unicode string)
          Sets the data type of the output dataset
          argument: ``-datum %s``
lin:     (a boolean)
          3 point linear filter: 0.15*a + 0.70*b + 0.15*c[This is the default
          smoother]
          argument: ``-lin``
med:     (a boolean)
          3 point median filter: median(a,b,c)
          argument: ``-med``
osf:     (a boolean)

```

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```

    3 point order statistics filter:0.15*min(a,b,c) + 0.70*median(a,b,c)
    + 0.15*max(a,b,c)
    argument: ``-osf``
lin3: (an integer (int or long))
    3 point linear filter: 0.5*(1-m)*a + m*b + 0.5*(1-m)*cHere, 'm' is a
    number strictly between 0 and 1.
    argument: ``-3lin %d``
hamming: (an integer (int or long))
    Use N point Hamming windows.(N must be odd and bigger than 1.)
    argument: ``-hamming %d``
blackman: (an integer (int or long))
    Use N point Blackman windows.(N must be odd and bigger than 1.)
    argument: ``-blackman %d``
custom: (a pathlike object or string representing a file)
    odd # of coefficients must be in a single column in ASCII file
    argument: ``-custom %s``
adaptive: (an integer (int or long))
    use adaptive mean filtering of width N (where N must be odd and
    bigger than 3).
    argument: ``-adaptive %d``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.3.35 Volreg[Link to code](#)

Wraps the executable command 3dvolreg.

Register input volumes to a base volume using AFNI 3dvolreg command

For complete details, see the [3dvolreg Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> volreg = afni.Volreg()
>>> volreg.inputs.in_file = 'functional.nii'
>>> volreg.inputs.args = '-Fourier -twopass'
>>> volreg.inputs.zpad = 4

```

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```
>>> volreg.inputs.outputtype = 'NIFTI'
>>> volreg.cmdline # doctest: +ELLIPSIS
'3dvolreg -Fourier -twopass -1Dfile functional.1D -1Dmatrix_save functional.aff12.
↪1D -prefix functional_volreg.nii -zpad 4 -maxdisp1D functional_md.1D functional.
↪nii'
>>> res = volreg.run() # doctest: +SKIP
```

```
>>> from nipy.interfaces import afni
>>> volreg = afni.Volreg()
>>> volreg.inputs.in_file = 'functional.nii'
>>> volreg.inputs.interp = 'cubic'
>>> volreg.inputs.verbose = True
>>> volreg.inputs.zpad = 1
>>> volreg.inputs.basefile = 'functional.nii'
>>> volreg.inputs.out_file = 'rm.epi.volreg.rl'
>>> volreg.inputs.oned_file = 'dfile.rl.1D'
>>> volreg.inputs.oned_matrix_save = 'mat.rl.tshift+orig.1D'
>>> volreg.cmdline
'3dvolreg -cubic -1Dfile dfile.rl.1D -1Dmatrix_save mat.rl.tshift+orig.1D -prefix_
↪rm.epi.volreg.rl -verbose -base functional.nii -zpad 1 -maxdisp1D functional_md.
↪1D functional.nii'
>>> res = volreg.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dvolreg
         argument: ``%s``, position: -1

[Optional]
in_weight_volume: (a tuple of the form: (a pathlike object or string
         representing an existing file, an integer (int or long)) or a
         pathlike object or string representing an existing file)
         weights for each voxel specified by a file with an optional volume
         number (defaults to 0)
         argument: ``-weight '%s[%d]''``
out_file: (a pathlike object or string representing a file)
         output image file name
         argument: ``-prefix %s``
basefile: (a pathlike object or string representing an existing file)
         base file for registration
         argument: ``-base %s``, position: -6
zpad: (an integer (int or long))
       Zeropad around the edges by 'n' voxels during rotations
       argument: ``-zpad %d``, position: -5
mdld_file: (a pathlike object or string representing a file)
           max displacement output file
           argument: ``-maxdisp1D %s``, position: -4
oned_file: (a pathlike object or string representing a file)
           1D movement parameters output file
           argument: ``-1Dfile %s``
verbose: (a boolean)
          more detailed description of the process
          argument: ``-verbose``
timeshift: (a boolean)
            time shift to mean slice time offset
```

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```

        argument: ``-tshift 0``
copyorigin: (a boolean)
    copy base file origin coords to output
    argument: ``-twodup``
oned_matrix_save: (a pathlike object or string representing a file)
    Save the matrix transformation
    argument: ``-lDmatrix_save %s``
interp: ('Fourier' or 'cubic' or 'heptic' or 'quintic' or 'linear')
    spatial interpolation methods [default = heptic]
    argument: ``-%s``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    registered file
mdld_file: (a pathlike object or string representing an existing
    file)
    max displacement info file
oned_file: (a pathlike object or string representing an existing
    file)
    movement parameters info file
oned_matrix_save: (a pathlike object or string representing an
    existing file)
    matrix transformation from base to input

```

References:

None None

51.3.36 Warp[Link to code](#)

Wraps the executable command 3dWarp.

Use 3dWarp for spatially transforming a dataset

For complete details, see the [3dWarp Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> warp = afni.Warp()
>>> warp.inputs.in_file = 'structural.nii'
>>> warp.inputs.deoblique = True
>>> warp.inputs.out_file = 'trans.nii.gz'
>>> warp.cmdline

```

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```
'3dWarp -deoblique -prefix trans.nii.gz structural.nii'
>>> res = warp.run() # doctest: +SKIP
```

```
>>> warp_2 = afni.Warp()
>>> warp_2.inputs.in_file = 'structural.nii'
>>> warp_2.inputs.newgrid = 1.0
>>> warp_2.inputs.out_file = 'trans.nii.gz'
>>> warp_2.cmdline
'3dWarp -newgrid 1.000000 -prefix trans.nii.gz structural.nii'
>>> res = warp_2.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input file to 3dWarp
        argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
        output image file name
        argument: ``-prefix %s``
tta2mni: (a boolean)
        transform dataset from Talairach to MNI152
        argument: ``-tta2mni``
mni2tta: (a boolean)
        transform dataset from MNI152 to Talairach
        argument: ``-mni2tta``
matparent: (a pathlike object or string representing an existing
        file)
        apply transformation from 3dWarpDrive
        argument: ``-matparent %s``
oblique_parent: (a pathlike object or string representing an existing
        file)
        Read in the oblique transformation matrix from an oblique dataset
        and make cardinal dataset oblique to match
        argument: ``-oblique_parent %s``
deoblique: (a boolean)
        transform dataset from oblique to cardinal
        argument: ``-deoblique``
interp: ('linear' or 'cubic' or 'NN' or 'quintic')
        spatial interpolation methods [default = linear]
        argument: ``-%s``
gridset: (a pathlike object or string representing an existing file)
        copy grid of specified dataset
        argument: ``-gridset %s``
newgrid: (a float)
        specify grid of this size (mm)
        argument: ``-newgrid %f``
zpad: (an integer (int or long))
        pad input dataset with N planes of zero on all sides.
        argument: ``-zpad %d``
verbose: (a boolean)
        Print out some information along the way.
        argument: ``-verb``
save_warp: (a boolean)
        save warp as .mat file
```

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```

        requires: verbose
num_threads: (an integer (int or long), nipy default value: 1)
        set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
        AFNI output filetype
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        Warped file.
warp_file: (a pathlike object or string representing a file)
        warp transform .mat file

```

References:

None None

51.4 interfaces.afni.svm

51.4.1 SVMTest

[Link to code](#)

Wraps the executable command 3dsvm.

Temporally predictive modeling with the support vector machine SVM Test Only For complete details, see the [3dsvm Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni as afni
>>> svmTest = afni.SVMTest()
>>> svmTest.inputs.in_file= 'run2+orig'
>>> svmTest.inputs.model= 'run1+orig_model'
>>> svmTest.inputs.testlabels= 'run2_categories.1D'
>>> svmTest.inputs.out_file= 'pred2_model1'
>>> res = svmTest.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
model: (a unicode string)
        modname is the basename for the brik containing the SVM model
        argument: ``-model %s``
in_file: (a pathlike object or string representing an existing file)
        A 3D or 3D+t AFNI brik dataset to be used for testing.
        argument: ``-testvol %s``

[Optional]
out_file: (a pathlike object or string representing a file)

```

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```

        filename for .1D prediction file(s).
        argument: ``-predictions %s``
testlabels: (a pathlike object or string representing an existing
            file)
            *true* class category .1D labels for the test dataset. It is used to
            calculate the prediction accuracy performance
            argument: ``-testlabels %s``
classout: (a boolean)
            Flag to specify that pname files should be integer-valued,
            corresponding to class category decisions.
            argument: ``-classout``
nopredcensord: (a boolean)
            Flag to prevent writing predicted values for censored time-points
            argument: ``-nopredcensord``
nodetrend: (a boolean)
            Flag to specify that pname files should not be linearly detrended
            argument: ``-nodetrend``
multiclass: (a boolean)
            Specifies multiclass algorithm for classification
            argument: ``-multiclass %s``
options: (a unicode string)
            additional options for SVM-light
            argument: ``%s``
num_threads: (an integer (int or long), nipy default value: 1)
            set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
            of class 'str' and with values which are a bytes or None or a
            value of class 'str', nipy default value: {})
            Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
            output file

```

References:

None None

51.4.2 SVMTrain[Link to code](#)

Wraps the executable command 3dsvm.

Temporally predictive modeling with the support vector machine SVM Train Only For complete details, see the [3dsvm Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni as afni
>>> svmTrain = afni.SVMTrain()

```

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```

>>> svmTrain.inputs.in_file = 'run1+orig'
>>> svmTrain.inputs.trainlabels = 'run1_categories.1D'
>>> svmTrain.inputs.ttype = 'regression'
>>> svmTrain.inputs.mask = 'mask.nii'
>>> svmTrain.inputs.model = 'model_run1'
>>> svmTrain.inputs.alphas = 'alphas_run1'
>>> res = svmTrain.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
ttype: (a unicode string)
    tname: classification or regression
    argument: ``-type %s``
in_file: (a pathlike object or string representing an existing file)
    A 3D+t AFNI brik dataset to be used for training.
    argument: ``-trainvol %s``

[Optional]
out_file: (a pathlike object or string representing a file)
    output sum of weighted linear support vectors file name
    argument: ``-bucket %s``
model: (a pathlike object or string representing a file)
    basename for the brik containing the SVM model
    argument: ``-model %s``
alphas: (a pathlike object or string representing a file)
    output alphas file name
    argument: ``-alpha %s``
mask: (a pathlike object or string representing an existing file)
    byte-format brik file used to mask voxels in the analysis
    argument: ``-mask %s``, position: -1
nomodelmask: (a boolean)
    Flag to enable the omission of a mask file
    argument: ``-nomodelmask``
trainlabels: (a pathlike object or string representing an existing
    file)
    .1D labels corresponding to the stimulus paradigm for the training
    data.
    argument: ``-trainlabels %s``
censor: (a pathlike object or string representing an existing file)
    .1D censor file that allows the user to ignore certain samples in
    the training data.
    argument: ``-censor %s``
kernel: (a unicode string)
    string specifying type of kernel function:linear, polynomial, rbf,
    sigmoid
    argument: ``-kernel %s``
max_iterations: (an integer (int or long))
    Specify the maximum number of iterations for the optimization.
    argument: ``-max_iterations %d``
w_out: (a boolean)
    output sum of weighted linear support vectors
    argument: ``-wout``
options: (a unicode string)
    additional options for SVM-light
    argument: ``%s``
num_threads: (an integer (int or long), nipy default value: 1)

```

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```

        set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
        AFNI output filetype
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
        sum of weighted linear support vectors file name
model: (a pathlike object or string representing a file)
        brik containing the SVM model file name
alphas: (a pathlike object or string representing a file)
        output alphas file name

```

References:

None None

51.5 interfaces.afni.utils

51.5.1 ABoverlap

[Link to code](#)

Wraps the executable command 3dABoverlap.

Output (to screen) is a count of various things about how the automasks of datasets A and B overlap or don't overlap.

For complete details, see the [3dABoverlap Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> aboverlap = afni.ABoverlap()
>>> aboverlap.inputs.in_file_a = 'functional.nii'
>>> aboverlap.inputs.in_file_b = 'structural.nii'
>>> aboverlap.inputs.out_file = 'out.mask_ae_overlap.txt'
>>> aboverlap.cmdline
'3dABoverlap functional.nii structural.nii |& tee out.mask_ae_overlap.txt'
>>> res = aboverlap.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file_a: (a pathlike object or string representing an existing
        file)
        input file A
        argument: ``%s``, position: -3
in_file_b: (a pathlike object or string representing an existing
        file)
        input file B

```

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```

        argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
    collect output to a file
    argument: ``|& tee %s``, position: -1
no_automask: (a boolean)
    consider input datasets as masks
    argument: ``-no_automask``
quiet: (a boolean)
    be as quiet as possible (without being entirely mute)
    argument: ``-quiet``
verb: (a boolean)
    print out some progress reports (to stderr)
    argument: ``-verb``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.5.2 AFNItoNIFTI[Link to code](#)

Wraps the executable command 3dAFNItoNIFTI.

Converts AFNI format files to NIFTI format. This can also convert 2D or 1D data, which you can `numpy.squeeze()` to remove extra dimensions.For complete details, see the [3dAFNItoNIFTI Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> a2n = afni.AFNItoNIFTI()
>>> a2n.inputs.in_file = 'afni_output.3D'
>>> a2n.inputs.out_file = 'afni_output.nii'
>>> a2n.cmdline
'3dAFNItoNIFTI -prefix afni_output.nii afni_output.3D'
>>> res = a2n.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    input file to 3dAFNIToNIFTI
    argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
    output image file name
    argument: ``-prefix %s``
pure: (a boolean)
    Do NOT write an AFNI extension field into the output file. Only use
    this option if needed. You can also use the 'nifti_tool' program to
    strip extensions from a file.
    argument: ``-pure``
denote: (a boolean)
    When writing the AFNI extension field, remove text notes that might
    contain subject identifying information.
    argument: ``-denote``
oldid: (a boolean)
    Give the new dataset the input datasets AFNI ID code.
    argument: ``-oldid``
    mutually_exclusive: newid
newid: (a boolean)
    Give the new dataset a new AFNI ID code, to distinguish it from the
    input dataset.
    argument: ``-newid``
    mutually_exclusive: oldid
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.5.3 Autobox[Link to code](#)

Wraps the executable command 3dAutobox.

Computes size of a box that fits around the volume. Also can be used to crop the volume to that box.

For complete details, see the [3dAutobox Documentation](#).

Examples

```
>>> from nipy.interfaces import afni
>>> abox = afni.Autobox()
>>> abox.inputs.in_file = 'structural.nii'
>>> abox.inputs.padding = 5
>>> abox.cmdline
'3dAutobox -input structural.nii -prefix structural_autobox -npad 5'
>>> res = abox.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input file
        argument: ``-input %s``

[Optional]
padding: (an integer (int or long))
        Number of extra voxels to pad on each side of box
        argument: ``-npad %d``
out_file: (a pathlike object or string representing a file)
        argument: ``-prefix %s``
no_clustering: (a boolean)
        Don't do any clustering to find box. Any non-zero voxel will be
        preserved in the cropped volume. The default method uses some
        clustering to find the cropping box, and will clip off small
        isolated blobs.
        argument: ``-noclust``
num_threads: (an integer (int or long), nipy default value: 1)
        set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
        AFNI output filetype
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables
```

Outputs:

```
x_min: (an integer (int or long))
x_max: (an integer (int or long))
y_min: (an integer (int or long))
y_max: (an integer (int or long))
z_min: (an integer (int or long))
z_max: (an integer (int or long))
out_file: (a pathlike object or string representing a file)
        output file
```

References:

None None

51.5.4 Axialize

[Link to code](#)

Wraps the executable command 3daxialize.

Read in a dataset and write it out as a new dataset with the data brick oriented as axial slices.

For complete details, see the [3dcopy Documenta  on](#).

Examples

```
>>> from nipy.interfaces import afni
>>> axial3d = afni.Axialize()
>>> axial3d.inputs.in_file = 'functional.nii'
>>> axial3d.inputs.out_file = 'axialized.nii'
>>> axial3d.cmdline
'3daxialize -prefix axialized.nii functional.nii'
>>> res = axial3d.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3daxialize
         argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
          output image file name
          argument: ``-prefix %s``
verb: (a boolean)
      Print out a progerss report
      argument: ``-verb``
sagittal: (a boolean)
          Do sagittal slice order [-orient ASL]
          argument: ``-sagittal``
          mutually_exclusive: coronal, axial
coronal: (a boolean)
          Do coronal slice order [-orient RSA]
          argument: ``-coronal``
          mutually_exclusive: sagittal, axial
axial: (a boolean)
        Do axial slice order [-orient RAI]This is the default AFNI axial
        order, andis the one currently required by thevolume rendering
        plugin; this is alsothe default orientation output by thisprogram
        (hence the program's name).
        argument: ``-axial``
        mutually_exclusive: coronal, sagittal
orientation: (a unicode string)
             new orientation code
             argument: ``-orient %s``
num_threads: (an integer (int or long), nipy default value: 1)
             set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          output file
```

References:

None None

51.5.5 BrickStat

[Link to code](#)

Wraps the executable command 3dBrickStat.

Computes maximum and/or minimum voxel values of an input dataset. TODO Add optional arguments.

For complete details, see the [3dBrickStat Documentation](#).

Examples

```
>>> from nipy.interfaces import afni
>>> brickstat = afni.BrickStat()
>>> brickstat.inputs.in_file = 'functional.nii'
>>> brickstat.inputs.mask = 'skeleton_mask.nii.gz'
>>> brickstat.inputs.min = True
>>> brickstat.cmdline
'3dBrickStat -min -mask skeleton_mask.nii.gz functional.nii'
>>> res = brickstat.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dmaskave
         argument: ``%s``, position: -1

[Optional]
mask: (a pathlike object or string representing an existing file)
      -mask dset = use dset as mask to include/exclude voxels
      argument: ``-mask %s``, position: 2
min: (a boolean)
      print the minimum value in dataset
      argument: ``-min``, position: 1
slow: (a boolean)
      read the whole dataset to find the min and max values
      argument: ``-slow``
max: (a boolean)
      print the maximum value in the dataset
      argument: ``-max``
mean: (a boolean)
      print the mean value in the dataset
      argument: ``-mean``
sum: (a boolean)
      print the sum of values in the dataset
      argument: ``-sum``
var: (a boolean)
      print the variance in the dataset
      argument: ``-var``
percentile: (a tuple of the form: (a float, a float, a float))
            p0 ps p1 write the percentile values starting at p0% and ending at
```

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```

    p1% at a step of ps%. only one sub-brick is accepted.
    argument: ``-percentile %.3f %.3f %.3f``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

min_val: (a float)
    output

```

51.5.6 Bucket[Link to code](#)

Wraps the executable command 3dbucket.

Concatenate sub-bricks from input datasets into one big 'bucket' dataset.

For complete details, see the [3dbucket Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> bucket = afni.Bucket()
>>> bucket.inputs.in_file = [('functional.nii',"{2..$}"), ('functional.nii',"{1}
↪")]
>>> bucket.inputs.out_file = 'vr_base'
>>> bucket.cmdline
"3dbucket -prefix vr_base functional.nii'{2..$}' functional.nii'{1}'"
>>> res = bucket.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a list of items which are a tuple of the form: (a pathlike
    object or string representing an existing file, a unicode string))
    List of tuples of input datasets and subbrick selection stringsas
    described in more detail in the following afni help stringInput
    dataset specified using one of these forms: 'prefix+view',
    'prefix+view.HEAD', or 'prefix+view.BRIK'.You can also add a sub-
    brick selection list after the end of thedataset name. This allows
    only a subset of the sub-bricks to beincluded into the output (by
    default, all of the input datasetis copied into the output). A sub-
    brick selection list looks likeone of the following forms:
    fred+orig[5] ==> use only sub-brick #5 fred+orig[5,9,17] ==> use #5,
    #9, and #17 fred+orig[5..8] or [5-8] ==> use #5, #6, #7, and #8
    fred+orig[5..13(2)] or [5-13(2)] ==> use #5, #7, #9, #11, and
    #13Sub-brick indexes start at 0. You can use the character '$'to
    indicate the last sub-brick in a dataset; for example, youcan select
    every third sub-brick by using the selection list
    fred+orig[0..$(3)]N.B.: The sub-bricks are output in the order
    specified, which may not be the order in the original datasets. For
    example, using fred+orig[0..$(2),1..$(2)] will cause the sub-bricks
    in fred+orig to be output into the new dataset in an interleaved

```

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fashion. Using `fred+orig[$..0]` will reverse the order of the sub-bricks in the output. N.B.: Bucket datasets have multiple sub-bricks, but do NOT have a time dimension. You can input sub-bricks from a 3D+time dataset into a bucket dataset. You can use the '3dinfo' program to see how many sub-bricks a 3D+time or a bucket dataset contains. N.B.: In non-bucket functional datasets (like the 'fico' datasets output by FIM, or the 'fitt' datasets output by 3dttest), sub-brick [0] is the 'intensity' and sub-brick [1] is the statistical parameter used as a threshold. Thus, to create a bucket dataset using the intensity from dataset A and the threshold from dataset B, and calling the output dataset C, you would type `3dbucket -prefix C -fbuc 'A+orig[0]' -fbuc 'B+orig[1]'` WARNING: using this program, it is possible to create a dataset that has different basic datum types for different sub-bricks (e.g., shorts for brick 0, floats for brick 1). Do NOT do this! Very few AFNI programs will work correctly with such datasets!

argument: ``%s``, position: -1

[Optional]

`out_file`: (a pathlike object or string representing a file)
 argument: ``-prefix %s``

`num_threads`: (an integer (int or long), nipy default value: 1)
 set number of threads

`outputtype`: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
 AFNI output filetype

`args`: (a unicode string)
 Additional parameters to the command
 argument: ``%s``

`environ`: (a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str', nipy default value: {})
 Environment variables

Outputs:

`out_file`: (a pathlike **object** **or** string representing an existing file)
 output file

References:

None None

51.5.7 Calc[Link to code](#)Wraps the executable command `3dcalc`.

This program does voxel-by-voxel arithmetic on 3D datasets.

For complete details, see the [3dcalc Documentation](#).**Examples**

```
>>> from nipy.interfaces import afni
>>> calc = afni.Calc()
>>> calc.inputs.in_file_a = 'functional.nii'
>>> calc.inputs.in_file_b = 'functional2.nii'
```

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```
>>> calc.inputs.expr='a*b'
>>> calc.inputs.out_file = 'functional_calc.nii.gz'
>>> calc.inputs.outputtype = 'NIFTI'
>>> calc.cmdline # doctest: +ELLIPSIS
'3dcalc -a functional.nii -b functional2.nii -expr "a*b" -prefix functional_calc.
↪nii.gz'
>>> res = calc.run() # doctest: +SKIP
```

```
>>> from nipy.interfaces import afni
>>> calc = afni.Calc()
>>> calc.inputs.in_file_a = 'functional.nii'
>>> calc.inputs.expr = '1'
>>> calc.inputs.out_file = 'rm.epi.all1'
>>> calc.inputs.overwrite = True
>>> calc.cmdline
'3dcalc -a functional.nii -expr "1" -prefix rm.epi.all1 -overwrite'
>>> res = calc.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file_a: (a pathlike object or string representing an existing
            file)
            input file to 3dcalc
            argument: ``-a %s``, position: 0
expr: (a unicode string)
      expr
      argument: ``-expr "%s"`, position: 3

[Optional]
in_file_b: (a pathlike object or string representing an existing
            file)
            operand file to 3dcalc
            argument: ``-b %s``, position: 1
in_file_c: (a pathlike object or string representing an existing
            file)
            operand file to 3dcalc
            argument: ``-c %s``, position: 2
out_file: (a pathlike object or string representing a file)
          output image file name
          argument: ``-prefix %s``
start_idx: (an integer (int or long))
           start index for in_file_a
           requires: stop_idx
stop_idx: (an integer (int or long))
          stop index for in_file_a
          requires: start_idx
single_idx: (an integer (int or long))
            volume index for in_file_a
overwrite: (a boolean)
           overwrite output
           argument: ``-overwrite``
other: (a pathlike object or string representing a file)
       other options
num_threads: (an integer (int or long), nipy default value: 1)
             set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
```

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```

    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.5.8 Cat[Link to code](#)

Wraps the executable command 1dcat.

1dcat takes as input one or more 1D files, and writes out a 1D file containing the side-by-side concatenation of all or a subset of the columns from the input files.

For complete details, see the [1dcat Documentations](#).

Examples

```

>>> from nipy.interfaces import afni
>>> cat1d = afni.Cat()
>>> cat1d.inputs.sel = "[0,2]"
>>> cat1d.inputs.in_files = ['f1.1D', 'f2.1D']
>>> cat1d.inputs.out_file = 'catout.1d'
>>> cat1d.cmdline
"1dcat -sel '[0,2]' f1.1D f2.1D > catout.1d"
>>> res = cat1d.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string
    representing an existing file)
    argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file, nipy
    default value: catout.1d)
    output (concatenated) file name
    argument: ``> %s``, position: -1

[Optional]
omitconst: (a boolean)
    Omit columns that are identically constant from output.
    argument: ``-nonconst``
keepfree: (a boolean)
    Keep only columns that are marked as 'free' in the 3dAllineate
    header from '-1Dparam_save'. If there is no such header, all columns
    are kept.

```

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```

    argument: ``-nonfixed``
out_format: ('int' or 'nice' or 'double' or 'fint' or 'cint')
    specify data type for output. Valid types are 'int', 'nice',
    'double', 'fint', and 'cint'.
    argument: ``-form %s``
    mutually_exclusive: out_int, out_nice, out_double, out_fint,
    out_cint
stack: (a boolean)
    Stack the columns of the resultant matrix in the output.
    argument: ``-stack``
sel: (a unicode string)
    Apply the same column/row selection string to all filenames on the
    command line.
    argument: ``-sel %s``
out_int: (a boolean)
    specify int data type for output
    argument: ``-i``
    mutually_exclusive: out_format, out_nice, out_double, out_fint,
    out_cint
out_nice: (a boolean)
    specify nice data type for output
    argument: ``-n``
    mutually_exclusive: out_format, out_int, out_double, out_fint,
    out_cint
out_double: (a boolean)
    specify double data type for output
    argument: ``-d``
    mutually_exclusive: out_format, out_nice, out_int, out_fint,
    out_cint
out_fint: (a boolean)
    specify int, rounded down, data type for output
    argument: ``-f``
    mutually_exclusive: out_format, out_nice, out_double, out_int,
    out_cint
out_cint: (a boolean)
    specify int, rounded up, data type for output
    mutually_exclusive: out_format, out_nice, out_double, out_fint,
    out_int
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.5.9 CatMatvec

[Link to code](#)

Wraps the executable command `cat_matvec`.

Catenates 3D rotation+shift matrix+vector transformations.

For complete details, see the [cat_matvec Documentation](#).

Examples

```
>>> from nipy.interfaces import afni
>>> cmv = afni.CatMatvec()
>>> cmv.inputs.in_file = [('structural.BRIK::WARP_DATA', 'I')]
>>> cmv.inputs.out_file = 'warp.anat.Xat.1D'
>>> cmv.cmdline
'cat_matvec structural.BRIK::WARP_DATA -I > warp.anat.Xat.1D'
>>> res = cmv.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a list of items which are a tuple of the form: (a unicode
          string, a unicode string))
          list of tuples of mfiles and associated opkeys
          argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file)
          File to write concatenated matvecs to
          argument: `` > %s``, position: -1

[Optional]
matrix: (a boolean)
          indicates that the resulting matrix will be written to outfile in the
          'MATRIX(...)' format (FORM 3). This feature could be used, with
          clever scripting, to input a matrix directly on the command line to
          program 3dWarp.
          argument: ``-MATRIX``
          mutually_exclusive: oneline, fourxfour
oneline: (a boolean)
          indicates that the resulting matrix will simply be written as 12
          numbers on one line.
          argument: ``-ONELINE``
          mutually_exclusive: matrix, fourxfour
fourxfour: (a boolean)
          Output matrix in augmented form (last row is 0 0 0 1) This option
          does not work with -MATRIX or -ONELINE
          argument: ``-4x4``
          mutually_exclusive: matrix, oneline
num_threads: (an integer (int or long), nipy default value: 1)
          set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
          AFNI output filetype
args: (a unicode string)
          Additional parameters to the command
          argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          output file
```

References:

None None

51.5.10 CenterMass

[Link to code](#)

Wraps the executable command 3dCM.

Computes center of mass using 3dCM command

Note: By default, the output is (x,y,z) values in DICOM coordinates. But as of Dec, 2016, there are now command line switches for other options.

For complete details, see the [3dCM Documentation](#).

Examples

```
>>> from nipy.interfaces import afni
>>> cm = afni.CenterMass()
>>> cm.inputs.in_file = 'structural.nii'
>>> cm.inputs.cm_file = 'cm.txt'
>>> cm.inputs.roi_vals = [2, 10]
>>> cm.cmdline
'3dCM -roi_vals 2 10 structural.nii > cm.txt'
>>> res = 3dcm.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dCM
         argument: ``%s``, position: -2

[Optional]
cm_file: (a pathlike object or string representing a file)
         File to write center of mass to
         argument: ``> %s``, position: -1
mask_file: (a pathlike object or string representing an existing
            file)
            Only voxels with nonzero values in the provided mask will be
            averaged.
            argument: ``-mask %s``
automask: (a boolean)
            Generate the mask automatically
            argument: ``-automask``
set_cm: (a tuple of the form: (a float, a float, a float))
         After computing the center of mass, set the origin fields in the
         header so that the center of mass will be at (x,y,z) in DICOM
         coords.
         argument: ``-set %f %f %f``
local_ijk: (a boolean)
            Output values as (i,j,k) in local orientation
            argument: ``-local_ijk``
```

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```

roi_vals: (a list of items which are an integer (int or long))
    Compute center of mass for each blob with voxel value of v0, v1, v2,
    etc. This option is handy for getting ROI centers of mass.
    argument: ``-roi_vals %s``
all_rois: (a boolean)
    Don't bother listing the values of ROIs you want: The program will
    find all of them and produce a full list
    argument: ``-all_rois``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file
cm_file: (a pathlike object or string representing a file)
    file with the center of mass coordinates
cm: (a list of items which are a tuple of the form: (a float, a
    float, a float))
    center of mass

```

51.5.11 ConvertDset[Link to code](#)

Wraps the executable command ConvertDset.

Converts a surface dataset from one format to another.

For complete details, see the [ConvertDset Documentation](#).**Examples**

```

>>> from nipype.interfaces import afni
>>> convert_dset = afni.ConvertDset()
>>> convert_dset.inputs.in_file = 'lh.pial_converted.gii'
>>> convert_dset.inputs.out_type = 'niml_asc'
>>> convert_dset.inputs.out_file = 'lh.pial_converted.niml.dset'
>>> convert_dset.cmdline
'ConvertDset -o_niml_asc -input lh.pial_converted.gii -prefix lh.pial_converted.
↳niml.dset'
>>> res = convert_dset.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    input file to ConvertDset
    argument: ``-input %s``, position: -2
out_file: (a pathlike object or string representing a file)
    output file for ConvertDset
    argument: ``-prefix %s``, position: -1
out_type: ('niml' or 'niml_asc' or 'niml_bi' or '1D' or '1Dp' or
    '1Dpt' or 'gii' or 'gii_asc' or 'gii_b64' or 'gii_b64gz')

```

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```

        output type
        argument: ``-o_%s``, position: 0

[Optional]
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

51.5.12 Copy[Link to code](#)

Wraps the executable command 3dcopy.

Copies an image of one type to an image of the same or different type using 3dcopy command

For complete details, see the [3dcopy Documenta**tion**](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> copy3d = afni.Copy()
>>> copy3d.inputs.in_file = 'functional.nii'
>>> copy3d.cmdline
'3dcopy functional.nii functional_copy'
>>> res = copy3d.run() # doctest: +SKIP

```

```

>>> from copy import deepcopy
>>> copy3d_2 = deepcopy(copy3d)
>>> copy3d_2.inputs.outputtype = 'NIFTI'
>>> copy3d_2.cmdline
'3dcopy functional.nii functional_copy.nii'
>>> res = copy3d_2.run() # doctest: +SKIP

```

```

>>> copy3d_3 = deepcopy(copy3d)
>>> copy3d_3.inputs.outputtype = 'NIFTI_GZ'
>>> copy3d_3.cmdline
'3dcopy functional.nii functional_copy.nii.gz'
>>> res = copy3d_3.run() # doctest: +SKIP

```

```

>>> copy3d_4 = deepcopy(copy3d)
>>> copy3d_4.inputs.out_file = 'new_func.nii'
>>> copy3d_4.cmdline
'3dcopy functional.nii new_func.nii'
>>> res = copy3d_4.run() # doctest: +SKIP

```


Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dcopy
         argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
         output image file name
         argument: ``%s``, position: -1
verbose: (a boolean)
         print progress reports
         argument: ``-verb``
num_threads: (an integer (int or long), nipy default value: 1)
             set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
         output file
```

References:

None None

51.5.13 Dot[Link to code](#)

Wraps the executable command 3dDot.

Correlation coefficient between sub-brick pairs. All datasets in in_files list will be concatenated. You can use sub-brick selectors in the file specification. Note: This program is not efficient when more than two subbricks are input. For complete details, see the [3ddot Documenta**tion**](#).

```
>>> from nipy.interfaces import afni
>>> dot = afni.Dot()
>>> dot.inputs.in_files = ['functional.nii[0]', 'structural.nii']
>>> dot.inputs.dodice = True
>>> dot.inputs.out_file = 'out.mask_ae_dice.txt'
>>> dot.cmdline
'3dDot -dodice functional.nii[0] structural.nii  |& tee out.mask_ae_dice.txt'
>>> res = copy3d.run()  # doctest: +SKIP
```

Inputs:

```
[Optional]
in_files: (a list of items which are a pathlike object or string
         representing a file)
         list of input files, possibly with subbrick selectors
```

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```

    argument: ``%s ...``, position: -2
out_file: (a pathlike object or string representing a file)
    collect output to a file
    argument: ``|& tee %s``, position: -1
mask: (a pathlike object or string representing a file)
    Use this dataset as a mask
    argument: ``-mask %s``
mrange: (a tuple of the form: (a float, a float))
    Means to further restrict the voxels from 'mset' so that only those
    mask values within this range (inclusive) will be used.
    argument: ``-mrange %s %s``
demean: (a boolean)
    Remove the mean from each volume prior to computing the correlation
    argument: ``-demean``
docor: (a boolean)
    Return the correlation coefficient (default).
    argument: ``-docor``
dodot: (a boolean)
    Return the dot product (unscaled).
    argument: ``-dodot``
docoef: (a boolean)
    Return the least square fit coefficients {{a,b}} so that dset2 is
    approximately  $a + b \cdot \text{dset1}$ 
    argument: ``-docoef``
dosums: (a boolean)
    Return the 6 numbers  $\bar{x} = \langle x \rangle$   $\bar{y} = \langle y \rangle$   $\langle (x - \bar{x})^2 \rangle$   $\langle (y - \bar{y})^2 \rangle$ 
     $\langle (x - \bar{x})(y - \bar{y}) \rangle$  and the correlation coefficient.
    argument: ``-dosums``
dodice: (a boolean)
    Return the Dice coefficient (the Sorensen-Dice index).
    argument: ``-dodice``
doeta2: (a boolean)
    Return eta-squared (Cohen, NeuroImage 2008).
    argument: ``-doeta2``
full: (a boolean)
    Compute the whole matrix. A waste of time, but handy for parsing.
    argument: ``-full``
show_labels: (a boolean)
    Print sub-brick labels to help identify what is being correlated.
    This option is useful when you have more than 2 sub-bricks at input.
    argument: ``-show_labels``
upper: (a boolean)
    Compute upper triangular matrix
    argument: ``-upper``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          output file
```

References:

None None

51.5.14 Edge3

[Link to code](#)

Wraps the executable command 3dedge3.

Does 3D Edge detection using the library 3DEdge by Gregoire Malandain (gregoire.malandain@sophia.inria.fr). For complete details, see the [3dedge3 Documentation](#).

```
references_ = [{'entry': BibTeX('@article{Deriche1987,'
                                'author={R. Deriche}, 'title={Optimal edge detection using recursive filtering}, 'jour-
                                nal={International Journal of Computer Vision}, 'volume={2}, 'pages={167-187},
                                'year={1987}, '}),
                 'tags': ['method'], },
               {'entry': BibTeX('@article{MongaDericheMalandainCocquerez1991,'
                                'author={O. Monga, R. Deriche, G. Malandain, J.P. Cocquerez}, 'title={Recursive filtering
                                and edge tracking: two primary tools for 3D edge detection}, 'journal={Image and vision
                                computing}, 'volume={9}, 'pages={203-214}, 'year={1991}, '}),
                 'tags': ['method'], },
               ~
```

Examples

```
>>> from nipy.interfaces import afni
>>> edge3 = afni.Edge3()
>>> edge3.inputs.in_file = 'functional.nii'
>>> edge3.inputs.out_file = 'edges.nii'
>>> edge3.inputs.datum = 'byte'
>>> edge3.cmdline
'3dedge3 -input functional.nii -datum byte -prefix edges.nii'
>>> res = edge3.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dedge3
         argument: ``-input %s``, position: 0

[Optional]
out_file: (a pathlike object or string representing a file)
          output image file name
          argument: ``-prefix %s``, position: -1
datum: ('byte' or 'short' or 'float')
        specify data type for output. Valid types are 'byte', 'short' and
        'float'.
        argument: ``-datum %s``
fscale: (a boolean)
        Force scaling of the output to the maximum integer range.
        argument: ``-fscale``
        mutually_exclusive: gscale, nscale, scale_floats
```

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```

gscale: (a boolean)
    Same as '-fscale', but also forces each output sub-brick to to get
    the same scaling factor.
    argument: ``-gscale``
    mutually_exclusive: fscale, nscale, scale_floats
nscale: (a boolean)
    Don't do any scaling on output to byte or short datasets.
    argument: ``-nscale``
    mutually_exclusive: fscale, gscale, scale_floats
scale_floats: (a float)
    Multiply input by VAL, but only if the input datum is float. This is
    needed when the input dataset has a small range, like 0 to 2.0 for
    instance. With such a range, very few edges are detected due to what
    I suspect to be truncation problems. Multiplying such a dataset by
    10000 fixes the problem and the scaling is undone at the output.
    argument: ``-scale_floats %f``
    mutually_exclusive: fscale, gscale, nscale
verbose: (a boolean)
    Print out some information along the way.
    argument: ``-verbose``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.5.15 Eval[Link to code](#)Wraps the executable command `ldeval`.

Evaluates an expression that may include columns of data from one or more text files.

For complete details, see the [ldeval Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> eval = afni.Eval()
>>> eval.inputs.in_file_a = 'seed.1D'
>>> eval.inputs.in_file_b = 'resp.1D'
>>> eval.inputs.expr = 'a*b'

```

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```
>>> eval.inputs.out1D = True
>>> eval.inputs.out_file = 'data_calc.1D'
>>> eval.cmdline
'ldeval -a seed.1D -b resp.1D -expr "a*b" -1D -prefix data_calc.1D'
>>> res = eval.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file_a: (a pathlike object or string representing an existing
            file)
            input file to ldeval
            argument: ``-a %s``, position: 0
expr: (a unicode string)
      expr
      argument: ``-expr "%s"`, position: 3

[Optional]
in_file_b: (a pathlike object or string representing an existing
            file)
            operand file to ldeval
            argument: ``-b %s``, position: 1
in_file_c: (a pathlike object or string representing an existing
            file)
            operand file to ldeval
            argument: ``-c %s``, position: 2
out_file: (a pathlike object or string representing a file)
           output image file name
           argument: ``-prefix %s``
out1D: (a boolean)
        output in 1D
        argument: ``-1D``
start_idx: (an integer (int or long))
            start index for in_file_a
            requires: stop_idx
stop_idx: (an integer (int or long))
           stop index for in_file_a
           requires: start_idx
single_idx: (an integer (int or long))
             volume index for in_file_a
other: (a pathlike object or string representing a file)
       other options
num_threads: (an integer (int or long), nipy default value: 1)
              set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
             AFNI output filetype
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          output file
```

References:

None None

51.5.16 FWHMx

[Link to code](#)

Wraps the executable command 3dFWHMx.

Unlike the older 3dFWHM, this program computes FWHMs for all sub-bricks in the input dataset, each one separately. The output for each one is written to the file specified by ‘-out’. The mean (arithmetic or geometric) of all the FWHMs along each axis is written to stdout. (A non-positive output value indicates something bad happened; e.g., FWHM in z is meaningless for a 2D dataset; the estimation method computed incoherent intermediate results.)

For complete details, see the [3dFWHMx Documentation](#).

Examples

```
>>> from nipy.interfaces import afni
>>> fwhm = afni.FWHMx()
>>> fwhm.inputs.in_file = 'functional.nii'
>>> fwhm.cmdline
'3dFWHMx -input functional.nii -out functional_subbricks.out > functional_fwhmx.
  -out'
>>> res = fwhm.run() # doctest: +SKIP
```

(Classic) METHOD:

- Calculate ratio of variance of first differences to data variance.
- Should be the same as 3dFWHM for a 1-brick dataset. (But the output format is simpler to use in a script.)

Note: IMPORTANT NOTE [AFNI > 16]

A completely new method for estimating and using noise smoothness values is now available in 3dFWHMx and 3dClustSim. This method is implemented in the ‘-acf’ options to both programs. ‘ACF’ stands for (spatial) AutoCorrelation Function, and it is estimated by calculating moments of differences out to a larger radius than before.

Notably, real FMRI data does not actually have a Gaussian-shaped ACF, so the estimated ACF is then fit (in 3dFWHMx) to a mixed model (Gaussian plus mono-exponential) of the form

$$ACF(r) = a * \exp(-r * r / (2 * b * b)) + (1 - a) * \exp(-r / c)$$

where r is the radius, and a, b, c are the fitted parameters. The apparent FWHM from this model is usually somewhat larger in real data than the FWHM estimated from just the nearest-neighbor differences used in the ‘classic’ analysis.

The longer tails provided by the mono-exponential are also significant. 3dClustSim has also been modified to use the ACF model given above to generate noise random fields.

Note: TL;DR or summary

The take-awaymessage is that the ‘classic’ 3dFWHMx and 3dClustSim analysis, using a pure Gaussian ACF, is not very correct for FMRI data – I cannot speak for PET or MEG data.

Warning: Do NOT use 3dFWHMx on the statistical results (e.g., ‘-bucket’) from 3dDeconvolve or 3dREMLfit!!! The function of 3dFWHMx is to estimate the smoothness of the time series NOISE, not of the statistics. This proscription is especially true if you plan to use 3dClustSim next!!

Note: Recommendations

- For FMRI statistical purposes, you DO NOT want the FWHM to reflect the spatial structure of the underlying anatomy. Rather, you want the FWHM to reflect the spatial structure of the noise. This means that the input dataset should not have anatomical (spatial) structure.
- One good form of input is the output of '3dDeconvolve -errts', which is the dataset of residuals left over after the GLM fitted signal model is subtracted out from each voxel's time series.
- If you don't want to go to that much trouble, use '-detrend' to approximately subtract out the anatomical spatial structure, OR use the output of 3dDetrend for the same purpose.
- If you do not use '-detrend', the program attempts to find non-zero spatial structure in the input, and will print a warning message if it is detected.

Note: Notes on -demed

- I recommend this option, and it is not the default only for historical compatibility reasons. It may become the default someday.
- It is already the default in program 3dBlurToFWHM. This is the same detrending as done in 3dDespike; using $2*q+3$ basis functions for $q > 0$.
- If you don't use '-detrend', the program now [Aug 2010] checks if a large number of voxels are have significant nonzero means. If so, the program will print a warning message suggesting the use of '-detrend', since inherent spatial structure in the image will bias the estimation of the FWHM of the image time series NOISE (which is usually the point of using 3dFWHMx).

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input dataset
        argument: ``-input %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output file
        argument: ``> %s``, position: -1
out_subbricks: (a pathlike object or string representing a file)
        output file listing the subbricks FWHM
        argument: ``-out %s``
mask: (a pathlike object or string representing an existing file)
        use only voxels that are nonzero in mask
        argument: ``-mask %s``
automask: (a boolean, nipy default value: False)
        compute a mask from THIS dataset, a la 3dAutomask
        argument: ``-automask``
detrend: (a boolean or an integer (int or long), nipy default
        value: False)
        instead of demed (0th order detrending), detrend to the specified
        order. If order is not given, the program picks  $q=NT/30$ . -detrend
        disables -demed, and includes -unif.
        argument: ``-detrend``
        mutually_exclusive: demed
demed: (a boolean)
        If the input dataset has more than one sub-brick (e.g., has a time
        axis), then subtract the median of each voxel's time series before
        processing FWHM. This will tend to remove intrinsic spatial
        structure and leave behind the noise.
        argument: ``-demed``
```

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```

        mutually_exclusive: detrend
unif: (a boolean)
    If the input dataset has more than one sub-brick, then normalize
    each voxel's time series to have the same MAD before processing
    FWHM.
    argument: ``-unif``
out_detrend: (a pathlike object or string representing a file)
    Save the detrended file into a dataset
    argument: ``-detprefix %s``
geom: (a boolean)
    if in_file has more than one sub-brick, compute the final estimate
    as the geometric mean of the individual sub-brick FWHM estimates
    argument: ``-geom``
    mutually_exclusive: arith
arith: (a boolean)
    if in_file has more than one sub-brick, compute the final estimate
    as the arithmetic mean of the individual sub-brick FWHM estimates
    argument: ``-arith``
    mutually_exclusive: geom
combine: (a boolean)
    combine the final measurements along each axis
    argument: ``-combine``
compat: (a boolean)
    be compatible with the older 3dFWHM
    argument: ``-compat``
acf: (a boolean or a pathlike object or string representing a file or
    a tuple of the form: (a pathlike object or string representing an
    existing file, a float), nipype default value: False)
    computes the spatial autocorrelation
    argument: ``-acf``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file
out_subbricks: (a pathlike object or string representing an existing
    file)
    output file (subbricks)
out_detrend: (a pathlike object or string representing a file)
    output file, detrended
fwhm: (a tuple of the form: (a float, a float, a float) or a tuple of
    the form: (a float, a float, a float, a float))
    FWHM along each axis
acf_param: (a tuple of the form: (a float, a float, a float) or a
    tuple of the form: (a float, a float, a float, a float))
    fitted ACF model parameters
out_acf: (a pathlike object or string representing an existing file)
    output acf file

```


References:

None

51.5.17 GCOR[Link to code](#)Wraps the executable command `@compute_gcor`.

Computes the average correlation between every voxel and every other voxel, over any given mask.

For complete details, see the [@compute_gcor Documentation](#).**Examples**

```
>>> from nipy.interfaces import afni
>>> gcor = afni.GCOR()
>>> gcor.inputs.in_file = 'structural.nii'
>>> gcor.inputs.nfirst = 4
>>> gcor.cmdline
'@compute_gcor -nfirst 4 -input structural.nii'
>>> res = gcor.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input dataset to compute the GCOR over
         argument: ``-input %s``, position: -1

[Optional]
mask: (a pathlike object or string representing an existing file)
      mask dataset, for restricting the computation
      argument: ``-mask %s``
nfirst: (an integer (int or long))
        specify number of initial TRs to ignore
        argument: ``-nfirst %d``
no_demean: (a boolean)
           do not (need to) demean as first step
           argument: ``-no_demean``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out: (a float)
     global correlation value
```

51.5.18 LocalBistat[Link to code](#)Wraps the executable command `3dLocalBistat`.`3dLocalBistat` - computes statistics between 2 datasets, at each voxel, based on a local neighborhood of that voxel.For complete details, see the [3dLocalBistat Documentation](#).

Examples

```

>>> from nipy.interfaces import afni
>>> bistat = afni.LocalBistat()
>>> bistat.inputs.in_file1 = 'functional.nii'
>>> bistat.inputs.in_file2 = 'structural.nii'
>>> bistat.inputs.neighborhood = ('SPHERE', 1.2)
>>> bistat.inputs.stat = 'pearson'
>>> bistat.inputs.outputtype = 'NIFTI'
>>> bistat.cmdline
"3dLocalBistat -prefix functional_bistat.nii -nbhd 'SPHERE(1.2)' -stat pearson_
↳functional.nii structural.nii"
>>> res = automask.run() # doctest: +SKIP

```

Inputs:

[Mandatory]

in_file1: (a pathlike object or string representing an existing file)
 Filename of the first image
 argument: ``%s``, position: -2

in_file2: (a pathlike object or string representing an existing file)
 Filename of the second image
 argument: ``%s``, position: -1

neighborhood: (a tuple of the form: ('SPHERE' or 'RHDD' or 'TOHD', a float) or a tuple of the form: ('RECT', a tuple of the form: (a float, a float, a float)))
 The region around each voxel that will be extracted for the statistics calculation. Possible regions are: 'SPHERE', 'RHDD' (rhombic dodecahedron), 'TOHD' (truncated octahedron) with a given radius in mm or 'RECT' (rectangular block) with dimensions to specify in mm.
 argument: ``-nbhd '%s(%s)''``

stat: (a list of items which are 'pearson' or 'spearman' or 'quadrant' or 'mutinfo' or 'normuti' or 'jointent' or 'hellinger' or 'crU' or 'crM' or 'crA' or 'L2slope' or 'L1slope' or 'num' or 'ALL')
 statistics to compute. Possible names are : * pearson = Pearson correlation coefficient * spearman = Spearman correlation coefficient * quadrant = Quadrant correlation coefficient * mutinfo = Mutual Information * normuti = Normalized Mutual Information * jointent = Joint entropy * hellinger= Hellinger metric * crU = Correlation ratio (Unsymmetric) * crM = Correlation ratio (symmetrized by Multiplication) * crA = Correlation ratio (symmetrized by Addition) * L2slope = slope of least-squares (L2) linear regression of the data from dataset1 vs. the dataset2 (i.e., $d2 = a + b*d1 \Rightarrow$ this is 'b') * L1slope = slope of least-absolute-sum (L1) linear regression of the data from dataset1 vs. the dataset2 * num = number of the values in the region: with the use of -mask or -automask, the size of the region around any given voxel will vary; this option lets you map that size. * ALL = all of the above, in that order
 More than one option can be used.
 argument: ``-stat %s...``

[Optional]

mask_file: (a pathlike object or string representing an existing file)
 mask image file name. Voxels NOT in the mask will not be used in the neighborhood of any voxel. Also, a voxel NOT in the mask will have

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```

        its statistic(s) computed as zero (0).
        argument: ``-mask %s``
automask: (a boolean)
        Compute the mask as in program 3dAutomask.
        argument: ``-automask``
        mutually_exclusive: weight_file
weight_file: (a pathlike object or string representing an existing
        file)
        File name of an image to use as a weight. Only applies to 'pearson'
        statistics.
        argument: ``-weight %s``
        mutually_exclusive: automask
out_file: (a pathlike object or string representing a file)
        Output dataset.
        argument: ``-prefix %s``, position: 0
num_threads: (an integer (int or long), nipy default value: 1)
        set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
        AFNI output filetype
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        output file

```

References:

None None

51.5.19 Localstat[Link to code](#)

Wraps the executable command 3dLocalstat.

3dLocalstat - computes statistics at each voxel, based on a local neighborhood of that voxel.

For complete details, see the [3dLocalstat Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> localstat = afni.Localstat()
>>> localstat.inputs.in_file = 'functional.nii'
>>> localstat.inputs.mask_file = 'skeleton_mask.nii.gz'
>>> localstat.inputs.neighborhood = ('SPHERE', 45)
>>> localstat.inputs.stat = 'mean'
>>> localstat.inputs.nonmask = True
>>> localstat.inputs.outputtype = 'NIFTI_GZ'
>>> localstat.cmdline

```

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```
"3dLocalstat -prefix functional_localstat.nii -mask skeleton_mask.nii.gz -nbhd
↳ 'SPHERE(45.0)' -use_nonmask -stat mean functional.nii"
>>> res = localstat.run() # doctest: +SKIP
```

Inputs:

[Mandatory]

in_file: (a pathlike object or string representing an existing file)
input dataset
argument: ``%s``, position: -1

neighborhood: (a tuple of the form: ('SPHERE' or 'RHDD' or 'TOHD', a float) or a tuple of the form: ('RECT', a tuple of the form: (a float, a float, a float)))
The region around each voxel that will be extracted for the statistics calculation. Possible regions are: 'SPHERE', 'RHDD' (rhombic dodecahedron), 'TOHD' (truncated octahedron) with a given radius in mm or 'RECT' (rectangular block) with dimensions to specify in mm.
argument: ``-nbhd '%s(%s)''``

stat: (a list of items which are 'mean' or 'stdev' or 'var' or 'cvar' or 'median' or 'MAD' or 'min' or 'max' or 'absmax' or 'num' or 'sum' or 'FWHM' or 'FWHMbar' or 'rank' or 'frank' or 'P2skew' or 'ALL' or 'mMP2s' or 'mmMP2s' or a tuple of the form: ('perc', a tuple of the form: (a float, a float, a float)))
statistics to compute. Possible names are :

- * mean = average of the values
- * stdev = standard deviation
- * var = variance (stdev*stdev)
- * cvar = coefficient of variation = stdev/fabs(mean)
- * median = median of the values
- * MAD = median absolute deviation
- * min = minimum
- * max = maximum
- * absmax = maximum of the absolute values
- * num = number of the values in the region:

with the use of -mask or -automask, the size of the region around any given voxel will vary; this option lets you map that size. It may be useful if you plan to compute a t-statistic (say) from the mean and stdev outputs.

- * sum = sum of the values in the region
- * FWHM = compute (like 3dFWHM) image smoothness inside each voxel's neighborhood. Results are in 3 sub-bricks: FWHMx, FWHMy, and FWHMz. Places where an output is -1 are locations where the FWHM value could not be computed (e.g., outside the mask).
- * FWHMbar= Compute just the average of the 3 FWHM values (normally would NOT do this with FWHM also).
- * perc:P0:P1:Pstep =
Compute percentiles between P0 and P1 with a step of Pstep. Default P1 is equal to P0 and default P2 = 1
- * rank = rank of the voxel's intensity
- * frank = rank / number of voxels in neighborhood
- * P2skew = Pearson's second skewness coefficient $3 * (\text{mean} - \text{median}) / \text{stdev}$
- * ALL = all of the above, in that order (except for FWHMbar and perc).
- * mMP2s = Exactly the same output as: median, MAD, P2skew, but a little faster

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```

    * mmMP2s = Exactly the same output as: mean, median, MAD, P2skew
    More than one option can be used.
    argument: ``-stat %s...``

[Optional]
mask_file: (a pathlike object or string representing an existing
            file)
            Mask image file name. Voxels NOT in the mask will not be used in the
            neighborhood of any voxel. Also, a voxel NOT in the mask will have
            its statistic(s) computed as zero (0) unless the parameter 'nonmask'
            is set to true.
            argument: ``-mask %s``
automask: (a boolean)
            Compute the mask as in program 3dAutomask.
            argument: ``-automask``
nonmask: (a boolean)
            Voxels not in the mask WILL have their local statistics computed
            from all voxels in their neighborhood that ARE in the mask.
            * For instance, this option can be used to compute the average
            local white matter time series, even at non-WM voxels.
            argument: ``-use_nonmask``
reduce_grid: (a float or a tuple of the form: (a float, a float, a
            float))
            Compute output on a grid that is reduced by the specified factors.
            If a single value is passed, output is resampled to the specified
            isotropic grid. Otherwise, the 3 inputs describe the reduction in
            the X, Y, and Z directions. This option speeds up computations at
            the expense of resolution. It should only be used when the nbhd is
            quite large with respect to the input's resolution, and the
            resultant stats are expected to be smooth.
            argument: ``-reduce_grid %s``
            mutually_exclusive: reduce_restore_grid, reduce_max_vox
reduce_restore_grid: (a float or a tuple of the form: (a float, a
            float, a float))
            Like reduce_grid, but also resample output back to inputgrid.
            argument: ``-reduce_restore_grid %s``
            mutually_exclusive: reduce_max_vox, reduce_grid
reduce_max_vox: (a float)
            Like reduce_restore_grid, but automatically set Rx Ry Rz sothat the
            computation grid is at a resolution of nbhd/MAX_VOXvoxels.
            argument: ``-reduce_max_vox %s``
            mutually_exclusive: reduce_restore_grid, reduce_grid
grid_rmode: ('NN' or 'Li' or 'Cu' or 'Bk')
            Interpolant to use when resampling the output with
            thereduce_restore_grid option. The resampling method string RESAM
            should come from the set {'NN', 'Li', 'Cu', 'Bk'}. These stand for
            'Nearest Neighbor', 'Linear', 'Cubic', and 'Blocky' interpolation,
            respectively.
            argument: ``-grid_rmode %s``
            requires: reduce_restore_grid
quiet: (a boolean)
            Stop the highly informative progress reports.
            argument: ``-quiet``
overwrite: (a boolean)
            overwrite output file if it already exists
            argument: ``-overwrite``
out_file: (a pathlike object or string representing a file)

```

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```

    Output dataset.
    argument: ``-prefix %s``, position: 0
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.5.20 MaskTool[Link to code](#)

Wraps the executable command 3dmask_tool.

3dmask_tool - for combining/dilating/eroding/filling masks

For complete details, see the [3dmask_tool Documenta**tion**](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> masktool = afni.MaskTool()
>>> masktool.inputs.in_file = 'functional.nii'
>>> masktool.inputs.outputtype = 'NIFTI'
>>> masktool.cmdline
'3dmask_tool -prefix functional_mask.nii -input functional.nii'
>>> res = automask.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a list of items which are a pathlike object or string
    representing an existing file)
    input file or files to 3dmask_tool
    argument: ``-input %s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
    output image file name
    argument: ``-prefix %s``
count: (a boolean)
    Instead of created a binary 0/1 mask dataset, create one with counts
    of voxel overlap, i.e., each voxel will contain the number of masks
    that it is set in.

```

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```

    argument: ``-count``, position: 2
datum: ('byte' or 'short' or 'float')
    specify data type for output. Valid types are 'byte', 'short' and
    'float'.
    argument: ``-datum %s``
dilate_inputs: (a unicode string)
    Use this option to dilate and/or erode datasets as they are read.
    ex. '5 -5' to dilate and erode 5 times
    argument: ``-dilate_inputs %s``
dilate_results: (a unicode string)
    dilate and/or erode combined mask at the given levels.
    argument: ``-dilate_results %s``
frac: (a float)
    When combining masks (across datasets and sub-bricks), use this
    option to restrict the result to a certain fraction of the set of
    volumes
    argument: ``-frac %s``
inter: (a boolean)
    intersection, this means -frac 1.0
    argument: ``-inter``
union: (a boolean)
    union, this means -frac 0
    argument: ``-union``
fill_holes: (a boolean)
    This option can be used to fill holes in the resulting mask, i.e.
    after all other processing has been done.
    argument: ``-fill_holes``
fill_dirs: (a unicode string)
    fill holes only in the given directions. This option is for use with
    -fill holes. should be a single string that specifies 1-3 of the
    axes using {x,y,z} labels (i.e. dataset axis order), or using the
    labels in {R,L,A,P,I,S}.
    argument: ``-fill_dirs %s``
    requires: fill_holes
verbose: (an integer (int or long))
    specify verbosity level, for 0 to 3
    argument: ``-verb %s``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    mask file

```

References:

None None

51.5.21 Merge

[Link to code](#)

Wraps the executable command 3dmerge.

Merge or edit volumes using AFNI 3dmerge command

For complete details, see the [3dmerge Documenta**tion**](#).

Examples

```
>>> from nipy.interfaces import afni
>>> merge = afni.Merge()
>>> merge.inputs.in_files = ['functional.nii', 'functional2.nii']
>>> merge.inputs.blurfwhm = 4
>>> merge.inputs.doall = True
>>> merge.inputs.out_file = 'e7.nii'
>>> merge.cmdline
'3dmerge -lblur_fwhm 4 -doall -prefix e7.nii functional.nii functional2.nii'
>>> res = merge.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
          representing an existing file)
          argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
          output image file name
          argument: ``-prefix %s``
doall: (a boolean)
        apply options to all sub-bricks in dataset
        argument: ``-doall``
blurfwhm: (an integer (int or long))
           FWHM blur value (mm)
           argument: ``-lblur_fwhm %d``
num_threads: (an integer (int or long), nipy default value: 1)
              set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
             AFNI output filetype
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          output file
```

References:

None None

51.5.22 Notes

[Link to code](#)

Wraps the executable command 3dNotes.

A program to add, delete, and show notes for AFNI datasets.

For complete details, see the [3dNotes Documentation](#).

Examples

```
>>> from nipyre.interfaces import afni
>>> notes = afni.Notes()
>>> notes.inputs.in_file = 'functional.HEAD'
>>> notes.inputs.add = 'This note is added.'
>>> notes.inputs.add_history = 'This note is added to history.'
>>> notes.cmdline
'3dNotes -a "This note is added." -h "This note is added to history." functional.
↪HEAD'
>>> res = notes.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input file to 3dNotes
        argument: ``%s``, position: -1

[Optional]
add: (a unicode string)
     note to add
     argument: ``-a "%s"``
add_history: (a unicode string)
             note to add to history
             argument: ``-h "%s"``
             mutually_exclusive: rep_history
rep_history: (a unicode string)
             note with which to replace history
             argument: ``-HH "%s"``
             mutually_exclusive: add_history
delete: (an integer (int or long))
        delete note number num
        argument: ``-d %d``
ses: (a boolean)
     print to stdout the expanded notes
     argument: ``-ses``
out_file: (a pathlike object or string representing a file)
          output image file name
          argument: ``%s``
num_threads: (an integer (int or long), nipyre default value: 1)
             set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyre default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          output file
```

51.5.23 NwarpAdjust

[Link to code](#)

Wraps the executable command 3dNwarpAdjust.

This program takes as input a bunch of 3D warps, averages them, and computes the inverse of this average warp. It then composes each input warp with this inverse average to ‘adjust’ the set of warps. Optionally, it can also read in a set of 1-brick datasets corresponding to the input warps, and warp each of them, and average those. For complete details, see the [3dNwarpAdjust Documenta  on](#).

Examples

```
>>> from nipy.interfaces import afni
>>> adjust = afni.NwarpAdjust()
>>> adjust.inputs.warps = ['func2anat_InverseWarp.nii.gz', 'func2anat_InverseWarp.
↪nii.gz', 'func2anat_InverseWarp.nii.gz', 'func2anat_InverseWarp.nii.gz',
↪'func2anat_InverseWarp.nii.gz']
>>> adjust.cmdline
'3dNwarpAdjust -nwarp func2anat_InverseWarp.nii.gz func2anat_InverseWarp.nii.gz_
↪func2anat_InverseWarp.nii.gz func2anat_InverseWarp.nii.gz func2anat_InverseWarp.
↪nii.gz'
>>> res = adjust.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
warps: (a list of at least 5 items which are a pathlike object or
       string representing an existing file)
       List of input 3D warp datasets
       argument: ``-nwarp %s``

[Optional]
in_files: (a list of at least 5 items which are a pathlike object or
          string representing an existing file)
          List of input 3D datasets to be warped by the adjusted warp
          datasets. There must be exactly as many of these datasets as there
          are input warps.
          argument: ``-source %s``
out_file: (a pathlike object or string representing a file)
          Output mean dataset, only needed if in_files are also given. The
          output dataset will be on the common grid shared by the source
          datasets.
          argument: ``-prefix %s``
          requires: in_files
num_threads: (an integer (int or long), nipy default value: 1)
             set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
```

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```
value of class 'str', nipy default value: {}
Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
output file
```

51.5.24 NwarpApply[Link to code](#)

Wraps the executable command 3dNwarpApply.

Program to apply a nonlinear 3D warp saved from 3dQwarp (or 3dNwarpCat, etc.) to a 3D dataset, to produce a warped version of the source dataset.

For complete details, see the [3dNwarpApply Documentation](#).

Examples

```
>>> from nipy.interfaces import afni
>>> nwarp = afni.NwarpApply()
>>> nwarp.inputs.in_file = 'Fred+orig'
>>> nwarp.inputs.master = 'NWARP'
>>> nwarp.inputs.warp = "'Fred_WARP+tlrc Fred.Xaff12.1D'"
>>> nwarp.cmdline
"3dNwarpApply -source Fred+orig -interp wsinc5 -master NWARP -prefix Fred+orig_
↳Nwarp -nwarp 'Fred_WARP+tlrc Fred.Xaff12.1D'"
>>> res = nwarp.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file
         or a list of items which are a pathlike object or string
         representing an existing file)
         the name of the dataset to be warped can be multiple datasets
         argument: ``-source %s``
warp: (a string)
      the name of the warp dataset. multiple warps can be concatenated
      (make sure they exist)
      argument: ``-nwarp %s``

[Optional]
inv_warp: (a boolean)
          After the warp specified in '-nwarp' is computed, invert it
          argument: ``-iwarpp``
master: (a pathlike object or string representing an existing file)
        the name of the master dataset, which defines the output grid
        argument: ``-master %s``
interp: ('wsinc5' or 'NN' or 'nearestneighbour' or 'nearestneighbor'
         or 'linear' or 'trilinear' or 'cubic' or 'tricubic' or 'quintic'
         or 'triquintic', nipy default value: wsinc5)
        defines interpolation method to use during warp
        argument: ``-interp %s``
ainterp: ('NN' or 'nearestneighbour' or 'nearestneighbor' or 'linear'
          or 'trilinear' or 'cubic' or 'tricubic' or 'quintic' or
          'triquintic' or 'wsinc5')
```

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```

        specify a different interpolation method than might be used for the
        warp
        argument: ``-ainterp %s``
out_file: (a pathlike object or string representing a file)
        output image file name
        argument: ``-prefix %s``
short: (a boolean)
        Write output dataset using 16-bit short integers, rather than the
        usual 32-bit floats.
        argument: ``-short``
quiet: (a boolean)
        don't be verbose :(
        argument: ``-quiet``
        mutually_exclusive: verb
verb: (a boolean)
        be extra verbose :)
        argument: ``-verb``
        mutually_exclusive: quiet
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        output file

```

51.5.25 NwarpCat[Link to code](#)

Wraps the executable command 3dNwarpCat.

Catenates (composes) 3D warps defined on a grid, OR via a matrix.

Note:

- All transformations are from DICOM xyz (in mm) to DICOM xyz.
- Matrix warps are in files that end in '.1D' or in '.txt'. A matrix warp file should have 12 numbers in it, as output (for example), by '3dAllineate -1Dmatrix_save'.
- Nonlinear warps are in dataset files (AFNI .HEAD/.BRIK or NIfTI .nii) with 3 sub-bricks giving the DICOM order xyz grid displacements in mm.
- If all the input warps are matrices, then the output is a matrix and will be written to the file 'prefix.aff12.1D'. Unless the prefix already contains the string '.1D', in which case the filename is just the prefix.
- If 'prefix' is just 'stdout', then the output matrix is written to standard output. In any of these cases, the output format is 12 numbers in one row.
- If any of the input warps are datasets, they must all be defined on the same 3D grid! And of course, then the output will be a dataset on the same grid. However, you can expand the grid using the '-expad' option.
- The order of operations in the final (output) warp is, for the case of 3 input warps:

$$\text{OUTPUT}(x) = \text{warp3}(\text{warp2}(\text{warp1}(x)))$$
 That is, warp1 is applied first, then warp2, et cetera. The 3D x coordinates are taken from each grid location in the first dataset defined on a grid.

For complete details, see the [3dNwarpCat Documentation](#).

Examples

```
>>> from nipy.interfaces import afni
>>> nwarpcat = afni.NwarpCat()
>>> nwarpcat.inputs.in_files = ['Q25_warp+tlrc.HEAD', ('IDENT', 'structural.nii')]
>>> nwarpcat.inputs.out_file = 'Fred_total_WARP'
>>> nwarpcat.cmdline
"3dNwarpCat -interp wsinc5 -prefix Fred_total_WARP Q25_warp+tlrc.HEAD
↳ 'IDENT(structural.nii)'"
>>> res = nwarpcat.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
           representing a file or a tuple of the form: ('IDENT' or 'INV' or
           'Sqrt' or 'SqrtINV', a pathlike object or string representing a
           file))
           list of tuples of 3D warps and associated functions
           argument: ``%s``, position: -1

[Optional]
space: (a string)
       string to attach to the output dataset as its atlas space marker.
       argument: ``-space %s``
inv_warp: (a boolean)
          invert the final warp before output
          argument: ``-iwarp``
interp: ('wsinc5' or 'linear' or 'quintic', nipy default value:
         wsinc5)
         specify a different interpolation method than might be used for the
         warp
         argument: ``-interp %s``
expad: (an integer (int or long))
        Pad the nonlinear warps by the given number of voxels voxels in all
        directions. The warp displacements are extended by linear
        extrapolation from the faces of the input grid..
        argument: ``-expad %d``
out_file: (a pathlike object or string representing a file)
          output image file name
          argument: ``-prefix %s``
verb: (a boolean)
       be verbose
       argument: ``-verb``
num_threads: (an integer (int or long), nipy default value: 1)
             set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          output file
```

References:

None None

51.5.26 OneDToolPy

[Link to code](#)

Wraps the executable command `1d_tool.py`.

This program is meant to read/manipulate/write/diagnose 1D datasets. Input can be specified using AFNI sub-brick[*/time*{} selectors.

```
>>> from nipy.interfaces import afni
>>> odt = afni.OneDToolPy()
>>> odt.inputs.in_file = 'f1.1D'
>>> odt.inputs.set_nruns = 3
>>> odt.inputs.demean = True
>>> odt.inputs.out_file = 'motion_dmean.1D'
>>> odt.cmdline # doctest: +ELLIPSIS
'python2 ...1d_tool.py -demean -infile f1.1D -write motion_dmean.1D -set_nruns 3'
>>> res = odt.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to OneDTool
         argument: ``-infile %s``

[Optional]
set_nruns: (an integer (int or long))
           treat the input data as if it has nruns
           argument: ``-set_nruns %d``
derivative: (a boolean)
            take the temporal derivative of each vector (done as first backward
            difference)
            argument: ``-derivative``
demean: (a boolean)
        demean each run (new mean of each run = 0.0)
        argument: ``-demean``
out_file: (a pathlike object or string representing a file)
         write the current 1D data to FILE
         argument: ``-write %s``
         mutually_exclusive: show_cormat_warnings
show_censor_count: (a boolean)
                  display the total number of censored TRs Note : if input is a valid
                  xmat.1D dataset, then the count will come from the header. Otherwise
                  the input is assumed to be a binary censorfile, and zeros are simply
                  counted.
                  argument: ``-show_censor_count``
censor_motion: (a tuple of the form: (a float, a pathlike object or
                  string representing a file))
               Tuple of motion limit and outfile prefix. need to also set set_nruns
               -r set_run_lengths
               argument: ``-censor_motion %f %s``
```

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```

censor_prev_TR: (a boolean)
    for each censored TR, also censor previous
    argument: ``-censor_prev_TR``
show_trs_uncensored: ('comma' or 'space' or 'encoded' or 'verbose')
    display a list of TRs which were not censored in the specified style
    argument: ``-show_trs_uncensored %s``
show_cormat_warnings: (a pathlike object or string representing a
    file)
    Write cormat warnings to a file
    argument: ``-show_cormat_warnings |& tee %s``, position: -1
    mutually_exclusive: out_file
show_indices_interest: (a boolean)
    display column indices for regs of interest
    argument: ``-show_indices_interest``
show_trs_run: (an integer (int or long))
    restrict -show_trs_[un]censored to the given 1-based run
    argument: ``-show_trs_run %d``
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
py27_path: (a pathlike object or string representing an existing file
    or 'python2', nipype default value: python2)
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    output of 1D_tool.py

```

References:

None None

51.5.27 ReHo[Link to code](#)

Wraps the executable command 3dReHo.

Compute regional homogeneity for a given neighbourhood.l, based on a local neighborhood of that voxel.

For complete details, see the [3dReHo Documentation](#).**Examples**

```

>>> from nipype.interfaces import afni
>>> reho = afni.ReHo()
>>> reho.inputs.in_file = 'functional.nii'
>>> reho.inputs.out_file = 'reho.nii.gz'
>>> reho.inputs.neighborhood = 'vertices'
>>> reho.cmdline
'3dReHo -prefix reho.nii.gz -inset functional.nii -nneigh 27'
>>> res = reho.run() # doctest: +SKIP

```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    input dataset
    argument: ``-inset %s``, position: 1

[Optional]
out_file: (a pathlike object or string representing a file)
    Output dataset.
    argument: ``-prefix %s``, position: 0
chi_sq: (a boolean)
    Output the Friedman chi-squared value in addition to the Kendall's
    W. This option is currently compatible only with the AFNI
    (BRIK/HEAD) output type; the chi-squared value will be the second
    sub-brick of the output dataset.
    argument: ``-chi_sq``
mask_file: (a pathlike object or string representing a file)
    Mask within which ReHo should be calculated voxelwise
    argument: ``-mask %s``
neighborhood: ('faces' or 'edges' or 'vertices')
    voxels in neighborhood. can be: * faces (for voxel and 6 facewise
    neighbors, only),
    * edges (for voxel and 18 face- and edge-wise neighbors),
    * vertices (for voxel and 26 face-, edge-, and node-wise neighbors).
    argument: ``-nneigh %s``
    mutually_exclusive: sphere, ellipsoid
sphere: (a float)
    for additional voxelwise neighborhood control, the radius R of a
    desired neighborhood can be put in; R is a floating point number,
    and must be >1. Examples of the numbers of voxels in a given radius
    are as follows (you can roughly approximate with the ol'
    4*PI*(R^3)/3 thing):
    R=2.0 -> V=33,
    R=2.3 -> V=57,
    R=2.9 -> V=93,
    R=3.1 -> V=123,
    R=3.9 -> V=251,
    R=4.5 -> V=389,
    R=6.1 -> V=949,
    but you can choose most any value.
    argument: ``-neigh_RAD %s``
    mutually_exclusive: neighborhood, ellipsoid
ellipsoid: (a tuple of the form: (a float, a float, a float))
    Tuple indicating the x, y, and z radius of an ellipsoid defining the
    neighbourhood of each voxel.
    The 'hood is then made according to the following relation: (i/A)^2 +
    (j/B)^2 + (k/C)^2 <=1.
    which will have approx. V=4*PI*A*B*C/3. The impetus for this freedom
    was for use with data having anisotropic voxel edge lengths.
    argument: ``-neigh_X %s -neigh_Y %s -neigh_Z %s``
    mutually_exclusive: sphere, neighborhood
label_set: (a pathlike object or string representing an existing
    file)
    a set of ROIs, each labelled with distinct integers. ReHo will then
    be calculated per ROI.
    argument: ``-in_rois %s``
overwrite: (a boolean)
    overwrite output file if it already exists
```

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```

        argument: ``-overwrite``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        Voxelwise regional homogeneity map
out_vals: (a pathlike object or string representing a file)
        Table of labelwise regional homogeneity values

```

51.5.28 Refit[Link to code](#)

Wraps the executable command 3drefit.

Changes some of the information inside a 3D dataset's header

For complete details, see the [3drefit Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> refit = afni.Refit()
>>> refit.inputs.in_file = 'structural.nii'
>>> refit.inputs.deoblique = True
>>> refit.cmdline
'3drefit -deoblique structural.nii'
>>> res = refit.run() # doctest: +SKIP

```

```

>>> refit_2 = afni.Refit()
>>> refit_2.inputs.in_file = 'structural.nii'
>>> refit_2.inputs.atrfloat = ("IJK_TO_DICOM_REAL", "'1 0.2 0 0 -0.2 1 0 0 0 0 1 0
↪'")
>>> refit_2.cmdline
"3drefit -atrfloat IJK_TO_DICOM_REAL '1 0.2 0 0 -0.2 1 0 0 0 0 1 0' structural.nii
↪"
>>> res = refit_2.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input file to 3drefit
        argument: ``%s``, position: -1

[Optional]
deoblique: (a boolean)
        replace current transformation matrix with cardinal matrix
        argument: ``-deoblique``
xorigin: (a unicode string)
        x distance for edge voxel offset

```

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```

        argument: ``-xorigin %s``
yorigin: (a unicode string)
        y distance for edge voxel offset
        argument: ``-yorigin %s``
zorigin: (a unicode string)
        z distance for edge voxel offset
        argument: ``-zorigin %s``
duporigin_file: (a pathlike object or string representing an existing
        file)
        Copies the xorigin, yorigin, and zorigin values from the header of
        the given dataset
        argument: ``-duporigin %s``
xdel: (a float)
        new x voxel dimension in mm
        argument: ``-xdel %f``
ydel: (a float)
        new y voxel dimension in mm
        argument: ``-ydel %f``
zdel: (a float)
        new z voxel dimension in mm
        argument: ``-zdel %f``
xyzscale: (a float)
        Scale the size of the dataset voxels by the given factor
        argument: ``-xyzscale %f``
space: ('TLRC' or 'MNI' or 'ORIG')
        Associates the dataset with a specific template type, e.g. TLRC,
        MNI, ORIG
        argument: ``-space %s``
atrcopy: (a tuple of the form: (a pathlike object or string
        representing an existing file, a unicode string))
        Copy AFNI header attribute from the given file into the header of
        the dataset(s) being modified. For more information on AFNI header
        attributes, see documentation file README.attributes. More than one
        '-atrcopy' option can be used. For AFNI advanced users only. Do NOT
        use -atrcopy or -atrstring with other modification options. See also
        -copyaux.
        argument: ``-atrcopy %s %s``
atrstring: (a tuple of the form: (a unicode string, a unicode
        string))
        Copy the last given string into the dataset(s) being modified,
        giving it the attribute name given by the last string. To be safe,
        the last string should be in quotes.
        argument: ``-atrstring %s %s``
atrfloat: (a tuple of the form: (a unicode string, a unicode string))
        Create or modify floating point attributes. The input values may be
        specified as a single string in quotes or as a 1D filename or
        string, example '1 0.2 0 0 -0.2 1 0 0 0 0 1 0' or flipZ.1D or
        '1D:1,0.2,2@0,-0.2,1,2@0,2@0,1,0'
        argument: ``-atrfloat %s %s``
atrint: (a tuple of the form: (a unicode string, a unicode string))
        Create or modify integer attributes. The input values may be
        specified as a single string in quotes or as a 1D filename or
        string, example '1 0 0 0 0 1 0 0 0 0 1 0' or flipZ.1D or
        '1D:1,0,2@0,-0,1,2@0,2@0,1,0'
        argument: ``-atrint %s %s``
saveatr: (a boolean)
        (default) Copy the attributes that are known to AFNI into the

```

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```

        dset->dbl structure thereby forcing changes to known attributes to
        be present in the output. This option only makes sense with
        -atrcopy.
        argument: ``-saveatr``
nosaveatr: (a boolean)
        Opposite of -saveatr
        argument: ``-nosaveatr``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        output file

```

51.5.29 Resample[Link to code](#)

Wraps the executable command 3dresample.

Resample or reorient an image using AFNI 3dresample command

For complete details, see the [3dresample Documenta**tion**](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> resample = afni.Resample()
>>> resample.inputs.in_file = 'functional.nii'
>>> resample.inputs.orientation= 'RPI'
>>> resample.inputs.outputtype = 'NIFTI'
>>> resample.cmdline
'3dresample -orient RPI -prefix functional_resample.nii -inset functional.nii'
>>> res = resample.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input file to 3dresample
        argument: ``-inset %s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
        output image file name
        argument: ``-prefix %s``
orientation: (a unicode string)
        new orientation code
        argument: ``-orient %s``
resample_mode: ('NN' or 'Li' or 'Cu' or 'Bk')
        resampling method from set {"NN", "Li", "Cu", "Bk"}. These are for
        "Nearest Neighbor", "Linear", "Cubic" and "Blocky" interpolation,
        respectively. Default is NN.

```

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```

        argument: ``-rmode %s``
voxel_size: (a tuple of the form: (a float, a float, a float))
    resample to new dx, dy and dz
    argument: ``-dxyz %f %f %f``
master: (a pathlike object or string representing a file)
    align dataset grid to a reference file
    argument: ``-master %s``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.5.30 TCat[Link to code](#)

Wraps the executable command 3dTcat.

Concatenate sub-bricks from input datasets into one big 3D+time dataset.

TODO Replace InputMultiPath in_files with Traits.List, if possible. Current version adds extra whitespace.

For complete details, see the [3dTcat Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> tcat = afni.TCat()
>>> tcat.inputs.in_files = ['functional.nii', 'functional2.nii']
>>> tcat.inputs.out_file= 'functional_tcat.nii'
>>> tcat.inputs.rlt = '+'
>>> tcat.cmdline
'3dTcat -rlt+ -prefix functional_tcat.nii functional.nii functional2.nii'
>>> res = tcat.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string
    representing an existing file)
    input file to 3dTcat
    argument: `` %s``, position: -1

[Optional]

```

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```

out_file: (a pathlike object or string representing a file)
    output image file name
    argument: ``-prefix %s``
rlt: ('' or '+' or '++')
    Remove linear trends in each voxel time series loaded from each
    input dataset, SEPARATELY. Option -rlt removes the least squares fit
    of 'a+b*t' to each voxel time series. Option -rlt+ adds dataset mean
    back in. Option -rlt++ adds overall mean of all dataset timeseries
    back in.
    argument: ``-rlt%s``, position: 1
verbose: (a boolean)
    Print out some verbose output as the program
    argument: ``-verb``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

51.5.31 TCatSubBrick[Link to code](#)

Wraps the executable command 3dTcat.

Hopefully a temporary function to allow sub-brick selection until afni file managment is improved.

For complete details, see the [3dTcat Documenta**tion**](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> tcsb = afni.TCatSubBrick()
>>> tcsb.inputs.in_files = [('functional.nii', "{2..$}"), ('functional2.nii', "
↳{2..$}")]
>>> tcsb.inputs.out_file= 'functional_tcat.nii'
>>> tcsb.inputs.rlt = '+'
>>> tcsb.cmdline
"3dTcat -rlt+ -prefix functional_tcat.nii functional.nii'{2..$}' functional2.nii'
↳{2..$}' "
>>> res = tcsb.run() # doctest: +SKIP

```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a tuple of the form: (a pathlike
            object or string representing an existing file, a unicode string))
            List of tuples of file names and subbrick selectors as strings. Don't
            forget to protect the single quotes in the subbrick selector so the
            contents are protected from the command line interpreter.
            argument: ``%s %s ...``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
            output image file name
            argument: ``-prefix %s``
rlt: ('' or '+' or '++')
            Remove linear trends in each voxel time series loaded from each
            input dataset, SEPARATELY. Option -rlt removes the least squares fit
            of 'a+b*t' to each voxel time series. Option -rlt+ adds dataset mean
            back in. Option -rlt++ adds overall mean of all dataset timeseries
            back in.
            argument: ``-rlt%s``, position: 1
num_threads: (an integer (int or long), nipy default value: 1)
            set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
            of class 'str' and with values which are a bytes or None or a
            value of class 'str', nipy default value: {})
            Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
            output file
```

References:

None None

51.5.32 TStat

[Link to code](#)

Wraps the executable command 3dTstat.

Compute voxel-wise statistics using AFNI 3dTstat command

For complete details, see the [3dTstat Documentation](#).

Examples

```
>>> from nipy.interfaces import afni
>>> tstat = afni.TStat()
>>> tstat.inputs.in_file = 'functional.nii'
>>> tstat.inputs.args = '-mean'
>>> tstat.inputs.out_file = 'stats'
>>> tstat.cmdline
'3dTstat -mean -prefix stats functional.nii'
>>> res = tstat.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dTstat
         argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
         output image file name
         argument: ``-prefix %s``
mask: (a pathlike object or string representing an existing file)
      mask file
      argument: ``-mask %s``
options: (a unicode string)
         selected statistical output
         argument: ``%s``
num_threads: (an integer (int or long), nipyre default value: 1)
             set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipyre default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
         output file
```

References:

None None

51.5.33 To3D

[Link to code](#)

Wraps the executable command `to3d`.

Create a 3D dataset from 2D image files using AFNI `to3d` command

For complete details, see the [to3d Documentation](#)

Examples

```
>>> from nipyre.interfaces import afni
>>> to3d = afni.To3D()
>>> to3d.inputs.datatype = 'float'
>>> to3d.inputs.in_folder = '.'
>>> to3d.inputs.out_file = 'dicomdir.nii'
>>> to3d.inputs.filetype = 'anat'
>>> to3d.cmdline # doctest: +ELLIPSIS
'to3d -datum float -anat -prefix dicomdir.nii ./*.dcm'
>>> res = to3d.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_folder: (a pathlike object or string representing an existing
           directory)
           folder with DICOM images to convert
           argument: ``%s/*.dcm``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
          output image file name
          argument: ``-prefix %s``
filetype: ('spgr' or 'fse' or 'epan' or 'anat' or 'ct' or 'spct' or
          'pet' or 'mra' or 'bmap' or 'diff' or 'omri' or 'abuc' or 'fim' or
          'fith' or 'fico' or 'fitt' or 'fift' or 'fizt' or 'fict' or 'fibt'
          or 'fibn' or 'figt' or 'fipt' or 'fbuc')
          type of datafile being converted
          argument: ``-%s``
skipoutliers: (a boolean)
              skip the outliers check
              argument: ``-skip_outliers``
assumemosaic: (a boolean)
              assume that Siemens image is mosaic
              argument: ``-assume_dicom_mosaic``
datatype: ('short' or 'float' or 'byte' or 'complex')
          set output file datatype
          argument: ``-datum %s``
funcparams: (a unicode string)
            parameters for functional data
            argument: ``-time:zt %s alt+z2``
num_threads: (an integer (int or long), nipy default value: 1)
            set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          output file
```

References:

None None

51.5.34 Undump

[Link to code](#)

Wraps the executable command 3dUndump.

3dUndump - Assembles a 3D dataset from an ASCII list of coordinates and (optionally) values.

The input file(s) are ASCII files, with one voxel specification per line. A voxel specification is 3 numbers (-ijk or -xyz coordinates), with an optional 4th number giving the voxel value. For example:
 1 2 3 3 2 1 5 5.3 6.2 3.7 // this line illustrates a comment

The first line puts a voxel (with value given by ‘-dval’) at point (1,2,3). The second line puts a voxel (with value 5) at point (3,2,1). The third line puts a voxel (with value given by ‘-dval’) at point (5.3,6.2,3.7). If -ijk is in effect, and fractional coordinates are given, they will be rounded to the nearest integers; for example, the third line would be equivalent to (i,j,k) = (5,6,4).

For complete details, see the [3dUndump Documentation](#).

Examples

```
>>> from nipy.interfaces import afni
>>> unndump = afni.Undump()
>>> unndump.inputs.in_file = 'structural.nii'
>>> unndump.inputs.out_file = 'structural_undumped.nii'
>>> unndump.cmdline
'3dUndump -prefix structural_undumped.nii -master structural.nii'
>>> res = unndump.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input file to 3dUndump, whose geometry will determinethe geometry of
        the output
        argument: ``-master %s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
        output image file name
        argument: ``-prefix %s``
mask_file: (a pathlike object or string representing a file)
        mask image file name. Only voxels that are nonzero in the mask can
        be set.
        argument: ``-mask %s``
datatype: ('short' or 'float' or 'byte')
        set output file datatype
        argument: ``-datum %s``
default_value: (a float)
        default value stored in each input voxel that does not have a value
        supplied in the input file
        argument: ``-dval %f``
fill_value: (a float)
        value, used for each voxel in the output dataset that is NOT listed
        in the input file
        argument: ``-fval %f``
coordinates_specification: ('ijk' or 'xyz')
        Coordinates in the input file as index triples (i, j, k) or spatial
        coordinates (x, y, z) in mm
        argument: ``-%s``
srad: (a float)
        radius in mm of the sphere that will be filled about each input
        (x,y,z) or (i,j,k) voxel. If the radius is not given, or is 0, then
        each input data line sets the value in only one voxel.
        argument: ``-srad %f``
orient: (a tuple of the form: ('R' or 'L', 'A' or 'P', 'I' or 'S'))
        Specifies the coordinate order used by -xyz. The code must be 3
        letters, one each from the pairs {R,L} {A,P} {I,S}. The first letter
        gives the orientation of the x-axis, the second the orientation of
        the y-axis, the third the z-axis: R = right-to-left L = left-to-
```

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```

    right A = anterior-to-posterior P = posterior-to-anterior I =
    inferior-to-superior S = superior-to-inferior If -orient isn't used,
    then the coordinate order of the -master (in_file) dataset is used
    to interpret (x,y,z) inputs.
    argument: ``-orient %s``
head_only: (a boolean)
    create only the .HEAD file which gets exploited by the AFNI matlab
    library function New_HEAD.m
    argument: ``-head_only``
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    assembled file

```

References:

None None

51.5.35 Unifize[Link to code](#)

Wraps the executable command 3dUnifize.

3dUnifize - for uniformizing image intensity

- The input dataset is supposed to be a T1-weighted volume, possibly already skull-stripped (e.g., via 3dSkullStrip). However, this program can be a useful step to take BEFORE 3dSkullStrip, since the latter program can fail if the input volume is strongly shaded – 3dUnifize will (mostly) remove such shading artifacts.
 - The output dataset has the white matter (WM) intensity approximately uniformized across space, and scaled to peak at about 1000.
 - The output dataset is always stored in float format!
 - If the input dataset has more than 1 sub-brick, only sub-brick #0 will be processed!
 - Want to correct EPI datasets for nonuniformity? You can try the new and experimental [Mar 2017] ‘-EPI’ option.
 - The principal motive for this program is for use in an image registration script, and it may or may not be useful otherwise.
 - This program replaces the older (and very different) 3dUniformize, which is no longer maintained and may subliminate at any moment. (In other words, we do not recommend the use of 3dUniformize.)
- For complete details, see the [3dUnifize Documentation](#).

Examples

```

>>> from nipy.interfaces import afni
>>> unifize = afni.Unifize()
>>> unifize.inputs.in_file = 'structural.nii'

```

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```
>>> unifiz.inputs.out_file = 'structural_unified.nii'
>>> unifiz.cmdline
'3dUnifiz -prefix structural_unified.nii -input structural.nii'
>>> res = unifiz.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dUnifiz
         argument: ``-input %s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
         output image file name
         argument: ``-prefix %s``

t2: (a boolean)
    Treat the input as if it were T2-weighted, rather than T1-weighted.
    This processing is done simply by inverting the image contrast,
    processing it as if that result were T1-weighted, and then re-
    inverting the results counts of voxel overlap, i.e., each voxel will
    contain the number of masks that it is set in.
    argument: ``-T2``

gm: (a boolean)
    Also scale to unifiz 'gray matter' = lower intensity voxels (to aid
    in registering images from different scanners).
    argument: ``-GM``

urad: (a float)
    Sets the radius (in voxels) of the ball used for the sneaky trick.
    Default value is 18.3, and should be changed proportionally if the
    dataset voxel size differs significantly from 1 mm.
    argument: ``-Urad %s``

scale_file: (a pathlike object or string representing a file)
            output file name to save the scale factor used at each voxel
            argument: ``-ssave %s``

no_duplo: (a boolean)
            Do NOT use the 'duplo down' step; this can be useful for lower
            resolution datasets.
            argument: ``-noduplo``

epi: (a boolean)
            Assume the input dataset is a T2 (or T2*) weighted EPI time series.
            After computing the scaling, apply it to ALL volumes (TRs) in the
            input dataset. That is, a given voxel will be scaled by the same
            factor at each TR. This option also implies '-noduplo' and
            '-T2'. This option turns off '-GM' if you turned it on.
            argument: ``-EPI``
            mutually_exclusive: gm
            requires: no_duplo, t2

rbt: (a tuple of the form: (a float, a float, a float))
            Option for AFNI experts only. Specify the 3 parameters for the
            algorithm:
            R = radius; same as given by option '-Urad', [default=18.3]
            b = bottom percentile of normalizing data range, [default=70.0]
            r = top percentile of normalizing data range, [default=80.0]
            argument: ``-rbt %f %f %f``

t2_up: (a float)
            Option for AFNI experts only. Set the upper percentile point used for
```

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```

T2-T1 inversion. Allowed to be anything between 90 and 100
(inclusive), with default to 98.5 (for no good reason).
argument: ``-T2up %f``
cl_frac: (a float)
Option for AFNI experts only. Set the automask 'clip level fraction'.
Must be between 0.1 and 0.9. A small fraction means to make the
initial threshold for clipping (a la 3dClipLevel) smaller, which
will tend to make the mask larger. [default=0.1]
argument: ``-clfrac %f``
quiet: (a boolean)
Don't print the progress messages.
argument: ``-quiet``
num_threads: (an integer (int or long), nipy default value: 1)
set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
AFNI output filetype
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

scale_file: (a pathlike object or string representing a file)
scale factor file
out_file: (a pathlike object or string representing an existing file)
unifized file

```

References:

None None

51.5.36 ZCutUp[Link to code](#)

Wraps the executable command 3dZcutup.

Cut z-slices from a volume using AFNI 3dZcutup command

For complete details, see the [3dZcutup Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> zcutup = afni.ZCutUp()
>>> zcutup.inputs.in_file = 'functional.nii'
>>> zcutup.inputs.out_file = 'functional_zcutup.nii'
>>> zcutup.inputs.keep= '0 10'
>>> zcutup.cmdline
'3dZcutup -keep 0 10 -prefix functional_zcutup.nii functional.nii'
>>> res = zcutup.run() # doctest: +SKIP

```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to 3dZcutup
         argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
          output image file name
          argument: ``-prefix %s``
keep: (a unicode string)
      slice range to keep in output
      argument: ``-keep %s``
num_threads: (an integer (int or long), nipy default value: 1)
             set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
            AFNI output filetype
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          output file
```

References:

None None

51.5.37 Zcat

[Link to code](#)

Wraps the executable command 3dZcat.

Copies an image of one type to an image of the same or different type using 3dZcat command

For complete details, see the [3dZcat Documentation](#).

Examples

```
>>> from nipy.interfaces import afni
>>> zcat = afni.Zcat()
>>> zcat.inputs.in_files = ['functional2.nii', 'functional3.nii']
>>> zcat.inputs.out_file = 'cat_functional.nii'
>>> zcat.cmdline
'3dZcat -prefix cat_functional.nii functional2.nii functional3.nii'
>>> res = zcat.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
          representing an existing file)
          argument: ``%s``, position: -1
```

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```
[Optional]
out_file: (a pathlike object or string representing a file)
    output dataset prefix name (default 'zcat')
    argument: ``-prefix %s``
datum: ('byte' or 'short' or 'float')
    specify data type for output. Valid types are 'byte', 'short' and
    'float'.
    argument: ``-datum %s``
verb: (a boolean)
    print out some verbatimness as the program proceeds.
    argument: ``-verb``
fscale: (a boolean)
    Force scaling of the output to the maximum integer range. This only
    has effect if the output datum is byte or short (either forced or
    defaulted). This option is sometimes necessary to eliminate
    unpleasant truncation artifacts.
    argument: ``-fscale``
    mutually_exclusive: nscale
nscale: (a boolean)
    Don't do any scaling on output to byte or short datasets. This may
    be especially useful when operating on mask datasets whose output
    values are only 0's and 1's.
    argument: ``-nscale``
    mutually_exclusive: fscale
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
    output file
```

References:

None None

51.5.38 Zeropad[Link to code](#)

Wraps the executable command 3dZeropad.

Adds planes of zeros to a dataset (i.e., pads it out).

For complete details, see the [3dZeropad Documentation](#).**Examples**

```

>>> from nipy.interfaces import afni
>>> zeropad = afni.Zeropad()
>>> zeropad.inputs.in_files = 'functional.nii'
>>> zeropad.inputs.out_file = 'pad_functional.nii'
>>> zeropad.inputs.I = 10
>>> zeropad.inputs.S = 10
>>> zeropad.inputs.A = 10
>>> zeropad.inputs.P = 10
>>> zeropad.inputs.R = 10
>>> zeropad.inputs.L = 10
>>> zeropad.cmdline
'3dZeropad -A 10 -I 10 -L 10 -P 10 -R 10 -S 10 -prefix pad_functional.nii_
↳functional.nii'
>>> res = zeropad.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a pathlike object or string representing an existing file)
          input dataset
          argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
          output dataset prefix name (default 'zeropad')
          argument: ``-prefix %s``

I: (an integer (int or long))
   adds 'n' planes of zero at the Inferior edge
   argument: ``-I %i``
   mutually_exclusive: master

S: (an integer (int or long))
   adds 'n' planes of zero at the Superior edge
   argument: ``-S %i``
   mutually_exclusive: master

A: (an integer (int or long))
   adds 'n' planes of zero at the Anterior edge
   argument: ``-A %i``
   mutually_exclusive: master

P: (an integer (int or long))
   adds 'n' planes of zero at the Posterior edge
   argument: ``-P %i``
   mutually_exclusive: master

L: (an integer (int or long))
   adds 'n' planes of zero at the Left edge
   argument: ``-L %i``
   mutually_exclusive: master

R: (an integer (int or long))
   adds 'n' planes of zero at the Right edge
   argument: ``-R %i``
   mutually_exclusive: master

z: (an integer (int or long))
   adds 'n' planes of zero on EACH of the dataset z-axis (slice-
   direction) faces
   argument: ``-z %i``
   mutually_exclusive: master

RL: (an integer (int or long))
     specify that planes should be added or cut symmetrically to make the
     resulting volume haveN slices in the right-left direction

```

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```

        argument: ``-RL %i``
        mutually_exclusive: master
AP: (an integer (int or long))
    specify that planes should be added or cut symmetrically to make the
    resulting volume haveN slices in the anterior-posterior direction
    argument: ``-AP %i``
    mutually_exclusive: master
IS: (an integer (int or long))
    specify that planes should be added or cut symmetrically to make the
    resulting volume haveN slices in the inferior-superior direction
    argument: ``-IS %i``
    mutually_exclusive: master
mm: (a boolean)
    pad counts 'n' are in mm instead of slices, where each 'n' is an
    integer and at least 'n' mm of slices will be added/removed; e.g., n
    = 3 and slice thickness = 2.5 mm ==> 2 slices added
    argument: ``-mm``
    mutually_exclusive: master
master: (a pathlike object or string representing a file)
    match the volume described in dataset 'mset', where mset must have
    the same orientation and grid spacing as dataset to be padded. the
    goal of -master is to make the output dataset from 3dZeropad match
    the spatial 'extents' of mset by adding or subtracting slices as
    needed. You can't use -I, -S, ..., or -mm with -master
    argument: ``-master %s``
    mutually_exclusive: I, S, A, P, L, R, z, RL, AP, IS, mm
num_threads: (an integer (int or long), nipy default value: 1)
    set number of threads
outputtype: ('NIFTI' or 'AFNI' or 'NIFTI_GZ')
    AFNI output filetype
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output file

```

References:

None None

52.1 interfaces.ants.legacy

52.1.1 GenWarpFields

[Link to code](#)

Wraps the executable command `antsIntroduction.sh`.

Inputs:

```
[Mandatory]
reference_image: (a pathlike object or string representing an
                  existing file)
                  template file to warp to
                  argument: ``-r %s``
input_image: (a pathlike object or string representing an existing
              file)
              input image to warp to template
              argument: ``-i %s``

[Optional]
dimension: (3 or 2, nipy default value: 3)
            image dimension (2 or 3)
            argument: ``-d %d``, position: 1
force_proceed: (a boolean)
                force script to proceed even if headers may be incompatible
                argument: ``-f 1``
inverse_warp_template_labels: (a boolean)
                               Applies inverse warp to the template labels to estimate label
                               positions in target space (use for template-based segmentation)
                               argument: ``-l``
max_iterations: (a list of items which are an integer (int or long))
                 maximum number of iterations (must be list of integers in the form
                 [J,K,L...]: J = coarsest resolution iterations, K = middle
                 resolution iterations, L = fine resolution iterations
                 argument: ``-m %s``
bias_field_correction: (a boolean)
                       Applies bias field correction to moving image
```

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```

        argument: ``-n 1``
similarity_metric: ('PR' or 'CC' or 'MI' or 'MSQ')
    Type of similartiy metric used for registration (CC = cross
    correlation, MI = mutual information, PR = probability mapping, MSQ
    = mean square difference)
    argument: ``-s %s``
transformation_model: ('GR' or 'EL' or 'SY' or 'S2' or 'EX' or 'DD'
    or 'RI' or 'RA', nipy default value: GR)
    Type of transofmrtaion model used for registration (EL = elastic
    transformation model, SY = SyN with time, arbitrary number of time
    points, S2 = SyN with time optimized for 2 time points, GR = greedy
    SyN, EX = exponential, DD = diffeomorphic demons style exponential
    mapping, RI = purely rigid, RA = affine rigid
    argument: ``-t %s``
out_prefix: (a unicode string, nipy default value: ants_)
    Prefix that is prepended to all output files (default = ants_)
    argument: ``-o %s``
quality_check: (a boolean)
    Perform a quality check of the result
    argument: ``-q 1``
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

affine_transformation: (a pathlike object or string representing an
    existing file)
    affine (prefix_Affine.txt)
warp_field: (a pathlike object or string representing an existing
    file)
    warp field (prefix_Warp.nii)
inverse_warp_field: (a pathlike object or string representing an
    existing file)
    inverse warp field (prefix_InverseWarp.nii)
input_file: (a pathlike object or string representing an existing
    file)
    input image (prefix_repaired.nii)
output_file: (a pathlike object or string representing an existing
    file)
    output image (prefix_deformed.nii)

```

52.1.2 antsIntroduction[Link to code](#)Wraps the executable command `antsIntroduction.sh`.

Uses ANTS to generate matrices to warp data from one space to another.

Examples

```
>>> from nipyne.interfaces.ants.legacy import antsIntroduction
>>> warp = antsIntroduction()
>>> warp.inputs.reference_image = 'Template_6.nii'
>>> warp.inputs.input_image = 'structural.nii'
>>> warp.inputs.max_iterations = [30,90,20]
>>> warp.cmdline
'antsIntroduction.sh -d 3 -i structural.nii -m 30x90x20 -o ants_ -r Template_6.
↪nii -t GR'
```

Inputs:

```
[Mandatory]
reference_image: (a pathlike object or string representing an
existing file)
template file to warp to
argument: ``-r %s``
input_image: (a pathlike object or string representing an existing
file)
input image to warp to template
argument: ``-i %s``

[Optional]
dimension: (3 or 2, nipyne default value: 3)
image dimension (2 or 3)
argument: ``-d %d``, position: 1
force_proceed: (a boolean)
force script to proceed even if headers may be incompatible
argument: ``-f 1``
inverse_warp_template_labels: (a boolean)
Applies inverse warp to the template labels to estimate label
positions in target space (use for template-based segmentation)
argument: ``-l``
max_iterations: (a list of items which are an integer (int or long))
maximum number of iterations (must be list of integers in the form
[J,K,L...]: J = coarsest resolution iterations, K = middle
resolution iterations, L = fine resolution iterations
argument: ``-m %s``
bias_field_correction: (a boolean)
Applies bias field correction to moving image
argument: ``-n 1``
similarity_metric: ('PR' or 'CC' or 'MI' or 'MSQ')
Type of similarity metric used for registration (CC = cross
correlation, MI = mutual information, PR = probability mapping, MSQ
= mean square difference)
argument: ``-s %s``
transformation_model: ('GR' or 'EL' or 'SY' or 'S2' or 'EX' or 'DD'
or 'RI' or 'RA', nipyne default value: GR)
Type of transformation model used for registration (EL = elastic
transformation model, SY = SyN with time, arbitrary number of time
points, S2 = SyN with time optimized for 2 time points, GR = greedy
SyN, EX = exponential, DD = diffeomorphic demons style exponential
mapping, RI = purely rigid, RA = affine rigid
argument: ``-t %s``
out_prefix: (a unicode string, nipyne default value: ants_)
Prefix that is prepended to all output files (default = ants_)
argument: ``-o %s``
```

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```

quality_check: (a boolean)
    Perform a quality check of the result
    argument: ``-q 1``
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

affine_transformation: (a pathlike object or string representing an
    existing file)
    affine (prefix_Affine.txt)
warp_field: (a pathlike object or string representing an existing
    file)
    warp field (prefix_Warp.nii)
inverse_warp_field: (a pathlike object or string representing an
    existing file)
    inverse warp field (prefix_InverseWarp.nii)
input_file: (a pathlike object or string representing an existing
    file)
    input image (prefix_repaired.nii)
output_file: (a pathlike object or string representing an existing
    file)
    output image (prefix_deformed.nii)

```

52.1.3 buildtemplateparallel[Link to code](#)

Wraps the executable command buildtemplateparallel.sh.

Generate a optimal average template

Warning: This can take a VERY long time to complete**Examples**

```

>>> from nipy.interfaces.ants.legacy import buildtemplateparallel
>>> tmp1 = buildtemplateparallel()
>>> tmp1.inputs.in_files = ['T1.nii', 'structural.nii']
>>> tmp1.inputs.max_iterations = [30, 90, 20]
>>> tmp1.cmdline
'buildtemplateparallel.sh -d 3 -i 4 -m 30x90x20 -o antsTMPL_ -c 0 -t GR T1.nii_
↳structural.nii'

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string
    representing an existing file)
    list of images to generate template from

```

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```

        argument: ``%s``, position: -1

[Optional]
dimension: (3 or 2 or 4, nipy default value: 3)
    image dimension (2, 3 or 4)
    argument: ``-d %d``, position: 1
out_prefix: (a unicode string, nipy default value: antsTMPL_)
    Prefix that is prepended to all output files (default = antsTMPL_)
    argument: ``-o %s``
parallelization: (0 or 1 or 2, nipy default value: 0)
    control for parallel processing (0 = serial, 1 = use PBS, 2 = use
    PEXEC, 3 = use Apple XGrid)
    argument: ``-c %d``
gradient_step_size: (a float)
    smaller magnitude results in more cautious steps (default = .25)
    argument: ``-g %f``
iteration_limit: (an integer (int or long), nipy default value: 4)
    iterations of template construction
    argument: ``-i %d``
num_cores: (an integer (int or long))
    Requires parallelization = 2 (PEXEC). Sets number of cpu cores to
    use
    argument: ``-j %d``
    requires: parallelization
max_iterations: (a list of items which are an integer (int or long))
    maximum number of iterations (must be list of integers in the form
    [J,K,L...]: J = coarsest resolution iterations, K = middle
    resolution iterations, L = fine resolution iterations
    argument: ``-m %s``
bias_field_correction: (a boolean)
    Applies bias field correction to moving image
    argument: ``-n 1``
rigid_body_registration: (a boolean)
    registers inputs before creating template (useful if no initial
    template available)
    argument: ``-r 1``
similarity_metric: ('PR' or 'CC' or 'MI' or 'MSQ')
    Type of similartiy metric used for registration (CC = cross
    correlation, MI = mutual information, PR = probability mapping, MSQ
    = mean square difference)
    argument: ``-s %s``
transformation_model: ('GR' or 'EL' or 'SY' or 'S2' or 'EX' or 'DD',
    nipy default value: GR)
    Type of transofmrtaion model used for registration (EL = elastic
    transformation model, SY = SyN with time, arbitrary number of time
    points, S2 = SyN with time optimized for 2 time points, GR = greedy
    SyN, EX = exponential, DD = diffeomorphic demons style exponential
    mapping
    argument: ``-t %s``
use_first_as_target: (a boolean)
    uses first volume as target of all inputs. When not used, an
    unbiased average image is used to start.
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``

```

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```
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
final_template_file: (a pathlike object or string representing an
                      existing file)
                      final ANTS template
template_files: (a list of items which are a pathlike object or
                 string representing an existing file)
                 Templates from different stages of iteration
subject_outfiles: (a list of items which are a pathlike object or
                   string representing an existing file)
                   Outputs for each input image. Includes warp field, inverse warp,
                   Affine, original image (repaired) and warped image (deformed)
```

52.2 interfaces.ants.registration

52.2.1 CompositeTransformUtil

[Link to code](#)

Wraps the executable command CompositeTransformUtil.

ANTs utility which can combine or break apart transform files into their individual constituent components.

Examples

```
>>> from nipy.interfaces.ants import CompositeTransformUtil
>>> tran = CompositeTransformUtil()
>>> tran.inputs.process = 'disassemble'
>>> tran.inputs.in_file = 'output_Composite.h5'
>>> tran.cmdline
'CompositeTransformUtil --disassemble output_Composite.h5 transform'
>>> tran.run() # doctest: +SKIP
```

example for assembling transformation files

```
>>> from nipy.interfaces.ants import CompositeTransformUtil
>>> tran = CompositeTransformUtil()
>>> tran.inputs.process = 'assemble'
>>> tran.inputs.out_file = 'my.h5'
>>> tran.inputs.in_file = ['AffineTransform.mat', 'DisplacementFieldTransform.nii.
↳gz']
>>> tran.cmdline
'CompositeTransformUtil --assemble my.h5 AffineTransform.mat_
↳DisplacementFieldTransform.nii.gz '
>>> tran.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a list of items which are a pathlike object or string
          representing an existing file)
          Input transform file(s)
          argument: ``%s...``, position: 3
```

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```
[Optional]
process: ('assemble' or 'disassemble', nipyne default value:
        assemble)
        What to do with the transform inputs (assemble or disassemble)
        argument: ``--%s``, position: 1
out_file: (a pathlike object or string representing a file)
        Output file path (only used for disassembly).
        argument: ``%s``, position: 2
output_prefix: (a unicode string, nipyne default value: transform)
        A prefix that is prepended to all output files (only used for
        assembly).
        argument: ``%s``, position: 4
num_threads: (an integer (int or long), nipyne default value: 1)
        Number of ITK threads to use
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipyne default value: {})
        Environment variables
```

Outputs:

```
affine_transform: (a pathlike object or string representing a file)
        Affine transform component
displacement_field: (a pathlike object or string representing a file)
        Displacement field component
out_file: (a pathlike object or string representing a file)
        Compound transformation file
```

52.2.2 MeasureImageSimilarity

[Link to code](#)

Wraps the executable command MeasureImageSimilarity.

Examples

```
>>> from nipyne.interfaces.ants import MeasureImageSimilarity
>>> sim = MeasureImageSimilarity()
>>> sim.inputs.dimension = 3
>>> sim.inputs.metric = 'MI'
>>> sim.inputs.fixed_image = 'T1.nii'
>>> sim.inputs.moving_image = 'resting.nii'
>>> sim.inputs.metric_weight = 1.0
>>> sim.inputs.radius_or_number_of_bins = 5
>>> sim.inputs.sampling_strategy = 'Regular'
>>> sim.inputs.sampling_percentage = 1.0
>>> sim.inputs.fixed_image_mask = 'mask.nii'
>>> sim.inputs.moving_image_mask = 'mask.nii.gz'
>>> sim.cmdline
'MeasureImageSimilarity --dimensionality 3 --masks ["mask.nii","mask.nii.gz"] --
↪metric MI["T1.nii","resting.nii",1.0,5,Regular,1.0]'
```

Inputs:

```

[Mandatory]
fixed_image: (a pathlike object or string representing an existing
              file)
              Image to which the moving image is warped
moving_image: (a pathlike object or string representing an existing
              file)
              Image to apply transformation to (generally a coregistered
              functional)
metric: ('CC' or 'MI' or 'Mattes' or 'MeanSquares' or 'Demons' or
         'GC')
         argument: ``%s``
radius_or_number_of_bins: (an integer (int or long))
                          The number of bins in each stage for the MI and Mattes metric, or
                          the radius for other metrics
                          requires: metric
sampling_percentage: (0.0 <= a floating point number <= 1.0)
                    Percentage of points accessible to the sampling strategy over which
                    to optimize the metric.
                    requires: metric

[Optional]
dimension: (2 or 3 or 4)
           Dimensionality of the fixed/moving image pair
           argument: ``--dimensionality %d``, position: 1
metric_weight: (a float, nipy default value: 1.0)
               The "metricWeight" variable is not used.
               requires: metric
sampling_strategy: ('None' or 'Regular' or 'Random', nipy default
                   value: None)
                   Manner of choosing point set over which to optimize the metric.
                   Defaults to "None" (i.e. a dense sampling of one sample per voxel).
                   requires: metric
fixed_image_mask: (a pathlike object or string representing an
                  existing file)
                  mask used to limit metric sampling region of the fixed image
                  argument: ``%s``
moving_image_mask: (a pathlike object or string representing an
                   existing file)
                   mask used to limit metric sampling region of the moving image
                   requires: fixed_image_mask
num_threads: (an integer (int or long), nipy default value: 1)
             Number of ITK threads to use
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables

```

Outputs:

```

similarity: (a float)

```

52.2.3 Registration

[Link to code](#)

Wraps the executable command `antsRegistration`.

ANTs Registration command for registration of images

`antsRegistration` registers a `moving_image` to a `fixed_image`, using a predefined (sequence of) cost function(s) and transformation operations. The cost function is defined using one or more ‘metrics’, specifically local cross-correlation (CC), Mean Squares (MeanSquares), Demons (Demons), global correlation (GC), or Mutual Information (Mattes or MI).

ANTS can use both linear (Translation, Rigid, Affine, CompositeAffine, or Translation) and non-linear transformations (BSpline, GaussianDisplacementField, TimeVaryingVelocityField, TimeVaryingBSplineVelocityField, SyN, BSplineSyN, Exponential, or BSplineExponential). Usually, registration is done in multiple *stages*. For example first an Affine, then a Rigid, and ultimately a non-linear (Syn)-transformation.

`antsRegistration` can be initialized using one or more transforms from `moving_image` to `fixed_image` with the `initial_moving_transform`-input. For example, when you already have a warpfield that corrects for geometrical distortions in an EPI (functional) image, that you want to apply before an Affine registration to a structural image. You could put this transform into ‘`initial_moving_transform`’.

The Registration-interface can output the resulting transform(s) that map `moving_image` to `fixed_image` in a single file as a `composite_transform` (if `write_composite_transform` is set to `True`), or a list of transforms as `forwards_transforms`. It can also output inverse transforms (from `fixed_image` to `moving_image`) in a similar fashion using `inverse_composite_transform`. Note that the order of `forward_transforms` is in ‘natural’ order: the first element should be applied first, the last element should be applied last.

Note, however, that ANTS tools always apply lists of transformations in reverse order (the last transformation in the list is applied first). Therefore, if the output `forward_transforms` is a list, one can not directly feed it into, for example, `ants.ApplyTransforms`. To make `ants.ApplyTransforms` apply the transformations in the same order as `ants.Registration`, you have to provide the list of transformations in reverse order from `forward_transforms`. `reverse_forward_transforms` outputs `forward_transforms` in reverse order and can be used for this purpose. Note also that, because `composite_transform` is always a single file, this output is preferred for most use-cases.

More information can be found in the [ANTS manual](#).

See below for some useful examples.

Examples

Set up a Registration node with some default settings. This Node registers ‘`fixed1.nii`’ to ‘`moving1.nii`’ by first fitting a linear ‘Affine’ transformation, and then a non-linear ‘SyN’ transformation, both using the Mutual Information-cost metric.

The registration is initialized by first applying the (linear) transform `trans.mat`.

```
>>> import copy, pprint
>>> from nipy.interfaces.ants import Registration
>>> reg = Registration()
>>> reg.inputs.fixed_image = 'fixed1.nii'
>>> reg.inputs.moving_image = 'moving1.nii'
>>> reg.inputs.output_transform_prefix = "output_"
>>> reg.inputs.initial_moving_transform = 'trans.mat'
>>> reg.inputs.transforms = ['Affine', 'SyN']
>>> reg.inputs.transform_parameters = [(2.0,), (0.25, 3.0, 0.0)]
>>> reg.inputs.number_of_iterations = [[1500, 200], [100, 50, 30]]
>>> reg.inputs.dimension = 3
>>> reg.inputs.write_composite_transform = True
>>> reg.inputs.collapse_output_transforms = False
>>> reg.inputs.initialize_transforms_per_stage = False
>>> reg.inputs.metric = ['Mattes']*2
>>> reg.inputs.metric_weight = [1]*2 # Default (value ignored currently by ANTs)
>>> reg.inputs.radius_or_number_of_bins = [32]*2
>>> reg.inputs.sampling_strategy = ['Random', None]
```

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```

>>> reg.inputs.sampling_percentage = [0.05, None]
>>> reg.inputs.convergence_threshold = [1.e-8, 1.e-9]
>>> reg.inputs.convergence_window_size = [20]*2
>>> reg.inputs.smoothing_sigmas = [[1,0], [2,1,0]]
>>> reg.inputs.sigma_units = ['vox'] * 2
>>> reg.inputs.shrink_factors = [[2,1], [3,2,1]]
>>> reg.inputs.use_estimate_learning_rate_once = [True, True]
>>> reg.inputs.use_histogram_matching = [True, True] # This is the default
>>> reg.inputs.output_warped_image = 'output_warped_image.nii.gz'
>>> reg.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-
↪moving-transform [ trans.mat, 0 ] --initialize-transforms-per-stage 0 --
↪interpolation Linear --output [ output_, output_warped_image.nii.gz ] --
↪transform Affine[ 2.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32, Random,
↪ 0.05 ] --convergence [ 1500x200, 1e-08, 20 ] --smoothing-sigmas 1.0x0.0vox --
↪shrink-factors 2x1 --use-estimate-learning-rate-once 1 --use-histogram-matching_
↪1 --transform SyN[ 0.25, 3.0, 0.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1,
↪ 32 ] --convergence [ 100x50x30, 1e-09, 20 ] --smoothing-sigmas 2.0x1.0x0.0vox -
↪shrink-factors 3x2x1 --use-estimate-learning-rate-once 1 --use-histogram-
↪matching 1 --winsorize-image-intensities [ 0.0, 1.0 ] --write-composite-
↪transform 1'
>>> reg.run() # doctest: +SKIP

```

Same as reg1, but first invert the initial transform ('trans.mat') before applying it.

```

>>> reg.inputs.invert_initial_moving_transform = True
>>> reg1 = copy.deepcopy(reg)
>>> reg1.inputs.winsorize_lower_quantile = 0.025
>>> reg1.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-
↪moving-transform [ trans.mat, 1 ] --initialize-transforms-per-stage 0 --
↪interpolation Linear --output [ output_, output_warped_image.nii.gz ] --
↪transform Affine[ 2.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32, Random,
↪ 0.05 ] --convergence [ 1500x200, 1e-08, 20 ] --smoothing-sigmas 1.0x0.0vox --
↪shrink-factors 2x1 --use-estimate-learning-rate-once 1 --use-histogram-matching_
↪1 --transform SyN[ 0.25, 3.0, 0.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1,
↪ 32 ] --convergence [ 100x50x30, 1e-09, 20 ] --smoothing-sigmas 2.0x1.0x0.0vox -
↪shrink-factors 3x2x1 --use-estimate-learning-rate-once 1 --use-histogram-
↪matching 1 --winsorize-image-intensities [ 0.025, 1.0 ] --write-composite-
↪transform 1'
>>> reg1.run() # doctest: +SKIP

```

Clip extremely high intensity data points using winsorize_upper_quantile. All data points higher than the 0.975 quantile are set to the value of the 0.975 quantile.

```

>>> reg2 = copy.deepcopy(reg)
>>> reg2.inputs.winsorize_upper_quantile = 0.975
>>> reg2.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-
↪moving-transform [ trans.mat, 1 ] --initialize-transforms-per-stage 0 --
↪interpolation Linear --output [ output_, output_warped_image.nii.gz ] --
↪transform Affine[ 2.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32, Random,
↪ 0.05 ] --convergence [ 1500x200, 1e-08, 20 ] --smoothing-sigmas 1.0x0.0vox --
↪shrink-factors 2x1 --use-estimate-learning-rate-once 1 --use-histogram-matching_
↪1 --transform SyN[ 0.25, 3.0, 0.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1,
↪ 32 ] --convergence [ 100x50x30, 1e-09, 20 ] --smoothing-sigmas 2.0x1.0x0.0vox -
↪shrink-factors 3x2x1 --use-estimate-learning-rate-once 1 --use-histogram-
↪matching 1 --winsorize-image-intensities [ 0.0, 0.975 ] --write-composite-
↪transform 1'

```

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Clip extremely low intensity data points using `winsorize_lower_quantile`. All data points lower than the 0.025 quantile are set to the original value at the 0.025 quantile.

```
>>> reg3 = copy.deepcopy(reg)
>>> reg3.inputs.winsorize_lower_quantile = 0.025
>>> reg3.inputs.winsorize_upper_quantile = 0.975
>>> reg3.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-
↳moving-transform [ trans.mat, 1 ] --initialize-transforms-per-stage 0 --
↳interpolation Linear --output [ output_, output_warped_image.nii.gz ] --
↳transform Affine[ 2.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32, Random,
↳0.05 ] --convergence [ 1500x200, 1e-08, 20 ] --smoothing-sigmas 1.0x0.0vox --
↳shrink-factors 2x1 --use-estimate-learning-rate-once 1 --use-histogram-matching_
↳1 --transform SyN[ 0.25, 3.0, 0.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1,
↳32 ] --convergence [ 100x50x30, 1e-09, 20 ] --smoothing-sigmas 2.0x1.0x0.0vox -
↳shrink-factors 3x2x1 --use-estimate-learning-rate-once 1 --use-histogram-
↳matching 1 --winsorize-image-intensities [ 0.025, 0.975 ] --write-composite-
↳transform 1'
```

Use float instead of double for computations (saves memory usage)

```
>>> reg3a = copy.deepcopy(reg)
>>> reg3a.inputs.float = True
>>> reg3a.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --float 1 --
↳initial-moving-transform [ trans.mat, 1 ] --initialize-transforms-per-stage 0 --
↳interpolation Linear --output [ output_, output_warped_image.nii.gz ] --
↳transform Affine[ 2.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32, Random,
↳0.05 ] --convergence [ 1500x200, 1e-08, 20 ] --smoothing-sigmas 1.0x0.0vox --
↳shrink-factors 2x1 --use-estimate-learning-rate-once 1 --use-histogram-matching_
↳1 --transform SyN[ 0.25, 3.0, 0.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1,
↳32 ] --convergence [ 100x50x30, 1e-09, 20 ] --smoothing-sigmas 2.0x1.0x0.0vox -
↳shrink-factors 3x2x1 --use-estimate-learning-rate-once 1 --use-histogram-
↳matching 1 --winsorize-image-intensities [ 0.0, 1.0 ] --write-composite-
↳transform 1'
```

Force to use double instead of float for computations (more precision and memory usage).

```
>>> reg3b = copy.deepcopy(reg)
>>> reg3b.inputs.float = False
>>> reg3b.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --float 0 --
↳initial-moving-transform [ trans.mat, 1 ] --initialize-transforms-per-stage 0 --
↳interpolation Linear --output [ output_, output_warped_image.nii.gz ] --
↳transform Affine[ 2.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32, Random,
↳0.05 ] --convergence [ 1500x200, 1e-08, 20 ] --smoothing-sigmas 1.0x0.0vox --
↳shrink-factors 2x1 --use-estimate-learning-rate-once 1 --use-histogram-matching_
↳1 --transform SyN[ 0.25, 3.0, 0.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1,
↳32 ] --convergence [ 100x50x30, 1e-09, 20 ] --smoothing-sigmas 2.0x1.0x0.0vox -
↳shrink-factors 3x2x1 --use-estimate-learning-rate-once 1 --use-histogram-
↳matching 1 --winsorize-image-intensities [ 0.0, 1.0 ] --write-composite-
↳transform 1'
```

'collapse_output_transforms' can be used to put all transformation in a single 'composite_transform'- file. Note that forward_transforms will now be an empty list.

```
>>> # Test collapse transforms flag
>>> reg4 = copy.deepcopy(reg)
>>> reg4.inputs.save_state = 'trans.mat'
>>> reg4.inputs.restore_state = 'trans.mat'
>>> reg4.inputs.initialize_transforms_per_stage = True
>>> reg4.inputs.collapse_output_transforms = True
>>> outputs = reg4._list_outputs()
>>> pprint.pprint(outputs) # doctest: +ELLIPSIS,
{'composite_transform': '...data/output_Composite.h5',
 'elapsed_time': <undefined>,
 'forward_invert_flags': [],
 'forward_transforms': [],
 'inverse_composite_transform': '...data/output_InverseComposite.h5',
 'inverse_warped_image': <undefined>,
 'metric_value': <undefined>,
 'reverse_invert_flags': [],
 'reverse_transforms': [],
 'save_state': '...data/trans.mat',
 'warped_image': '...data/output_warped_image.nii.gz'}
>>> reg4.cmdline
'antsRegistration --collapse-output-transforms 1 --dimensionality 3 --initial-
moving-transform [ trans.mat, 1 ] --initialize-transforms-per-stage 1 --
interpolation Linear --output [ output_, output_warped_image.nii.gz ] --restore-
state trans.mat --save-state trans.mat --transform Affine[ 2.0 ] --metric_
Mattes[ fixed1.nii, moving1.nii, 1, 32, Random, 0.05 ] --convergence [ 1500x200,
1e-08, 20 ] --smoothing-sigmas 1.0x0.0vox --shrink-factors 2x1 --use-estimate-
learning-rate-once 1 --use-histogram-matching 1 --transform SyN[ 0.25, 3.0, 0.0_
] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32 ] --convergence [ 100x50x30,
1e-09, 20 ] --smoothing-sigmas 2.0x1.0x0.0vox --shrink-factors 3x2x1 --use-
estimate-learning-rate-once 1 --use-histogram-matching 1 --winsorize-image-
intensities [ 0.0, 1.0 ] --write-composite-transform 1'
```

```
>>> # Test collapse transforms flag
>>> reg4b = copy.deepcopy(reg4)
>>> reg4b.inputs.write_composite_transform = False
>>> outputs = reg4b._list_outputs()
>>> pprint.pprint(outputs) # doctest: +ELLIPSIS,
{'composite_transform': <undefined>,
 'elapsed_time': <undefined>,
 'forward_invert_flags': [False, False],
 'forward_transforms': ['...data/output_0GenericAffine.mat',
 '...data/output_1Warp.nii.gz'],
 'inverse_composite_transform': <undefined>,
 'inverse_warped_image': <undefined>,
 'metric_value': <undefined>,
 'reverse_invert_flags': [True, False],
 'reverse_transforms': ['...data/output_0GenericAffine.mat',
 '...data/output_1InverseWarp.nii.gz'],
 'save_state': '...data/trans.mat',
 'warped_image': '...data/output_warped_image.nii.gz'}
>>> reg4b.aggregate_outputs() # doctest: +SKIP
>>> reg4b.cmdline
'antsRegistration --collapse-output-transforms 1 --dimensionality 3 --initial-
moving-transform [ trans.mat, 1 ] --initialize-transforms-per-stage 1 --
interpolation Linear --output [ output_, output_warped_image.nii.gz ] --restore-
state trans.mat --save-state trans.mat --transform Affine[ 2.0 ] --metric_
Mattes[ fixed1.nii, moving1.nii, 1, 32, Random, 0.05 ] --convergence [ 1500x200,
1e-08, 20 ] --smoothing-sigmas 1.0x0.0vox --shrink-factors 2x1 --use-estimate-
learning-rate-once 1 --use-histogram-matching 1 --transform SyN[ 0.25, 3.0, 0.0_
] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32 ] --convergence [ 100x50x30,
1e-09, 20 ] --smoothing-sigmas 2.0x1.0x0.0vox --shrink-factors 3x2x1 --use-
estimate-learning-rate-once 1 --use-histogram-matching 1 --winsorize-image-
intensities [ 0.0, 1.0 ] --write-composite-transform 0'
```

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One can use multiple similarity metrics in a single registration stage. The Node below first performs a linear registration using only the Mutual Information ('Mattes')-metric. In a second stage, it performs a non-linear registration ('Syn') using both a Mutual Information and a local cross-correlation ('CC')-metric. Both metrics are weighted equally ('metric_weight' is .5 for both). The Mutual Information- metric uses 32 bins. The local cross-correlations (correlations between every voxel's neighborhoods) is computed with a radius of 4.

```
>>> # Test multiple metrics per stage
>>> reg5 = copy.deepcopy(reg)
>>> reg5.inputs.fixed_image = 'fixed1.nii'
>>> reg5.inputs.moving_image = 'moving1.nii'
>>> reg5.inputs.metric = ['Mattes', ['Mattes', 'CC']]
>>> reg5.inputs.metric_weight = [1, [.5, .5]]
>>> reg5.inputs.radius_or_number_of_bins = [32, [32, 4]]
>>> reg5.inputs.sampling_strategy = ['Random', None] # use default strategy in
↳second stage
>>> reg5.inputs.sampling_percentage = [0.05, [0.05, 0.10]]
>>> reg5.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-
↳moving-transform [ trans.mat, 1 ] --initialize-transforms-per-stage 0 --
↳interpolation Linear --output [ output_, output_warped_image.nii.gz ] --
↳transform Affine[ 2.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32, Random,
↳0.05 ] --convergence [ 1500x200, 1e-08, 20 ] --smoothing-sigmas 1.0x0.0vox --
↳shrink-factors 2x1 --use-estimate-learning-rate-once 1 --use-histogram-matching_
↳1 --transform SyN[ 0.25, 3.0, 0.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 0.
↳5, 32, None, 0.05 ] --metric CC[ fixed1.nii, moving1.nii, 0.5, 4, None, 0.1 ] --
↳convergence [ 100x50x30, 1e-09, 20 ] --smoothing-sigmas 2.0x1.0x0.0vox --shrink-
↳factors 3x2x1 --use-estimate-learning-rate-once 1 --use-histogram-matching 1 --
↳winsorize-image-intensities [ 0.0, 1.0 ] --write-composite-transform 1'
```

ANTs Registration can also use multiple modalities to perform the registration. Here it is assumed that fixed1.nii and fixed2.nii are in the same space, and so are moving1.nii and moving2.nii. First, a linear registration is performed matching fixed1.nii to moving1.nii, then a non-linear registration is performed to match fixed2.nii to moving2.nii, starting from the transformation of the first step.

```
>>> # Test multiple inputs
>>> reg6 = copy.deepcopy(reg5)
>>> reg6.inputs.fixed_image = ['fixed1.nii', 'fixed2.nii']
>>> reg6.inputs.moving_image = ['moving1.nii', 'moving2.nii']
>>> reg6.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-
↳moving-transform [ trans.mat, 1 ] --initialize-transforms-per-stage 0 --
↳interpolation Linear --output [ output_, output_warped_image.nii.gz ] --
↳transform Affine[ 2.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32, Random,
↳0.05 ] --convergence [ 1500x200, 1e-08, 20 ] --smoothing-sigmas 1.0x0.0vox --
↳shrink-factors 2x1 --use-estimate-learning-rate-once 1 --use-histogram-matching_
↳1 --transform SyN[ 0.25, 3.0, 0.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 0.
↳5, 32, None, 0.05 ] --metric CC[ fixed2.nii, moving2.nii, 0.5, 4, None, 0.1 ] --
↳convergence [ 100x50x30, 1e-09, 20 ] --smoothing-sigmas 2.0x1.0x0.0vox --shrink-
↳factors 3x2x1 --use-estimate-learning-rate-once 1 --use-histogram-matching 1 --
↳winsorize-image-intensities [ 0.0, 1.0 ] --write-composite-transform 1'
```

Different methods can be used for the interpolation when applying transformations.

```
>>> # Test Interpolation Parameters (BSpline)
>>> reg7a = copy.deepcopy(reg)
>>> reg7a.inputs.interpolation = 'BSpline'
```

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```
>>> reg7a.inputs.interpolation_parameters = (3,)
>>> reg7a.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-
↪moving-transform [ trans.mat, 1 ] --initialize-transforms-per-stage 0 --
↪interpolation BSpline[ 3 ] --output [ output_, output_warped_image.nii.gz ] --
↪transform Affine[ 2.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32, Random,
↪0.05 ] --convergence [ 1500x200, 1e-08, 20 ] --smoothing-sigmas 1.0x0.0vox --
↪shrink-factors 2x1 --use-estimate-learning-rate-once 1 --use-histogram-matching_
↪1 --transform SyN[ 0.25, 3.0, 0.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1,
↪32 ] --convergence [ 100x50x30, 1e-09, 20 ] --smoothing-sigmas 2.0x1.0x0.0vox -
↪shrink-factors 3x2x1 --use-estimate-learning-rate-once 1 --use-histogram-
↪matching 1 --winsorize-image-intensities [ 0.0, 1.0 ] --write-composite-
↪transform 1'
```

```
>>> # Test Interpolation Parameters (MultiLabel/Gaussian)
>>> reg7b = copy.deepcopy(reg)
>>> reg7b.inputs.interpolation = 'Gaussian'
>>> reg7b.inputs.interpolation_parameters = (1.0, 1.0)
>>> reg7b.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-
↪moving-transform [ trans.mat, 1 ] --initialize-transforms-per-stage 0 --
↪interpolation Gaussian[ 1.0, 1.0 ] --output [ output_, output_warped_image.nii.
↪gz ] --transform Affine[ 2.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32,
↪Random, 0.05 ] --convergence [ 1500x200, 1e-08, 20 ] --smoothing-sigmas 1.0x0.
↪0vox --shrink-factors 2x1 --use-estimate-learning-rate-once 1 --use-histogram-
↪matching 1 --transform SyN[ 0.25, 3.0, 0.0 ] --metric Mattes[ fixed1.nii,
↪moving1.nii, 1, 32 ] --convergence [ 100x50x30, 1e-09, 20 ] --smoothing-sigmas_
↪2.0x1.0x0.0vox --shrink-factors 3x2x1 --use-estimate-learning-rate-once 1 --use-
↪histogram-matching 1 --winsorize-image-intensities [ 0.0, 1.0 ] --write-
↪composite-transform 1'
```

BSplineSyN non-linear registration with custom parameters.

```
>>> # Test Extended Transform Parameters
>>> reg8 = copy.deepcopy(reg)
>>> reg8.inputs.transforms = ['Affine', 'BSplineSyN']
>>> reg8.inputs.transform_parameters = [(2.0,), (0.25, 26, 0, 3)]
>>> reg8.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-
↪moving-transform [ trans.mat, 1 ] --initialize-transforms-per-stage 0 --
↪interpolation Linear --output [ output_, output_warped_image.nii.gz ] --
↪transform Affine[ 2.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32, Random,
↪0.05 ] --convergence [ 1500x200, 1e-08, 20 ] --smoothing-sigmas 1.0x0.0vox --
↪shrink-factors 2x1 --use-estimate-learning-rate-once 1 --use-histogram-matching_
↪1 --transform BSplineSyN[ 0.25, 26, 0, 3 ] --metric Mattes[ fixed1.nii, moving1.
↪nii, 1, 32 ] --convergence [ 100x50x30, 1e-09, 20 ] --smoothing-sigmas 2.0x1.
↪0x0.0vox --shrink-factors 3x2x1 --use-estimate-learning-rate-once 1 --use-
↪histogram-matching 1 --winsorize-image-intensities [ 0.0, 1.0 ] --write-
↪composite-transform 1'
```

Mask the fixed image in the second stage of the registration (but not the first).

```
>>> # Test masking
>>> reg9 = copy.deepcopy(reg)
>>> reg9.inputs.fixed_image_masks = ['NULL', 'fixed1.nii']
>>> reg9.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-
↪moving-transform [ trans.mat, 1 ] --initialize-transforms-per-stage 0 --
↪interpolation Linear --output [ output_, output_warped_image.nii.gz ] --
↪transform Affine[ 2.0 ] --metric Mattes[ fixed1.nii, moving1.nii, 1, 32, Random,
↪0.05 ] --convergence [ 1500x200, 1e-08, 20 ] --smoothing-sigmas 1.0x0.0vox --
↪shrink-factors 2x1 --use-estimate-learning-rate-once 1 --use-histogram-matching_
↪1 --masks [ NULL, NULL ] --transform SyN[ 0.25, 3.0, 0.0 ] --metric Mattes[
↪fixed1.nii, moving1.nii, 1, 32 ] --convergence [ 100x50x30, 1e-09, 20 ] --
↪smoothing-sigmas 2.0x1.0x0.0vox --shrink-factors 3x2x1 --use-estimate-learning-
```

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Here we use both a warpfield and a linear transformation, before registration commences. Note that the first transformation that needs to be applied ('ants_Warp.nii.gz') is last in the list of 'initial_moving_transform'.

```
>>> # Test initialization with multiple transforms matrices (e.g., unwarp and
    ↪ affine transform)
>>> reg10 = copy.deepcopy(reg)
>>> reg10.inputs.initial_moving_transform = ['func_to_struct.mat', 'ants_Warp.nii.
    ↪ gz']
>>> reg10.inputs.invert_initial_moving_transform = [False, False]
>>> reg10.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-
    ↪ moving-transform [ func_to_struct.mat, 0 ] [ ants_Warp.nii.gz, 0 ] --initialize-
    ↪ transforms-per-stage 0 --interpolation Linear --output [ output_, output_warped_
    ↪ image.nii.gz ] --transform Affine[ 2.0 ] --metric Mattes[ fixed1.nii, moving1.
    ↪ nii, 1, 32, Random, 0.05 ] --convergence [ 1500x200, 1e-08, 20 ] --smoothing-
    ↪ sigmas 1.0x0.0vox --shrink-factors 2x1 --use-estimate-learning-rate-once 1 --
    ↪ use-histogram-matching 1 --transform SyN[ 0.25, 3.0, 0.0 ] --metric Mattes[
    ↪ fixed1.nii, moving1.nii, 1, 32 ] --convergence [ 100x50x30, 1e-09, 20 ] --
    ↪ smoothing-sigmas 2.0x1.0x0.0vox --shrink-factors 3x2x1 --use-estimate-learning-
    ↪ rate-once 1 --use-histogram-matching 1 --winsorize-image-intensities [ 0.0, 1.0
    ↪ ] --write-composite-transform 1'
```

Inputs:

```
[Mandatory]
fixed_image: (a list of items which are a pathlike object or string
    representing an existing file)
    Image to which the moving_image should be transformed(usually a
    structural image)
moving_image: (a list of items which are a pathlike object or string
    representing an existing file)
    Image that will be registered to the space of fixed_image. This is
    the image on which the transformations will be applied to
metric: (a list of items which are 'CC' or 'MeanSquares' or 'Demons'
    or 'GC' or 'MI' or 'Mattes' or a list of items which are 'CC' or
    'MeanSquares' or 'Demons' or 'GC' or 'MI' or 'Mattes')
    the metric(s) to use for each stage. Note that multiple metrics per
    stage are not supported in ANTS 1.9.1 and earlier.
metric_weight: (a list of items which are a float or a list of items
    which are a float, nipy default value: [1.0])
    the metric weight(s) for each stage. The weights must sum to 1 per
    stage.
    requires: metric
transforms: (a list of items which are 'Rigid' or 'Affine' or
    'CompositeAffine' or 'Similarity' or 'Translation' or 'BSpline' or
    'GaussianDisplacementField' or 'TimeVaryingVelocityField' or
    'TimeVaryingBSplineVelocityField' or 'SyN' or 'BSplineSyN' or
    'Exponential' or 'BSplineExponential')
    argument: ``%s``
smoothing_sigmas: (a list of items which are a list of items which
    are a float)
shrink_factors: (a list of items which are a list of items which are
    an integer (int or long))

[Optional]
dimension: (3 or 2, nipy default value: 3)
```

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```

    image dimension (2 or 3)
    argument: ``--dimensionality %d``
fixed_image_mask: (a pathlike object or string representing an
    existing file)
    Mask used to limit metric sampling region of the fixed image in all
    stages
    argument: ``%s``
    mutually_exclusive: fixed_image_masks
fixed_image_masks: (a list of items which are a pathlike object or
    string representing an existing file or 'NULL')
    Masks used to limit metric sampling region of the fixed image,
    defined per registration stage (Use "NULL" to omit a mask at a given
    stage)
    mutually_exclusive: fixed_image_mask
moving_image_mask: (a pathlike object or string representing an
    existing file)
    mask used to limit metric sampling region of the moving image in all
    stages
    mutually_exclusive: moving_image_masks
    requires: fixed_image_mask
moving_image_masks: (a list of items which are a pathlike object or
    string representing an existing file or 'NULL')
    Masks used to limit metric sampling region of the moving image,
    defined per registration stage (Use "NULL" to omit a mask at a given
    stage)
    mutually_exclusive: moving_image_mask
save_state: (a pathlike object or string representing a file)
    Filename for saving the internal restorable state of the
    registration
    argument: ``--save-state %s``
restore_state: (a pathlike object or string representing an existing
    file)
    Filename for restoring the internal restorable state of the
    registration
    argument: ``--restore-state %s``
initial_moving_transform: (a list of items which are a pathlike
    object or string representing an existing file)
    A transform or a list of transforms that should be applied before
    the registration begins. Note that, when a list is given, the
    transformations are applied in reverse order.
    argument: ``%s``
    mutually_exclusive: initial_moving_transform_com
invert_initial_moving_transform: (a list of items which are a
    boolean)
    One boolean or a list of booleans that indicate whether the
    inverse(s) of the transform(s) defined in initial_moving_transform
    should be used.
    mutually_exclusive: initial_moving_transform_com
    requires: initial_moving_transform
initial_moving_transform_com: (0 or 1 or 2)
    Align the moving_image and fixed_image before registration using the
    geometric center of the images (=0), the image intensities (=1), or
    the origin of the images (=2).
    argument: ``%s``
    mutually_exclusive: initial_moving_transform
metric_item_trait: ('CC' or 'MeanSquares' or 'Demons' or 'GC' or 'MI'
    or 'Mattes')
```

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```

metric_stage_trait: ('CC' or 'MeanSquares' or 'Demons' or 'GC' or
                    'MI' or 'Mattes' or a list of items which are 'CC' or
                    'MeanSquares' or 'Demons' or 'GC' or 'MI' or 'Mattes')
metric_weight_item_trait: (a float, nipy default value: 1.0)
metric_weight_stage_trait: (a float or a list of items which are a
                             float)
radius_bins_item_trait: (an integer (int or long), nipy default
                        value: 5)
radius_bins_stage_trait: (an integer (int or long) or a list of items
                        which are an integer (int or long))
radius_or_number_of_bins: (a list of items which are an integer (int
                        or long) or a list of items which are an integer (int or long),
                        nipy default value: [5])
                        the number of bins in each stage for the MI and Mattes metric, the
                        radius for other metrics
                        requires: metric_weight
sampling_strategy_item_trait: ('None' or 'Regular' or 'Random' or
                             None)
sampling_strategy_stage_trait: ('None' or 'Regular' or 'Random' or
                             None or a list of items which are 'None' or 'Regular' or 'Random'
                             or None)
sampling_strategy: (a list of items which are 'None' or 'Regular' or
                  'Random' or None or a list of items which are 'None' or 'Regular'
                  or 'Random' or None)
                  the metric sampling strategy (strategies) for each stage
                  requires: metric_weight
sampling_percentage_item_trait: (0.0 <= a floating point number <=
                                1.0 or None)
sampling_percentage_stage_trait: (0.0 <= a floating point number <=
                                1.0 or None or a list of items which are 0.0 <= a floating point
                                number <= 1.0 or None)
sampling_percentage: (a list of items which are 0.0 <= a floating
                    point number <= 1.0 or None or a list of items which are 0.0 <= a
                    floating point number <= 1.0 or None)
                    the metric sampling percentage(s) to use for each stage
                    requires: sampling_strategy
use_estimate_learning_rate_once: (a list of items which are a
                                boolean)
use_histogram_matching: (a boolean or a list of items which are a
                        boolean, nipy default value: True)
                        Histogram match the images before registration.
interpolation: ('Linear' or 'NearestNeighbor' or 'CosineWindowedSinc'
               or 'WelchWindowedSinc' or 'HammingWindowedSinc' or
               'LanczosWindowedSinc' or 'BSpline' or 'MultiLabel' or 'Gaussian',
               nipy default value: Linear)
               argument: ``%s``
interpolation_parameters: (a tuple of the form: (an integer (int or
                                long)) or a tuple of the form: (a float, a float))
write_composite_transform: (a boolean, nipy default value: False)
                        argument: ``--write-composite-transform %d``
collapse_output_transforms: (a boolean, nipy default value: True)
                        Collapse output transforms. Specifically, enabling this option
                        combines all adjacent linear transforms and composes all adjacent
                        displacement field transforms before writing the results to disk.
                        argument: ``--collapse-output-transforms %d``
initialize_transforms_per_stage: (a boolean, nipy default value:
                                False)

```

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```

Initialize linear transforms from the previous stage. By enabling
this option, the current linear stage transform is directly
intialized from the previous stages linear transform; this allows
multiple linear stages to be run where each stage directly updates
the estimated linear transform from the previous stage. (e.g.
Translation -> Rigid -> Affine).
argument: ``--initialize-transforms-per-stage %d``
float: (a boolean)
Use float instead of double for computations.
argument: ``--float %d``
transform_parameters: (a list of items which are a tuple of the form:
    (a float) or a tuple of the form: (a float, a float, a float) or a
    tuple of the form: (a float, an integer (int or long), an integer
    (int or long), an integer (int or long)) or a tuple of the form:
    (a float, an integer (int or long), a float, a float, a float, a
    float) or a tuple of the form: (a float, a float, a float, an
    integer (int or long)) or a tuple of the form: (a float, an
    integer (int or long), an integer (int or long), an integer (int
    or long), an integer (int or long))
restrict_deformation: (a list of items which are a list of items
    which are 0 or 1)
This option allows the user to restrict the optimization of the
displacement field, translation, rigid or affine transform on a per-
component basis. For example, if one wants to limit the deformation
or rotation of 3-D volume to the first two dimensions, this is
possible by specifying a weight vector of '1x1x0' for a deformation
field or '1x1x0x1x1x0' for a rigid transformation. Low-dimensional
restriction only works if there are no preceding transformations.
number_of_iterations: (a list of items which are a list of items
    which are an integer (int or long))
sigma_units: (a list of items which are 'mm' or 'vox')
    units for smoothing sigmas
    requires: smoothing_sigmas
convergence_threshold: (a list of at least 1 items which are a float,
    nipy default value: [1e-06])
    requires: number_of_iterations
convergence_window_size: (a list of at least 1 items which are an
    integer (int or long), nipy default value: [10])
    requires: convergence_threshold
output_transform_prefix: (a unicode string, nipy default value:
    transform)
    argument: ``%s``
output_warped_image: (a boolean or a pathlike object or string
    representing a file)
output_inverse_warped_image: (a boolean or a pathlike object or
    string representing a file)
    requires: output_warped_image
winsorize_upper_quantile: (0.0 <= a floating point number <= 1.0,
    nipy default value: 1.0)
    The Upper quantile to clip image ranges
    argument: ``%s``
winsorize_lower_quantile: (0.0 <= a floating point number <= 1.0,
    nipy default value: 0.0)
    The Lower quantile to clip image ranges
    argument: ``%s``
verbose: (a boolean, nipy default value: False)
    argument: ``-v``

```

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```

num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

forward_transforms: (a list of items which are a pathlike object or
    string representing an existing file)
    List of output transforms for forward registration
reverse_transforms: (a list of items which are a pathlike object or
    string representing an existing file)
    List of output transforms for reverse registration
forward_invert_flags: (a list of items which are a boolean)
    List of flags corresponding to the forward transforms
reverse_invert_flags: (a list of items which are a boolean)
    List of flags corresponding to the reverse transforms
composite_transform: (a pathlike object or string representing an
    existing file)
    Composite transform file
inverse_composite_transform: (a pathlike object or string
    representing a file)
    Inverse composite transform file
warped_image: (a pathlike object or string representing a file)
    Outputs warped image
inverse_warped_image: (a pathlike object or string representing a
    file)
    Outputs the inverse of the warped image
save_state: (a pathlike object or string representing a file)
    The saved registration state to be restored
metric_value: (a float)
    the final value of metric
elapsed_time: (a float)
    the total elapsed time as reported by ANTs

```

52.2.4 RegistrationSynQuick[Link to code](#)Wraps the executable command `antsRegistrationSynQuick.sh`.Registration using a symmetric image normalization method (SyN). You can read more in Avants et al.; Med Image Anal., 2008 (<https://www.ncbi.nlm.nih.gov/pubmed/17659998>).**Examples**

```

>>> from nipy.interfaces.ants import RegistrationSynQuick
>>> reg = RegistrationSynQuick()
>>> reg.inputs.fixed_image = 'fixed1.nii'
>>> reg.inputs.moving_image = 'moving1.nii'
>>> reg.inputs.num_threads = 2
>>> reg.cmdline

```

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```
'antsRegistrationSynQuick.sh -d 3 -f fixed1.nii -r 32 -m moving1.nii -n 2 -o_
↳transform -p d -s 26 -t s'
>>> reg.run() # doctest: +SKIP
```

example for multiple images

```
>>> from nipyte.interfaces.ants import RegistrationSynQuick
>>> reg = RegistrationSynQuick()
>>> reg.inputs.fixed_image = ['fixed1.nii', 'fixed2.nii']
>>> reg.inputs.moving_image = ['moving1.nii', 'moving2.nii']
>>> reg.inputs.num_threads = 2
>>> reg.cmdline
'antsRegistrationSynQuick.sh -d 3 -f fixed1.nii -f fixed2.nii -r 32 -m moving1.
↳nii -m moving2.nii -n 2 -o transform -p d -s 26 -t s'
>>> reg.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
fixed_image: (a list of items which are a pathlike object or string
              representing an existing file)
              Fixed image or source image or reference image
              argument: ``-f %s...``
moving_image: (a list of items which are a pathlike object or string
              representing an existing file)
              Moving image or target image
              argument: ``-m %s...``

[Optional]
dimension: (3 or 2, nipyte default value: 3)
            image dimension (2 or 3)
            argument: ``-d %d``
output_prefix: (a unicode string, nipyte default value: transform)
                A prefix that is prepended to all output files
                argument: ``-o %s``
num_threads: (an integer (int or long), nipyte default value: 1)
              Number of threads (default = 1)
              argument: ``-n %d``
transform_type: ('s' or 't' or 'r' or 'a' or 'sr' or 'b' or 'br',
                 nipyte default value: s)
                transform type
                t: translation
                r: rigid
                a: rigid + affine
                s: rigid + affine + deformable syn (default)
                sr: rigid + deformable syn
                b: rigid + affine + deformable b-spline syn
                br: rigid + deformable b-spline syn
                argument: ``-t %s``
use_histogram_matching: (a boolean)
                        use histogram matching
                        argument: ``-j %d``
histogram_bins: (an integer (int or long), nipyte default value: 32)
                 histogram bins for mutual information in SyN stage (default = 32)
                 argument: ``-r %d``
spline_distance: (an integer (int or long), nipyte default value: 26)
                  spline distance for deformable B-spline SyN transform (default = 26)
                  argument: ``-s %d``
```

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```
precision_type: ('double' or 'float', nipy default value: double)
    precision type (default = double)
    argument: ``-p %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
warped_image: (a pathlike object or string representing an existing
    file)
    Warped image
inverse_warped_image: (a pathlike object or string representing an
    existing file)
    Inverse warped image
out_matrix: (a pathlike object or string representing an existing
    file)
    Affine matrix
forward_warp_field: (a pathlike object or string representing an
    existing file)
    Forward warp field
inverse_warp_field: (a pathlike object or string representing an
    existing file)
    Inverse warp field
```

52.3 interfaces.ants.resampling

52.3.1 ApplyTransforms

[Link to code](#)

Wraps the executable command antsApplyTransforms.

ApplyTransforms, applied to an input image, transforms it according to a reference image and a transform (or a set of transforms).

Examples

```
>>> from nipy.interfaces.ants import ApplyTransforms
>>> at = ApplyTransforms()
>>> at.inputs.input_image = 'moving1.nii'
>>> at.inputs.reference_image = 'fixed1.nii'
>>> at.inputs.transforms = 'identity'
>>> at.cmdline
'antsApplyTransforms --default-value 0 --float 0 --input moving1.nii --
↪interpolation Linear --output moving1_trans.nii --reference-image fixed1.nii -t_
↪identity'
```

```
>>> at = ApplyTransforms()
>>> at.inputs.dimension = 3
>>> at.inputs.input_image = 'moving1.nii'
>>> at.inputs.reference_image = 'fixed1.nii'
```

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```
>>> at.inputs.output_image = 'deformed_moving1.nii'
>>> at.inputs.interpolation = 'Linear'
>>> at.inputs.default_value = 0
>>> at.inputs.transforms = ['ants_Warp.nii.gz', 'trans.mat']
>>> at.inputs.invert_transform_flags = [False, False]
>>> at.cmdline
'antsApplyTransforms --default-value 0 --dimensionality 3 --float 0 --input_
↪moving1.nii --interpolation Linear --output deformed_moving1.nii --reference-
↪image fixed1.nii --transform [ ants_Warp.nii.gz, 0 ] --transform [ trans.mat, 0_
↪]'
```

```
>>> at1 = ApplyTransforms()
>>> at1.inputs.dimension = 3
>>> at1.inputs.input_image = 'moving1.nii'
>>> at1.inputs.reference_image = 'fixed1.nii'
>>> at1.inputs.output_image = 'deformed_moving1.nii'
>>> at1.inputs.interpolation = 'BSpline'
>>> at1.inputs.interpolation_parameters = (5,)
>>> at1.inputs.default_value = 0
>>> at1.inputs.transforms = ['ants_Warp.nii.gz', 'trans.mat']
>>> at1.inputs.invert_transform_flags = [False, False]
>>> at1.cmdline
'antsApplyTransforms --default-value 0 --dimensionality 3 --float 0 --input_
↪moving1.nii --interpolation BSpline[ 5 ] --output deformed_moving1.nii --
↪reference-image fixed1.nii --transform [ ants_Warp.nii.gz, 0 ] --transform [_
↪trans.mat, 0 ]'
```

Inputs:

[Mandatory]

input_image: (a pathlike object or string representing an existing file)
 image to apply transformation to (generally a coregistered functional)
 argument: ``--input %s``

reference_image: (a pathlike object or string representing an existing file)
 reference image space that you wish to warp INTO
 argument: ``--reference-image %s``

transforms: (a list of items which are a pathlike object or string representing an existing file or 'identity')
 transform files: will be applied in reverse order. For example, the last specified transform will be applied first.
 argument: ``%s``

[Optional]

dimension: (2 or 3 or 4)
 This option forces the image to be treated as a specified-dimensional image. If not specified, antsWarp tries to infer the dimensionality from the input image.
 argument: ``--dimensionality %d``

input_image_type: (0 or 1 or 2 or 3)
 Option specifying the input image type of scalar (default), vector, tensor, or time series.
 argument: ``--input-image-type %d``

output_image: (a unicode string)
 output file name

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```

        argument: ``--output %s``
out_postfix: (a unicode string, nipy default value: _trans)
    Postfix that is appended to all output files (default = _trans)
interpolation: ('Linear' or 'NearestNeighbor' or 'CosineWindowedSinc'
    or 'WelchWindowedSinc' or 'HammingWindowedSinc' or
    'LanczosWindowedSinc' or 'MultiLabel' or 'Gaussian' or 'BSpline',
    nipy default value: Linear)
        argument: ``%s``
interpolation_parameters: (a tuple of the form: (an integer (int or
    long)) or a tuple of the form: (a float, a float))
invert_transform_flags: (a list of items which are a boolean)
default_value: (a float, nipy default value: 0.0)
        argument: ``--default-value %g``
print_out_composite_warp_file: (a boolean)
    output a composite warp file instead of a transformed image
    requires: output_image
float: (a boolean, nipy default value: False)
    Use float instead of double for computations.
        argument: ``--float %d``
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

output_image: (a pathlike object or string representing an existing
    file)
    Warped image

```

52.3.2 ApplyTransformsToPoints[Link to code](#)

Wraps the executable command antsApplyTransformsToPoints.

ApplyTransformsToPoints, applied to an CSV file, transforms coordinates using provided transform (or a set of transforms).

Examples

```

>>> from nipy.interfaces.ants import ApplyTransforms
>>> at = ApplyTransformsToPoints()
>>> at.inputs.dimension = 3
>>> at.inputs.input_file = 'moving.csv'
>>> at.inputs.transforms = ['trans.mat', 'ants_Warp.nii.gz']
>>> at.inputs.invert_transform_flags = [False, False]
>>> at.cmdline
'antsApplyTransformsToPoints --dimensionality 3 --input moving.csv --output_
↪moving_transformed.csv --transform [ trans.mat, 0 ] --transform [ ants_Warp.nii.
↪gz, 0 ]'

```

Inputs:

```
[Mandatory]
input_file: (a pathlike object or string representing an existing
            file)
            Currently, the only input supported is a csv file with columns
            including x,y (2D), x,y,z (3D) or x,y,z,t,label (4D) column headers.
            The points should be defined in physical space. If in doubt how to
            convert coordinates from your files to the space required by
            antsApplyTransformsToPoints try creating/drawing a simple label
            volume with only one voxel set to 1 and all others set to 0. Write
            down the voxel coordinates. Then use ImageMaths LabelStats to find
            out what coordinates for this voxel antsApplyTransformsToPoints is
            expecting.
            argument: ``--input %s``
transforms: (a list of items which are a pathlike object or string
            representing an existing file)
            transforms that will be applied to the points
            argument: ``%s``

[Optional]
dimension: (2 or 3 or 4)
            This option forces the image to be treated as a specified-
            dimensional image. If not specified, antsWarp tries to infer the
            dimensionality from the input image.
            argument: ``--dimensionality %d``
output_file: (a unicode string)
            Name of the output CSV file
            argument: ``--output %s``
invert_transform_flags: (a list of items which are a boolean)
            list indicating if a transform should be reversed
num_threads: (an integer (int or long), nipy default value: 1)
            Number of ITK threads to use
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
            file)
            csv file with transformed coordinates
```

52.3.3 WarpImageMultiTransform[Link to code](#)

Wraps the executable command WarpImageMultiTransform.

Warp an image from one space to another

Examples

```
>>> from nipy.interfaces.ants import WarpImageMultiTransform
>>> wimt = WarpImageMultiTransform()
>>> wimt.inputs.input_image = 'structural.nii'
```

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```
>>> wimt.inputs.reference_image = 'ants_deformed.nii.gz'
>>> wimt.inputs.transformation_series = ['ants_Warp.nii.gz', 'ants_Affine.txt']
>>> wimt.cmdline
'WarpImageMultiTransform 3 structural.nii structural_wimt.nii -R ants_deformed.
↪nii.gz ants_Warp.nii.gz ants_Affine.txt'
```

```
>>> wimt = WarpImageMultiTransform()
>>> wimt.inputs.input_image = 'diffusion_weighted.nii'
>>> wimt.inputs.reference_image = 'functional.nii'
>>> wimt.inputs.transformation_series = ['func2anat_coreg_Affine.txt', 'func2anat_
↪InverseWarp.nii.gz', 'dwi2anat_Warp.nii.gz', 'dwi2anat_coreg_Affine.txt']
>>> wimt.inputs.invert_affine = [1] # this will invert the 1st Affine file:
↪'func2anat_coreg_Affine.txt'
>>> wimt.cmdline
'WarpImageMultiTransform 3 diffusion_weighted.nii diffusion_weighted_wimt.nii -R_
↪functional.nii -i func2anat_coreg_Affine.txt func2anat_InverseWarp.nii.gz_
↪dwi2anat_Warp.nii.gz dwi2anat_coreg_Affine.txt'
```

Inputs:

[Mandatory]

input_image: (a pathlike object or string representing a file)
 image to apply transformation to (generally a coregistered functional)
 argument: ``%s``, position: 2

transformation_series: (a list of items which are a pathlike object or string representing an existing file)
 transformation file(s) to be applied
 argument: ``%s``, position: -1

[Optional]

dimension: (3 or 2, nipy default value: 3)
 image dimension (2 or 3)
 argument: ``%d``, position: 1

output_image: (a pathlike object or string representing a file)
 name of the output warped image
 argument: ``%s``, position: 3
 mutually_exclusive: out_postfix

out_postfix: (a pathlike object or string representing a file, nipy default value: _wimt)
 Postfix that is prepended to all output files (default = _wimt)
 mutually_exclusive: output_image

reference_image: (a pathlike object or string representing a file)
 reference image space that you wish to warp INTO
 argument: ``-R %s``
 mutually_exclusive: tightest_box

tightest_box: (a boolean)
 computes tightest bounding box (overridden by reference_image if given)
 argument: ``--tightest-bounding-box``
 mutually_exclusive: reference_image

reslice_by_header: (a boolean)
 Uses orientation matrix and origin encoded in reference image file header. Not typically used with additional transforms
 argument: ``--reslice-by-header``

use_nearest: (a boolean)
 Use nearest neighbor interpolation

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```

        argument: ``--use-NN``
use_bspline: (a boolean)
    Use 3rd order B-Spline interpolation
    argument: ``--use-BSpline``
invert_affine: (a list of items which are an integer (int or long))
    List of Affine transformations to invert.E.g.: [1,4,5] inverts the
    1st, 4th, and 5th Affines found in transformation_series. Note that
    indexing starts with 1 and does not include warp fields. Affine
    transformations are distinguished from warp fields by the word
    "affine" included in their filenames.
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

output_image: (a pathlike object or string representing an existing
    file)
    Warped image

```

52.3.4 WarpTimeSeriesImageMultiTransform[Link to code](#)

Wraps the executable command WarpTimeSeriesImageMultiTransform.

Warpes a time-series from one space to another

Examples

```

>>> from nipy.interfaces.ants import WarpTimeSeriesImageMultiTransform
>>> wtsimt = WarpTimeSeriesImageMultiTransform()
>>> wtsimt.inputs.input_image = 'resting.nii'
>>> wtsimt.inputs.reference_image = 'ants_deformed.nii.gz'
>>> wtsimt.inputs.transformation_series = ['ants_Warp.nii.gz','ants_Affine.txt']
>>> wtsimt.cmdline
'WarpTimeSeriesImageMultiTransform 4 resting.nii resting_wtsimt.nii -R ants_
↳deformed.nii.gz ants_Warp.nii.gz ants_Affine.txt'

```

```

>>> wtsimt = WarpTimeSeriesImageMultiTransform()
>>> wtsimt.inputs.input_image = 'resting.nii'
>>> wtsimt.inputs.reference_image = 'ants_deformed.nii.gz'
>>> wtsimt.inputs.transformation_series = ['ants_Warp.nii.gz','ants_Affine.txt']
>>> wtsimt.inputs.invert_affine = [1] # # this will invert the 1st Affine file:
↳ants_Affine.txt
>>> wtsimt.cmdline
'WarpTimeSeriesImageMultiTransform 4 resting.nii resting_wtsimt.nii -R ants_
↳deformed.nii.gz ants_Warp.nii.gz -i ants_Affine.txt'

```

Inputs:

```

[Mandatory]
input_image: (a pathlike object or string representing a file)
    image to apply transformation to (generally a coregistered
    functional)
    argument: ``%s``
transformation_series: (a list of items which are a pathlike object
    or string representing an existing file)
    transformation file(s) to be applied
    argument: ``%s``

[Optional]
dimension: (4 or 3, nipy default value: 4)
    image dimension (3 or 4)
    argument: ``%d``, position: 1
out_postfix: (a unicode string, nipy default value: _wtsimt)
    Postfix that is prepended to all output files (default = _wtsimt)
    argument: ``%s``
reference_image: (a pathlike object or string representing a file)
    reference image space that you wish to warp INTO
    argument: ``-R %s``
    mutually_exclusive: tightest_box
tightest_box: (a boolean)
    computes tightest bounding box (overridden by reference_image if
    given)
    argument: ``--tightest-bounding-box``
    mutually_exclusive: reference_image
reslice_by_header: (a boolean)
    Uses orientation matrix and origin encoded in reference image file
    header. Not typically used with additional transforms
    argument: ``--reslice-by-header``
use_nearest: (a boolean)
    Use nearest neighbor interpolation
    argument: ``--use-NN``
use_bspline: (a boolean)
    Use 3rd order B-Spline interpolation
    argument: ``--use-Bspline``
invert_affine: (a list of items which are an integer (int or long))
    List of Affine transformations to invert.E.g.: [1,4,5] inverts the
    1st, 4th, and 5th Affines found in transformation_series. Note that
    indexing starts with 1 and does not include warp fields. Affine
    transformations are distinguished from warp fields by the word
    "affine" included in their filenames.
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

output_image: (a pathlike object or string representing an existing
    file)
    Warped image

```

52.4 interfaces.ants.segmentation

52.4.1 AntsJointFusion

[Link to code](#)

Wraps the executable command antsJointFusion.

Examples

```
>>> from nipy.interfaces.ants import AntsJointFusion
>>> antsjointfusion = AntsJointFusion()
>>> antsjointfusion.inputs.out_label_fusion = 'ants_fusion_label_output.nii'
>>> antsjointfusion.inputs.atlas_image = [ ['rc1s1.nii', 'rc1s2.nii'] ]
>>> antsjointfusion.inputs.atlas_segmentation_image = ['segmentation0.nii.gz']
>>> antsjointfusion.inputs.target_image = ['im1.nii']
>>> antsjointfusion.cmdline
"antsJointFusion -a 0.1 -g ['rc1s1.nii', 'rc1s2.nii'] -l segmentation0.nii.gz -b_
↪2.0 -o ants_fusion_label_output.nii -s 3x3x3 -t ['im1.nii']"
```

```
>>> antsjointfusion.inputs.target_image = [ ['im1.nii', 'im2.nii'] ]
>>> antsjointfusion.cmdline
"antsJointFusion -a 0.1 -g ['rc1s1.nii', 'rc1s2.nii'] -l segmentation0.nii.gz -b_
↪2.0 -o ants_fusion_label_output.nii -s 3x3x3 -t ['im1.nii', 'im2.nii']"
```

```
>>> antsjointfusion.inputs.atlas_image = [ ['rc1s1.nii', 'rc1s2.nii'],
...                                         ['rc2s1.nii', 'rc2s2.nii'] ]
>>> antsjointfusion.inputs.atlas_segmentation_image = ['segmentation0.nii.gz',
...                                                    'segmentation1.nii.gz']
>>> antsjointfusion.cmdline
"antsJointFusion -a 0.1 -g ['rc1s1.nii', 'rc1s2.nii'] -g ['rc2s1.nii', 'rc2s2.nii
↪'] -l segmentation0.nii.gz -l segmentation1.nii.gz -b 2.0 -o ants_fusion_label_
↪output.nii -s 3x3x3 -t ['im1.nii', 'im2.nii']"
```

```
>>> antsjointfusion.inputs.dimension = 3
>>> antsjointfusion.inputs.alpha = 0.5
>>> antsjointfusion.inputs.beta = 1.0
>>> antsjointfusion.inputs.patch_radius = [3,2,1]
>>> antsjointfusion.inputs.search_radius = [3]
>>> antsjointfusion.cmdline
"antsJointFusion -a 0.5 -g ['rc1s1.nii', 'rc1s2.nii'] -g ['rc2s1.nii', 'rc2s2.nii
↪'] -l segmentation0.nii.gz -l segmentation1.nii.gz -b 1.0 -d 3 -o ants_fusion_
↪label_output.nii -p 3x2x1 -s 3 -t ['im1.nii', 'im2.nii']"
```

```
>>> antsjointfusion.inputs.search_radius = ['mask.nii']
>>> antsjointfusion.inputs.verbose = True
>>> antsjointfusion.inputs.exclusion_image = ['roi01.nii', 'roi02.nii']
>>> antsjointfusion.inputs.exclusion_image_label = ['1', '2']
>>> antsjointfusion.cmdline
"antsJointFusion -a 0.5 -g ['rc1s1.nii', 'rc1s2.nii'] -g ['rc2s1.nii', 'rc2s2.nii
↪'] -l segmentation0.nii.gz -l segmentation1.nii.gz -b 1.0 -d 3 -e 1[roi01.nii] -
↪e 2[roi02.nii] -o ants_fusion_label_output.nii -p 3x2x1 -s mask.nii -t ['im1.nii
↪', 'im2.nii'] -v"
```

```
>>> antsjointfusion.inputs.out_label_fusion = 'ants_fusion_label_output.nii'
>>> antsjointfusion.inputs.out_intensity_fusion_name_format = 'ants_joint_fusion_
↪intensity_%d.nii.gz'
```

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```
>>> antsjointfusion.inputs.out_label_post_prob_name_format = 'ants_joint_fusion_
↳posterior_%d.nii.gz'
>>> antsjointfusion.inputs.out_atlas_voting_weight_name_format = 'ants_joint_
↳fusion_voting_weight_%d.nii.gz'
>>> antsjointfusion.cmdline
"antsJointFusion -a 0.5 -g ['rc1s1.nii', 'rc1s2.nii'] -g ['rc2s1.nii', 'rc2s2.nii
↳'] -l segmentation0.nii.gz -l segmentation1.nii.gz -b 1.0 -d 3 -e 1[roi01.nii] -
↳e 2[roi02.nii] -o [ants_fusion_label_output.nii, ants_joint_fusion_intensity_
↳%d.nii.gz, ants_joint_fusion_posterior_%d.nii.gz, ants_joint_fusion_voting_
↳weight_%d.nii.gz] -p 3x2x1 -s mask.nii -t ['im1.nii', 'im2.nii'] -v"
```

Inputs:

```
[Mandatory]
target_image: (a list of items which are a list of items which are a
    pathlike object or string representing an existing file)
    The target image (or multimodal target images) assumed to be aligned
    to a common image domain.
    argument: ``-t %s``

atlas_image: (a list of items which are a list of items which are a
    pathlike object or string representing an existing file)
    The atlas image (or multimodal atlas images) assumed to be aligned
    to a common image domain.
    argument: ``-g %s...``

atlas_segmentation_image: (a list of items which are a pathlike
    object or string representing an existing file)
    The atlas segmentation images. For performing label fusion the
    number of specified segmentations should be identical to the number
    of atlas image sets.
    argument: ``-l %s...``

[Optional]
dimension: (3 or 2 or 4)
    This option forces the image to be treated as a specified-
    dimensional image. If not specified, the program tries to infer the
    dimensionality from the input image.
    argument: ``-d %d``

alpha: (a float, nipy default value: 0.1)
    Regularization term added to matrix Mx for calculating the inverse.
    Default = 0.1
    argument: ``-a %s``

beta: (a float, nipy default value: 2.0)
    Exponent for mapping intensity difference to the joint error.
    Default = 2.0
    argument: ``-b %s``

retain_label_posterior_images: (a boolean, nipy default value:
    False)
    Retain label posterior probability images. Requires atlas
    segmentations to be specified. Default = false
    argument: ``-r``
    requires: atlas_segmentation_image

retain_atlas_voting_images: (a boolean, nipy default value: False)
    Retain atlas voting images. Default = false
    argument: ``-f``

constrain_nonnegative: (a boolean, nipy default value: False)
    Constrain solution to non-negative weights.
    argument: ``-c``
```

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```

patch_radius: (a list of items which are a value of class 'int')
    Patch radius for similarity measures.Default: 2x2x2
    argument: ``-p %s``
patch_metric: ('PC' or 'MSQ')
    Metric to be used in determining the most similar neighborhood
    patch. Options include Pearson's correlation (PC) and mean squares
    (MSQ). Default = PC (Pearson correlation).
    argument: ``-m %s``
search_radius: (a list of from 1 to 3 items which are any value,
    nipy default value: [3, 3, 3])
    Search radius for similarity measures. Default = 3x3x3. One can also
    specify an image where the value at the voxel specifies the
    isotropic search radius at that voxel.
    argument: ``-s %s``
exclusion_image_label: (a list of items which are a unicode string)
    Specify a label for the exclusion region.
    argument: ``-e %s``
    requires: exclusion_image
exclusion_image: (a list of items which are a pathlike object or
    string representing an existing file)
    Specify an exclusion region for the given label.
mask_image: (a pathlike object or string representing an existing
    file)
    If a mask image is specified, fusion is only performed in the mask
    region.
    argument: ``-x %s``
out_label_fusion: (a pathlike object or string representing a file)
    The output label fusion image.
    argument: ``%s``
out_intensity_fusion_name_format: (a unicode string)
    Optional intensity fusion image file name format. (e.g.
    "antsJointFusionIntensity_%d.nii.gz")
out_label_post_prob_name_format: (a unicode string)
    Optional label posterior probability image file name format.
    requires: out_label_fusion, out_intensity_fusion_name_format
out_atlas_voting_weight_name_format: (a unicode string)
    Optional atlas voting weight image file name format.
    requires: out_label_fusion, out_intensity_fusion_name_format,
    out_label_post_prob_name_format
verbose: (a boolean)
    Verbose output.
    argument: ``-v``
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_label_fusion: (a pathlike object or string representing an
    existing file)
out_intensity_fusion_name_format: (a unicode string)

```

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```

out_label_post_prob_name_format: (a unicode string)
out_atlas_voting_weight_name_format: (a unicode string)

```

52.4.2 Atropos

[Link to code](#)

Wraps the executable command Atropos.

A finite mixture modeling (FMM) segmentation approach with possibilities for specifying prior constraints. These prior constraints include the specification of a prior label image, prior probability images (one for each class), and/or an MRF prior to enforce spatial smoothing of the labels. Similar algorithms include FAST and SPM.

Examples

```

>>> from nipy.interfaces.ants import Atropos
>>> at = Atropos()
>>> at.inputs.dimension = 3
>>> at.inputs.intensity_images = 'structural.nii'
>>> at.inputs.mask_image = 'mask.nii'
>>> at.inputs.initialization = 'PriorProbabilityImages'
>>> at.inputs.prior_probability_images = ['rc1s1.nii', 'rc1s2.nii']
>>> at.inputs.number_of_tissue_classes = 2
>>> at.inputs.prior_weighting = 0.8
>>> at.inputs.prior_probability_threshold = 0.0000001
>>> at.inputs.likelihood_model = 'Gaussian'
>>> at.inputs.mrf_smoothing_factor = 0.2
>>> at.inputs.mrf_radius = [1, 1, 1]
>>> at.inputs.icm_use_synchronous_update = True
>>> at.inputs.maximum_number_of_icm_terminations = 1
>>> at.inputs.n_terminations = 5
>>> at.inputs.convergence_threshold = 0.000001
>>> at.inputs.posterior_formulation = 'Socrates'
>>> at.inputs.use_mixture_model_proportions = True
>>> at.inputs.save_posteriors = True
>>> at.cmdline
'Atropos --image-dimensionality 3 --icm [1,1] --initialization_
↳PriorProbabilityImages[2,priors/priorProbImages%02d.nii,0.8,1e-07] --intensity-
↳image structural.nii --likelihood-model Gaussian --mask-image mask.nii --mrf [0.
↳2,1x1x1] --convergence [5,1e-06] --output [structural_labeled.nii,POSTERIOR_
↳%02d.nii.gz] --posterior-formulation Socrates[1] --use-random-seed 1'

```

Inputs:

```

[Mandatory]
intensity_images: (a list of items which are a pathlike object or
    string representing an existing file)
    argument: ``--intensity-image %s...``
mask_image: (a pathlike object or string representing an existing
    file)
    argument: ``--mask-image %s``
initialization: ('Random' or 'Otsu' or 'KMeans' or
    'PriorProbabilityImages' or 'PriorLabelImage')
    argument: ``%s``
    requires: number_of_tissue_classes
number_of_tissue_classes: (an integer (int or long))

```

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```

[Optional]
dimension: (3 or 2 or 4, nipy default value: 3)
            image dimension (2, 3, or 4)
            argument: ``--image-dimensionality %d``
prior_probability_images: (a list of items which are a pathlike
                           object or string representing an existing file)
prior_weighting: (a float)
prior_probability_threshold: (a float)
                        requires: prior_weighting
likelihood_model: (a unicode string)
            argument: ``--likelihood-model %s``
mrf_smoothing_factor: (a float)
            argument: ``%s``
mrf_radius: (a list of items which are an integer (int or long))
            requires: mrf_smoothing_factor
icm_use_synchronous_update: (a boolean)
            argument: ``%s``
maximum_number_of_icm_teraions: (an integer (int or long))
            requires: icm_use_synchronous_update
n_teraions: (an integer (int or long))
            argument: ``%s``
convergence_threshold: (a float)
            requires: n_teraions
posterior_formulation: (a unicode string)
            argument: ``%s``
use_random_seed: (a boolean, nipy default value: True)
            use random seed value over constant
            argument: ``--use-random-seed %d``
use_mixture_model_proportions: (a boolean)
            requires: posterior_formulation
out_classified_image_name: (a pathlike object or string representing
                           a file)
            argument: ``%s``
save_posteriors: (a boolean)
output_posteriors_name_template: (a unicode string, nipy default
                                value: POSTERIOR_%02d.nii.gz)
num_threads: (an integer (int or long), nipy default value: 1)
            Number of ITK threads to use
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

classified_image: (a pathlike object or string representing an
                  existing file)
posteriors: (a list of items which are a pathlike object or string
            representing a file)

```

52.4.3 BrainExtraction[Link to code](#)

Wraps the executable command `antsBrainExtraction.sh`.

Examples

```
>>> from nipyee.interfaces.ants.segmentation import BrainExtraction
>>> brainextraction = BrainExtraction()
>>> brainextraction.inputs.dimension = 3
>>> brainextraction.inputs.anatomical_image = 'T1.nii.gz'
>>> brainextraction.inputs.brain_template = 'study_template.nii.gz'
>>> brainextraction.inputs.brain_probability_mask =
↳ 'ProbabilityMaskOfStudyTemplate.nii.gz'
>>> brainextraction.cmdline
'antsBrainExtraction.sh -a T1.nii.gz -m ProbabilityMaskOfStudyTemplate.nii.gz -e_
↳ study_template.nii.gz -d 3 -s nii.gz -o highres001_'
```

Inputs:

[Mandatory]

`anatomical_image`: (a pathlike object or string representing an existing file)
Structural image, typically T1. If more than one anatomical image is specified, subsequently specified images are used during the segmentation process. However, only the first image is used in the registration of priors. Our suggestion would be to specify the T1 as the first image. Anatomical template created using e.g. LPBA40 data set with `buildtemplateparallel.sh` in ANTs.
argument: ```-a %s```

`brain_template`: (a pathlike object or string representing an existing file)
Anatomical template created using e.g. LPBA40 data set with `buildtemplateparallel.sh` in ANTs.
argument: ```-e %s```

`brain_probability_mask`: (a pathlike object or string representing an existing file)
Brain probability mask created using e.g. LPBA40 data set which have brain masks defined, and warped to anatomical template and averaged resulting in a probability image.
argument: ```-m %s```

[Optional]

`dimension`: (3 or 2, nipyee default value: 3)
image dimension (2 or 3)
argument: ```-d %d```

`out_prefix`: (a unicode string, nipyee default value: `highres001_`)
Prefix that is prepended to all output files (default = `highres001_`)
argument: ```-o %s```

`extraction_registration_mask`: (a pathlike object or string representing an existing file)
Mask (defined in the template space) used during registration for brain extraction. To limit the metric computation to a specific region.
argument: ```-f %s```

`image_suffix`: (a unicode string, nipyee default value: `nii.gz`)
any of standard ITK formats, `nii.gz` is default
argument: ```-s %s```

`use_random_seeding`: (0 or 1)
Use random number generated from system clock in Atropos (default =

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```

1)
argument: ``-u %d``
keep_temporary_files: (an integer (int or long))
    Keep brain extraction/segmentation warps, etc (default = 0).
    argument: ``-k %d``
use_floatingpoint_precision: (0 or 1)
    Use floating point precision in registrations (default = 0)
    argument: ``-q %d``
debug: (a boolean)
    If > 0, runs a faster version of the script. Only for testing.
    Implies -u 0. Requires single thread computation for complete
    reproducibility.
    argument: ``-z 1``
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

BrainExtractionMask: (a pathlike object or string representing an
    existing file)
    brain extraction mask
BrainExtractionBrain: (a pathlike object or string representing an
    existing file)
    brain extraction image
BrainExtractionCSF: (a pathlike object or string representing an
    existing file)
    segmentation mask with only CSF
BrainExtractionGM: (a pathlike object or string representing an
    existing file)
    segmentation mask with only grey matter
BrainExtractionInitialAffine: (a pathlike object or string
    representing an existing file)
BrainExtractionInitialAffineFixed: (a pathlike object or string
    representing an existing file)
BrainExtractionInitialAffineMoving: (a pathlike object or string
    representing an existing file)
BrainExtractionLaplacian: (a pathlike object or string representing
    an existing file)
BrainExtractionPrior0GenericAffine: (a pathlike object or string
    representing an existing file)
BrainExtractionPrior1InverseWarp: (a pathlike object or string
    representing an existing file)
BrainExtractionPrior1Warp: (a pathlike object or string representing
    an existing file)
BrainExtractionPriorWarped: (a pathlike object or string representing
    an existing file)
BrainExtractionSegmentation: (a pathlike object or string
    representing an existing file)
    segmentation mask with CSF, GM, and WM
BrainExtractionTemplateLaplacian: (a pathlike object or string

```

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```

        representing an existing file)
BrainExtractionTmp: (a pathlike object or string representing an
    existing file)
BrainExtractionWM: (a pathlike object or string representing an
    existing file)
    segmenration mask with only white matter
N4Corrected0: (a pathlike object or string representing an existing
    file)
    N4 bias field corrected image
N4Truncated0: (a pathlike object or string representing an existing
    file)

```

52.4.4 CorticalThickness

[Link to code](#)

Wraps the executable command `antsCorticalThickness.sh`.

Examples

```

>>> from nipy.interfaces.ants.segmentation import CorticalThickness
>>> corticalthickness = CorticalThickness()
>>> corticalthickness.inputs.dimension = 3
>>> corticalthickness.inputs.anatomical_image = 'T1.nii.gz'
>>> corticalthickness.inputs.brain_template = 'study_template.nii.gz'
>>> corticalthickness.inputs.brain_probability_mask =
    ↳ 'ProbabilityMaskOfStudyTemplate.nii.gz'
>>> corticalthickness.inputs.segmentation_priors = ['BrainSegmentationPrior01.nii.
    ↳ gz',
    ...
    ↳ 'BrainSegmentationPrior02.nii.
    ↳ gz',
    ...
    ↳ 'BrainSegmentationPrior03.nii.
    ↳ gz',
    ...
    ↳ 'BrainSegmentationPrior04.nii.
    ↳ gz']
>>> corticalthickness.inputs.t1_registration_template = 'brain_study_template.nii.
    ↳ gz'
>>> corticalthickness.cmdline
'antsCorticalThickness.sh -a T1.nii.gz -m ProbabilityMaskOfStudyTemplate.nii.gz -
    ↳ e study_template.nii.gz -d 3 -s nii.gz -o antsCT_ -p nipy_priors/
    ↳ BrainSegmentationPrior%02d.nii.gz -t brain_study_template.nii.gz'

```

Inputs:

```

[Mandatory]
anatomical_image: (a pathlike object or string representing an
    existing file)
    Structural *intensity* image, typically T1. If more than one
    anatomical image is specified, subsequently specified images are
    used during the segmentation process. However, only the first image
    is used in the registration of priors. Our suggestion would be to
    specify the T1 as the first image.
    argument: ``-a %s``
brain_template: (a pathlike object or string representing an existing
    file)
    Anatomical *intensity* template (possibly created using a population
    data set with buildtemplateparallel.sh in ANTs). This template is

```

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```

    *not* skull-stripped.
    argument: ``-e %s``
brain_probability_mask: (a pathlike object or string representing an
    existing file)
    brain probability mask in template space
    argument: ``-m %s``
segmentation_priors: (a list of items which are a pathlike object or
    string representing an existing file)
    argument: ``-p %s``
t1_registration_template: (a pathlike object or string representing
    an existing file)
    Anatomical *intensity* template (assumed to be skull-stripped). A
    common case would be where this would be the same template as
    specified in the -e option which is not skull stripped.
    argument: ``-t %s``

[Optional]
dimension: (3 or 2, nipy default value: 3)
    image dimension (2 or 3)
    argument: ``-d %d``
out_prefix: (a unicode string, nipy default value: antsCT_)
    Prefix that is prepended to all output files (default = antsCT_)
    argument: ``-o %s``
image_suffix: (a unicode string, nipy default value: nii.gz)
    any of standard ITK formats, nii.gz is default
    argument: ``-s %s``
extraction_registration_mask: (a pathlike object or string
    representing an existing file)
    Mask (defined in the template space) used during registration for
    brain extraction.
    argument: ``-f %s``
keep_temporary_files: (an integer (int or long))
    Keep brain extraction/segmentation warps, etc (default = 0).
    argument: ``-k %d``
max_iterations: (an integer (int or long))
    ANTS registration max iterations (default = 100x100x70x20)
    argument: ``-i %d``
prior_segmentation_weight: (a float)
    Atropos spatial prior *probability* weight for the segmentation
    argument: ``-w %f``
segmentation_iterations: (an integer (int or long))
    N4 -> Atropos -> N4 iterations during segmentation (default = 3)
    argument: ``-n %d``
posterior_formulation: (a unicode string)
    Atropos posterior formulation and whether or not to use mixture
    model proportions. e.g 'Socrates[1]' (default) or 'Aristotle[1]'.
    Choose the latter if you want use the distance priors (see also the
    -l option for label propagation control).
    argument: ``-b %s``
use_floatingpoint_precision: (0 or 1)
    Use floating point precision in registrations (default = 0)
    argument: ``-j %d``
use_random_seeding: (0 or 1)
    Use random number generated from system clock in Atropos (default =
    1)
    argument: ``-u %d``
b_spline_smoothing: (a boolean)

```

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```

        Use B-spline SyN for registrations and B-spline exponential mapping
        in DiReCT.
        argument: ``-v``
cortical_label_image: (a pathlike object or string representing an
    existing file)
    Cortical ROI labels to use as a prior for ATITH.
label_propagation: (a unicode string)
    Incorporate a distance prior one the posterior formulation. Should
    be of the form 'label[lambda,boundaryProbability]' where label is a
    value of 1,2,3,... denoting label ID. The label probability for
    anything outside the current label = boundaryProbability * exp(
    -lambda * distanceFromBoundary ) Intuitively, smaller lambda values
    will increase the spatial capture range of the distance prior. To
    apply to all label values, simply omit specifying the label, i.e. -1
    [lambda,boundaryProbability].
    argument: ``-l %s``
quick_registration: (a boolean)
    If = 1, use antsRegistrationSyNQuick.sh as the basis for
    registration during brain extraction, brain segmentation, and
    (optional) normalization to a template. Otherwise use
    antsRegistrationSyN.sh (default = 0).
    argument: ``-q 1``
debug: (a boolean)
    If > 0, runs a faster version of the script. Only for testing.
    Implies -u 0. Requires single thread computation for complete
    reproducibility.
    argument: ``-z 1``
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

BrainExtractionMask: (a pathlike object or string representing an
    existing file)
    brain extraction mask
ExtractedBrainN4: (a pathlike object or string representing an
    existing file)
    extracted brain from N4 image
BrainSegmentation: (a pathlike object or string representing an
    existing file)
    brain segmentaion image
BrainSegmentationN4: (a pathlike object or string representing an
    existing file)
    N4 corrected image
BrainSegmentationPosteriors: (a list of items which are a pathlike
    object or string representing an existing file)
    Posterior probability images
CorticalThickness: (a pathlike object or string representing an
    existing file)
    cortical thickness file

```

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```

TemplateToSubject1GenericAffine: (a pathlike object or string
    representing an existing file)
    Template to subject affine
TemplateToSubject0Warp: (a pathlike object or string representing an
    existing file)
    Template to subject warp
SubjectToTemplate1Warp: (a pathlike object or string representing an
    existing file)
    Template to subject inverse warp
SubjectToTemplate0GenericAffine: (a pathlike object or string
    representing an existing file)
    Template to subject inverse affine
SubjectToTemplateLogJacobian: (a pathlike object or string
    representing an existing file)
    Template to subject log jacobian
CorticalThicknessNormedToTemplate: (a pathlike object or string
    representing an existing file)
    Normalized cortical thickness
BrainVolumes: (a pathlike object or string representing an existing
    file)
    Brain volumes as text

```

52.4.5 DenoiseImage

[Link to code](#)

Wraps the executable command DenoiseImage.

Examples

```

>>> import copy
>>> from nipy.interfaces.ants import DenoiseImage
>>> denoise = DenoiseImage()
>>> denoise.inputs.dimension = 3
>>> denoise.inputs.input_image = 'im1.nii'
>>> denoise.cmdline
'DenoiseImage -d 3 -i im1.nii -n Gaussian -o im1_noise_corrected.nii -s 1'

```

```

>>> denoise_2 = copy.deepcopy(denoise)
>>> denoise_2.inputs.output_image = 'output_corrected_image.nii.gz'
>>> denoise_2.inputs.noise_model = 'Rician'
>>> denoise_2.inputs.shrink_factor = 2
>>> denoise_2.cmdline
'DenoiseImage -d 3 -i im1.nii -n Rician -o output_corrected_image.nii.gz -s 2'

```

```

>>> denoise_3 = DenoiseImage()
>>> denoise_3.inputs.input_image = 'im1.nii'
>>> denoise_3.inputs.save_noise = True
>>> denoise_3.cmdline
'DenoiseImage -i im1.nii -n Gaussian -o [ im1_noise_corrected.nii, im1_noise.nii_
↪ ] -s 1'

```

Inputs:

```

[Mandatory]
input_image: (a pathlike object or string representing an existing

```

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```

    file)
    A scalar image is expected as input for noise correction.
    argument: ``-i %s``
save_noise: (a boolean, nipyre default value: False)
    True if the estimated noise should be saved to file.
    mutually_exclusive: noise_image

[Optional]
dimension: (2 or 3 or 4)
    This option forces the image to be treated as a specified-
    dimensional image. If not specified, the program tries to infer the
    dimensionality from the input image.
    argument: ``-d %d``
noise_model: ('Gaussian' or 'Rician', nipyre default value: Gaussian)
    Employ a Rician or Gaussian noise model.
    argument: ``-n %s``
shrink_factor: (an integer (int or long), nipyre default value: 1)
    Running noise correction on large images can be time consuming. To
    lessen computation time, the input image can be resampled. The
    shrink factor, specified as a single integer, describes this
    resampling. Shrink factor = 1 is the default.
    argument: ``-s %s``
output_image: (a pathlike object or string representing a file)
    The output consists of the noise corrected version of the input
    image.
    argument: ``-o %s``
noise_image: (a pathlike object or string representing a file)
    Filename for the estimated noise.
verbose: (a boolean)
    Verbose output.
    argument: ``-v``
num_threads: (an integer (int or long), nipyre default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyre default value: {})
    Environment variables

```

Outputs:

```

output_image: (a pathlike object or string representing an existing
    file)
noise_image: (a pathlike object or string representing a file)

```

52.4.6 JointFusion

[Link to code](#)

Wraps the executable command jointfusion.

Examples

```

>>> from nipyre.interfaces.ants import JointFusion
>>> at = JointFusion()

```

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```

>>> at.inputs.dimension = 3
>>> at.inputs.modalities = 1
>>> at.inputs.method = 'Joint[0.1,2]'
>>> at.inputs.output_label_image = 'fusion_labelimage_output.nii'
>>> at.inputs.warped_intensity_images = ['im1.nii',
...                                     'im2.nii',
...                                     'im3.nii']
>>> at.inputs.warped_label_images = ['segmentation0.nii.gz',
...                                  'segmentation1.nii.gz',
...                                  'segmentation1.nii.gz']
>>> at.inputs.target_image = 'T1.nii'
>>> at.cmdline
'jointfusion 3 1 -m Joint[0.1,2] -tg T1.nii -g im1.nii -g im2.nii -g im3.nii -l_
↪segmentation0.nii.gz -l segmentation1.nii.gz -l segmentation1.nii.gz fusion_
↪labelimage_output.nii'

```

```

>>> at.inputs.method = 'Joint'
>>> at.inputs.alpha = 0.5
>>> at.inputs.beta = 1
>>> at.inputs.patch_radius = [3,2,1]
>>> at.inputs.search_radius = [1,2,3]
>>> at.cmdline
'jointfusion 3 1 -m Joint[0.5,1] -rp 3x2x1 -rs 1x2x3 -tg T1.nii -g im1.nii -g im2.
↪nii -g im3.nii -l segmentation0.nii.gz -l segmentation1.nii.gz -l segmentation1.
↪nii.gz fusion_labelimage_output.nii'

```

Inputs:

```

[Mandatory]
dimension: (3 or 2 or 4, nipy default value: 3)
    image dimension (2, 3, or 4)
    argument: ``%d``, position: 0
modalities: (an integer (int or long))
    Number of modalities or features
    argument: ``%d``, position: 1
warped_intensity_images: (a list of items which are a pathlike object
    or string representing an existing file)
    Warped atlas images
    argument: ``-g %s...``
target_image: (a list of items which are a pathlike object or string
    representing an existing file)
    Target image(s)
    argument: ``-tg %s...``
warped_label_images: (a list of items which are a pathlike object or
    string representing an existing file)
    Warped atlas segmentations
    argument: ``-l %s...``
output_label_image: (a pathlike object or string representing a file)
    Output fusion label map image
    argument: ``%s``, position: -1

[Optional]
method: (a unicode string, nipy default value: )
    Select voting method. Options: Joint (Joint Label Fusion). May be
    followed by optional parameters in brackets, e.g., -m Joint[0.1,2]
    argument: ``-m %s``
alpha: (a float, nipy default value: 0.0)

```

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```

        Regularization term added to matrix Mx for inverse
        requires: method
    beta: (an integer (int or long), nipy default value: 0)
        Exponent for mapping intensity difference to joint error
        requires: method
    patch_radius: (a list of items which are a value of class 'int')
        Patch radius for similarity measures, scalar or vector. Default:
        2x2x2
        argument: ``-rp %s``
    search_radius: (a list of items which are a value of class 'int')
        Local search radius. Default: 3x3x3
        argument: ``-rs %s``
    exclusion_region: (a pathlike object or string representing an
        existing file)
        Specify an exclusion region for the given label.
        argument: ``-x %s``
    atlas_group_id: (a list of items which are a value of class 'int')
        Assign a group ID for each atlas
        argument: ``-gp %d...``
    atlas_group_weights: (a list of items which are a value of class
        'int')
        Assign the voting weights to each atlas group
        argument: ``-gpw %d...``
    num_threads: (an integer (int or long), nipy default value: 1)
        Number of ITK threads to use
    args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
    environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

output_label_image: (a pathlike object or string representing an
    existing file)

```

52.4.7 KellyKapowski[Link to code](#)

Wraps the executable command KellyKapowski.

Nipy Interface to ANTs' KellyKapowski, also known as DiReCT.

DiReCT is a registration based estimate of cortical thickness. It was published in S. R. Das, B. B. Avants, M. Grossman, and J. C. Gee, Registration based cortical thickness measurement, Neuroimage 2009, 45:867–879.

Examples

```

>>> from nipy.interfaces.ants.segmentation import KellyKapowski
>>> kk = KellyKapowski()
>>> kk.inputs.dimension = 3
>>> kk.inputs.segmentation_image = "segmentation0.nii.gz"
>>> kk.inputs.convergence = "[45,0.0,10]"
>>> kk.inputs.thickness_prior_estimate = 10
>>> kk.cmdline

```

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```
'KellyKapowski --convergence "[45,0.0,10]" --output "[segmentation0_cortical_
→thickness.nii.gz,segmentation0_warped_white_matter.nii.gz]" --image-
→dimensionality 3 --gradient-step 0.025000 --maximum-number-of-invert-
→displacement-field-iterations 20 --number-of-integration-points 10 --
→segmentation-image "[segmentation0.nii.gz,2,3]" --smoothing-variance 1.000000 --
→smoothing-velocity-field-parameter 1.500000 --thickness-prior-estimate 10.000000
→'
```

Inputs:

```
[Mandatory]
segmentation_image: (a pathlike object or string representing an
    existing file)
    A segmentation image must be supplied labeling the gray and white
    matters. Default values = 2 and 3, respectively.
    argument: ``--segmentation-image "%s"``

[Optional]
dimension: (3 or 2, nipy default value: 3)
    image dimension (2 or 3)
    argument: ``--image-dimensionality %d``
gray_matter_label: (an integer (int or long), nipy default value:
    2)
    The label value for the gray matter label in the segmentation_image.
white_matter_label: (an integer (int or long), nipy default value:
    3)
    The label value for the white matter label in the
    segmentation_image.
gray_matter_prob_image: (a pathlike object or string representing an
    existing file)
    In addition to the segmentation image, a gray matter probability
    image can be used. If no such image is supplied, one is created
    using the segmentation image and a variance of 1.0 mm.
    argument: ``--gray-matter-probability-image "%s"``
white_matter_prob_image: (a pathlike object or string representing an
    existing file)
    In addition to the segmentation image, a white matter probability
    image can be used. If no such image is supplied, one is created
    using the segmentation image and a variance of 1.0 mm.
    argument: ``--white-matter-probability-image "%s"``
convergence: (a unicode string, nipy default value: )
    Convergence is determined by fitting a line to the normalized energy
    profile of the last N iterations (where N is specified by the window
    size) and determining the slope which is then compared with the
    convergence threshold.
    argument: ``--convergence "%s"``
thickness_prior_estimate: (a float, nipy default value: 10)
    Provides a prior constraint on the final thickness measurement in
    mm.
    argument: ``--thickness-prior-estimate %f``
thickness_prior_image: (a pathlike object or string representing an
    existing file)
    An image containing spatially varying prior thickness values.
    argument: ``--thickness-prior-image "%s"``
gradient_step: (a float, nipy default value: 0.025)
    Gradient step size for the optimization.
    argument: ``--gradient-step %f``
```

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```

smoothing_variance: (a float, nipy default value: 1.0)
    Defines the Gaussian smoothing of the hit and total images.
    argument: ``--smoothing-variance %f``
smoothing_velocity_field: (a float, nipy default value: 1.5)
    Defines the Gaussian smoothing of the velocity field (default =
    1.5). If the b-spline smoothing option is chosen, then this defines
    the isotropic mesh spacing for the smoothing spline (default = 15).
    argument: ``--smoothing-velocity-field-parameter %f``
use_bspline_smoothing: (a boolean)
    Sets the option for B-spline smoothing of the velocity field.
    argument: ``--use-bspline-smoothing 1``
number_integration_points: (an integer (int or long), nipy default
    value: 10)
    Number of compositions of the diffeomorphism per iteration.
    argument: ``--number-of-integration-points %d``
max_invert_displacement_field_iters: (an integer (int or long),
    nipy default value: 20)
    Maximum number of iterations for estimating the invert displacement
    field.
    argument: ``--maximum-number-of-invert-displacement-field-iterations
    %d``
cortical_thickness: (a pathlike object or string representing a file)
    Filename for the cortical thickness.
    argument: ``--output "%s"``
warped_white_matter: (a pathlike object or string representing a
    file)
    Filename for the warped white matter file.
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

cortical_thickness: (a pathlike object or string representing a file)
    A thickness map defined in the segmented gray matter.
warped_white_matter: (a pathlike object or string representing a
    file)
    A warped white matter image.

```

References:

None

52.4.8 LaplacianThickness[Link to code](#)

Wraps the executable command LaplacianThickness.

Calculates the cortical thickness from an anatomical image

Examples

```
>>> from nipy.interfaces.ants import LaplacianThickness
>>> cort_thick = LaplacianThickness()
>>> cort_thick.inputs.input_wm = 'white_matter.nii.gz'
>>> cort_thick.inputs.input_gm = 'gray_matter.nii.gz'
>>> cort_thick.cmdline
'LaplacianThickness white_matter.nii.gz gray_matter.nii.gz white_matter_thickness.
↪nii.gz'
```

```
>>> cort_thick.inputs.output_image = 'output_thickness.nii.gz'
>>> cort_thick.cmdline
'LaplacianThickness white_matter.nii.gz gray_matter.nii.gz output_thickness.nii.gz
↪'
```

Inputs:

```
[Mandatory]
input_wm: (a pathlike object or string representing a file)
    white matter segmentation image
    argument: ``%s``, position: 1
input_gm: (a pathlike object or string representing a file)
    gray matter segmentation image
    argument: ``%s``, position: 2

[Optional]
output_image: (a pathlike object or string representing a file)
    name of output file
    argument: ``%s``, position: 3
smooth_param: (a float)
    Sigma of the Laplacian Recursive Image Filter (defaults to 1)
    argument: ``%s``, position: 4
prior_thickness: (a float)
    Prior thickness (defaults to 500)
    argument: ``%s``, position: 5
    requires: smooth_param
dT: (a float)
    Time delta used during integration (defaults to 0.01)
    argument: ``%s``, position: 6
    requires: prior_thickness
sulcus_prior: (a float)
    Positive floating point number for sulcus prior. Authors said that
    0.15 might be a reasonable value
    argument: ``%s``, position: 7
    requires: dT
tolerance: (a float)
    Tolerance to reach during optimization (defaults to 0.001)
    argument: ``%s``, position: 8
    requires: sulcus_prior
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
output_image: (a pathlike object or string representing an existing
               file)
               Cortical thickness
```

52.4.9 N4BiasFieldCorrection

[Link to code](#)

Wraps the executable command N4BiasFieldCorrection.

Bias field correction.

N4 is a variant of the popular N3 (nonparameteric nonuniform normalization) retrospective bias correction algorithm. Based on the assumption that the corruption of the low frequency bias field can be modeled as a convolution of the intensity histogram by a Gaussian, the basic algorithmic protocol is to iterate between deconvolving the intensity histogram by a Gaussian, remapping the intensities, and then spatially smoothing this result by a B-spline modeling of the bias field itself. The modifications from and improvements obtained over the original N3 algorithm are described in [Tustison2010].

Examples

```
>>> import copy
>>> from nipy.interfaces.ants import N4BiasFieldCorrection
>>> n4 = N4BiasFieldCorrection()
>>> n4.inputs.dimension = 3
>>> n4.inputs.input_image = 'structural.nii'
>>> n4.inputs.bspline_fitting_distance = 300
>>> n4.inputs.shrink_factor = 3
>>> n4.inputs.n_iterations = [50,50,30,20]
>>> n4.cmdline
'N4BiasFieldCorrection --bspline-fitting [ 300 ] -d 3 --input-image structural.
↪nii --convergence [ 50x50x30x20 ] --output structural_corrected.nii --shrink-
↪factor 3'
```

```
>>> n4_2 = copy.deepcopy(n4)
>>> n4_2.inputs.convergence_threshold = 1e-6
>>> n4_2.cmdline
'N4BiasFieldCorrection --bspline-fitting [ 300 ] -d 3 --input-image structural.
↪nii --convergence [ 50x50x30x20, 1e-06 ] --output structural_corrected.nii --
↪shrink-factor 3'
```

```
>>> n4_3 = copy.deepcopy(n4_2)
>>> n4_3.inputs.bspline_order = 5
>>> n4_3.cmdline
'N4BiasFieldCorrection --bspline-fitting [ 300, 5 ] -d 3 --input-image structural.
↪nii --convergence [ 50x50x30x20, 1e-06 ] --output structural_corrected.nii --
↪shrink-factor 3'
```

```
>>> n4_4 = N4BiasFieldCorrection()
>>> n4_4.inputs.input_image = 'structural.nii'
>>> n4_4.inputs.save_bias = True
>>> n4_4.inputs.dimension = 3
>>> n4_4.cmdline
'N4BiasFieldCorrection -d 3 --input-image structural.nii --output [ structural_
↪corrected.nii, structural_bias.nii ]'
```

```
>>> n4_5 = N4BiasFieldCorrection()
>>> n4_5.inputs.input_image = 'structural.nii'
>>> n4_5.inputs.dimension = 3
>>> n4_5.inputs.histogram_sharpening = (0.12, 0.02, 200)
>>> n4_5.cmdline
'N4BiasFieldCorrection -d 3 --histogram-sharpening [0.12,0.02,200] --input-image_
↳ structural.nii --output structural_corrected.nii'
```

Inputs:

```
[Mandatory]
input_image: (a pathlike object or string representing a file)
    input for bias correction. Negative values or values close to zero
    should be processed prior to correction
    argument: ``--input-image %s``
save_bias: (a boolean, nipy default value: False)
    True if the estimated bias should be saved to file.
    mutually_exclusive: bias_image
copy_header: (a boolean, nipy default value: False)
    copy headers of the original image into the output (corrected) file

[Optional]
dimension: (3 or 2 or 4, nipy default value: 3)
    image dimension (2, 3 or 4)
    argument: ``-d %d``
mask_image: (a pathlike object or string representing a file)
    image to specify region to perform final bias correction in
    argument: ``--mask-image %s``
weight_image: (a pathlike object or string representing a file)
    image for relative weighting (e.g. probability map of the white
    matter) of voxels during the B-spline fitting.
    argument: ``--weight-image %s``
output_image: (a unicode string)
    output file name
    argument: ``--output %s``
bspline_fitting_distance: (a float)
    argument: ``--bspline-fitting %s``
bspline_order: (an integer (int or long))
    requires: bspline_fitting_distance
shrink_factor: (an integer (int or long))
    argument: ``--shrink-factor %d``
n_iterations: (a list of items which are an integer (int or long))
    argument: ``--convergence %s``
convergence_threshold: (a float)
    requires: n_iterations
bias_image: (a pathlike object or string representing a file)
    Filename for the estimated bias.
rescale_intensities: (a boolean, nipy default value: False)
    [NOTE: Only ANTs>=2.1.0]
    At each iteration, a new intensity mapping is calculated and applied
    but there
    is nothing which constrains the new intensity range to be within
    certain values.
    The result is that the range can "drift" from the original at each
    iteration.
    This option rescales to the [min,max] range of the original image
    intensities
    within the user-specified mask.
```

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```

    argument: ``-r``
    histogram_sharpening: (a tuple of the form: (a float, a float, an
        integer (int or long)))
        Three-values tuple of histogram sharpening parameters (FWHM,
        wienerNose, numberOfHistogramBins).
        These options describe the histogram sharpening parameters, i.e. the
        deconvolution step parameters described in the original N3
        algorithm.
        The default values have been shown to work fairly well.
    argument: ``--histogram-sharpening [%g,%g,%d]``
    num_threads: (an integer (int or long), nipy default value: 1)
        Number of ITK threads to use
    args: (a unicode string)
        Additional parameters to the command
    argument: ``%s``
    environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

    output_image: (a pathlike object or string representing an existing
        file)
        Warped image
    bias_image: (a pathlike object or string representing an existing
        file)
        Estimated bias

```

52.5 interfaces.ants.utils

52.5.1 AffineInitializer

[Link to code](#)

Wraps the executable command antsAffineInitializer.

Initialize an affine transform (as in antsBrainExtraction.sh)

```

>>> from nipy.interfaces.ants import AffineInitializer
>>> init = AffineInitializer()
>>> init.inputs.fixed_image = 'fixed1.nii'
>>> init.inputs.moving_image = 'moving1.nii'
>>> init.cmdline
'antsAffineInitializer 3 fixed1.nii moving1.nii transform.mat 15.000000 0.100000_
↪0 10'

```

Inputs:

```

[Mandatory]
    fixed_image: (a pathlike object or string representing an existing
        file)
        reference image
        argument: ``%s``, position: 1
    moving_image: (a pathlike object or string representing an existing
        file)
        moving image
        argument: ``%s``, position: 2

```

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```
[Optional]
dimension: (3 or 2, nipy default value: 3)
    dimension
    argument: ``%s``, position: 0
out_file: (a pathlike object or string representing a file, nipy
    default value: transform.mat)
    output transform file
    argument: ``%s``, position: 3
search_factor: (a float, nipy default value: 15.0)
    increments (degrees) for affine search
    argument: ``%f``, position: 4
radian_fraction: (0.0 <= a floating point number <= 1.0, nipy
    default value: 0.1)
    search this arc +/- principal axes
    argument: ``%f``, position: 5
principal_axes: (a boolean, nipy default value: False)
    whether the rotation is searched around an initial principal axis
    alignment.
    argument: ``%d``, position: 6
local_search: (an integer (int or long), nipy default value: 10)
    determines if a local optimization is run at each search point for
    the set number of iterations
    argument: ``%d``, position: 7
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
    output transform file
```

52.5.2 AverageAffineTransform[Link to code](#)

Wraps the executable command AverageAffineTransform.

Examples

```
>>> from nipy.interfaces.ants import AverageAffineTransform
>>> avg = AverageAffineTransform()
>>> avg.inputs.dimension = 3
>>> avg.inputs.transforms = ['trans.mat', 'func_to_struct.mat']
>>> avg.inputs.output_affine_transform = 'MYtemplatewarp.mat'
>>> avg.cmdline
'AverageAffineTransform 3 MYtemplatewarp.mat trans.mat func_to_struct.mat'
```

Inputs:


```
[Mandatory]
dimension: (3 or 2)
    image dimension (2 or 3)
    argument: ``%d``, position: 0
output_affine_transform: (a pathlike object or string representing a
    file)
    Outputfname.txt: the name of the resulting transform.
    argument: ``%s``, position: 1
transforms: (a list of items which are a pathlike object or string
    representing an existing file)
    transforms to average
    argument: ``%s``, position: 3

[Optional]
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
affine_transform: (a pathlike object or string representing an
    existing file)
    average transform file
```

52.5.3 Average**Images**[Link to code](#)

Wraps the executable command AverageImages.

Examples

```
>>> from nipy.interfaces.ants import AverageImages
>>> avg = AverageImages()
>>> avg.inputs.dimension = 3
>>> avg.inputs.output_average_image = "average.nii.gz"
>>> avg.inputs.normalize = True
>>> avg.inputs.images = ['rclsl.nii', 'rclsl.nii']
>>> avg.cmdline
'AverageImages 3 average.nii.gz 1 rclsl.nii rclsl.nii'
```

Inputs:

```
[Mandatory]
dimension: (3 or 2)
    image dimension (2 or 3)
    argument: ``%d``, position: 0
normalize: (a boolean)
    Normalize: if true, the 2nd image is divided by its mean. This will
    select the largest image to average into.
    argument: ``%d``, position: 2
images: (a list of items which are a pathlike object or string
```

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```

        representing an existing file)
        image to apply transformation to (generally a coregistered
        functional)
        argument: ``%s``, position: 3

[Optional]
output_average_image: (a pathlike object or string representing a
        file, nipy default value: average.nii)
        the name of the resulting image.
        argument: ``%s``, position: 1
num_threads: (an integer (int or long), nipy default value: 1)
        Number of ITK threads to use
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

output_average_image: (a pathlike object or string representing an
        existing file)
        average image file

```

52.5.4 ComposeMultiTransform[Link to code](#)

Wraps the executable command ComposeMultiTransform.

Take a set of transformations and convert them to a single transformation matrix/warfield.

Examples

```

>>> from nipy.interfaces.ants import ComposeMultiTransform
>>> compose_transform = ComposeMultiTransform()
>>> compose_transform.inputs.dimension = 3
>>> compose_transform.inputs.transforms = ['struct_to_template.mat', 'func_to_
↳ struct.mat']
>>> compose_transform.cmdline
'ComposeMultiTransform 3 struct_to_template_composed.mat struct_to_template.mat_
↳ func_to_struct.mat '

```

Inputs:

```

[Mandatory]
transforms: (a list of items which are a pathlike object or string
        representing an existing file)
        transforms to average
        argument: ``%s``, position: 3

[Optional]
dimension: (3 or 2, nipy default value: 3)
        image dimension (2 or 3)
        argument: ``%d``, position: 0
output_transform: (a pathlike object or string representing a file)

```

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```

        the name of the resulting transform.
        argument: ``%s``, position: 1
reference_image: (a pathlike object or string representing a file)
        Reference image (only necessary when output is warpfield)
        argument: ``%s``, position: 2
num_threads: (an integer (int or long), nipy default value: 1)
        Number of ITK threads to use
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

output_transform: (a pathlike object or string representing an
        existing file)
        Composed transform file

```

52.5.5 CreateJacobianDeterminantImage[Link to code](#)

Wraps the executable command CreateJacobianDeterminantImage.

Examples

```

>>> from nipy.interfaces.ants import CreateJacobianDeterminantImage
>>> jacobian = CreateJacobianDeterminantImage()
>>> jacobian.inputs.imageDimension = 3
>>> jacobian.inputs.deformationField = 'ants_Warp.nii.gz'
>>> jacobian.inputs.outputImage = 'out_name.nii.gz'
>>> jacobian.cmdline
'CreateJacobianDeterminantImage 3 ants_Warp.nii.gz out_name.nii.gz'

```

Inputs:

```

[Mandatory]
imageDimension: (3 or 2)
        image dimension (2 or 3)
        argument: ``%d``, position: 0
deformationField: (a pathlike object or string representing an
        existing file)
        deformation transformation file
        argument: ``%s``, position: 1
outputImage: (a pathlike object or string representing a file)
        output filename
        argument: ``%s``, position: 2

[Optional]
doLogJacobian: (0 or 1)
        return the log jacobian
        argument: ``%d``, position: 3
useGeometric: (0 or 1)
        return the geometric jacobian

```

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```

        argument: ``%d``, position: 4
num_threads: (an integer (int or long), nipyte default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables

```

Outputs:

```

jacobian_image: (a pathlike object or string representing an existing
    file)
    jacobian image

```

52.5.6 LabelGeometry

[Link to code](#)

Wraps the executable command LabelGeometryMeasures.

Extracts geometry measures using a label file and an optional image file

Examples

```

>>> from nipyte.interfaces.ants import LabelGeometry
>>> label_extract = LabelGeometry()
>>> label_extract.inputs.dimension = 3
>>> label_extract.inputs.label_image = 'atlas.nii.gz'
>>> label_extract.cmdline
'LabelGeometryMeasures 3 atlas.nii.gz [] atlas.csv'

```

```

>>> label_extract.inputs.intensity_image = 'ants_Warp.nii.gz'
>>> label_extract.cmdline
'LabelGeometryMeasures 3 atlas.nii.gz ants_Warp.nii.gz atlas.csv'

```

Inputs:

```

[Mandatory]
label_image: (a pathlike object or string representing a file)
    label image to use for extracting geometry measures
    argument: ``%s``, position: 1
intensity_image: (a pathlike object or string representing an
    existing file, nipyte default value: [])
    Intensity image to extract values from. This is an optional input
    argument: ``%s``, position: 2

[Optional]
dimension: (3 or 2, nipyte default value: 3)
    image dimension (2 or 3)
    argument: ``%d``, position: 0
output_file: (a unicode string)
    name of output file
    argument: ``%s``, position: 3
num_threads: (an integer (int or long), nipyte default value: 1)
    Number of ITK threads to use

```

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```
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
    file)
    CSV file of geometry measures
```

52.5.7 MultiplyImages[Link to code](#)

Wraps the executable command MultiplyImages.

Examples

```
>>> from nipy.interfaces.ants import MultiplyImages
>>> test = MultiplyImages()
>>> test.inputs.dimension = 3
>>> test.inputs.first_input = 'moving2.nii'
>>> test.inputs.second_input = 0.25
>>> test.inputs.output_product_image = "out.nii"
>>> test.cmdline
'MultiplyImages 3 moving2.nii 0.25 out.nii'
```

Inputs:

```
[Mandatory]
dimension: (3 or 2)
    image dimension (2 or 3)
    argument: ``%d``, position: 0
first_input: (a pathlike object or string representing an existing
    file)
    image 1
    argument: ``%s``, position: 1
second_input: (a pathlike object or string representing an existing
    file or a float)
    image 2 or multiplication weight
    argument: ``%s``, position: 2
output_product_image: (a pathlike object or string representing a
    file)
    Outputfname.nii.gz: the name of the resulting image.
    argument: ``%s``, position: 3

[Optional]
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
```

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```

of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

output_product_image: (a pathlike object or string representing an
existing file)
average image file

```

52.6 interfaces.ants.visualization

52.6.1 ConvertScalarImageToRGB

[Link to code](#)

Wraps the executable command ConvertScalarImageToRGB.

Examples

```

>>> from nipy.interfaces.ants.visualization import ConvertScalarImageToRGB
>>> converter = ConvertScalarImageToRGB()
>>> converter.inputs.dimension = 3
>>> converter.inputs.input_image = 'T1.nii.gz'
>>> converter.inputs.colormap = 'jet'
>>> converter.inputs.minimum_input = 0
>>> converter.inputs.maximum_input = 6
>>> converter.cmdline
'ConvertScalarImageToRGB 3 T1.nii.gz rgb.nii.gz none jet none 0 6 0 255'

```

Inputs:

```

[Mandatory]
dimension: (3 or 2, nipy default value: 3)
    image dimension (2 or 3)
    argument: ``%d``, position: 0
input_image: (a pathlike object or string representing an existing
file)
    Main input is a 3-D grayscale image.
    argument: ``%s``, position: 1
colormap: (a unicode string, nipy default value: )
    Possible colormaps: grey, red, green, blue, copper, jet, hsv,
spring, summer, autumn, winter, hot, cool, overunder, custom
    argument: ``%s``, position: 4
minimum_input: (an integer (int or long))
    minimum input
    argument: ``%d``, position: 6
maximum_input: (an integer (int or long))
    maximum input
    argument: ``%d``, position: 7

[Optional]
output_image: (a unicode string, nipy default value: rgb.nii.gz)
    rgb output image
    argument: ``%s``, position: 2
mask_image: (a pathlike object or string representing an existing

```

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```

        file, nipy default value: none)
    mask image
        argument: ``%s``, position: 3
custom_color_map_file: (a unicode string, nipy default value: none)
    custom color map file
        argument: ``%s``, position: 5
minimum_RGB_output: (an integer (int or long), nipy default value:
    0)
        argument: ``%d``, position: 8
maximum_RGB_output: (an integer (int or long), nipy default value:
    255)
        argument: ``%d``, position: 9
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

output_image: (a pathlike object or string representing an existing
    file)
    converted RGB image

```

52.6.2 CreateTiledMosaic

[Link to code](#)

Wraps the executable command CreateTiledMosaic.

The program CreateTiledMosaic in conjunction with ConvertScalarImageToRGB provides useful functionality for common image analysis tasks. The basic usage of CreateTiledMosaic is to tile a 3-D image volume slice-wise into a 2-D image.

Examples

```

>>> from nipy.interfaces.ants.visualization import CreateTiledMosaic
>>> mosaic_slicer = CreateTiledMosaic()
>>> mosaic_slicer.inputs.input_image = 'T1.nii.gz'
>>> mosaic_slicer.inputs.rgb_image = 'rgb.nii.gz'
>>> mosaic_slicer.inputs.mask_image = 'mask.nii.gz'
>>> mosaic_slicer.inputs.output_image = 'output.png'
>>> mosaic_slicer.inputs.alpha_value = 0.5
>>> mosaic_slicer.inputs.direction = 2
>>> mosaic_slicer.inputs.pad_or_crop = '[-15x -50 , -15x -30 ,0]'
>>> mosaic_slicer.inputs.slices = '[2 ,100 ,160]'
>>> mosaic_slicer.cmdline
'CreateTiledMosaic -a 0.50 -d 2 -i T1.nii.gz -x mask.nii.gz -o output.png -p [ -
  ↪15x -50 , -15x -30 ,0] -r rgb.nii.gz -s [2 ,100 ,160]'

```

Inputs:

```

[Mandatory]
input_image: (a pathlike object or string representing an existing

```

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```

    file)
    Main input is a 3-D grayscale image.
    argument: ``-i %s``
rgb_image: (a pathlike object or string representing an existing
    file)
    An optional Rgb image can be added as an overlay.It must have the
    same imagegeometry as the input grayscale image.
    argument: ``-r %s``

[Optional]
mask_image: (a pathlike object or string representing an existing
    file)
    Specifies the ROI of the RGB voxels used.
    argument: ``-x %s``
alpha_value: (a float)
    If an Rgb image is provided, render the overlay using the specified
    alpha parameter.
    argument: ``-a %.2f``
output_image: (a unicode string, nipy default value: output.png)
    The output consists of the tiled mosaic image.
    argument: ``-o %s``
tile_geometry: (a unicode string)
    The tile geometry specifies the number of rows and columns in the
    output image. For example, if the user specifies "5x10", then 5 rows
    by 10 columns of slices are rendered. If R < 0 and C > 0 (or vice
    versa), the negative value is selected based on direction.
    argument: ``-t %s``
direction: (an integer (int or long))
    Specifies the direction of the slices. If no direction is specified,
    the direction with the coarsest spacing is chosen.
    argument: ``-d %d``
pad_or_crop: (a unicode string)
    argument passed to -p flag:[padVoxelWidth,<constantValue=0>][lowerPa
    dding[0]xlowerPadding[1],upperPadding[0]xupperPadding[1],constantVal
    ue]The user can specify whether to pad or crop a specified voxel-
    width boundary of each individual slice. For this program, cropping
    is simply padding with negative voxel-widths.If one pads (+), the
    user can also specify a constant pad value (default = 0). If a mask
    is specified, the user can use the mask to define the region, by
    using the keyword "mask" plus an offset, e.g. "-p mask+3".
    argument: ``-p %s``
slices: (a unicode string)
    Number of slices to increment Slice1xSlice2xSlice3[numberOfSlicesToI
    ncrement,<minSlice=0>,<maxSlice=lastSlice>]
    argument: ``-s %s``
flip_slice: (a unicode string)
    flipXxflipY
    argument: ``-f %s``
permute_axes: (a boolean)
    doPermute
    argument: ``-g``
num_threads: (an integer (int or long), nipy default value: 1)
    Number of ITK threads to use
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value

```

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```
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipyype default value: {}))
Environment variables
```

Outputs:

```
output_image: (a pathlike object or string representing an existing
               file)
               image file
```


53.1 interfaces.base.core

53.1.1 BaseInterface

[Link to code](#)

Implements common interface functionality.

Implements

- Initializes inputs/outputs from input_spec/output_spec
- Provides help based on input_spec and output_spec
- Checks for mandatory inputs before running an interface
- Runs an interface and returns results
- Determines which inputs should be copied or linked to cwd

This class does not implement aggregate_outputs, input_spec or output_spec. These should be defined by derived classes.

This class cannot be instantiated.

Relevant Interface attributes

input_spec points to the traitled class for the inputs output_spec points to the traitled class for the outputs
_redirect_x should be set to True when the interface requires
connecting to a \$DISPLAY (default is False).

resource_monitor if **False** prevents resource-monitoring this interface, if True monitoring will be enabled IFF the general Nipype config is set on (resource_monitor = true).

Inputs:

None

Outputs:

None

53.1.2 CommandLine

[Link to code](#)

Implements functionality to interact with command line programs class must be instantiated with a command argument

Parameters

command [string] define base immutable *command* you wish to run

args [string, optional] optional arguments passed to base *command*

Examples

```
>>> import pprint
>>> from nipyne.interfaces.base import CommandLine
>>> cli = CommandLine(command='ls', environ={'DISPLAY': ':1'})
>>> cli.inputs.args = '-al'
>>> cli.cmdline
'ls -al'
```

```
# Use get_traitsfree() to check all inputs set >>> pprint.pprint(cli.inputs.get_traitsfree()) # doctest: {'args': '-al',
'environ': {'DISPLAY': ':1'}}
```

```
>>> cli.inputs.get_hashval()[0][0]
('args', '-al')
>>> cli.inputs.get_hashval()[1]
'11c37f97649cd61627f4afe5136af8c0'
```

Inputs:

```
[Optional]
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyne default value: {})
          Environment variables
```

Outputs:

```
None
```

53.1.3 LibraryBaseInterface

[Link to code](#)

Inputs:

```
None
```

Outputs:

```
None
```

53.1.4 MpiCommandLine

[Link to code](#)

Implements functionality to interact with command line programs that can be run with MPI (i.e. using 'mpiexec').

Examples

```
>>> from nipyte.interfaces.base import MpiCommandLine
>>> mpi_cli = MpiCommandLine(command='my_mpi_prog')
>>> mpi_cli.inputs.args = '-v'
>>> mpi_cli.cmdline
'my_mpi_prog -v'
```

```
>>> mpi_cli.inputs.use_mpi = True
>>> mpi_cli.inputs.n_procs = 8
>>> mpi_cli.cmdline
'mpiexec -n 8 my_mpi_prog -v'
```

Inputs:

```
[Optional]
use_mpi: (a boolean, nipyte default value: False)
    Whether or not to run the command with mpiexec
n_procs: (an integer (int or long))
    Num processors to specify to mpiexec. Do not specify if this is
    managed externally (e.g. through SGE)
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables
```

Outputs:

None

53.1.5 SEMLikeCommandLine

[Link to code](#)

In SEM derived interface all outputs have corresponding inputs. However, some SEM commands create outputs that are not defined in the XML. In those cases one has to create a subclass of the autogenerated one and overload the `_list_outputs` method. `_outputs_from_inputs` should still be used but only for the reduced (by excluding those that do not have corresponding inputs list of outputs).

Inputs:

```
[Optional]
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables
```

Outputs:

None

53.1.6 SimpleInterface

[Link to code](#)

An interface pattern that allows outputs to be set in a dictionary called `_results` that is automatically interpreted by `_list_outputs()` to find the outputs.

When implementing `_run_interface`, set outputs with:

```
self._results[out_name] = out_value
```

This can be a way to upgrade a Function interface to do type checking.

Examples

```
>>> from nipyne.interfaces.base import (
...     SimpleInterface, BaseInterfaceInputSpec, TraitedSpec)
```

```
>>> def double(x):
...     return 2 * x
...
>>> class DoubleInputSpec(BaseInterfaceInputSpec):
...     x = traits.Float(mandatory=True)
...
>>> class DoubleOutputSpec(TraitdSpec):
...     doubled = traits.Float()
...
>>> class Double(SimpleInterface):
...     input_spec = DoubleInputSpec
...     output_spec = DoubleOutputSpec
...
...     def _run_interface(self, runtime):
...         self._results['doubled'] = double(self.inputs.x)
...         return runtime
```

```
>>> dbl = Double()
>>> dbl.inputs.x = 2
>>> dbl.run().outputs.doubled
4.0
```

Inputs:

```
None
```

Outputs:

```
None
```

53.1.7 StdOutCommandLine

[Link to code](#)

Inputs:

```
[Optional]
out_file: (a pathlike object or string representing a file)
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables
```

Outputs:

None

53.2 interfaces.base.specs

53.2.1 get_filecopy_info()

[Link to code](#)

Provides information about file inputs to copy or link to cwd. Necessary for pipeline operation

53.3 interfaces.base.support

53.3.1 format_help()

[Link to code](#)

Prints help text of a Nipype interface

```

>>> from nipype.interfaces.afni import GCOR
>>> GCOR.help() # doctest: +ELLIPSIS, +NORMALIZE_WHITESPACE
Wraps the executable command ``@compute_gcor``.
<BLANKLINE>
Computes the average correlation between every voxel
and ever other voxel, over any give mask.
<BLANKLINE>
<BLANKLINE>
For complete details, ...

```

53.3.2 get_trait_desc()

[Link to code](#)

Parses a HasTraits object into a nipype documentation string

53.4 interfaces.base.traits_extension

53.4.1 has_metadata()

[Link to code](#)

Checks if a given trait has a metadata (and optionally if it is set to particular value)

53.4.2 isdefined()

[Link to code](#)

53.4.3 rebase_path_traits()

[Link to code](#)

Rebase a BasePath-derived trait given an interface spec.

53.4.4 resolve_path_traits()

[Link to code](#)

Resolve a BasePath-derived trait given an interface spec.

54.1 interfaces.brainsuite.brainsuite

54.1.1 BDP

[Link to code](#)

Wraps the executable command `bdp.sh`.

BrainSuite Diffusion Pipeline (BDP) enables fusion of diffusion and structural MRI information for advanced image and connectivity analysis. It provides various methods for distortion correction, co-registration, diffusion modeling (DTI and ODF) and basic ROI-wise statistic. BDP is a flexible and diverse tool which supports wide variety of diffusion datasets. For more information, please see:

<http://brainsuite.org/processing/diffusion/>

Examples

```
>>> from nipype.interfaces import brainsuite
>>> bdp = brainsuite.BDP()
>>> bdp.inputs.bfcFile = '/directory/subdir/prefix.bfc.nii.gz'
>>> bdp.inputs.inputDiffusionData = '/directory/subdir/prefix.dwi.nii.gz'
>>> bdp.inputs.BVecBValPair = ['/directory/subdir/prefix.dwi.bvec', '/directory/
↳subdir/prefix.dwi.bval']
>>> results = bdp.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
bfcFile: (a pathlike object or string representing a file)
    Specify absolute path to file produced by bfc. By default, bfc
    produces the file in the format: prefix.bfc.nii.gz
    argument: ``%s``, position: 0
    mutually_exclusive: noStructuralRegistration
noStructuralRegistration: (a boolean)
    Allows BDP to work without any structural input. This can useful
    when one is only interested in diffusion modelling part of BDP. With
    this flag only fieldmap-based distortion correction is supported.
    outPrefix can be used to specify fileprefix of the output filenames.
    Change dwiMask to define region of interest for diffusion modelling.
```

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```

        argument: ``--no-structural-registration``, position: 0
        mutually_exclusive: bfcFile
inputDiffusionData: (a pathlike object or string representing a file)
    Specifies the absolute path and filename of the input diffusion data
    in 4D NIfTI-1 format. The flag must be followed by the filename.
    Only NIfTI-1 files with extension .nii or .nii.gz are supported.
    Furthermore, either bMatrixFile, or a combination of both bValueFile
    and diffusionGradientFile must be used to provide the necessary
    b-matrices/b-values and gradient vectors.
    argument: ``--nii %s``, position: -2
bMatrixFile: (a pathlike object or string representing a file)
    Specifies the absolute path and filename of the file containing
    b-matrices for diffusion-weighted scans. The flag must be followed
    by the filename. This file must be a plain text file containing 3x3
    matrices for each diffusion encoding direction. It should contain
    zero matrices corresponding to b=0 images. This file usually has
    ".bmat" as its extension, and can be used to provide BDP with the
    more-accurate b-matrices as saved by some proprietary scanners. The
    b-matrices specified by the file must be in the voxel coordinates of
    the input diffusion weighted image (NIfTI file). In case b-matrices
    are not known/calculated, bvec and .bval files can be used instead
    (see diffusionGradientFile and bValueFile).
    argument: ``--bmat %s``, position: -1
    mutually_exclusive: BVecBValPair
BVecBValPair: (a list of from 2 to 2 items which are a unicode
    string)
    Must input a list containing first the BVector file, then the BValue
    file (both must be absolute paths)
    Example: bdp.inputs.BVecBValPair =
    ['/directory/subdir/prefix.dwi.bvec',
     '/directory/subdir/prefix.dwi.bval'] The first item in the list
    specifies the filename of the file containing b-values for the
    diffusion scan. The b-value file must be a plain-text file and
    usually has an extension of .bval
    The second item in the list specifies the filename of the file
    containing the diffusion gradient directions (specified in the voxel
    coordinates of the input diffusion-weighted image)The b-vectors file
    must be a plain text file and usually has an extension of .bvec
    argument: ``--bvec %s --bval %s``, position: -1
    mutually_exclusive: bMatrixFile

[Optional]
dataSinkDelay: (a list of items which are a unicode string)
    For use in parallel processing workflows including Brainsuite
    Cortical Surface Extraction sequence. Connect datasink out_file to
    dataSinkDelay to delay execution of BDP until dataSink has finished
    sinking outputs. In particular, BDP may be run after BFC has
    finished. For more information see
    http://brainsuite.org/processing/diffusion/pipeline/
    argument: ``%s``
phaseEncodingDirection: ('x' or 'x-' or 'y' or 'y-' or 'z' or 'z-')
    Specifies the phase-encoding direction of the EPI (diffusion)
    images. It is same as the dominant direction of distortion in the
    images. This information is used to constrain the distortion
    correction along the specified direction. Directions are represented
    by any one of x, x-, y, y-, z or z-. "x" direction increases towards
    the right side of the subject, while "x-" increases towards the left

```

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```

side of the subject. Similarly, "y" and "y-" are along the anterior-
posterior direction of the subject, and "z" & "z-" are along the
inferior-superior direction. When this flag is not used, BDP uses
"y" as the default phase-encoding direction.
argument: ``--dir=%s``
echoSpacing: (a float)
Sets the echo spacing to t seconds, which is used for fieldmap-based
distortion correction. This flag is required when using
fieldmapCorrection
argument: ``--echo-spacing=%f``
bValRatioThreshold: (a float)
Sets a threshold which is used to determine b=0 images. When there
are no diffusion weighted image with b-value of zero, then BDP tries
to use diffusion weighted images with a low b-value in place of b=0
image. The diffusion images with minimum b-value is used as b=0
image only if the ratio of the maximum and minimum b-value is more
than the specified threshold. A lower value of threshold will allow
diffusion images with higher b-value to be used as b=0 image. The
default value of this threshold is set to 45, if this trait is not
set.
argument: ``--bval-ratio-threshold %f``
estimateTensors: (a boolean)
Estimates diffusion tensors using a weighted log-linear estimation
and saves derived diffusion tensor parameters (FA, MD, axial,
radial, L2, L3). This is the default behavior if no diffusion
modeling flags are specified. The estimated diffusion tensors can be
visualized by loading the saved *.eig.nii.gz file in BrainSuite. BDP
reports diffusivity (MD, axial, radial, L2 and L3) in a unit which
is reciprocal inverse of the unit of input b-value.
argument: ``--tensors``
estimateODF_FRACT: (a boolean)
Estimates ODFs using the Funk-Radon and Cosine Transformation
(FRACT). The outputs are saved in a separate directory with name
"FRACT" and the ODFs can be visualized by loading the saved ".odf"
file in BrainSuite.
argument: ``--FRACT``
estimateODF_FRT: (a boolean)
Estimates ODFs using Funk-Radon Transformation (FRT). The
coefficient maps for ODFs are saved in a separate directory with
name "FRT" and the ODFs can be visualized by loading the saved
".odf" file in BrainSuite. The derived generalized-FA (GFA) maps are
also saved in the output directory.
argument: ``--FRT``
estimateODF_3DShore: (a float)
Estimates ODFs using 3Dshore. Pass in diffusion time, in ms
argument: ``--3dshore --diffusion_time_ms %f``
odfLambda: (a boolean)
Sets the regularization parameter, lambda, of the Laplace-Beltrami
operator while estimating ODFs. The default value is set to 0.006 .
This can be used to set the appropriate regularization for the input
diffusion data.
argument: ``--odf-lambda <L>``
t1Mask: (a pathlike object or string representing a file)
Specifies the filename of the brain-mask file for input T1-weighted
image. This mask can be same as the brain mask generated during
BrainSuite extraction sequence. For best results, the mask should
not include any extra-meningial tissues from T1-weighted image. The

```

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mask must be in the same coordinates as input T1-weighted image (i.e. should overlay correctly with input <fileprefix>.bfc.nii.gz file in BrainSuite). This mask is used for co-registration and defining brain boundary for statistics computation. The mask can be generated and/or edited in BrainSuite. In case outputDiffusionCoordinates is also used, this mask is first transformed to diffusion coordinate and the transformed mask is used for defining brain boundary in diffusion coordinates. When t1Mask is not set, BDP will try to use fileprefix>.mask.nii.gz as brain-mask. If <fileprefix>.mask.nii.gz is not found, then BDP will use the input <fileprefix>.bfc.nii.gz itself as mask (i.e. all non-zero voxels in <fileprefix>.bfc.nii.gz is assumed to constitute brain mask).

argument: ``--t1-mask %s``

dwiMask: (a pathlike object or string representing a file)
Specifies the filename of the brain-mask file for diffusion data. This mask is used only for co-registration purposes and can affect overall quality of co-registration (see t1Mask for definition of brain mask for statistics computation). The mask must be a 3D volume and should be in the same coordinates as input Diffusion file/data (i.e. should overlay correctly with input diffusion data in BrainSuite). For best results, the mask should include only brain voxels (CSF voxels around brain is also acceptable). When this flag is not used, BDP will generate a pseudo mask using first b=0 image volume and would save it as fileprefix>.dwi.RSA.mask.nii.gz. In case co-registration is not accurate with automatically generated pseudo mask, BDP should be re-run with a refined diffusion mask. The mask can be generated and/or edited in BrainSuite.

argument: ``--dwi-mask %s``

rigidRegMeasure: ('MI' or 'INVERSION' or 'BDP')
Defines the similarity measure to be used for rigid registration. Possible measures are "MI", "INVERSION" and "BDP". MI measure uses normalized mutual information based cost function. INVERSION measure uses simpler cost function based on sum of squared difference by exploiting the approximate inverse-contrast relationship in T1- and T2-weighted images. BDP measure combines MI and INVERSION. It starts with INVERSION measure and refines the result with MI measure. BDP is the default measure when this trait is not set.

argument: ``--rigid-reg-measure %s``

dcorrRegMeasure: ('MI' or 'INVERSION-EPI' or 'INVERSION-T1' or 'INVERSION-BOTH' or 'BDP')
Defines the method for registration-based distortion correction. Possible methods are "MI", "INVERSION-EPI", "INVERSION-T1", "INVERSION-BOTH", and "BDP". MI method uses normalized mutual information based cost-function while estimating the distortion field. INVERSION-based method uses simpler cost function based on sum of squared difference by exploiting the known approximate contrast relationship in T1- and T2-weighted images. T2-weighted EPI is inverted when INVERSION-EPI is used; T1-image is inverted when INVERSION-T1 is used; and both are inverted when INVERSION-BOTH is used. BDP method add the MI-based refinement after the correction using INVERSION-BOTH method. BDP is the default method when this trait is not set.

argument: ``--dcorr-reg-method %s``

dcorrWeight: (a float)
Sets the (scalar) weighting parameter for regularization penalty in registration-based distortion correction. Set this trait to a

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single, non-negative number which specifies the weight. A large regularization weight encourages smoother distortion field at the cost of low measure of image similarity after distortion correction. On the other hand, a smaller regularization weight can result into higher measure of image similarity but with unrealistic and unsmooth distortion field. A weight of 0.5 would reduce the penalty to half of the default regularization penalty (By default, this weight is set to 1.0). Similarly, a weight of 2.0 would increase the penalty to twice of the default penalty.

argument: ``--dcorr-regularization-wt %f``

skipDistortionCorr: (a boolean)

Skips distortion correction completely and performs only a rigid registration of diffusion and T1-weighted image. This can be useful when the input diffusion images do not have any distortion or they have been corrected for distortion.

argument: ``--no-distortion-correction``

skipNonuniformityCorr: (a boolean)

Skips intensity non-uniformity correction in b=0 image for registration-based distortion correction. The intensity non-uniformity correction does not affect any diffusion modeling.

argument: ``--no-nonuniformity-correction``

skipIntensityCorr: (a boolean)

Disables intensity correction when performing distortion correction. Intensity correction can change the noise distribution in the corrected image, but it does not affect estimated diffusion parameters like FA, etc.

argument: ``--no-intensity-correction``

mutually_exclusive: fieldmapCorrectionMethod

fieldmapCorrection: (a pathlike object or string representing a file)

Use an acquired fieldmap for distortion correction. The fieldmap must have units of radians/second. Specify the filename of the fieldmap file. The field of view (FOV) of the fieldmap scan must cover the FOV of the diffusion scan. BDP will try to check the overlap of the FOV of the two scans and will issue a warning/error if the diffusion scan's FOV is not fully covered by the fieldmap's FOV. BDP uses all of the information saved in the NIfTI header to compute the FOV. If you get this error and think that it is incorrect, then it can be suppressed using the flag ignore-fieldmap-FOV. Neither the image matrix size nor the imaging grid resolution of the fieldmap needs to be the same as that of the diffusion scan, but the fieldmap must be pre-registered to the diffusion scan. BDP does NOT align the fieldmap to the diffusion scan, nor does it check the alignment of the fieldmap and diffusion scans. Only NIfTI files with extension of .nii or .nii.gz are supported. Fieldmap-based distortion correction also requires the echoSpacing. Also fieldmapCorrectionMethod allows you to define method for distortion correction. least squares is the default method.

argument: ``--fieldmap-correction %s``

requires: echoSpacing

fieldmapCorrectionMethod: ('pixelshift' or 'leastsq')

Defines the distortion correction method while using fieldmap. Possible methods are "pixelshift" and "leastsq". leastsq is the default method when this flag is not used. Pixel-shift (pixelshift) method uses image interpolation to un-distort the distorted diffusion images. Least squares (leastsq) method uses a physical model of distortion which is more accurate (and more computationally expensive) than pixel-shift method.

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```

    argument: ``--fieldmap-correction-method %s``
    mutually_exclusive: skipIntensityCorr
ignoreFieldmapFOV: (a boolean)
    Supresses the error generated by an insufficient field of view of
    the input fieldmap and continues with the processing. It is useful
    only when used with fieldmap-based distortion correction. See
    fieldmap-correction for a detailed explanation.
    argument: ``--ignore-fieldmap-fov``
fieldmapSmooth: (a float)
    Applies 3D Gaussian smoothing with a standard deviation of S
    millimeters (mm) to the input fieldmap before applying distortion
    correction. This trait is only useful with fieldmapCorrection. Skip
    this trait for no smoothing.
    argument: ``--fieldmap-smooth3=%f``
transformDiffusionVolume: (a pathlike object or string representing a
    file)
    This flag allows to define custom volumes in diffusion coordinate
    which would be transformed into T1 coordinate in a rigid fashion.
    The flag must be followed by the name of either a NIfTI file or of a
    folder that contains one or more NIfTI files. All of the files must
    be in diffusion coordinate, i.e. the files should overlay correctly
    with the diffusion scan in BrainSuite. Only NIfTI files with an
    extension of .nii or .nii.gz are supported. The transformed files
    are written to the output directory with suffix ".T1_coord" in the
    filename and will not be corrected for distortion, if any. The trait
    transformInterpolation can be used to define the type of
    interpolation that would be used (default is set to linear). If you
    are attempting to transform a label file or mask file, use "nearest"
    interpolation method with transformInterpolation. See also
    transformT1Volume and transformInterpolation
    argument: ``--transform-diffusion-volume %s``
transformT1Volume: (a pathlike object or string representing a file)
    Same as transformDiffusionVolume except that files specified must be
    in T1 coordinate, i.e. the files should overlay correctly with the
    input <fileprefix>.bfc.nii.gz files in BrainSuite. BDP transforms
    these data/images from T1 coordinate to diffusion coordinate. The
    transformed files are written to the output directory with suffix
    ".D_coord" in the filename. See also transformDiffusionVolume and
    transformInterpolation.
    argument: ``--transform-t1-volume %s``
transformInterpolation: ('linear' or 'nearest' or 'cubic' or
    'spline')
    Defines the type of interpolation method which would be used while
    transforming volumes defined by transformT1Volume and
    transformDiffusionVolume. Possible methods are "linear", "nearest",
    "cubic" and "spline". By default, "linear" interpolation is used.
    argument: ``--transform-interpolation %s``
transformT1Surface: (a pathlike object or string representing a file)
    Similar to transformT1Volume, except that this flag allows
    transforming surfaces (instead of volumes) in T1 coordinate into
    diffusion coordinate in a rigid fashion. The flag must be followed
    by the name of either a .dfs file or of a folder that contains one
    or more dfs files. All of the files must be in T1 coordinate, i.e.
    the files should overlay correctly with the T1-weighted scan in
    BrainSuite. The transformed files are written to the output
    directory with suffix D_coord" in the filename.
    argument: ``--transform-t1-surface %s``

```

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```

transformDiffusionSurface: (a pathlike object or string representing
    a file)
    Same as transformT1Volume, except that the .dfs files specified must
    be in diffusion coordinate, i.e. the surface files should overlay
    correctly with the diffusion scan in BrainSuite. The transformed
    files are written to the output directory with suffix ".T1_coord" in
    the filename. See also transformT1Volume.
    argument: ``--transform-diffusion-surface %s``

transformDataOnly: (a boolean)
    Skip all of the processing (co-registration, distortion correction
    and tensor/ODF estimation) and directly start transformation of
    defined custom volumes, mask and labels (using transformT1Volume,
    transformDiffusionVolume, transformT1Surface,
    transformDiffusionSurface, customDiffusionLabel, customT1Label).
    This flag is useful when BDP was previously run on a subject (or
    <fileprefix>) and some more data (volumes, mask or labels) need to
    be transformed across the T1-diffusion coordinate spaces. This
    assumes that all the necessary files were generated earlier and all
    of the other flags MUST be used in the same way as they were in the
    initial BDP run that processed the data.
    argument: ``--transform-data-only``

generateStats: (a boolean)
    Generate ROI-wise statistics of estimated diffusion tensor
    parameters. Units of the reported statistics are same as that of the
    estimated tensor parameters (see estimateTensors). Mean, variance,
    and voxel counts of white matter(WM), grey matter(GM), and both WM
    and GM combined are written for each estimated parameter in a
    separate comma-seperated value csv) file. BDP uses the ROI labels
    generated by Surface-Volume Registration (SVReg) in the BrainSuite
    extraction sequence. Specifically, it looks for labels saved in
    either fileprefix>.svreg.corr.label.nii.gz or
    <fileprefix>.svreg.label.nii.gz. In case both files are present,
    only the first file is used. Also see customDiffusionLabel and
    customT1Label for specifying your own ROIs. It is also possible to
    forgo computing the SVReg ROI-wise statistics and only compute stats
    with custom labels if SVReg label is missing. BDP also transfers
    (and saves) the label/mask files to appropriate coordinates before
    computing statistics. Also see outputDiffusionCoordinates for
    outputs in diffusion coordinate and forcePartialROIStats for an
    important note about field of view of diffusion and T1-weighted
    scans.
    argument: ``--generate-stats``

onlyStats: (a boolean)
    Skip all of the processing (co-registration, distortion correction
    and tensor/ODF estimation) and directly start computation of
    statistics. This flag is useful when BDP was previously run on a
    subject (or fileprefix>) and statistics need to be (re-)computed
    later. This assumes that all the necessary files were generated
    earlier. All of the other flags MUST be used in the same way as they
    were in the initial BDP run that processed the data.
    argument: ``--generate-only-stats``

forcePartialROIStats: (a boolean)
    The field of view (FOV) of the diffusion and T1-weighted scans may
    differ significantly in some situations. This may result in partial
    acquisitions of some ROIs in the diffusion scan. By default, BDP
    does not compute statistics for partially acquired ROIs and shows
    warnings. This flag forces computation of statistics for all ROIs,

```

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including those which are partially acquired. When this flag is used, number of missing voxels are also reported for each ROI in statistics files. Number of missing voxels are reported in the same coordinate system as the statistics file.

argument: ``--force-partial-roi-stats``

customDiffusionLabel: (a pathlike object or string representing a file)

BDP supports custom ROIs in addition to those generated by BrainSuite SVReg) for ROI-wise statistics calculation. The flag must be followed by the name of either a file (custom ROI file) or of a folder that contains one or more ROI files. All of the files must be in diffusion coordinate, i.e. the label files should overlay correctly with the diffusion scan in BrainSuite. These input label files are also transferred (and saved) to T1 coordinate for statistics in T1 coordinate. BDP uses nearest-neighborhood interpolation for this transformation. Only NIfTI files, with an extension of .nii or .nii.gz are supported. In order to avoid confusion with other ROI IDs in the statistic files, a 5-digit ROI ID is generated for each custom label found and the mapping of ID to label file is saved in the file `fileprefix>.BDP_ROI_MAP.xml`. Custom label files can also be generated by using the label painter tool in BrainSuite. See also `customLabelXML`

argument: ``--custom-diffusion-label %s``

customT1Label: (a pathlike object or string representing a file)

Same as `customDiffusionLabel` except that the label files specified must be in T1 coordinate, i.e. the label files should overlay correctly with the T1-weighted scan in BrainSuite. If the trait `outputDiffusionCoordinates` is also used then these input label files are also transferred (and saved) to diffusion coordinate for statistics in diffusion coordinate. BDP uses nearest-neighborhood interpolation for this transformation. See also `customLabelXML`.

argument: ``--custom-t1-label %s``

customLabelXML: (a pathlike object or string representing a file)

BrainSuite saves a descriptions of the SVReg labels (ROI name, ID, color, and description) in an .xml file (`brainsuite_labeldescription.xml`). BDP uses the ROI ID"s from this xml file to report statistics. This flag allows for the use of a custom label description xml file. The flag must be followed by an xml filename. This can be useful when you want to limit the ROIs for which you compute statistics. You can also use custom xml files to name your own ROIs (assign ID"s) for custom labels. BrainSuite can save a label description in .xml format after using the label painter tool to create a ROI label. The xml file MUST be in the same format as BrainSuite"s label description file (see `brainsuite_labeldescription.xml` for an example). When this flag is used, NO 5-digit ROI ID is generated for custom label files and NO Statistics will be calculated for ROIs not identified in the custom xml file. See also `customDiffusionLabel` and `customT1Label`.

argument: ``--custom-label-xml %s``

outputSubdir: (a unicode string)

By default, BDP writes out all the output (and intermediate) files in the same directory (or folder) as the BFC file. This flag allows to specify a sub-directory name in which output (and intermediate) files would be written. BDP will create the sub-directory in the same directory as BFC file. `<directory_name>` should be the name of the sub-directory without any path. This can be useful to organize all outputs generated by BDP in a separate sub-directory.

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```

    argument: ``--output-subdir %s``
outputDiffusionCoordinates: (a boolean)
    Enables estimation of diffusion tensors and/or ODFs (and statistics
    if applicable) in the native diffusion coordinate in addition to the
    default T1-coordinate. All native diffusion coordinate files are
    saved in a seperate folder named "diffusion_coord_outputs". In case
    statistics computation is required, it will also transform/save all
    label/mask files required to diffusion coordinate (see generateStats
    for details).
    argument: ``--output-diffusion-coordinate``
flagConfigFile: (a pathlike object or string representing a file)
    Uses the defined file to specify BDP flags which can be useful for
    batch processing. A flag configuration file is a plain text file
    which can contain any number of BDP's optional flags (and their
    parameters) separated by whitespace. Everything coming after # until
    end-of-line is treated as comment and is ignored. If a flag is
    defined in configuration file and is also specified in the command
    used to run BDP, then the later get preference and overrides the
    definition in configuration file.
    argument: ``--flag-conf-file %s``
outPrefix: (a unicode string)
    Specifies output fileprefix when noStructuralRegistration is used.
    The fileprefix can not start with a dash (-) and should be a simple
    string reflecting the absolute path to desired location, along with
    outPrefix. When this flag is not specified (and
    noStructuralRegistration is used) then the output files have same
    file-base as the input diffusion file. This trait is ignored when
    noStructuralRegistration is not used.
    argument: ``--output-fileprefix %s``
threads: (an integer (int or long))
    Sets the number of parallel process threads which can be used for
    computations to N, where N must be an integer. Default value of N is
    argument: ``--threads=%d``
lowMemory: (a boolean)
    Activates low-memory mode. This will run the registration-based
    distortion correction at a lower resolution, which could result in a
    less-accurate correction. This should only be used when no other
    alternative is available.
    argument: ``--low-memory``
ignoreMemory: (a boolean)
    Deactivates the inbuilt memory checks and forces BDP to run
    registration-based distortion correction at its default resolution
    even on machines with a low amount of memory. This may result in an
    out-of-memory error when BDP cannot allocate sufficient memory.
    argument: ``--ignore-memory``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

None

54.1.2 Bfc

[Link to code](#)

Wraps the executable command `bfc`.

bias field corrector (BFC) This program corrects gain variation in T1-weighted MRI.

<http://brainsuite.org/processing/surfaceextraction/bfc/>

Examples

```
>>> from nipy.interfaces import brainsuite
>>> from nipy.testing import example_data
>>> bfc = brainsuite.Bfc()
>>> bfc.inputs.inputMRIFile = example_data('structural.nii')
>>> bfc.inputs.inputMaskFile = example_data('mask.nii')
>>> results = bfc.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
inputMRIFile: (a pathlike object or string representing a file)
    input skull-stripped MRI volume
    argument: ``-i %s``

[Optional]
inputMaskFile: (a pathlike object or string representing a file)
    mask file
    argument: ``-m %s``
outputMRIVolume: (a pathlike object or string representing a file)
    output bias-corrected MRI volume.If unspecified, output file name
    will be auto generated.
    argument: ``-o %s``
outputBiasField: (a pathlike object or string representing a file)
    save bias field estimate
    argument: ``--bias %s``
outputMaskedBiasField: (a pathlike object or string representing a
    file)
    save bias field estimate (masked)
    argument: ``--maskedbias %s``
histogramRadius: (an integer (int or long))
    histogram radius (voxels)
    argument: ``-r %d``
biasEstimateSpacing: (an integer (int or long))
    bias sample spacing (voxels)
    argument: ``-s %d``
controlPointSpacing: (an integer (int or long))
    control point spacing (voxels)
    argument: ``-c %d``
splineLambda: (a float)
    spline stiffness weighting parameter
    argument: ``-w %f``
histogramType: ('ellipse' or 'block')
    Options for type of histogram
    ellipse: use ellipsoid for ROI histogram
    block :use block for ROI histogram
    argument: ``%s``
iterativeMode: (a boolean)
    iterative mode (overrides -r, -s, -c, -w settings)
    argument: ``--iterate``
```

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```

correctionScheduleFile: (a pathlike object or string representing a
    file)
    list of parameters
    argument: ``--schedule %s``
biasFieldEstimatesOutputPrefix: (a unicode string)
    save iterative bias field estimates as <prefix>.n.field.nii.gz
    argument: ``--biasprefix %s``
correctedImagesOutputPrefix: (a unicode string)
    save iterative corrected images as <prefix>.n.bfc.nii.gz
    argument: ``--prefix %s``
correctWholeVolume: (a boolean)
    apply correction field to entire volume
    argument: ``--extrapolate``
minBias: (a float, nipy default value: 0.5)
    minimum allowed bias value
    argument: ``-L %f``
maxBias: (a float, nipy default value: 1.5)
    maximum allowed bias value
    argument: ``-U %f``
biasRange: ('low' or 'medium' or 'high')
    Preset options for bias_model
    low: small bias model [0.95,1.05]
    medium: medium bias model [0.90,1.10]
    high: high bias model [0.80,1.20]
    argument: ``%s``
intermediate_file_type: ('analyze' or 'nifti' or 'gzippedAnalyze' or
    'gzippedNifti')
    Options for the format in which intermediate files are generated
    argument: ``%s``
convergenceThreshold: (a float)
    convergence threshold
    argument: ``--eps %f``
biasEstimateConvergenceThreshold: (a float)
    bias estimate convergence threshold (values > 0.1 disable)
    argument: ``--beps %f``
verbosityLevel: (an integer (int or long))
    verbosity level (0=silent)
    argument: ``-v %d``
timer: (a boolean)
    display timing information
    argument: ``--timer``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputMRIVolume: (a pathlike object or string representing a file)
    path/name of output file
outputBiasField: (a pathlike object or string representing a file)
    path/name of bias field output file
outputMaskedBiasField: (a pathlike object or string representing a
    file)

```

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```

    path/name of masked bias field output
correctionScheduleFile: (a pathlike object or string representing a
    file)
    path/name of schedule file

```

54.1.3 Bse

[Link to code](#)

Wraps the executable command bse.

brain surface extractor (BSE) This program performs automated skull and scalp removal on T1-weighted MRI volumes.

<http://brainsuite.org/processing/surfaceextraction/bse/>

Examples

```

>>> from nipy.interfaces import brainsuite
>>> from nipy.testing import example_data
>>> bse = brainsuite.Bse()
>>> bse.inputs.inputMRIFile = example_data('structural.nii')
>>> results = bse.run() #doctest: +SKIP

```

Inputs:

```

[Mandatory]
inputMRIFile: (a pathlike object or string representing a file)
    input MRI volume
    argument: ``-i %s``

[Optional]
outputMRIVolume: (a pathlike object or string representing a file)
    output brain-masked MRI volume. If unspecified, output file name
    will be auto generated.
    argument: ``-o %s``
outputMaskFile: (a pathlike object or string representing a file)
    save smooth brain mask. If unspecified, output file name will be
    auto generated.
    argument: ``--mask %s``
diffusionConstant: (a float, nipy default value: 25)
    diffusion constant
    argument: ``-d %f``
diffusionIterations: (an integer (int or long), nipy default value:
    3)
    diffusion iterations
    argument: ``-n %d``
edgeDetectionConstant: (a float, nipy default value: 0.64)
    edge detection constant
    argument: ``-s %f``
radius: (a float, nipy default value: 1)
    radius of erosion/dilation filter
    argument: ``-r %f``
dilateFinalMask: (a boolean, nipy default value: True)
    dilate final mask
    argument: ``-p``
trim: (a boolean, nipy default value: True)
    trim brainstem

```

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```

        argument: ``--trim``
outputDiffusionFilter: (a pathlike object or string representing a
    file)
    diffusion filter output
    argument: ``--adf %s``
outputEdgeMap: (a pathlike object or string representing a file)
    edge map output
    argument: ``--edge %s``
outputDetailedBrainMask: (a pathlike object or string representing a
    file)
    save detailed brain mask
    argument: ``--hires %s``
outputCortexFile: (a pathlike object or string representing a file)
    cortex file
    argument: ``--cortex %s``
verbosityLevel: (a float, nipy default value: 1)
    verbosity level (0=silent)
    argument: ``-v %f``
noRotate: (a boolean)
    retain original orientation (default behavior will auto-rotate input
    NII files to LPI orientation)
    argument: ``--norotate``
timer: (a boolean)
    show timing
    argument: ``--timer``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputMRIVolume: (a pathlike object or string representing a file)
    path/name of brain-masked MRI volume
outputMaskFile: (a pathlike object or string representing a file)
    path/name of smooth brain mask
outputDiffusionFilter: (a pathlike object or string representing a
    file)
    path/name of diffusion filter output
outputEdgeMap: (a pathlike object or string representing a file)
    path/name of edge map output
outputDetailedBrainMask: (a pathlike object or string representing a
    file)
    path/name of detailed brain mask
outputCortexFile: (a pathlike object or string representing a file)
    path/name of cortex file

```

54.1.4 Cerebro[Link to code](#)

Wraps the executable command cerebro.

Cerebrum/cerebellum labeling tool This program performs automated labeling of cerebellum and cerebrum in T1 MRI. Input MRI should be skull-stripped or a brain-only mask should be provided.

<http://brainsuite.org/processing/surfaceextraction/cerebrum/>

Examples

```
>>> from nipyre.interfaces import brainsuite
>>> from nipyre.testing import example_data
>>> cerebro = brainsuite.Cerebro()
>>> cerebro.inputs.inputMRIFile = example_data('structural.nii')
>>> cerebro.inputs.inputAtlasMRIFile = 'atlasMRIVolume.img'
>>> cerebro.inputs.inputAtlasLabelFile = 'atlasLabels.img'
>>> cerebro.inputs.inputBrainMaskFile = example_data('mask.nii')
>>> results = cerebro.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
inputMRIFile: (a pathlike object or string representing a file)
    input 3D MRI volume
    argument: ``-i %s``
inputAtlasMRIFile: (a pathlike object or string representing a file)
    atlas MRI volume
    argument: ``--atlas %s``
inputAtlasLabelFile: (a pathlike object or string representing a
    file)
    atlas labeling
    argument: ``--atlaslabels %s``

[Optional]
inputBrainMaskFile: (a pathlike object or string representing a file)
    brain mask file
    argument: ``-m %s``
outputCerebrumMaskFile: (a pathlike object or string representing a
    file)
    output cerebrum mask volume. If unspecified, output file name will
    be auto generated.
    argument: ``-o %s``
outputLabelVolumeFile: (a pathlike object or string representing a
    file)
    output labeled hemisphere/cerebrum volume. If unspecified, output
    file name will be auto generated.
    argument: ``-l %s``
costFunction: (an integer (int or long), nipyre default value: 2)
    0,1,2
    argument: ``-c %d``
useCentroids: (a boolean)
    use centroids of data to initialize position
    argument: ``--centroids``
outputAffineTransformFile: (a pathlike object or string representing
    a file)
    save affine transform to file.
    argument: ``--air %s``
outputWarpTransformFile: (a pathlike object or string representing a
    file)
    save warp transform to file.
    argument: ``--warp %s``
verbosity: (an integer (int or long))
    verbosity level (0=silent)
    argument: ``-v %d``
linearConvergence: (a float)
    linear convergence
```

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```

        argument: ``--linconv %f``
warpLabel: (an integer (int or long))
        warp order (2,3,4,5,6,7,8)
        argument: ``--warplevel %d``
warpConvergence: (a float)
        warp convergence
        argument: ``--warpconv %f``
keepTempFiles: (a boolean)
        don't remove temporary files
        argument: ``--keep``
tempDirectory: (a unicode string)
        specify directory to use for temporary files
        argument: ``--tempdir %s``
tempDirectoryBase: (a unicode string)
        create a temporary directory within this directory
        argument: ``--tempdirbase %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

outputCerebrumMaskFile: (a pathlike object or string representing a
        file)
        path/name of cerebrum mask file
outputLabelVolumeFile: (a pathlike object or string representing a
        file)
        path/name of label mask file
outputAffineTransformFile: (a pathlike object or string representing
        a file)
        path/name of affine transform file
outputWarpTransformFile: (a pathlike object or string representing a
        file)
        path/name of warp transform file

```

54.1.5 Cortex[Link to code](#)Wraps the executable command `cortex`.`cortex` extractor This program produces a cortical mask using tissue fraction estimates and a co-registered cerebellum/hemisphere mask.<http://brainsuite.org/processing/surfaceextraction/cortex/>**Examples**

```

>>> from nipy.interfaces import brainsuite
>>> from nipy.testing import example_data
>>> cortex = brainsuite.Cortex()
>>> cortex.inputs.inputHemisphereLabelFile = example_data('mask.nii')
>>> cortex.inputs.inputTissueFractionFile = example_data('tissues.nii.gz')
>>> results = cortex.run() #doctest: +SKIP

```

Inputs:

```

[Mandatory]
inputHemisphereLabelFile: (a pathlike object or string representing a
    file)
    hemisphere / lobe label volume
    argument: ``-h %s``
inputTissueFractionFile: (a pathlike object or string representing a
    file)
    tissue fraction file (32-bit float)
    argument: ``-f %s``

[Optional]
outputCerebrumMask: (a pathlike object or string representing a file)
    output structure mask. If unspecified, output file name will be auto
    generated.
    argument: ``-o %s``
tissueFractionThreshold: (a float, nipy default value: 50.0)
    tissue fraction threshold (percentage)
    argument: ``-p %f``
computeWGBoundary: (a boolean, nipy default value: True)
    compute WM/GM boundary
    argument: ``-w``
computeGCBoundary: (a boolean)
    compute GM/CSF boundary
    argument: ``-g``
includeAllSubcorticalAreas: (a boolean, nipy default value: True)
    include all subcortical areas in WM mask
    argument: ``-a``
verbosity: (an integer (int or long))
    verbosity level
    argument: ``-v %d``
timer: (a boolean)
    timing function
    argument: ``--timer``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputCerebrumMask: (a pathlike object or string representing a file)
    path/name of cerebrum mask

```

54.1.6 Dewisp[Link to code](#)

Wraps the executable command dewisp.

dewisp removes wispy tendril structures from cortex model binary masks. It does so based on graph theoretic analysis of connected components, similar to TCA. Each branch of the structure graph is analyzed to determine pinch points that indicate a likely error in segmentation that attaches noise to the image. The pinch threshold determines how many voxels the cross-section can be before it is considered part of the image.

<http://brainsuite.org/processing/surfaceextraction/dewisp/>

Examples

```
>>> from nipy.interfaces import brainsuite
>>> from nipy.testing import example_data
>>> dewisp = brainsuite.Dewisp()
>>> dewisp.inputs.inputMaskFile = example_data('mask.nii')
>>> results = dewisp.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
inputMaskFile: (a pathlike object or string representing a file)
    input file
    argument: ``-i %s``

[Optional]
outputMaskFile: (a pathlike object or string representing a file)
    output file. If unspecified, output file name will be auto
    generated.
    argument: ``-o %s``
verbosity: (an integer (int or long))
    verbosity
    argument: ``-v %d``
sizeThreshold: (an integer (int or long))
    size threshold
    argument: ``-t %d``
maximumIterations: (an integer (int or long))
    maximum number of iterations
    argument: ``-n %d``
timer: (a boolean)
    time processing
    argument: ``--timer``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outputMaskFile: (a pathlike object or string representing a file)
    path/name of mask file
```

54.1.7 Dfs

Link to code

Wraps the executable command dfs.

Surface Generator Generates mesh surfaces using an isosurface algorithm.

<http://brainsuite.org/processing/surfaceextraction/inner-cortical-surface/>

Examples

```
>>> from nipy.interfaces import brainsuite
>>> from nipy.testing import example_data
>>> dfs = brainsuite.Dfs()
```

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```
>>> dfs.inputs.inputVolumeFile = example_data('structural.nii')
>>> results = dfs.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
inputVolumeFile: (a pathlike object or string representing a file)
    input 3D volume
    argument: ``-i %s``

[Optional]
outputSurfaceFile: (a pathlike object or string representing a file)
    output surface mesh file. If unspecified, output file name will be
    auto generated.
    argument: ``-o %s``
inputShadingVolume: (a pathlike object or string representing a file)
    shade surface model with data from image volume
    argument: ``-c %s``
smoothingIterations: (an integer (int or long), nipype default value:
    10)
    number of smoothing iterations
    argument: ``-n %d``
smoothingConstant: (a float, nipype default value: 0.5)
    smoothing constant
    argument: ``-a %f``
curvatureWeighting: (a float, nipype default value: 5.0)
    curvature weighting
    argument: ``-w %f``
scalingPercentile: (a float)
    scaling percentile
    argument: ``-f %f``
nonZeroTessellation: (a boolean)
    tessellate non-zero voxels
    argument: ``-nz``
    mutually_exclusive: nonZeroTessellation, specialTessellation
tessellationThreshold: (a float)
    To be used with specialTessellation. Set this value first, then set
    specialTessellation value.
    Usage: tessellate voxels greater_than, less_than, or equal_to
    <tessellationThreshold>
    argument: ``%f``
specialTessellation: ('greater_than' or 'less_than' or 'equal_to')
    To avoid throwing a UserWarning, set tessellationThreshold first.
    Then set this attribute.
    Usage: tessellate voxels greater_than, less_than, or equal_to
    <tessellationThreshold>
    argument: ``%s``, position: -1
    mutually_exclusive: nonZeroTessellation, specialTessellation
    requires: tessellationThreshold
zeroPadFlag: (a boolean)
    zero-pad volume (avoids clipping at edges)
    argument: ``-z``
noNormalsFlag: (a boolean)
    do not compute vertex normals
    argument: ``--nonormals``
postSmoothFlag: (a boolean)
    smooth vertices after coloring
```

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```

        argument: ``--postsmooth``
    verbosity: (an integer (int or long))
        verbosity (0 = quiet)
        argument: ``-v %d``
    timer: (a boolean)
        timing function
        argument: ``--timer``
    args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
    environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipype default value: {})
        Environment variables

```

Outputs:

```

outputSurfaceFile: (a pathlike object or string representing a file)
    path/name of surface file

```

54.1.8 Hemisplit[Link to code](#)

Wraps the executable command hemisplit.

Hemisphere splitter Splits a surface object into two separate surfaces given an input label volume. Each vertex is labeled left or right based on the labels being odd (left) or even (right). The largest contour on the split surface is then found and used as the separation between left and right.

Examples

```

>>> from nipype.interfaces import brainsuite
>>> from nipype.testing import example_data
>>> hemisplit = brainsuite.Hemisplit()
>>> hemisplit.inputs.inputSurfaceFile = 'input_surf.dfs'
>>> hemisplit.inputs.inputHemisphereLabelFile = 'label.nii'
>>> hemisplit.inputs.pialSurfaceFile = 'pial.dfs'
>>> results = hemisplit.run() #doctest: +SKIP

```

Inputs:

```

[Mandatory]
inputSurfaceFile: (a pathlike object or string representing a file)
    input surface
    argument: ``-i %s``
inputHemisphereLabelFile: (a pathlike object or string representing a
    file)
    input hemisphere label volume
    argument: ``-l %s``

[Optional]
outputLeftHemisphere: (a pathlike object or string representing a
    file)
    output surface file, left hemisphere. If unspecified, output file
    name will be auto generated.
    argument: ``--left %s``
outputRightHemisphere: (a pathlike object or string representing a

```

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```

    file)
    output surface file, right hemisphere. If unspecified, output file
    name will be auto generated.
    argument: ``--right %s``
pialSurfaceFile: (a pathlike object or string representing a file)
    pial surface file -- must have same geometry as input surface
    argument: ``-p %s``
outputLeftPialHemisphere: (a pathlike object or string representing a
    file)
    output pial surface file, left hemisphere. If unspecified, output
    file name will be auto generated.
    argument: ``-pl %s``
outputRightPialHemisphere: (a pathlike object or string representing
    a file)
    output pial surface file, right hemisphere. If unspecified, output
    file name will be auto generated.
    argument: ``-pr %s``
verbosity: (an integer (int or long))
    verbosity (0 = silent)
    argument: ``-v %d``
timer: (a boolean)
    timing function
    argument: ``--timer``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputLeftHemisphere: (a pathlike object or string representing a
    file)
    path/name of left hemisphere
outputRightHemisphere: (a pathlike object or string representing a
    file)
    path/name of right hemisphere
outputLeftPialHemisphere: (a pathlike object or string representing a
    file)
    path/name of left pial hemisphere
outputRightPialHemisphere: (a pathlike object or string representing
    a file)
    path/name of right pial hemisphere

```

54.1.9 Pialmesh[Link to code](#)

Wraps the executable command pialmesh.

pialmesh computes a pial surface model using an inner WM/GM mesh and a tissue fraction map.

<http://brainsuite.org/processing/surfaceextraction/pial/>

Examples

```

>>> from nipy.interfaces import brainsuite
>>> from nipy.testing import example_data
>>> pialmesh = brainsuite.Pialmesh()
>>> pialmesh.inputs.inputSurfaceFile = 'input_mesh.dfs'
>>> pialmesh.inputs.inputTissueFractionFile = 'frac_file.nii.gz'
>>> pialmesh.inputs.inputMaskFile = example_data('mask.nii')
>>> results = pialmesh.run() #doctest: +SKIP

```

Inputs:

```

[Mandatory]
inputSurfaceFile: (a pathlike object or string representing a file)
    input file
    argument: ``-i %s``
inputTissueFractionFile: (a pathlike object or string representing a
    file)
    floating point (32) tissue fraction image
    argument: ``-f %s``
inputMaskFile: (a pathlike object or string representing a file)
    restrict growth to mask file region
    argument: ``-m %s``

[Optional]
outputSurfaceFile: (a pathlike object or string representing a file)
    output file. If unspecified, output file name will be auto
    generated.
    argument: ``-o %s``
verbosity: (an integer (int or long))
    verbosity
    argument: ``-v %d``
numIterations: (an integer (int or long), nipy default value: 100)
    number of iterations
    argument: ``-n %d``
searchRadius: (a float, nipy default value: 1)
    search radius
    argument: ``-r %f``
stepSize: (a float, nipy default value: 0.4)
    step size
    argument: ``-s %f``
maxThickness: (a float, nipy default value: 20)
    maximum allowed tissue thickness
    argument: ``--max %f``
tissueThreshold: (a float, nipy default value: 1.05)
    tissue threshold
    argument: ``-t %f``
outputInterval: (an integer (int or long), nipy default value: 10)
    output interval
    argument: ``--interval %d``
exportPrefix: (a unicode string)
    prefix for exporting surfaces if interval is set
    argument: ``--prefix %s``
laplacianSmoothing: (a float, nipy default value: 0.025)
    apply Laplacian smoothing
    argument: ``--smooth %f``
timer: (a boolean)
    show timing

```

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```

        argument: ``--timer``
recomputeNormals: (a boolean)
    recompute normals at each iteration
    argument: ``--norm``
normalSmoother: (a float, nipy default value: 0.2)
    strength of normal smoother.
    argument: ``--nc %f``
tangentSmoother: (a float)
    strength of tangential smoother.
    argument: ``--tc %f``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputSurfaceFile: (a pathlike object or string representing a file)
    path/name of surface file

```

54.1.10 Pvc[Link to code](#)

Wraps the executable command pvc.

partial volume classifier (PVC) tool. This program performs voxel-wise tissue classification T1-weighted MRI. Image should be skull-stripped and bias-corrected before tissue classification.

<http://brainsuite.org/processing/surfaceextraction/pvc/>

Examples

```

>>> from nipy.interfaces import brainsuite
>>> from nipy.testing import example_data
>>> pvc = brainsuite.Pvc()
>>> pvc.inputs.inputMRIFile = example_data('structural.nii')
>>> pvc.inputs.inputMaskFile = example_data('mask.nii')
>>> results = pvc.run() #doctest: +SKIP

```

Inputs:

```

[Mandatory]
inputMRIFile: (a pathlike object or string representing a file)
    MRI file
    argument: ``-i %s``

[Optional]
inputMaskFile: (a pathlike object or string representing a file)
    brain mask file
    argument: ``-m %s``
outputLabelFile: (a pathlike object or string representing a file)
    output label file. If unspecified, output file name will be auto
    generated.
    argument: ``-o %s``
outputTissueFractionFile: (a pathlike object or string representing a

```

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```

        file)
        output tissue fraction file
        argument: ``-f %s``
spatialPrior: (a float)
        spatial prior strength
        argument: ``-l %f``
verbosity: (an integer (int or long))
        verbosity level (0 = silent)
        argument: ``-v %d``
threeClassFlag: (a boolean)
        use a three-class (CSF=0,GM=1,WM=2) labeling
        argument: ``-3``
timer: (a boolean)
        time processing
        argument: ``--timer``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

outputLabelFile: (a pathlike object or string representing a file)
        path/name of label file
outputTissueFractionFile: (a pathlike object or string representing a
        file)
        path/name of tissue fraction file

```

54.1.11 SVReg**Link to code**

Wraps the executable command `svreg.sh`.

surface and volume registration (svreg) This program registers a subject's BrainSuite-processed volume and surfaces to an atlas, allowing for automatic labelling of volume and surface ROIs.

For more information, please see: <http://brainsuite.org/processing/svreg/usage/>

Examples

```

>>> from nipy.interfaces import brainsuite
>>> svreg = brainsuite.SVReg()
>>> svreg.inputs.subjectFilePrefix = 'home/user/btestsubject/testsubject'
>>> svreg.inputs.refineOutputs = True
>>> svreg.inputs.skipToVolumeReg = False
>>> svreg.inputs.keepIntermediates = True
>>> svreg.inputs.verbosity2 = True
>>> svreg.inputs.displayTimestamps = True
>>> svreg.inputs.useSingleThreading = True
>>> results = svreg.run() #doctest: +SKIP

```

Inputs:

```

[Mandatory]
subjectFilePrefix: (a unicode string)

```

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```

    Absolute path and filename prefix of the subjects output from
    BrainSuite Cortical Surface Extraction Sequence
    argument: ``'%s'``, position: 0

[Optional]
dataSinkDelay: (a list of items which are a unicode string)
    Connect datasink out_file to dataSinkDelay to delay execution of
    SVReg until dataSink has finished sinking CSE outputs. For use with
    parallel processing workflows including Brainsuites Cortical Surface
    Extraction sequence (SVReg requires certain files from Brainsuite
    CSE, which must all be in the pathway specified by
    subjectFilePrefix. see http://brainsuite.org/processing/svreg/usage/
    for list of required inputs
    argument: ``'%s'``
atlasFilePrefix: (a unicode string)
    Optional: Absolute Path and filename prefix of atlas files and
    labels to which the subject will be registered. If unspecified,
    SVReg will use its own included atlas files
    argument: ``'%s'``, position: 1
iterations: (an integer (int or long))
    Assigns a number of iterations in the intensity registration step. if
    unspecified, performs 100 iterations
    argument: ``'-H %d'``
refineOutputs: (a boolean)
    Refine outputs at the expense of more processing time.
    argument: ``'-r'``
skipToVolumeReg: (a boolean)
    If surface registration was already performed at an earlier time and
    the user would not like to redo this step, then this flag may be
    used to skip ahead to the volumetric registration. Necessary input
    files will need to be present in the input directory called by the
    command.
    argument: ``'-s'``
skipToIntensityReg: (a boolean)
    If the p-harmonic volumetric registration was already performed at
    an earlier time and the user would not like to redo this step, then
    this flag may be used to skip ahead to the intensity registration
    and label transfer step.
    argument: ``'-p'``
useManualMaskFile: (a boolean)
    Can call a manually edited cerebrum mask to limit boundaries. Will
    use file: subbasename.cerebrum.mask.nii.gz Make sure to correctly
    replace your manually edited mask file in your input folder with the
    correct subbasename.
    argument: ``'-cbm'``
curveMatchingInstructions: (a unicode string)
    Used to take control of the curve matching process between the atlas
    and subject. One can specify the name of the .dfc file <subname.dfc>
    and the sulcal numbers <#sul> to be used as constraints. example:
    curveMatchingInstructions = "subbasename.right.dfc 1 2 20"
    argument: ``'-cur %s'``
useCerebrumMask: (a boolean)
    The cerebrum mask <subbasename.cerebrum.mask.nii.gz> will be used
    for masking the final labels instead of the default pial surface
    mask. Every voxel will be labeled within the cerebrum mask
    regardless of the boundaries of the pial surface.
    argument: ``'-C'``

```

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```

pialSurfaceMaskDilation: (an integer (int or long))
    Cortical volume labels found in file output
    subbasename.svreg.label.nii.gz find its boundaries by using the pial
    surface then dilating by 1 voxel. Use this flag in order to control
    the number of pial surface mask dilation. (ie. -D 0 will assign no
    voxel dilation)
    argument: ``'-D %d'``
keepIntermediates: (a boolean)
    Keep the intermediate files after the svreg sequence is complete.
    argument: ``'-k'``
verbosity0: (a boolean)
    no messages will be reported
    argument: ``'-v0'``
    mutually_exclusive: verbosity0, verbosity1, verbosity2
verbosity1: (a boolean)
    messages will be reported but not the iteration-wise detailed
    messages
    argument: ``'-v1'``
    mutually_exclusive: verbosity0, verbosity1, verbosity2
verbosity2: (a boolean)
    all the messages, including per-iteration, will be displayed
    argument: ``'-v2'``
    mutually_exclusive: verbosity0, verbosity1, verbosity2
shortMessages: (a boolean)
    Short messages instead of detailed messages
    argument: ``'-gui'``
displayModuleName: (a boolean)
    Module name will be displayed in the messages
    argument: ``'-m'``
displayTimestamps: (a boolean)
    Timestamps will be displayed in the messages
    argument: ``'-t'``
skipVolumetricProcessing: (a boolean)
    Only surface registration and labeling will be performed. Volumetric
    processing will be skipped.
    argument: ``'-S'``
useMultiThreading: (a boolean)
    If multiple CPUs are present on the system, the code will try to use
    multithreading to make the execution fast.
    argument: ``'-P'``
useSingleThreading: (a boolean)
    Use single threaded mode.
    argument: ``'-U'``
args: (a unicode string)
    Additional parameters to the command
    argument: ``'%s'``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:**None**

54.1.12 Scrubmask

[Link to code](#)

Wraps the executable command `scrubmask`.

ScrubMask tool `scrubmask` filters binary masks to trim loosely connected voxels that may result from segmentation errors and produce bumps on tessellated surfaces.

<http://brainsuite.org/processing/surfaceextraction/scrubmask/>

Examples

```
>>> from nipy.interfaces import brainsuite
>>> from nipy.testing import example_data
>>> scrubmask = brainsuite.Scrubmask()
>>> scrubmask.inputs.inputMaskFile = example_data('mask.nii')
>>> results = scrubmask.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
inputMaskFile: (a pathlike object or string representing a file)
    input structure mask file
    argument: ``-i %s``

[Optional]
outputMaskFile: (a pathlike object or string representing a file)
    output structure mask file. If unspecified, output file name will be
    auto generated.
    argument: ``-o %s``
backgroundFillThreshold: (an integer (int or long), nipy default
    value: 2)
    background fill threshold
    argument: ``-b %d``
foregroundTrimThreshold: (an integer (int or long), nipy default
    value: 0)
    foreground trim threshold
    argument: ``-f %d``
numberIterations: (an integer (int or long))
    number of iterations
    argument: ``-n %d``
verbosity: (an integer (int or long))
    verbosity (0=silent)
    argument: ``-v %d``
timer: (a boolean)
    timing function
    argument: ``--timer``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outputMaskFile: (a pathlike object or string representing a file)
    path/name of mask file
```

54.1.13 Skullfinder

[Link to code](#)

Wraps the executable command skullfinder.

Skull and scalp segmentation algorithm.

Examples

```
>>> from nipy.interfaces import brainsuite
>>> from nipy.testing import example_data
>>> skullfinder = brainsuite.Skullfinder()
>>> skullfinder.inputs.inputMRIFile = example_data('structural.nii')
>>> skullfinder.inputs.inputMaskFile = example_data('mask.nii')
>>> results = skullfinder.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
inputMRIFile: (a pathlike object or string representing a file)
    input file
    argument: ``-i %s``
inputMaskFile: (a pathlike object or string representing a file)
    A brain mask file, 8-bit image (0=non-brain, 255=brain)
    argument: ``-m %s``

[Optional]
outputLabelFile: (a pathlike object or string representing a file)
    output multi-colored label volume segmenting brain, scalp, inner
    skull & outer skull If unspecified, output file name will be auto
    generated.
    argument: ``-o %s``
verbosity: (an integer (int or long))
    verbosity
    argument: ``-v %d``
lowerThreshold: (an integer (int or long))
    Lower threshold for segmentation
    argument: ``-l %d``
upperThreshold: (an integer (int or long))
    Upper threshold for segmentation
    argument: ``-u %d``
surfaceFilePrefix: (a unicode string)
    if specified, generate surface files for brain, skull, and scalp
    argument: ``-s %s``
bgLabelValue: (an integer (int or long))
    background label value (0-255)
    argument: ``--bglabel %d``
scalpLabelValue: (an integer (int or long))
    scalp label value (0-255)
    argument: ``--scalplabel %d``
skullLabelValue: (an integer (int or long))
    skull label value (0-255)
    argument: ``--skulllabel %d``
spaceLabelValue: (an integer (int or long))
    space label value (0-255)
    argument: ``--spacelabel %d``
brainLabelValue: (an integer (int or long))
    brain label value (0-255)
    argument: ``--brainlabel %d``
```

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```

performFinalOpening: (a boolean)
    perform a final opening operation on the scalp mask
    argument: ``--finalOpening``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputLabelFile: (a pathlike object or string representing a file)
    path/name of label file

```

54.1.14 Tca[Link to code](#)Wraps the executable command `tca`.

topological correction algorithm (TCA) This program removes topological handles from a binary object.

<http://brainsuite.org/processing/surfaceextraction/tca/>**Examples**

```

>>> from nipy.interfaces import brainsuite
>>> from nipy.testing import example_data
>>> tca = brainsuite.Tca()
>>> tca.inputs.inputMaskFile = example_data('mask.nii')
>>> results = tca.run() #doctest: +SKIP

```

Inputs:

```

[Mandatory]
inputMaskFile: (a pathlike object or string representing a file)
    input mask volume
    argument: ``-i %s``

[Optional]
outputMaskFile: (a pathlike object or string representing a file)
    output mask volume. If unspecified, output file name will be auto
    generated.
    argument: ``-o %s``
minCorrectionSize: (an integer (int or long), nipy default value:
    2500)
    maximum correction size
    argument: ``-m %d``
maxCorrectionSize: (an integer (int or long))
    minimum correction size
    argument: ``-n %d``
foregroundDelta: (an integer (int or long), nipy default value: 20)
    foreground delta
    argument: ``--delta %d``
verbosity: (an integer (int or long))
    verbosity (0 = quiet)
    argument: ``-v %d``

```

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```

timer: (a boolean)
        timing function
        argument: ``--timer``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables

```

Outputs:

```

outputMaskFile: (a pathlike object or string representing a file)
                 path/name of mask file

```

54.1.15 ThicknessPVC

[Link to code](#)

Wraps the executable command `thicknessPVC.sh`.

ThicknessPVC computes cortical thickness using partial tissue fractions. This thickness measure is then transferred to the atlas surface to facilitate population studies. It also stores the computed thickness into separate hemisphere files and subject thickness mapped to the atlas hemisphere surfaces. ThicknessPVC is not run through the main SVReg sequence, and should be used after executing the BrainSuite and SVReg sequence. For more information, please see:

http://brainsuite.org/processing/svreg/svreg_modules/

Examples

```

>>> from nipype.interfaces import brainsuite
>>> thicknessPVC = brainsuite.ThicknessPVC()
>>> thicknessPVC.inputs.subjectFilePrefix = 'home/user/btestsubject/testsubject'
>>> results = thicknessPVC.run() #doctest: +SKIP

```

Inputs:

```

[Mandatory]
subjectFilePrefix: (a unicode string)
                   Absolute path and filename prefix of the subject data
                   argument: ``%s``

[Optional]
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables

```

Outputs:

None

54.1.16 `getFileName()`

[Link to code](#)

54.1.17 `l_outputs()`

[Link to code](#)

55.1 interfaces.camino.calib

55.1.1 SFLUTGen

[Link to code](#)

Wraps the executable command `sflutgen`.

Generates PICO lookup tables (LUT) for multi-fibre methods such as PASMRI and Q-Ball.

SFLUTGen creates the lookup tables for the generalized multi-fibre implementation of the PICO tractography algorithm. The outputs of this utility are either surface or line coefficients up to a given order. The calibration can be performed for different distributions, such as the Bingham and Watson distributions.

This utility uses calibration data generated from SFPICOCalibData and peak information created by SFPeaks. The utility outputs two lut's, `*_oneFibreSurfaceCoeffs.Bdouble` and `*_twoFibreSurfaceCoeffs.Bdouble`. Each of these files contains big- endian doubles as standard. The format of the output is:

```
dimensions      (1 for Watson, 2 for Bingham)
order           (the order of the polynomial)
coefficient_1
coefficient_2
...
coefficient_N
```

In the case of the Watson, there is a single set of coefficients, which are ordered:

```
constant, x, x^2, ..., x^order.
```

In the case of the Bingham, there are two sets of coefficients (one for each surface), ordered so that:

```
for j = 1 to order
  for k = 1 to order
    coeff_i = x^j * y^k
  where j+k < order
```

Example

To create a calibration dataset using the default settings

```
>>> import nipyne.interfaces.camino as cam
>>> lutgen = cam.SFLUTGen()
>>> lutgen.inputs.in_file = 'QSH_peaks.Bdouble'
>>> lutgen.inputs.info_file = 'PICO_calib.info'
>>> lutgen.run()           # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        Voxel-order data of the spherical functions peaks.
        argument: ``-inputfile %s``
info_file: (a pathlike object or string representing a file)
        The Info file that corresponds to the calibration datafile used in
        the reconstruction.
        argument: ``-infofile %s``

[Optional]
outputstem: (a unicode string, nipyne default value: LUT)
        Define the name of the generated luts. The form of the filenames
        will be [outputstem]_oneFibreSurfaceCoeffs.Bdouble and
        [outputstem]_twoFibreSurfaceCoeffs.Bdouble
        argument: ``-outputstem %s``
pdf: ('bingham' or 'watson', nipyne default value: bingham)
        Sets the distribution to use for the calibration. The default is the
        Bingham distribution, which allows elliptical probability density
        contours. Currently supported options are: bingham - The Bingham
        distribution, which allows elliptical probability density contours.
        watson - The Watson distribution. This distribution is rotationally
        symmetric.
        argument: ``-pdf %s``
binincsize: (an integer (int or long))
        Sets the size of the bins. In the case of 2D histograms such as the
        Bingham, the bins are always square. Default is 1.
        argument: ``-binincsize %d``
minvectsperbin: (an integer (int or long))
        Specifies the minimum number of fibre-orientation estimates a bin
        must contain before it is used in the lut line/surface generation.
        Default is 50. If you get the error "no fibre-orientation estimates
        in histogram!", the calibration data set is too small to get enough
        samples in any of the histogram bins. You can decrease the minimum
        number per bin to get things running in quick tests, but the sta-
        tistics will not be reliable and for serious applications, you need
        to increase the size of the calibration data set until the error
        goes.
        argument: ``-minvectsperbin %d``
directmap: (a boolean)
        Use direct mapping between the eigenvalues and the distribution
        parameters instead of the log of the eigenvalues.
        argument: ``-directmap``
order: (an integer (int or long))
        The order of the polynomial fitting the surface. Order 1 is linear.
        Order 2 (default) is quadratic.
        argument: ``-order %d``
out_file: (a pathlike object or string representing a file)
        argument: ``> %s``, position: -1
args: (a unicode string)
        Additional parameters to the command
```

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```

argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyne default value: {})
Environment variables

```

Outputs:

```

lut_one_fibre: (a pathlike object or string representing an existing
               file)
               PICO lut for one-fibre model
lut_two_fibres: (a pathlike object or string representing an existing
                file)
                PICO lut for two-fibre model

```

55.1.2 SFPICOCalibData

[Link to code](#)

Wraps the executable command `sfpicocalibdata`.

Generates Spherical Function PICO Calibration Data.

SFPICOCalibData creates synthetic data for use with SFLUTGen. The synthetic data is generated using a mixture of gaussians, in the same way `datasynth` generates data. Each voxel of data models a slightly different fibre configuration (varying FA and fibre- crossings) and undergoes a random rotation to help account for any directional bias in the chosen acquisition scheme. A second file, which stores information about the datafile, is generated along with the datafile.

Example 1

To create a calibration dataset using the default settings

```

>>> import nipyne.interfaces.camino as cam
>>> calib = cam.SFPICOCalibData()
>>> calib.inputs.scheme_file = 'A.scheme'
>>> calib.inputs.snr = 20
>>> calib.inputs.info_file = 'PICO_calib.info'
>>> calib.run()                # doctest: +SKIP

```

The default settings create a large dataset (249,231 voxels), of which 3401 voxels contain a single fibre population per voxel and the rest of the voxels contain two fibre-populations. The amount of data produced can be varied by specifying the ranges and steps of the parameters for both the one and two fibre datasets used.

Example 2

To create a custom calibration dataset

```

>>> import nipyne.interfaces.camino as cam
>>> calib = cam.SFPICOCalibData()
>>> calib.inputs.scheme_file = 'A.scheme'
>>> calib.inputs.snr = 20
>>> calib.inputs.info_file = 'PICO_calib.info'
>>> calib.inputs.twodtfarange = [0.3, 0.9]
>>> calib.inputs.twodtfastep = 0.02
>>> calib.inputs.twodtanglerange = [0, 0.785]
>>> calib.inputs.twodtanglestep = 0.03925
>>> calib.inputs.twodtmixmax = 0.8
>>> calib.inputs.twodtmixstep = 0.1
>>> calib.run()                # doctest: +SKIP

```

This would provide 76,313 voxels of synthetic data, where 3401 voxels simulate the one fibre cases and 72,912 voxels simulate the various two fibre cases. However, care should be taken to ensure that enough data is generated for calculating the LUT. # doctest: +SKIP

Inputs:

```
[Mandatory]
scheme_file: (a pathlike object or string representing an existing
              file)
              Specifies the scheme file for the diffusion MRI data
              argument: ``-schemefile %s``
info_file: (a pathlike object or string representing a file)
            The name to be given to the information output filename.
            argument: ``-infooutputfile %s``

[Optional]
snr: (a float)
     Specifies the signal-to-noise ratio of the non-diffusion-weighted
     measurements to use in simulations.
     argument: ``-snr %f``
trace: (a float)
        Trace of the diffusion tensor(s) used in the test function.
        argument: ``-trace %f``
onedtfarange: (a list of from 2 to 2 items which are a float)
               Minimum and maximum FA for the single tensor synthetic data.
               argument: ``-onedtfarange %s``
onedtfaststep: (a float)
                FA step size controlling how many steps there are between the
                minimum and maximum FA settings.
                argument: ``-onedtfaststep %f``
twodtfarange: (a list of from 2 to 2 items which are a float)
               Minimum and maximum FA for the two tensor synthetic data. FA is
               varied for both tensors to give all the different permutations.
               argument: ``-twodtfarange %s``
twodtfaststep: (a float)
                FA step size controlling how many steps there are between the
                minimum and maximum FA settings for the two tensor cases.
                argument: ``-twodtfaststep %f``
twodtanglerange: (a list of from 2 to 2 items which are a float)
                  Minimum and maximum crossing angles between the two fibres.
                  argument: ``-twodtanglerange %s``
twodtanglestep: (a float)
                  Angle step size controlling how many steps there are between the
                  minimum and maximum crossing angles for the two tensor cases.
                  argument: ``-twodtanglestep %f``
twodtmixmax: (a float)
              Mixing parameter controlling the proportion of one fibre population
              to the other. The minimum mixing parameter is (1 - twodtmixmax).
              argument: ``-twodtmixmax %f``
twodtmixstep: (a float)
               Mixing parameter step size for the two tensor cases. Specify how
               many mixing parameter increments to use.
               argument: ``-twodtmixstep %f``
seed: (a float)
       Specifies the random seed to use for noise generation in simulation
       trials.
       argument: ``-seed %f``
out_file: (a pathlike object or string representing a file)
           argument: ``> %s``, position: -1
```

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```
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
PICOCalib: (a pathlike object or string representing an existing
    file)
    Calibration dataset
calib_info: (a pathlike object or string representing an existing
    file)
    Calibration dataset
```

55.2 interfaces.camino.connectivity

55.2.1 Conmat

[Link to code](#)

Wraps the executable command `conmat`.

Creates a connectivity matrix using a 3D label image (the target image) and a set of streamlines. The connectivity matrix records how many stream- lines connect each pair of targets, and optionally the mean tractwise statistic (eg tract-averaged FA, or length).

The output is a comma separated variable file or files. The first row of the output matrix is label names. Label names may be defined by the user, otherwise they are assigned based on label intensity.

Starting from the seed point, we move along the streamline until we find a point in a labeled region. This is done in both directions from the seed point. Streamlines are counted if they connect two target regions, one on either side of the seed point. Only the labeled region closest to the seed is counted, for example if the input contains two streamlines:

```
1: A-----B-----SEED---C
2: A-----SEED-----
```

then the output would be

```
A,B,C
0,0,0
0,0,1
0,1,0
```

There are zero connections to A because in streamline 1, the connection to B is closer to the seed than the connection to A, and in streamline 2 there is no region reached in the other direction.

The connected target regions can have the same label, as long as the seed point is outside of the labeled region and both ends connect to the same label (which may be in different locations). Therefore this is allowed:

```
A-----SEED-----A
```

Such fibers will add to the diagonal elements of the matrix. To remove these entries, run `procstreamlines` with `-endpointfile` before running `conmat`.

If the seed point is inside a labeled region, it counts as one end of the connection. So

```
----[SEED inside A]-----B
```

counts as a connection between A and B, while

```
C----[SEED inside A]-----B
```

counts as a connection between A and C, because C is closer to the seed point. In all cases, distance to the seed point is defined along the streamline path.

Example 1

To create a standard connectivity matrix based on streamline counts.

```
>>> import nipy.interfaces.camino as cam
>>> conmat = cam.Conmat()
>>> conmat.inputs.in_file = 'tracts.Bdouble'
>>> conmat.inputs.target_file = 'atlas.nii.gz'
>>> conmat.run()           # doctest: +SKIP
```

Example 1

To create a standard connectivity matrix and mean tractwise FA statistics.

```
>>> import nipy.interfaces.camino as cam
>>> conmat = cam.Conmat()
>>> conmat.inputs.in_file = 'tracts.Bdouble'
>>> conmat.inputs.target_file = 'atlas.nii.gz'
>>> conmat.inputs.scalar_file = 'fa.nii.gz'
>>> conmat.tract_stat = 'mean'
>>> conmat.run()           # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         Streamlines as generated by the Track interface
         argument: ``-inputfile %s``
target_file: (a pathlike object or string representing an existing
              file)
              An image containing targets, as used in ProcStreamlines interface.
              argument: ``-targetfile %s``

[Optional]
scalar_file: (a pathlike object or string representing an existing
              file)
              Optional scalar file for computing tract-based statistics. Must be
              in the same space as the target file.
              argument: ``-scalarfile %s``
              requires: tract_stat
targetname_file: (a pathlike object or string representing an
                  existing file)
                  Optional names of targets. This file should contain one entry per
                  line, with the target intensity followed by the name, separated by
                  white space. For example: 1 some_brain_region 2 some_other_region
                  These names will be used in the output. The names themselves should
                  not contain spaces or commas. The labels may be in any order but the
                  output matrices will be ordered by label intensity.
                  argument: ``-targetnamefile %s``
tract_stat: ('mean' or 'min' or 'max' or 'sum' or 'median' or 'var')
              Tract statistic to use. See TractStats for other options.
              argument: ``-tractstat %s``
              mutually_exclusive: tract_prop
```

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```

    requires: scalar_file
tract_prop: ('length' or 'endpointsep')
    Tract property average to compute in the connectivity matrix. See
    TractStats for details.
    argument: ``-tractstat %s``
    mutually_exclusive: tract_stat
output_root: (a pathlike object or string representing a file)
    filename root prepended onto the names of the output files. The
    extension will be determined from the input.
    argument: ``-outputroot %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

conmat_sc: (a pathlike object or string representing an existing
    file)
    Connectivity matrix in CSV file.
conmat_ts: (a pathlike object or string representing a file)
    Tract statistics in CSV file.

```

55.3 interfaces.camino.convert

55.3.1 AnalyzeHeader

[Link to code](#)

Wraps the executable command analyzeheader.

Create or read an Analyze 7.5 header file.

Analyze image header, provides support for the most common header fields. Some fields, such as patient_id, are not currently supported. The program allows three nonstandard options: the field image_dimension.funused1 is the image scale. The intensity of each pixel in the associated .img file is (image value from file) * scale. Also, the origin of the Talairach coordinates (midline of the anterior commissure) are encoded in the field data_history.originator. These changes are included for compatibility with SPM.

All headers written with this program are big endian by default.

Example

```

>>> import nipy.interfaces.camino as cmon
>>> hdr = cmon.AnalyzeHeader()
>>> hdr.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> hdr.inputs.scheme_file = 'A.scheme'
>>> hdr.inputs.data_dims = [256,256,256]
>>> hdr.inputs.voxel_dims = [1,1,1]
>>> hdr.run()                                # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Tensor-fitted data filename

```

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```

    argument: ``< %s``, position: 1
datatype: ('byte' or 'char' or '[u]short' or '[u]int' or 'float' or
    'complex' or 'double')
    The char datatype is 8 bit (not the 16 bit char of Java), as
    specified by the Analyze 7.5 standard. The byte, ushort and uint
    types are not part of the Analyze specification but are supported by
    SPM.
    argument: ``-datatype %s``

[Optional]
scheme_file: (a pathlike object or string representing an existing
    file)
    Camino scheme file (b values / vectors, see camino.fsl2scheme)
    argument: ``%s``, position: 2
readheader: (a pathlike object or string representing an existing
    file)
    Reads header information from file and prints to stdout. If this
    option is not specified, then the program writes a header based on
    the other arguments.
    argument: ``-readheader %s``, position: 3
printimagedims: (a pathlike object or string representing an existing
    file)
    Prints image data and voxel dimensions as Camino arguments and
    exits.
    argument: ``-printimagedims %s``, position: 3
printprogargs: (a pathlike object or string representing an existing
    file)
    Prints data dimension (and type, if relevant) arguments for a
    specific Camino program, where prog is one of shredder,
    scanner2voxel, vctreshselect, pdview, track.
    argument: ``-printprogargs %s``, position: 3
printintelbyteorder: (a pathlike object or string representing an
    existing file)
    Prints 1 if the header is little-endian, 0 otherwise.
    argument: ``-printintelbyteorder %s``, position: 3
printbigendian: (a pathlike object or string representing an existing
    file)
    Prints 1 if the header is big-endian, 0 otherwise.
    argument: ``-printbigendian %s``, position: 3
initfromheader: (a pathlike object or string representing an existing
    file)
    Reads header information from file and initializes a new header with
    the values read from the file. You may replace any combination of
    fields in the new header by specifying subsequent options.
    argument: ``-initfromheader %s``, position: 3
data_dims: (a list of from 3 to 3 items which are an integer (int or
    long))
    data dimensions in voxels
    argument: ``-datadims %s``
voxel_dims: (a list of from 3 to 3 items which are a float)
    voxel dimensions in mm
    argument: ``-voxeldims %s``
centre: (a list of from 3 to 3 items which are an integer (int or
    long))
    Voxel specifying origin of Talairach coordinate system for SPM,
    default [0 0 0].
    argument: ``-centre %s``

```

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```

picoseed: (a list of from 3 to 3 items which are an integer (int or
          long))
          Voxel specifying the seed (for PICO maps), default [0 0 0].
          argument: ``-picoseed %s``
nimages: (an integer (int or long))
          Number of images in the img file. Default 1.
          argument: ``-nimages %d``
offset: (an integer (int or long))
          According to the Analyze 7.5 standard, this is the byte offset in
          the .img file at which voxels start. This value can be negative to
          specify that the absolute value is applied for every image in the
          file.
          argument: ``-offset %d``
greylevels: (a list of from 2 to 2 items which are an integer (int or
            long))
            Minimum and maximum greylevels. Stored as shorts in the header.
            argument: ``-gl %s``
scaleslope: (a float)
            Intensities in the image are scaled by this factor by SPM and
            MRICro. Default is 1.0.
            argument: ``-scaleslope %d``
scaleinter: (a float)
            Constant to add to the image intensities. Used by SPM and MRICro.
            argument: ``-scaleinter %d``
description: (a string)
            Short description - No spaces, max length 79 bytes. Will be null
            terminated automatically.
            argument: ``-description %s``
intelbyteorder: (a boolean)
            Write header in intel byte order (little-endian).
            argument: ``-intelbyteorder``
networkbyteorder: (a boolean)
            Write header in network byte order (big-endian). This is the default
            for new headers.
            argument: ``-networkbyteorder``
out_file: (a pathlike object or string representing a file)
            argument: ``> %s``, position: -1
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

header: (a pathlike object or string representing an existing file)
        Analyze header

```

55.3.2 DT2Nifti[Link to code](#)

Wraps the executable command dt2nii.

Converts camino tensor data to Nifti format

Reads Camino diffusion tensors, and converts them to NIFTI format as three .nii files.

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         tract file
         argument: ``-inputfile %s``, position: 1
header_file: (a pathlike object or string representing an existing
              file)
              A Nifti .nii or .hdr file containing the header information
              argument: ``-header %s``, position: 3

[Optional]
output_root: (a pathlike object or string representing a file)
              filename root prepended onto the names of three output files.
              argument: ``-outputroot %s``, position: 2
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
dt: (a pathlike object or string representing an existing file)
     diffusion tensors in NIFTI format
exitcode: (a pathlike object or string representing an existing file)
           exit codes from Camino reconstruction in NIFTI format
lns0: (a pathlike object or string representing an existing file)
       estimated lns0 from Camino reconstruction in NIFTI format
```

55.3.3 Image2Voxel[Link to code](#)

Wraps the executable command image2voxel.

Converts Analyze / NIFTI / MHA files to voxel order.

Converts scanner-order data in a supported image format to voxel-order data. Either takes a 4D file (all measurements in single image) or a list of 3D images.

Examples

```
>>> import nipy.interfaces.camino as cmon
>>> img2vox = cmon.Image2Voxel()
>>> img2vox.inputs.in_file = '4d_dwi.nii'
>>> img2vox.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         4d image file
         argument: ``-4dimage %s``, position: 1

[Optional]
out_type: ('float' or 'char' or 'short' or 'int' or 'long' or
           'double', nipy default value: float)
           "i.e. Bfloat". Can be "char", "short", "int", "long", "float" or
```

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```

    "double"
    argument: ``-outputdatatype %s``, position: 2
out_file: (a pathlike object or string representing a file)
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

voxel_order: (a pathlike object or string representing an existing
    file)
    path/name of 4D volume in voxel order

```

55.3.4 NiftiDT2Camino[Link to code](#)

Wraps the executable command `niftidt2camino`.

Converts NIFTI-1 diffusion tensors to Camino format. The program reads the NIFTI header but does not apply any spatial transformations to the data. The NIFTI intensity scaling parameters are applied.

The output is the tensors in Camino voxel ordering: [exit, ln(S0), dxx, dxy, dxz, dyy, dyz, dzz].

The exit code is set to 0 unless a background mask is supplied, in which case the code is 0 in brain voxels and -1 in background voxels.

The value of ln(S0) in the output is taken from a file if one is supplied, otherwise it is set to 0.

NOTE FOR FSL USERS - FSL's `dtfit` can output NIFTI tensors, but they are not stored in the usual way (which is using `NIFTI_INTENT_SYMMATRIX`). FSL's tensors follow the ITK / VTK "upper-triangular" convention, so you will need to use the `-uppertriangular` option to convert these correctly.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    A NIFTI-1 dataset containing diffusion tensors. The tensors are
    assumed to be in lower-triangular order as specified by the NIFTI
    standard for the storage of symmetric matrices. This file should be
    either a .nii or a .hdr file.
    argument: ``-inputfile %s``, position: 1

[Optional]
s0_file: (a pathlike object or string representing an existing file)
    File containing the unweighted signal for each voxel, may be a raw
    binary file (specify type with -inputdatatype) or a supported image
    file.
    argument: ``-s0 %s``
lns0_file: (a pathlike object or string representing an existing
    file)
    File containing the log of the unweighted signal for each voxel, may
    be a raw binary file (specify type with -inputdatatype) or a
    supported image file.
    argument: ``-lns0 %s``
bgmask: (a pathlike object or string representing an existing file)
    Binary valued brain / background segmentation, may be a raw binary
    file (specify type with -maskdatatype) or a supported image file.

```

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```

    argument: ``-bgmask %s``
scaleslope: (a float)
    A value v in the diffusion tensor is scaled to  $v * s + i$ . This is
    applied after any scaling specified by the input image. Default is
    1.0.
    argument: ``-scaleslope %s``
scaleinter: (a float)
    A value v in the diffusion tensor is scaled to  $v * s + i$ . This is
    applied after any scaling specified by the input image. Default is
    0.0.
    argument: ``-scaleinter %s``
uppertriangular: (a boolean)
    Specifies input in upper-triangular (VTK style) order.
    argument: ``-uppertriangular %s``
out_file: (a pathlike object or string representing a file)
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    diffusion tensors data in Camino format

```

55.3.5 ProcStreamlines

[Link to code](#)Wraps the executable command `procstreamlines`.

Process streamline data

This program does post-processing of streamline output from track. It can either output streamlines or connection probabilities.<http://web4.cs.ucl.ac.uk/research/medic/camino/pmwiki/pmwiki.php?n=Man.procstreamlines>**Examples**

```

>>> import nipy.interfaces.camino as cmon
>>> proc = cmon.ProcStreamlines()
>>> proc.inputs.in_file = 'tract_data.Bfloat'
>>> proc.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    data file
    argument: ``-inputfile %s``, position: 1

[Optional]
inputmodel: ('raw' or 'voxels', nipy default value: raw)
    input model type (raw or voxels)
    argument: ``-inputmodel %s``

```

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```

maxtractpoints: (an integer (int or long))
    maximum number of tract points
    argument: ``-maxtractpoints %d``
mintractpoints: (an integer (int or long))
    minimum number of tract points
    argument: ``-mintractpoints %d``
maxtractlength: (an integer (int or long))
    maximum length of tracts
    argument: ``-maxtractlength %d``
mintractlength: (an integer (int or long))
    minimum length of tracts
    argument: ``-mintractlength %d``
datadims: (a list of from 3 to 3 items which are an integer (int or
    long))
    data dimensions in voxels
    argument: ``-datadims %s``
voxeldims: (a list of from 3 to 3 items which are an integer (int or
    long))
    voxel dimensions in mm
    argument: ``-voxeldims %s``
seedpointmm: (a list of from 3 to 3 items which are an integer (int
    or long))
    The coordinates of a single seed point for tractography in mm
    argument: ``-seedpointmm %s``
seedpointvox: (a list of from 3 to 3 items which are an integer (int
    or long))
    The coordinates of a single seed point for tractography in voxels
    argument: ``-seedpointvox %s``
seedfile: (a pathlike object or string representing a file)
    Image Containing Seed Points
    argument: ``-seedfile %s``
regionindex: (an integer (int or long))
    index of specific region to process
    argument: ``-regionindex %d``
iterations: (a float)
    Number of streamlines generated for each seed. Not required when
    outputting streamlines, but needed to create PICO images. The
    default is 1 if the output is streamlines, and 5000 if the output is
    connection probability images.
    argument: ``-iterations %d``
targetfile: (a pathlike object or string representing a file)
    Image containing target volumes.
    argument: ``-targetfile %s``
allowmultitargets: (a boolean)
    Allows streamlines to connect to multiple target volumes.
    argument: ``-allowmultitargets``
directional: (a list of from 3 to 3 items which are an integer (int
    or long))
    Splits the streamlines at the seed point and computes separate
    connection probabilities for each segment. Streamline segments are
    grouped according to their dot product with the vector (X, Y, Z).
    The ideal vector will be tangential to the streamline trajectory at
    the seed, such that the streamline projects from the seed along (X,
    Y, Z) and -(X, Y, Z). However, it is only necessary for the
    streamline trajectory to not be orthogonal to (X, Y, Z).
    argument: ``-directional %s``
waypointfile: (a pathlike object or string representing a file)

```

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```

    Image containing waypoints. Waypoints are defined as regions of the
    image with the same intensity, where 0 is background and any value >
    0 is a waypoint.
    argument: ``-waypointfile %s``
truncateloops: (a boolean)
    This option allows streamlines to enter a waypoint exactly once.
    After the streamline leaves the waypoint, it is truncated upon a
    second entry to the waypoint.
    argument: ``-truncateloops``
discardloops: (a boolean)
    This option allows streamlines to enter a waypoint exactly once.
    After the streamline leaves the waypoint, the entire streamline is
    discarded upon a second entry to the waypoint.
    argument: ``-discardloops``
exclusionfile: (a pathlike object or string representing a file)
    Image containing exclusion ROIs. This should be an Analyze 7.5
    header / image file.hdr and file.img.
    argument: ``-exclusionfile %s``
truncateinexclusion: (a boolean)
    Retain segments of a streamline before entry to an exclusion ROI.
    argument: ``-truncateinexclusion``
endpointfile: (a pathlike object or string representing a file)
    Image containing endpoint ROIs. This should be an Analyze 7.5 header
    / image file.hdr and file.img.
    argument: ``-endpointfile %s``
resamplestepsize: (a float)
    Each point on a streamline is tested for entry into target,
    exclusion or waypoint volumes. If the length between points on a
    tract is not much smaller than the voxel length, then streamlines
    may pass through part of a voxel without being counted. To avoid
    this, the program resamples streamlines such that the step size is
    one tenth of the smallest voxel dimension in the image. This
    increases the size of raw or oogl streamline output and incurs some
    performance penalty. The resample resolution can be controlled with
    this option or disabled altogether by passing a negative step size
    or by passing the -noresample option.
    argument: ``-resamplestepsize %d``
noresample: (a boolean)
    Disables resampling of input streamlines. Resampling is
    automatically disabled if the input model is voxels.
    argument: ``-noresample``
outputtracts: (a boolean)
    Output streamlines in raw binary format.
    argument: ``-outputtracts``
outputroot: (a pathlike object or string representing a file)
    Prepended onto all output file names.
    argument: ``-outputroot %s``
gzip: (a boolean)
    save the output image in gzip format
    argument: ``-gzip``
outputtcp: (a boolean)
    output the connection probability map (Analyze image, float)
    argument: ``-outputtcp``
    requires: outputroot, seedfile
outputsc: (a boolean)
    output the connection probability map (raw streamlines, int)
    argument: ``-outputsc``

```

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```

        requires: outputroot, seedfile
outputacm: (a boolean)
    output all tracts in a single connection probability map (Analyze
    image)
    argument: ``-outputacm``
    requires: outputroot, seedfile
outputcbs: (a boolean)
    outputs connectivity-based segmentation maps; requires target
    outputfile
    argument: ``-outputcbs``
    requires: outputroot, targetfile, seedfile
out_file: (a pathlike object or string representing a file)
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables

```

Outputs:

```

proc: (a pathlike object or string representing an existing file)
    Processed Streamlines
outputroot_files: (a list of items which are a pathlike object or
    string representing an existing file)

```

55.3.6 Shredder

[Link to code](#)

Wraps the executable command shredder.

Extracts periodic chunks from a data stream.

Shredder makes an initial offset of offset bytes. It then reads and outputs chunksize bytes, skips space bytes, and repeats until there is no more input.

If the chunksize is negative, chunks of size chunksize are read and the byte ordering of each chunk is reversed. The whole chunk will be reversed, so the chunk must be the same size as the data type, otherwise the order of the values in the chunk, as well as their endianness, will be reversed.

Examples

```

>>> import nipyte.interfaces.camino as cam
>>> shred = cam.Shredder()
>>> shred.inputs.in_file = 'SubjectA.Bfloat'
>>> shred.inputs.offset = 0
>>> shred.inputs.chunksize = 1
>>> shred.inputs.space = 2
>>> shred.run()                                # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    raw binary data file
    argument: ``< %s``, position: -2

```

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```
[Optional]
offset: (an integer (int or long))
    initial offset of offset bytes
    argument: ``%d``, position: 1
chunksize: (an integer (int or long))
    reads and outputs a chunk of chunksize bytes
    argument: ``%d``, position: 2
space: (an integer (int or long))
    skips space bytes
    argument: ``%d``, position: 3
out_file: (a pathlike object or string representing a file)
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyre default value: {})
    Environment variables
```

Outputs:

```
shredded: (a pathlike object or string representing an existing file)
    Shredded binary data file
```

55.3.7 TractShredder

[Link to code](#)

Wraps the executable command `tractshredder`.

Extracts bunches of streamlines.

`tractshredder` works in a similar way to `shredder`, but processes streamlines instead of scalar data. The input is raw streamlines, in the format produced by `track` or `procstreamlines`.

The program first makes an initial offset of offset tracts. It then reads and outputs a group of bunchsize tracts, skips space tracts, and repeats until there is no more input.

Examples

```
>>> import nipyre.interfaces.camino as cmon
>>> shred = cmon.TractShredder()
>>> shred.inputs.in_file = 'tract_data.Bfloat'
>>> shred.inputs.offset = 0
>>> shred.inputs.bunchsize = 1
>>> shred.inputs.space = 2
>>> shred.run()                                # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    tract file
    argument: ``< %s``, position: -2

[Optional]
offset: (an integer (int or long))
    initial offset of offset tracts
```

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```

        argument: ``%d``, position: 1
bunchsize: (an integer (int or long))
            reads and outputs a group of bunchsize tracts
            argument: ``%d``, position: 2
space: (an integer (int or long))
        skips space tracts
        argument: ``%d``, position: 3
out_file: (a pathlike object or string representing a file)
            argument: ``> %s``, position: -1
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables

```

Outputs:

```

shredded: (a pathlike object or string representing an existing file)
          Shredded tract file

```

55.3.8 VtkStreamlines[Link to code](#)

Wraps the executable command vtkstreamlines.

Use vtkstreamlines to convert raw or voxel format streamlines to VTK polydata

Examples

```

>>> import nipype.interfaces.camino as cmon
>>> vtk = cmon.VtkStreamlines()
>>> vtk.inputs.in_file = 'tract_data.Bfloat'
>>> vtk.inputs.voxeldims = [1,1,1]
>>> vtk.run()                                # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         data file
         argument: `` < %s``, position: -2

[Optional]
inputmodel: ('raw' or 'voxels', nipype default value: raw)
            input model type (raw or voxels)
            argument: ``-inputmodel %s``
voxeldims: (a list of from 3 to 3 items which are an integer (int or
            long))
            voxel dimensions in mm
            argument: ``-voxeldims %s``, position: 4
seed_file: (a pathlike object or string representing a file)
            image containing seed points
            argument: ``-seedfile %s``, position: 1
target_file: (a pathlike object or string representing a file)
             image containing integer-valued target regions

```

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```

        argument: ``-targetfile %s``, position: 2
scalar_file: (a pathlike object or string representing a file)
    image that is in the same physical space as the tracts
    argument: ``-scalarfile %s``, position: 3
colourorient: (a boolean)
    Each point on the streamline is coloured by the local orientation.
    argument: ``-colourorient``
interpolatescalars: (a boolean)
    the scalar value at each point on the streamline is calculated by
    trilinear interpolation
    argument: ``-interpolatescalars``
interpolate: (a boolean)
    the scalar value at each point on the streamline is calculated by
    trilinear interpolation
    argument: ``-interpolate``
out_file: (a pathlike object or string representing a file)
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

vtk: (a pathlike object or string representing an existing file)
    Streamlines in VTK format

```

55.4 interfaces.camino.dti

55.4.1 ComputeEigensystem

[Link to code](#)Wraps the executable command `dteig`.

Computes the eigensystem from tensor fitted data.

Reads diffusion tensor (single, two-tensor, three-tensor or multitensor) data from the standard input, computes the eigenvalues and eigenvectors of each tensor and outputs the results to the standard output. For multiple-tensor data the program outputs the eigensystem of each tensor. For each tensor the program outputs: $\{l_1, e_{11}, e_{12}, e_{13}, l_2, e_{21}, e_{22}, e_{23}, l_3, e_{31}, e_{32}, e_{33}\}$, where $l_1 \geq l_2 \geq l_3$ and $e_i = (e_{i1}, e_{i2}, e_{i3})$ is the eigenvector with eigenvalue l_i . For three-tensor data, for example, the output contains thirty-six values per voxel.

Example

```

>>> import nipy.interfaces.camino as cmon
>>> dteig = cmon.ComputeEigensystem()
>>> dteig.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> dteig.run()                                # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)

```

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```

    Tensor-fitted data filename
    argument: ``< %s``, position: 1

[Optional]
inputmodel: ('dt' or 'multitensor')
    Specifies the model that the input data contains parameters for.
    Possible model types are: "dt" (diffusion-tensor data) and
    "multitensor"
    argument: ``-inputmodel %s``
maxcomponents: (an integer (int or long))
    The maximum number of tensor components in a voxel of the input
    data.
    argument: ``-maxcomponents %d``
inputdatatype: ('double' or 'float' or 'long' or 'int' or 'short' or
    'char', nipy default value: double)
    Specifies the data type of the input data. The data type can be any
    of the following strings: "char", "short", "int", "long", "float" or
    "double". Default is double data type
    argument: ``-inputdatatype %s``
outputdatatype: ('double' or 'float' or 'long' or 'int' or 'short' or
    'char', nipy default value: double)
    Specifies the data type of the output data. The data type can be any
    of the following strings: "char", "short", "int", "long", "float" or
    "double". Default is double data type
    argument: ``-outputdatatype %s``
out_file: (a pathlike object or string representing a file)
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

eigen: (a pathlike object or string representing an existing file)
    Trace of the diffusion tensor

```

55.4.2 ComputeFractionalAnisotropy[Link to code](#)

Wraps the executable command `fa`.

Computes the fractional anisotropy of tensors.

Reads diffusion tensor (single, two-tensor or three-tensor) data from the standard input, computes the fractional anisotropy (FA) of each tensor and outputs the results to the standard output. For multiple-tensor data the program outputs the FA of each tensor, so for three-tensor data, for example, the output contains three fractional anisotropy values per voxel.

Example

```

>>> import nipy.interfaces.camino as cmon
>>> fa = cmon.ComputeFractionalAnisotropy()
>>> fa.inputs.in_file = 'tensor_fitted_data.Bdouble'

```

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```
>>> fa.inputs.scheme_file = 'A.scheme'
>>> fa.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        Tensor-fitted data filename
        argument: ``< %s``, position: 1

[Optional]
scheme_file: (a pathlike object or string representing an existing
             file)
             Camino scheme file (b values / vectors, see camino.fsl2scheme)
             argument: ``%s``, position: 2
inputmodel: ('dt' or 'twotensor' or 'threetensor' or 'multitensor')
            Specifies the model that the input tensor data contains parameters
            for. Possible model types are: "dt" (diffusion-tensor data),
            "twotensor" (two-tensor data), "threetensor" (three-tensor data). By
            default, the program assumes that the input data contains a single
            diffusion tensor in each voxel.
            argument: ``-inputmodel %s``
inputdatatype: ('char' or 'short' or 'int' or 'long' or 'float' or
               'double')
               Specifies the data type of the input file. The data type can be any
               of the following strings: "char", "short", "int", "long", "float" or
               "double".
               argument: ``-inputdatatype %s``
outputdatatype: ('char' or 'short' or 'int' or 'long' or 'float' or
                'double')
                Specifies the data type of the output data. The data type can be any
                of the following strings: "char", "short", "int", "long", "float" or
                "double".
                argument: ``-outputdatatype %s``
out_file: (a pathlike object or string representing a file)
          argument: ``> %s``, position: -1
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipype default value: {})
         Environment variables
```

Outputs:

```
fa: (a pathlike object or string representing an existing file)
    Fractional Anisotropy Map
```

55.4.3 ComputeMeanDiffusivity

[Link to code](#)Wraps the executable command `md`.

Computes the mean diffusivity (trace/3) from diffusion tensors.

Example

```
>>> import nipy.interfaces.camino as cmon
>>> md = cmon.ComputeMeanDiffusivity()
>>> md.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> md.inputs.scheme_file = 'A.scheme'
>>> md.run()                                # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        Tensor-fitted data filename
        argument: ``< %s``, position: 1

[Optional]
scheme_file: (a pathlike object or string representing an existing
             file)
             Camino scheme file (b values / vectors, see camino.fsl2scheme)
             argument: ``%s``, position: 2
out_file: (a pathlike object or string representing a file)
          argument: ``> %s``, position: -1
inputmodel: ('dt' or 'twotensor' or 'threetensor')
            Specifies the model that the input tensor data contains parameters
            for. Possible model types are: "dt" (diffusion-tensor data),
            "twotensor" (two-tensor data), "threetensor" (three-tensor data). By
            default, the program assumes that the input data contains a single
            diffusion tensor in each voxel.
            argument: ``-inputmodel %s``
inputdatatype: ('char' or 'short' or 'int' or 'long' or 'float' or
               'double')
              Specifies the data type of the input file. The data type can be any
              of the following strings: "char", "short", "int", "long", "float" or
              "double".
              argument: ``-inputdatatype %s``
outputdatatype: ('char' or 'short' or 'int' or 'long' or 'float' or
                'double')
              Specifies the data type of the output data. The data type can be any
              of the following strings: "char", "short", "int", "long", "float" or
              "double".
              argument: ``-outputdatatype %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
        Environment variables
```

Outputs:

```
md: (a pathlike object or string representing an existing file)
    Mean Diffusivity Map
```

55.4.4 ComputeTensorTrace

[Link to code](#)

Wraps the executable command `trd`.

Computes the trace of tensors.

Reads diffusion tensor (single, two-tensor or three-tensor) data from the standard input, computes the trace of each tensor, i.e., three times the mean diffusivity, and outputs the results to the standard output. For multiple-tensor data the program outputs the trace of each tensor, so for three-tensor data, for example, the output contains three values per voxel.

Divide the output by three to get the mean diffusivity.

Example

```
>>> import nipyype.interfaces.camino as cmon
>>> trace = cmon.ComputeTensorTrace()
>>> trace.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> trace.inputs.scheme_file = 'A.scheme'
>>> trace.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        Tensor-fitted data filename
        argument: ``< %s``, position: 1

[Optional]
scheme_file: (a pathlike object or string representing an existing
             file)
             Camino scheme file (b values / vectors, see camino.fsl2scheme)
             argument: ``%s``, position: 2
inputmodel: ('dt' or 'twotensor' or 'threetensor' or 'multitensor')
            Specifies the model that the input tensor data contains parameters
            for. Possible model types are: "dt" (diffusion-tensor data),
            "twotensor" (two-tensor data), "threetensor" (three-tensor data). By
            default, the program assumes that the input data contains a single
            diffusion tensor in each voxel.
            argument: ``-inputmodel %s``
inputdatatype: ('char' or 'short' or 'int' or 'long' or 'float' or
               'double')
               Specifies the data type of the input file. The data type can be any
               of the following strings: "char", "short", "int", "long", "float" or
               "double".
               argument: ``-inputdatatype %s``
outputdatatype: ('char' or 'short' or 'int' or 'long' or 'float' or
                'double')
                Specifies the data type of the output data. The data type can be any
                of the following strings: "char", "short", "int", "long", "float" or
                "double".
                argument: ``-outputdatatype %s``
out_file: (a pathlike object or string representing a file)
          argument: ``> %s``, position: -1
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipyype default value: {})
         Environment variables
```

Outputs:

```
trace: (a pathlike object or string representing an existing file)
        Trace of the diffusion tensor
```

55.4.5 DTIFit

[Link to code](#)

Wraps the executable command dtfit.

Reads diffusion MRI data, acquired using the acquisition scheme detailed in the scheme file, from the data file. Use non-linear fitting instead of the default linear regression to the log measurements. The data file stores the diffusion MRI data in voxel order with the measurements stored in big-endian format and ordered as in the scheme file. The default input data type is four-byte float. The default output data type is eight-byte double. See modelfit and Camino for the format of the data file and scheme file. The program fits the diffusion tensor to each voxel and outputs the results, in voxel order and as big-endian eight-byte doubles, to the standard output. The program outputs eight values in each voxel: [exit code, $\ln(S(0))$, D_{xx} , D_{xy} , D_{xz} , D_{yy} , D_{yz} , D_{zz}]. An exit code of zero indicates no problems. For a list of other exit codes, see modelfit(1). The entry $S(0)$ is an estimate of the signal at $q=0$.

Example

```
>>> import nipy.interfaces.camino as cmon
>>> fit = cmon.DTIFit()
>>> fit.inputs.scheme_file = 'A.scheme'
>>> fit.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> fit.run()                                # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        voxel-order data filename
        argument: ``%s``, position: 1
scheme_file: (a pathlike object or string representing an existing
             file)
             Camino scheme file (b values / vectors, see Camino.fsl2scheme)
             argument: ``%s``, position: 2

[Optional]
bgmask: (a pathlike object or string representing an existing file)
        Provides the name of a file containing a background mask computed
        using, for example, FSL bet2 program. The mask file contains zero in
        background voxels and non-zero in foreground.
        argument: ``-bgmask %s``
non_linear: (a boolean)
            Use non-linear fitting instead of the default linear regression to
            the log measurements.
            argument: ``-nonlinear``, position: 3
out_file: (a pathlike object or string representing a file)
          argument: ``> %s``, position: -1
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```

tensor_fitted: (a pathlike object or string representing an existing
                file)
                path/name of 4D volume in voxel order

```

55.4.6 DTLUTGen

[Link to code](#)

Wraps the executable command `dtlutgen`.

Calibrates the PDFs for PICO probabilistic tractography.

This program needs to be run once for every acquisition scheme. It outputs a lookup table that is used by the `dtpicoparams` program to find PICO PDF parameters for an image. The default single tensor LUT contains parameters of the Bingham distribution and is generated by supplying a scheme file and an estimated signal to noise in white matter regions of the ($q=0$) image. The default inversion is linear (inversion index 1).

Advanced users can control several options, including the extent and resolution of the LUT, the inversion index, and the type of PDF. See `dtlutgen(1)` for details.

Example

```

>>> import nipy.interfaces.camino as cmon
>>> dtl = cmon.DTLUTGen()
>>> dtl.inputs.snr = 16
>>> dtl.inputs.scheme_file = 'A.scheme'
>>> dtl.run()                                # doctest: +SKIP

```

Inputs:

```

[Mandatory]
scheme_file: (a pathlike object or string representing a file)
              The scheme file of the images to be processed using this LUT.
              argument: ``-schemefile %s``, position: 2

[Optional]
lrange: (a list of from 2 to 2 items which are a float)
        Index to one-tensor LUTs. This is the ratio  $L1/L3$  and  $L2 / L3$ . The
        LUT is square, with half the values calculated (because  $L2 / L3$ 
        cannot be less than  $L1 / L3$  by definition). The minimum must be  $\geq 1$ .
        For comparison, a ratio  $L1 / L3 = 10$  with  $L2 / L3 = 1$  corresponds to
        an FA of 0.891, and  $L1 / L3 = 15$  with  $L2 / L3 = 1$  corresponds to an
        FA of 0.929. The default range is 1 to 10.
        argument: ``-lrange %s``, position: 1
frange: (a list of from 2 to 2 items which are a float)
        Index to two-tensor LUTs. This is the fractional anisotropy of the
        two tensors. The default is 0.3 to 0.94
        argument: ``-frange %s``, position: 1
step: (a float)
        Distance between points in the LUT. For example, if lrange is 1 to 10
        and the step is 0.1, LUT entries will be computed at  $L1 / L3 = 1$ ,
        1.1, 1.2 ... 10.0 and at  $L2 / L3 = 1.0$ , 1.1 ...  $L1 / L3$ . For single
        tensor LUTs, the default step is 0.2, for two-tensor LUTs it is
        0.02.
        argument: ``-step %f``
samples: (an integer (int or long))
        The number of synthetic measurements to generate at each point in
        the LUT. The default is 2000.
        argument: ``-samples %d``
snr: (a float)

```

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```

    The signal to noise ratio of the unweighted (q = 0)
    measurements. This should match the SNR (in white matter) of the
    images that the LUTs are used with.
    argument: ``-snr %f``
bingham: (a boolean)
    Compute a LUT for the Bingham PDF. This is the default.
    argument: ``-bingham``
acg: (a boolean)
    Compute a LUT for the ACG PDF.
    argument: ``-acg``
watson: (a boolean)
    Compute a LUT for the Watson PDF.
    argument: ``-watson``
inversion: (an integer (int or long))
    Index of the inversion to use. The default is 1 (linear single
    tensor inversion).
    argument: ``-inversion %d``
trace: (a float)
    Trace of the diffusion tensor(s) used in the test function in the
    LUT generation. The default is 2100E-12 m^2 s^-1.
    argument: ``-trace %G``
out_file: (a pathlike object or string representing a file)
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

dtLUT: (a pathlike object or string representing an existing file)
    Lookup Table

```

55.4.7 DTMetric[Link to code](#)

Wraps the executable command dtshape.

Computes tensor metric statistics based on the eigenvalues $\lambda_1 \geq \lambda_2 \geq \lambda_3$ typically obtained from ComputeEigensystem.

The full list of statistics is:

- $\langle cl \rangle = (\lambda_1 - \lambda_2) / \lambda_1$, a measure of linearity
- $\langle cp \rangle = (\lambda_2 - \lambda_3) / \lambda_1$, a measure of planarity
- $\langle cs \rangle = \lambda_3 / \lambda_1$, a measure of isotropy with: $cl + cp + cs = 1$
- $\langle l1 \rangle$ = first eigenvalue
- $\langle l2 \rangle$ = second eigenvalue
- $\langle l3 \rangle$ = third eigenvalue
- $\langle tr \rangle = \lambda_1 + \lambda_2 + \lambda_3$
- $\langle md \rangle = tr / 3$
- $\langle rd \rangle = (\lambda_2 + \lambda_3) / 2$
- $\langle fa \rangle$ = fractional anisotropy. (Basser et al, J Magn Reson B 1996)
- $\langle ra \rangle$ = relative anisotropy (Basser et al, J Magn Reson B 1996)
- $\langle 2dfa \rangle$ = 2D FA of the two minor eigenvalues λ_2 and λ_3 i.e. $\sqrt{2 * [(\lambda_2 - \langle l \rangle)^2 + (\lambda_3 - \langle l \rangle)^2] / (\lambda_2^2 + \lambda_3^2)}$ with: $\langle l \rangle = (\lambda_2 + \lambda_3) / 2$

Example

Compute the CP planar metric as float data type.

```
>>> import nipy.interfaces.camino as cam
>>> dtmetric = cam.DTMetric()
>>> dtmetric.inputs.eigen_data = 'dteig.Bdouble'
>>> dtmetric.inputs.metric = 'cp'
>>> dtmetric.inputs.outputdatatype = 'float'
>>> dtmetric.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
eigen_data: (a pathlike object or string representing an existing
             file)
             voxel-order data filename
             argument: ``-inputfile %s``
metric: ('fa' or 'md' or 'rd' or 'l1' or 'l2' or 'l3' or 'tr' or 'ra'
         or '2dfa' or 'cl' or 'cp' or 'cs')
         Specifies the metric to compute. Possible choices are: "fa", "md",
         "rd", "l1", "l2", "l3", "tr", "ra", "2dfa", "cl", "cp" or "cs".
         argument: ``-stat %s``

[Optional]
inputdatatype: ('double' or 'float' or 'long' or 'int' or 'short' or
                'char', nipy default value: double)
                Specifies the data type of the input data. The data type can be any
                of the following strings: "char", "short", "int", "long", "float" or
                "double". Default is double data type
                argument: ``-inputdatatype %s``
outputdatatype: ('double' or 'float' or 'long' or 'int' or 'short' or
                 'char', nipy default value: double)
                 Specifies the data type of the output data. The data type can be any
                 of the following strings: "char", "short", "int", "long", "float" or
                 "double". Default is double data type
                 argument: ``-outputdatatype %s``
data_header: (a pathlike object or string representing an existing
              file)
              A Nifti .nii or .nii.gz file containing the header information.
              Usually this will be the header of the raw data file from which the
              diffusion tensors were reconstructed.
              argument: ``-header %s``
outputfile: (a pathlike object or string representing a file)
            Output name. Output will be a .nii.gz file if data_header is
            provided and in voxel order with outputdatatype datatype (default:
            double) otherwise.
            argument: ``-outputfile %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
metric_stats: (a pathlike object or string representing an existing
```

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```
file)
Diffusion Tensor statistics of the chosen metric
```

55.4.8 ModelFit

[Link to code](#)

Wraps the executable command `modelfit`.

Fits models of the spin-displacement density to diffusion MRI measurements.

This is an interface to various model fitting routines for diffusion MRI data that fit models of the spin-displacement density function. In particular, it will fit the diffusion tensor to a set of measurements as well as various other models including two or three-tensor models. The program can read input data from a file or can generate synthetic data using various test functions for testing and simulations.

Example

```
>>> import nipy.interfaces.camino as cmon
>>> fit = cmon.ModelFit()
>>> fit.model = 'dt'
>>> fit.inputs.scheme_file = 'A.scheme'
>>> fit.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> fit.run()                                # doctest: +SKIP
```

Inputs:

```
[Mandatory]
model: ('dt' or 'restore' or 'algdt' or 'nldt_pos' or 'nldt' or
        'ldt_wtd' or 'adc' or 'ball_stick' or 'cylcyl dt' or 'cylcyl
        restore' or 'cylcyl algdt' or 'cylcyl nldt_pos' or 'cylcyl nldt'
        or 'cylcyl ldt_wtd' or 'cylcyl adc' or 'cylcyl ball_stick' or
        'cylcyl_eq dt' or 'cylcyl_eq restore' or 'cylcyl_eq algdt' or
        'cylcyl_eq nldt_pos' or 'cylcyl_eq nldt' or 'cylcyl_eq ldt_wtd' or
        'cylcyl_eq adc' or 'cylcyl_eq ball_stick' or 'pospos dt' or
        'pospos restore' or 'pospos algdt' or 'pospos nldt_pos' or 'pospos
        nldt' or 'pospos ldt_wtd' or 'pospos adc' or 'pospos ball_stick'
        or 'pospos_eq dt' or 'pospos_eq restore' or 'pospos_eq algdt' or
        'pospos_eq nldt_pos' or 'pospos_eq nldt' or 'pospos_eq ldt_wtd' or
        'pospos_eq adc' or 'pospos_eq ball_stick' or 'poscyl dt' or
        'poscyl restore' or 'poscyl algdt' or 'poscyl nldt_pos' or 'poscyl
        nldt' or 'poscyl ldt_wtd' or 'poscyl adc' or 'poscyl ball_stick'
        or 'poscyl_eq dt' or 'poscyl_eq restore' or 'poscyl_eq algdt' or
        'poscyl_eq nldt_pos' or 'poscyl_eq nldt' or 'poscyl_eq ldt_wtd' or
        'poscyl_eq adc' or 'poscyl_eq ball_stick' or 'cylcylcyl dt' or
        'cylcylcyl restore' or 'cylcylcyl algdt' or 'cylcylcyl nldt_pos'
        or 'cylcylcyl nldt' or 'cylcylcyl ldt_wtd' or 'cylcylcyl adc' or
        'cylcylcyl ball_stick' or 'cylcylcyl_eq dt' or 'cylcylcyl_eq
        restore' or 'cylcylcyl_eq algdt' or 'cylcylcyl_eq nldt_pos' or
        'cylcylcyl_eq nldt' or 'cylcylcyl_eq ldt_wtd' or 'cylcylcyl_eq
        adc' or 'cylcylcyl_eq ball_stick' or 'pospospos dt' or 'pospospos
        restore' or 'pospospos algdt' or 'pospospos nldt_pos' or
        'pospospos nldt' or 'pospospos ldt_wtd' or 'pospospos adc' or
        'pospospos ball_stick' or 'pospospos_eq dt' or 'pospospos_eq
        restore' or 'pospospos_eq algdt' or 'pospospos_eq nldt_pos' or
        'pospospos_eq nldt' or 'pospospos_eq ldt_wtd' or 'pospospos_eq
        adc' or 'pospospos_eq ball_stick' or 'posposcyl dt' or 'posposcyl
        restore' or 'posposcyl algdt' or 'posposcyl nldt_pos' or
```

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```

'posposcyl nldt' or 'posposcyl ldt_wtd' or 'posposcyl adc' or
'posposcyl ball_stick' or 'posposcyl_eq dt' or 'posposcyl_eq
restore' or 'posposcyl_eq algt' or 'posposcyl_eq nldt_pos' or
'posposcyl_eq nldt' or 'posposcyl_eq ldt_wtd' or 'posposcyl_eq
adc' or 'posposcyl_eq ball_stick' or 'poscylcyl dt' or 'poscylcyl
restore' or 'poscylcyl algt' or 'poscylcyl nldt_pos' or
'poscylcyl nldt' or 'poscylcyl ldt_wtd' or 'poscylcyl adc' or
'poscylcyl ball_stick' or 'poscylcyl_eq dt' or 'poscylcyl_eq
restore' or 'poscylcyl_eq algt' or 'poscylcyl_eq nldt_pos' or
'poscylcyl_eq nldt' or 'poscylcyl_eq ldt_wtd' or 'poscylcyl_eq
adc' or 'poscylcyl_eq ball_stick')
Specifies the model to be fit to the data.
argument: ``-model %s``
in_file: (a pathlike object or string representing an existing file)
voxel-order data filename
argument: ``-inputfile %s``
scheme_file: (a pathlike object or string representing an existing
file)
Camino scheme file (b values / vectors, see camino.fsl2scheme)
argument: ``-schemefile %s``

[Optional]
inputdatatype: ('float' or 'char' or 'short' or 'int' or 'long' or
'double')
Specifies the data type of the input file: "char", "short", "int",
"long", "float" or "double". The input file must have BIG-ENDIAN
ordering. By default, the input type is "float".
argument: ``-inputdatatype %s``
outputfile: (a pathlike object or string representing a file)
Filename of the output file.
argument: ``-outputfile %s``
outlier: (a pathlike object or string representing an existing file)
Specifies the name of the file to contain the outlier map generated
by the RESTORE algorithm.
argument: ``-outliermmap %s``
noisemap: (a pathlike object or string representing an existing file)
Specifies the name of the file to contain the estimated noise
variance on the diffusion-weighted signal, generated by a weighted
tensor fit. The data type of this file is big-endian double.
argument: ``-noisemap %s``
residualmap: (a pathlike object or string representing an existing
file)
Specifies the name of the file to contain the weighted residual
errors after computing a weighted linear tensor fit. One value is
produced per measurement, in voxel order. The data type of this file
is big-endian double. Images of the residuals for each measurement
can be extracted with shredder.
argument: ``-residualmap %s``
sigma: (a float)
Specifies the standard deviation of the noise in the data. Required
by the RESTORE algorithm.
argument: ``-sigma %G``
bgthresh: (a float)
Sets a threshold on the average q=0 measurement to separate
foreground and background. The program does not process background
voxels, but outputs the same number of values in background voxels
and foreground voxels. Each value is zero in background voxels apart

```

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```

from the exit code which is -1.
argument: ``-bgthresh %G``
bgmask: (a pathlike object or string representing an existing file)
Provides the name of a file containing a background mask computed
using, for example, FSL's bet2 program. The mask file contains zero
in background voxels and non-zero in foreground.
argument: ``-bgmask %s``
cfthresh: (a float)
Sets a threshold on the average q=0 measurement to determine which
voxels are CSF. This program does not treat CSF voxels any different
to other voxels.
argument: ``-csfthresh %G``
fixedmodq: (a list of from 4 to 4 items which are a float)
Specifies <M> <N> <Q> <tau> a spherical acquisition scheme with M
measurements with q=0 and N measurements with |q|=Q and diffusion
time tau. The N measurements with |q|=Q have unique directions. The
program reads in the directions from the files in directory
PointSets.
argument: ``-fixedmod %s``
fixedbvalue: (a list of from 3 to 3 items which are a float)
As above, but specifies <M> <N> <b>. The resulting scheme is the
same whether you specify b directly or indirectly using -fixedmodq.
argument: ``-fixedbvalue %s``
tau: (a float)
Sets the diffusion time separately. This overrides the diffusion
time specified in a scheme file or by a scheme index for both the
acquisition scheme and in the data synthesis.
argument: ``-tau %G``
out_file: (a pathlike object or string representing a file)
argument: ``> %s``, position: -1
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipype default value: {})
Environment variables

```

Outputs:

```

fitted_data: (a pathlike object or string representing an existing
file)
output file of 4D volume in voxel order

```

55.4.9 PicoPDFs

[Link to code](#)

Wraps the executable command picopdfs.

Constructs a spherical PDF in each voxel for probabilistic tractography.

Example

```

>>> import nipype.interfaces.camino as cmon
>>> pdf = cmon.PicoPDFs()
>>> pdf.inputs.inputmodel = 'dt'

```

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```
>>> pdf.inputs.luts = ['lut_file']
>>> pdf.inputs.in_file = 'voxel-order_data.Bfloat'
>>> pdf.run()                # doctest: +SKIP
```

Inputs:

[Mandatory]

in_file: (a pathlike object or string representing an existing file)
voxel-order data filename
argument: ``< %s``, position: 1

luts: (a list of items which are a pathlike object or string
representing an existing file)
Files containing the lookup tables. For tensor data, one lut must be
specified for each type of inversion used in the image (one-tensor,
two-tensor, three-tensor). For pds, the number of LUTs must match
-numpds (it is acceptable to use the same LUT several times - see
example, above). These LUTs may be generated with dtlutgen.
argument: ``-luts %s``

[Optional]

inputmodel: ('dt' or 'multitensor' or 'pds', nipy default value:
dt)
input model type
argument: ``-inputmodel %s``, position: 2

pdf: ('bingham' or 'watson' or 'acg', nipy default value: bingham)
Specifies the PDF to use. There are three choices: watson - The
Watson distribution. This distribution is rotationally
symmetric. bingham - The Bingham distribution, which allows
elliptical probability density contours. acg - The Angular Central
Gaussian distribution, which also allows elliptical probability
density contours
argument: ``-pdf %s``, position: 4

directmap: (a boolean)
Only applicable when using pds as the inputmodel. Use direct mapping
between the eigenvalues and the distribution parameters instead of
the log of the eigenvalues.
argument: ``-directmap``

maxcomponents: (an integer (int or long))
The maximum number of tensor components in a voxel (default 2) for
multitensor data. Currently, only the default is supported, but
future releases may allow the input of three-tensor data using this
option.
argument: ``-maxcomponents %d``

numpds: (an integer (int or long))
The maximum number of PDs in a voxel (default 3) for PD data. This
option determines the size of the input and output voxels. This means
that the data file may be large enough to accomodate three or more
PDs, but does not mean that any of the voxels are classified as
containing three or more PDs.
argument: ``-numpds %d``

out_file: (a pathlike object or string representing a file)
argument: ``> %s``, position: -1

args: (a unicode string)
Additional parameters to the command
argument: ``%s``

environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a

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```
value of class 'str', nipyne default value: {}
Environment variables
```

Outputs:

```
pdfs: (a pathlike object or string representing an existing file)
      path/name of 4D volume in voxel order
```

55.4.10 Track[Link to code](#)

Wraps the executable command track.

Performs tractography using one of the following models: 'dt', 'multitensor', 'pds', 'pico', 'bootstrap', 'ballstick', 'bayesdirac'

Example

```
>>> import nipyne.interfaces.camino as cmon
>>> track = cmon.Track()
>>> track.inputs.inputmodel = 'dt'
>>> track.inputs.in_file = 'data.Bfloat'
>>> track.inputs.seed_file = 'seed_mask.nii'
>>> track.run()                                # doctest: +SKIP
```

Inputs:

```
[Optional]
in_file: (a pathlike object or string representing an existing file)
         input data file
         argument: ``-inputfile %s``, position: 1
seed_file: (a pathlike object or string representing an existing
            file)
            seed file
            argument: ``-seedfile %s``, position: 2
inputmodel: ('dt' or 'multitensor' or 'sfpeak' or 'pico' or
             'repbs_dt' or 'repbs_multitensor' or 'ballstick' or 'wildbs_dt' or
             'bayesdirac' or 'bayesdirac_dt' or 'bedpostx_dyad' or 'bedpostx',
             nipyne default value: dt)
            input model type
            argument: ``-inputmodel %s``
tracker: ('fact' or 'euler' or 'rk4', nipyne default value: fact)
         The tracking algorithm controls streamlines are generated from the
         data. The choices are: - FACT, which follows the local fibre
         orientation in each voxel. No interpolation is used.- EULER, which
         uses a fixed step size along the local fibre orientation. With
         nearest-neighbour interpolation, this method may be very similar to
         FACT, except that the step size is fixed, whereas FACT steps extend
         to the boundary of the next voxel (distance variable depending on
         the entry and exit points to the voxel).- RK4: Fourth-order Runge-
         Kutta method. The step size is fixed, however the eventual direction
         of the step is determined by taking and averaging a series of
         partial steps.
         argument: ``-tracker %s``
interpolator: ('nn' or 'prob_nn' or 'linear')
              The interpolation algorithm determines how the fiber orientation(s)
              are defined at a given continuous point within the input image.
```

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```

Interpolators are only used when the tracking algorithm is not FACT.
The choices are: - NN: Nearest-neighbour interpolation, just uses
the local voxel data directly.- PROB_NN: Probabilistic nearest-
neighbor interpolation, similar to the method pro- posed by Behrens
et al [Magnetic Resonance in Medicine, 50:1077-1088, 2003]. The data
is not interpolated, but at each point we randomly choose one of the
8 voxels sur- rounding a point. The probability of choosing a
particular voxel is based on how close the point is to the centre of
that voxel.- LINEAR: Linear interpolation of the vector field
containing the principal directions at each point.
argument: ``-interpolator %s``

stepsize: (a float)
    Step size for EULER and RK4 tracking. The default is 1mm.
    argument: ``-stepsize %f``
    requires: tracker

inputdatatype: ('float' or 'double')
    input file type
    argument: ``-inputdatatype %s``

gzip: (a boolean)
    save the output image in gzip format
    argument: ``-gzip``

maxcomponents: (an integer (int or long))
    The maximum number of tensor components in a voxel. This determines
    the size of the input file and does not say anything about the voxel
    classification. The default is 2 if the input model is multitensor
    and 1 if the input model is dt.
    argument: ``-maxcomponents %d``

numpds: (an integer (int or long))
    The maximum number of PDs in a voxel for input models sfpeak and
    pico. The default is 3 for input model sfpeak and 1 for input model
    pico. This option determines the size of the voxels in the input
    file and does not affect tracking. For tensor data, use the
    -maxcomponents option.
    argument: ``-numpds %d``

data_dims: (a list of from 3 to 3 items which are an integer (int or
    long))
    data dimensions in voxels
    argument: ``-datadims %s``

voxel_dims: (a list of from 3 to 3 items which are a float)
    voxel dimensions in mm
    argument: ``-voxeldims %s``

ipthresh: (a float)
    Curvature threshold for tracking, expressed as the minimum dot
    product between two streamline orientations calculated over the
    length of a voxel. If the dot product between the previous and
    current directions is less than this threshold, then the streamline
    terminates. The default setting will terminate fibres that curve by
    more than 80 degrees. Set this to -1.0 to disable curvature checking
    completely.
    argument: ``-ipthresh %f``

curvethresh: (a float)
    Curvature threshold for tracking, expressed as the maximum angle (in
    degrees) between between two streamline orientations calculated over
    the length of a voxel. If the angle is greater than this, then the
    streamline terminates.
    argument: ``-curvethresh %f``

curveinterval: (a float)

```

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```

Interval over which the curvature threshold should be evaluated, in
mm. The default is 5mm. When using the default curvature threshold
of 90 degrees, this means that streamlines will terminate if they
curve by more than 90 degrees over a path length of 5mm.
argument: ``-curveinterval %f``
requires: curvethresh
anisthresh: (a float)
    Terminate fibres that enter a voxel with lower anisotropy than the
    threshold.
    argument: ``-anisthresh %f``
anisfile: (a pathlike object or string representing an existing file)
    File containing the anisotropy map. This is required to apply an
    anisotropy threshold with non tensor data. If the map is supplied it
    is always used, even in tensor data.
    argument: ``-anisfile %s``
outputtracts: ('float' or 'double' or 'oogl')
    output tract file type
    argument: ``-outputtracts %s``
out_file: (a pathlike object or string representing a file)
    output data file
    argument: ``-outputfile %s``, position: -1
output_root: (a pathlike object or string representing a file)
    root directory for output
    argument: ``-outputroot %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyype default value: {})
    Environment variables

```

Outputs:

```

tracked: (a pathlike object or string representing an existing file)
    output file containing reconstructed tracts

```

55.4.11 TrackBallStick[Link to code](#)Wraps the executable command `track`.

Performs streamline tractography using ball-stick fitted data

Example

```

>>> import nipyype.interfaces.camino as cmon
>>> track = cmon.TrackBallStick()
>>> track.inputs.in_file = 'ballstickfit_data.Bfloat'
>>> track.inputs.seed_file = 'seed_mask.nii'
>>> track.run() # doctest: +SKIP

```

Inputs:

```

[Optional]
in_file: (a pathlike object or string representing an existing file)
    input data file

```

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```

    argument: ``-inputfile %s``, position: 1
seed_file: (a pathlike object or string representing an existing
    file)
    seed file
    argument: ``-seedfile %s``, position: 2
inputmodel: ('dt' or 'multitensor' or 'sfpeak' or 'pico' or
    'repbs_dt' or 'repbs_multitensor' or 'ballstick' or 'wilddb DT' or
    'bayesdirac' or 'bayesdirac_dt' or 'bedpostx_dyad' or 'bedpostx',
    nipy default value: dt)
    input model type
    argument: ``-inputmodel %s``
tracker: ('fact' or 'euler' or 'rk4', nipy default value: fact)
    The tracking algorithm controls streamlines are generated from the
    data. The choices are: - FACT, which follows the local fibre
    orientation in each voxel. No interpolation is used.- EULER, which
    uses a fixed step size along the local fibre orientation. With
    nearest-neighbour interpolation, this method may be very similar to
    FACT, except that the step size is fixed, whereas FACT steps extend
    to the boundary of the next voxel (distance variable depending on
    the entry and exit points to the voxel).- RK4: Fourth-order Runge-
    Kutta method. The step size is fixed, however the eventual direction
    of the step is determined by taking and averaging a series of
    partial steps.
    argument: ``-tracker %s``
interpolator: ('nn' or 'prob_nn' or 'linear')
    The interpolation algorithm determines how the fiber orientation(s)
    are defined at a given continuous point within the input image.
    Interpolators are only used when the tracking algorithm is not FACT.
    The choices are: - NN: Nearest-neighbour interpolation, just uses
    the local voxel data directly.- PROB_NN: Probabilistic nearest-
    neighbor interpolation, similar to the method pro- posed by Behrens
    et al [Magnetic Resonance in Medicine, 50:1077-1088, 2003]. The data
    is not interpolated, but at each point we randomly choose one of the
    8 voxels sur- rounding a point. The probability of choosing a
    particular voxel is based on how close the point is to the centre of
    that voxel.- LINEAR: Linear interpolation of the vector field
    containing the principal directions at each point.
    argument: ``-interpolator %s``
stepsize: (a float)
    Step size for EULER and RK4 tracking. The default is 1mm.
    argument: ``-stepsize %f``
    requires: tracker
inputdatatype: ('float' or 'double')
    input file type
    argument: ``-inputdatatype %s``
gzip: (a boolean)
    save the output image in gzip format
    argument: ``-gzip``
maxcomponents: (an integer (int or long))
    The maximum number of tensor components in a voxel. This determines
    the size of the input file and does not say anything about the voxel
    classification. The default is 2 if the input model is multitensor
    and 1 if the input model is dt.
    argument: ``-maxcomponents %d``
numpds: (an integer (int or long))
    The maximum number of PDs in a voxel for input models sfpeak and
    pico. The default is 3 for input model sfpeak and 1 for input model

```

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```

    pico. This option determines the size of the voxels in the input
    file and does not affect tracking. For tensor data, use the
    -maxcomponents option.
    argument: ``-numpds %d``
data_dims: (a list of from 3 to 3 items which are an integer (int or
    long))
    data dimensions in voxels
    argument: ``-datadims %s``
voxel_dims: (a list of from 3 to 3 items which are a float)
    voxel dimensions in mm
    argument: ``-voxeldims %s``
ipthresh: (a float)
    Curvature threshold for tracking, expressed as the minimum dot
    product between two streamline orientations calculated over the
    length of a voxel. If the dot product between the previous and
    current directions is less than this threshold, then the streamline
    terminates. The default setting will terminate fibres that curve by
    more than 80 degrees. Set this to -1.0 to disable curvature checking
    completely.
    argument: ``-ipthresh %f``
curvethresh: (a float)
    Curvature threshold for tracking, expressed as the maximum angle (in
    degrees) between between two streamline orientations calculated over
    the length of a voxel. If the angle is greater than this, then the
    streamline terminates.
    argument: ``-curvethresh %f``
curveinterval: (a float)
    Interval over which the curvature threshold should be evaluated, in
    mm. The default is 5mm. When using the default curvature threshold
    of 90 degrees, this means that streamlines will terminate if they
    curve by more than 90 degrees over a path length of 5mm.
    argument: ``-curveinterval %f``
    requires: curvethresh
anisthresh: (a float)
    Terminate fibres that enter a voxel with lower anisotropy than the
    threshold.
    argument: ``-anisthresh %f``
anisfile: (a pathlike object or string representing an existing file)
    File containing the anisotropy map. This is required to apply an
    anisotropy threshold with non tensor data. If the map issupplied it
    is always used, even in tensor data.
    argument: ``-anisfile %s``
outputtracts: ('float' or 'double' or 'oogl')
    output tract file type
    argument: ``-outputtracts %s``
out_file: (a pathlike object or string representing a file)
    output data file
    argument: ``-outputfile %s``, position: -1
output_root: (a pathlike object or string representing a file)
    root directory for output
    argument: ``-outputroot %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})

```

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Environment variables

Outputs:

tracked: (a pathlike `object` or string representing an existing file)
 output file containing reconstructed tracts

55.4.12 TrackBayesDirac

[Link to code](#)

Wraps the executable command `track`.

Performs streamline tractography using a Bayesian tracking with Dirac priors

Example

```
>>> import nipy.interfaces.camino as cmon
>>> track = cmon.TrackBayesDirac()
>>> track.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> track.inputs.seed_file = 'seed_mask.nii'
>>> track.inputs.scheme_file = 'bvecs.scheme'
>>> track.run() # doctest: +SKIP
```

Inputs:

[Mandatory]

scheme_file: (a pathlike object or string representing an existing file)
 The scheme file corresponding to the data being processed.
 argument: ``-schemefile %s``

[Optional]

iterations: (an integer (int or long))
 Number of streamlines to generate at each seed point. The default is 5000.
 argument: ``-iterations %d``

pdf: ('bingham' or 'watson' or 'acg')
 Specifies the model for PICO priors (not the curvature priors). The default is "bingham".
 argument: ``-pdf %s``

pointset: (an integer (int or long))
 Index to the point set to use for Bayesian likelihood calculation. The index specifies a set of evenly distributed points on the unit sphere, where each point `x` defines two possible step directions (`x` or `-x`) for the streamline path. A larger number indexes a larger point set, which gives higher angular resolution at the expense of computation time. The default is index 1, which gives 1922 points, index 0 gives 1082 points, index 2 gives 3002 points.
 argument: ``-pointset %s``

datamodel: ('cylsymmmt' or 'ballstick')
 Model of the data for Bayesian tracking. The default model is "cylsymmmt", a diffusion tensor with cylindrical symmetry about `e_1`, ie `L1 >= L2 = L3`. The other model is "ballstick", the partial volume model (see `ballstickfit`).
 argument: ``-datamodel %s``

curvepriork: (a float)
 Concentration parameter for the prior distribution on fibre

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```

orientations given the fibre orientation at the previous step.
Larger values of k make curvature less likely.
argument: ``-curvepriork %G``
curvepriorg: (a float)
Concentration parameter for the prior distribution on fibre
orientations given the fibre orientation at the previous step.
Larger values of g make curvature less likely.
argument: ``-curvepriorg %G``
extpriorfile: (a pathlike object or string representing an existing
file)
Path to a PICO image produced by picopdfs. The PDF in each voxel is
used as a prior for the fibre orientation in Bayesian tracking. The
prior image must be in the same space as the diffusion data.
argument: ``-extpriorfile %s``
extpriordatatype: ('float' or 'double')
Datatype of the prior image. The default is "double".
argument: ``-extpriordatatype %s``
in_file: (a pathlike object or string representing an existing file)
input data file
argument: ``-inputfile %s``, position: 1
seed_file: (a pathlike object or string representing an existing
file)
seed file
argument: ``-seedfile %s``, position: 2
inputmodel: ('dt' or 'multitensor' or 'sfpeak' or 'pico' or
'repbs_dt' or 'repbs_multitensor' or 'ballstick' or 'wildbs_dt' or
'bayesdirac' or 'bayesdirac_dt' or 'bedpostx_dyad' or 'bedpostx',
nipy default value: dt)
input model type
argument: ``-inputmodel %s``
tracker: ('fact' or 'euler' or 'rk4', nipy default value: fact)
The tracking algorithm controls streamlines are generated from the
data. The choices are: - FACT, which follows the local fibre
orientation in each voxel. No interpolation is used.- EULER, which
uses a fixed step size along the local fibre orientation. With
nearest-neighbour interpolation, this method may be very similar to
FACT, except that the step size is fixed, whereas FACT steps extend
to the boundary of the next voxel (distance variable depending on
the entry and exit points to the voxel).- RK4: Fourth-order Runge-
Kutta method. The step size is fixed, however the eventual direction
of the step is determined by taking and averaging a series of
partial steps.
argument: ``-tracker %s``
interpolator: ('nn' or 'prob_nn' or 'linear')
The interpolation algorithm determines how the fiber orientation(s)
are defined at a given continuous point within the input image.
Interpolators are only used when the tracking algorithm is not FACT.
The choices are: - NN: Nearest-neighbour interpolation, just uses
the local voxel data directly.- PROB_NN: Probabilistic nearest-
neighbor interpolation, similar to the method pro- posed by Behrens
et al [Magnetic Resonance in Medicine, 50:1077-1088, 2003]. The data
is not interpolated, but at each point we randomly choose one of the
8 voxels sur- rounding a point. The probability of choosing a
particular voxel is based on how close the point is to the centre of
that voxel.- LINEAR: Linear interpolation of the vector field
containing the principal directions at each point.
argument: ``-interpolator %s``

```

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```

stepsize: (a float)
    Step size for EULER and RK4 tracking. The default is 1mm.
    argument: ``-stepsize %f``
    requires: tracker
inputdatatype: ('float' or 'double')
    input file type
    argument: ``-inputdatatype %s``
gzip: (a boolean)
    save the output image in gzip format
    argument: ``-gzip``
maxcomponents: (an integer (int or long))
    The maximum number of tensor components in a voxel. This determines
    the size of the input file and does not say anything about the voxel
    classification. The default is 2 if the input model is multitensor
    and 1 if the input model is dt.
    argument: ``-maxcomponents %d``
numpds: (an integer (int or long))
    The maximum number of PDs in a voxel for input models sfpeak and
    pico. The default is 3 for input model sfpeak and 1 for input model
    pico. This option determines the size of the voxels in the input
    file and does not affect tracking. For tensor data, use the
    -maxcomponents option.
    argument: ``-numpds %d``
data_dims: (a list of from 3 to 3 items which are an integer (int or
    long))
    data dimensions in voxels
    argument: ``-datadims %s``
voxel_dims: (a list of from 3 to 3 items which are a float)
    voxel dimensions in mm
    argument: ``-voxeldims %s``
ipthresh: (a float)
    Curvature threshold for tracking, expressed as the minimum dot
    product between two streamline orientations calculated over the
    length of a voxel. If the dot product between the previous and
    current directions is less than this threshold, then the streamline
    terminates. The default setting will terminate fibres that curve by
    more than 80 degrees. Set this to -1.0 to disable curvature checking
    completely.
    argument: ``-ipthresh %f``
curvethresh: (a float)
    Curvature threshold for tracking, expressed as the maximum angle (in
    degrees) between between two streamline orientations calculated over
    the length of a voxel. If the angle is greater than this, then the
    streamline terminates.
    argument: ``-curvethresh %f``
curveinterval: (a float)
    Interval over which the curvature threshold should be evaluated, in
    mm. The default is 5mm. When using the default curvature threshold
    of 90 degrees, this means that streamlines will terminate if they
    curve by more than 90 degrees over a path length of 5mm.
    argument: ``-curveinterval %f``
    requires: curvethresh
anisthresh: (a float)
    Terminate fibres that enter a voxel with lower anisotropy than the
    threshold.
    argument: ``-anisthresh %f``
anisfile: (a pathlike object or string representing an existing file)

```

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```

    File containing the anisotropy map. This is required to apply an
    anisotropy threshold with non tensor data. If the map is supplied it
    is always used, even in tensor data.
    argument: ``-anisfile %s``
outputtracts: ('float' or 'double' or 'oogl')
    output tract file type
    argument: ``-outputtracts %s``
out_file: (a pathlike object or string representing a file)
    output data file
    argument: ``-outputfile %s``, position: -1
output_root: (a pathlike object or string representing a file)
    root directory for output
    argument: ``-outputroot %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

tracked: (a pathlike object or string representing an existing file)
    output file containing reconstructed tracts

```

55.4.13 TrackBedpostxDeter[Link to code](#)

Wraps the executable command `track`.

Data from FSL's `bedpostx` can be imported into Camino for deterministic tracking. (Use `TrackBedpostxProba` for `bedpostx` probabilistic tractography.)

The tracking is based on the vector images `dyads1.nii.gz`, ..., `dyadsN.nii.gz`, where there are a maximum of `N` compartments (corresponding to each fiber population) in each voxel.

It also uses the `N` images `mean_f1samples.nii.gz`, ..., `mean_fNsamples.nii.gz`, normalized such that the sum of all compartments is 1. Compartments where the `mean_f` is less than a threshold are discarded and not used for tracking. The default value is 0.01. This can be changed with the `min_vol_frac` option.

Example

```

>>> import nipy.interfaces.camino as cam
>>> track = cam.TrackBedpostxDeter()
>>> track.inputs.bedpostxdir = 'bedpostxout'
>>> track.inputs.seed_file = 'seed_mask.nii'
>>> track.run()                                # doctest: +SKIP

```

Inputs:

```

[Mandatory]
bedpostxdir: (a pathlike object or string representing an existing
    directory)
    Directory containing bedpostx output
    argument: ``-bedpostxdir %s``

[Optional]

```

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```

min_vol_frac: (a float)
    Zeros out compartments in bedpostx data with a mean volume fraction
    f of less than min_vol_frac. The default is 0.01.
    argument: ``-bedpostxminf %d``
in_file: (a pathlike object or string representing an existing file)
    input data file
    argument: ``-inputfile %s``, position: 1
seed_file: (a pathlike object or string representing an existing
    file)
    seed file
    argument: ``-seedfile %s``, position: 2
inputmodel: ('dt' or 'multitensor' or 'sfpeak' or 'pico' or
    'repbs_dt' or 'repbs_multitensor' or 'ballstick' or 'wildbs_dt' or
    'bayesdirac' or 'bayesdirac_dt' or 'bedpostx_dyad' or 'bedpostx',
    nipy default value: dt)
    input model type
    argument: ``-inputmodel %s``
tracker: ('fact' or 'euler' or 'rk4', nipy default value: fact)
    The tracking algorithm controls streamlines are generated from the
    data. The choices are: - FACT, which follows the local fibre
    orientation in each voxel. No interpolation is used.- EULER, which
    uses a fixed step size along the local fibre orientation. With
    nearest-neighbour interpolation, this method may be very similar to
    FACT, except that the step size is fixed, whereas FACT steps extend
    to the boundary of the next voxel (distance variable depending on
    the entry and exit points to the voxel).- RK4: Fourth-order Runge-
    Kutta method. The step size is fixed, however the eventual direction
    of the step is determined by taking and averaging a series of
    partial steps.
    argument: ``-tracker %s``
interpolator: ('nn' or 'prob_nn' or 'linear')
    The interpolation algorithm determines how the fiber orientation(s)
    are defined at a given continuous point within the input image.
    Interpolators are only used when the tracking algorithm is not FACT.
    The choices are: - NN: Nearest-neighbour interpolation, just uses
    the local voxel data directly.- PROB_NN: Probabilistic nearest-
    neighbor interpolation, similar to the method pro- posed by Behrens
    et al [Magnetic Resonance in Medicine, 50:1077-1088, 2003]. The data
    is not interpolated, but at each point we randomly choose one of the
    8 voxels sur- rounding a point. The probability of choosing a
    particular voxel is based on how close the point is to the centre of
    that voxel.- LINEAR: Linear interpolation of the vector field
    containing the principal directions at each point.
    argument: ``-interpolator %s``
stepsize: (a float)
    Step size for EULER and RK4 tracking. The default is 1mm.
    argument: ``-stepsize %f``
    requires: tracker
inputdatatype: ('float' or 'double')
    input file type
    argument: ``-inputdatatype %s``
gzip: (a boolean)
    save the output image in gzip format
    argument: ``-gzip``
maxcomponents: (an integer (int or long))
    The maximum number of tensor components in a voxel. This determines
    the size of the input file and does not say anything about the voxel

```

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```

classification. The default is 2 if the input model is multitensor
and 1 if the input model is dt.
argument: ``-maxcomponents %d``
numpds: (an integer (int or long))
The maximum number of PDs in a voxel for input models sfpeak and
pico. The default is 3 for input model sfpeak and 1 for input model
pico. This option determines the size of the voxels in the input
file and does not affect tracking. For tensor data, use the
-maxcomponents option.
argument: ``-numpds %d``
data_dims: (a list of from 3 to 3 items which are an integer (int or
long))
data dimensions in voxels
argument: ``-datadims %s``
voxel_dims: (a list of from 3 to 3 items which are a float)
voxel dimensions in mm
argument: ``-voxeldims %s``
ipthresh: (a float)
Curvature threshold for tracking, expressed as the minimum dot
product between two streamline orientations calculated over the
length of a voxel. If the dot product between the previous and
current directions is less than this threshold, then the streamline
terminates. The default setting will terminate fibres that curve by
more than 80 degrees. Set this to -1.0 to disable curvature checking
completely.
argument: ``-ipthresh %f``
curvethresh: (a float)
Curvature threshold for tracking, expressed as the maximum angle (in
degrees) between between two streamline orientations calculated over
the length of a voxel. If the angle is greater than this, then the
streamline terminates.
argument: ``-curvethresh %f``
curveinterval: (a float)
Interval over which the curvature threshold should be evaluated, in
mm. The default is 5mm. When using the default curvature threshold
of 90 degrees, this means that streamlines will terminate if they
curve by more than 90 degrees over a path length of 5mm.
argument: ``-curveinterval %f``
requires: curvethresh
anisthresh: (a float)
Terminate fibres that enter a voxel with lower anisotropy than the
threshold.
argument: ``-anisthresh %f``
anisfile: (a pathlike object or string representing an existing file)
File containing the anisotropy map. This is required to apply an
anisotropy threshold with non tensor data. If the map issupplied it
is always used, even in tensor data.
argument: ``-anisfile %s``
outputtracts: ('float' or 'double' or 'oogl')
output tract file type
argument: ``-outputtracts %s``
out_file: (a pathlike object or string representing a file)
output data file
argument: ``-outputfile %s``, position: -1
output_root: (a pathlike object or string representing a file)
root directory for output
argument: ``-outputroot %s``, position: -1

```

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```
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
tracked: (a pathlike object or string representing an existing file)
    output file containing reconstructed tracts
```

55.4.14 TrackBedpostxProba[Link to code](#)

Wraps the executable command `track`.

Data from FSL's bedpostx can be imported into Camino for probabilistic tracking. (Use `TrackBedpostxDeter` for bedpostx deterministic tractography.)

The tracking uses the files `merged_th1samples.nii.gz`, `merged_ph1samples.nii.gz`, ..., `merged_thNsamples.nii.gz`, `merged_phNsamples.nii.gz` where there are a maximum of `N` compartments (corresponding to each fiber population) in each voxel. These images contain `M` samples of theta and phi, the polar coordinates describing the “stick” for each compartment. At each iteration, a random number `X` between 1 and `M` is drawn and the `X`th samples of theta and phi become the principal directions in the voxel.

It also uses the `N` images `mean_f1samples.nii.gz`, ..., `mean_fNsamples.nii.gz`, normalized such that the sum of all compartments is 1. Compartments where the `mean_f` is less than a threshold are discarded and not used for tracking. The default value is 0.01. This can be changed with the `min_vol_frac` option.

Example

```
>>> import nipy.interfaces.camino as cam
>>> track = cam.TrackBedpostxProba()
>>> track.inputs.bedpostxdir = 'bedpostxout'
>>> track.inputs.seed_file = 'seed_mask.nii'
>>> track.inputs.iterations = 100
>>> track.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
bedpostxdir: (a pathlike object or string representing an existing
    directory)
    Directory containing bedpostx output
    argument: ``-bedpostxdir %s``

[Optional]
min_vol_frac: (a float)
    Zeros out compartments in bedpostx data with a mean volume fraction
    f of less than min_vol_frac. The default is 0.01.
    argument: ``-bedpostxminf %d``
iterations: (an integer (int or long))
    Number of streamlines to generate at each seed point. The default is
    1.
    argument: ``-iterations %d``
in_file: (a pathlike object or string representing an existing file)
```

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```

    input data file
    argument: ``-inputfile %s``, position: 1
seed_file: (a pathlike object or string representing an existing
    file)
    seed file
    argument: ``-seedfile %s``, position: 2
inputmodel: ('dt' or 'multitensor' or 'sfpeak' or 'pico' or
    'repbs_dt' or 'repbs_multitensor' or 'ballstick' or 'wildbs_dt' or
    'bayesdirac' or 'bayesdirac_dt' or 'bedpostx_dyad' or 'bedpostx',
    nipy default value: dt)
    input model type
    argument: ``-inputmodel %s``
tracker: ('fact' or 'euler' or 'rk4', nipy default value: fact)
    The tracking algorithm controls streamlines are generated from the
    data. The choices are: - FACT, which follows the local fibre
    orientation in each voxel. No interpolation is used.- EULER, which
    uses a fixed step size along the local fibre orientation. With
    nearest-neighbour interpolation, this method may be very similar to
    FACT, except that the step size is fixed, whereas FACT steps extend
    to the boundary of the next voxel (distance variable depending on
    the entry and exit points to the voxel).- RK4: Fourth-order Runge-
    Kutta method. The step size is fixed, however the eventual direction
    of the step is determined by taking and averaging a series of
    partial steps.
    argument: ``-tracker %s``
interpolator: ('nn' or 'prob_nn' or 'linear')
    The interpolation algorithm determines how the fiber orientation(s)
    are defined at a given continuous point within the input image.
    Interpolators are only used when the tracking algorithm is not FACT.
    The choices are: - NN: Nearest-neighbour interpolation, just uses
    the local voxel data directly.- PROB_NN: Probabilistic nearest-
    neighbor interpolation, similar to the method pro- posed by Behrens
    et al [Magnetic Resonance in Medicine, 50:1077-1088, 2003]. The data
    is not interpolated, but at each point we randomly choose one of the
    8 voxels sur- rounding a point. The probability of choosing a
    particular voxel is based on how close the point is to the centre of
    that voxel.- LINEAR: Linear interpolation of the vector field
    containing the principal directions at each point.
    argument: ``-interpolator %s``
stepsize: (a float)
    Step size for EULER and RK4 tracking. The default is 1mm.
    argument: ``-stepsize %f``
    requires: tracker
inputdatatype: ('float' or 'double')
    input file type
    argument: ``-inputdatatype %s``
gzip: (a boolean)
    save the output image in gzip format
    argument: ``-gzip``
maxcomponents: (an integer (int or long))
    The maximum number of tensor components in a voxel. This determines
    the size of the input file and does not say anything about the voxel
    classification. The default is 2 if the input model is multitensor
    and 1 if the input model is dt.
    argument: ``-maxcomponents %d``
numpds: (an integer (int or long))
    The maximum number of PDs in a voxel for input models sfpeak and

```

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```

    pico. The default is 3 for input model sfpeak and 1 for input model
    pico. This option determines the size of the voxels in the input
    file and does not affect tracking. For tensor data, use the
    -maxcomponents option.
    argument: ``-numpds %d``
data_dims: (a list of from 3 to 3 items which are an integer (int or
    long))
    data dimensions in voxels
    argument: ``-datadims %s``
voxel_dims: (a list of from 3 to 3 items which are a float)
    voxel dimensions in mm
    argument: ``-voxeldims %s``
ipthresh: (a float)
    Curvature threshold for tracking, expressed as the minimum dot
    product between two streamline orientations calculated over the
    length of a voxel. If the dot product between the previous and
    current directions is less than this threshold, then the streamline
    terminates. The default setting will terminate fibres that curve by
    more than 80 degrees. Set this to -1.0 to disable curvature checking
    completely.
    argument: ``-ipthresh %f``
curvethresh: (a float)
    Curvature threshold for tracking, expressed as the maximum angle (in
    degrees) between between two streamline orientations calculated over
    the length of a voxel. If the angle is greater than this, then the
    streamline terminates.
    argument: ``-curvethresh %f``
curveinterval: (a float)
    Interval over which the curvature threshold should be evaluated, in
    mm. The default is 5mm. When using the default curvature threshold
    of 90 degrees, this means that streamlines will terminate if they
    curve by more than 90 degrees over a path length of 5mm.
    argument: ``-curveinterval %f``
    requires: curvethresh
anisthresh: (a float)
    Terminate fibres that enter a voxel with lower anisotropy than the
    threshold.
    argument: ``-anisthresh %f``
anisfile: (a pathlike object or string representing an existing file)
    File containing the anisotropy map. This is required to apply an
    anisotropy threshold with non tensor data. If the map is supplied it
    is always used, even in tensor data.
    argument: ``-anisfile %s``
outputtracts: ('float' or 'double' or 'oogl')
    output tract file type
    argument: ``-outputtracts %s``
out_file: (a pathlike object or string representing a file)
    output data file
    argument: ``-outputfile %s``, position: -1
output_root: (a pathlike object or string representing a file)
    root directory for output
    argument: ``-outputroot %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a

```

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```
value of class 'str', nipy default value: {}
Environment variables
```

Outputs:

```
tracked: (a pathlike object or string representing an existing file)
output file containing reconstructed tracts
```

55.4.15 TrackBootstrap[Link to code](#)

Wraps the executable command track.

Performs bootstrap streamline tractography using multiple scans of the same subject

Example

```
>>> import nipy.interfaces.camino as cmon
>>> track = cmon.TrackBootstrap()
>>> track.inputs.inputmodel='repbs_dt'
>>> track.inputs.scheme_file = 'bvecs.scheme'
>>> track.inputs.bsdatafiles = ['fitted_data1.Bfloat', 'fitted_data2.Bfloat']
>>> track.inputs.seed_file = 'seed_mask.nii'
>>> track.run()                                # doctest: +SKIP
```

Inputs:

```
[Mandatory]
scheme_file: (a pathlike object or string representing an existing
file)
The scheme file corresponding to the data being processed.
argument: ``-schemefile %s``
bsdatafiles: (a list of items which are a pathlike object or string
representing an existing file)
Specifies files containing raw data for repetition bootstrapping.
Use -inputfile for wild bootstrap data.
argument: ``-bsdatafile %s``

[Optional]
iterations: (an integer (int or long))
Number of streamlines to generate at each seed point.
argument: ``-iterations %d``
inversion: (an integer (int or long))
Tensor reconstruction algorithm for repetition bootstrapping.
Default is 1 (linear reconstruction, single tensor).
argument: ``-inversion %s``
bgmask: (a pathlike object or string representing an existing file)
Provides the name of a file containing a background mask computed
using, for example, FSL's bet2 program. The mask file contains zero
in background voxels and non-zero in foreground.
argument: ``-bgmask %s``
in_file: (a pathlike object or string representing an existing file)
input data file
argument: ``-inputfile %s``, position: 1
seed_file: (a pathlike object or string representing an existing
file)
seed file
```

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```

    argument: ``-seedfile %s``, position: 2
inputmodel: ('dt' or 'multitensor' or 'sfpeak' or 'pico' or
            'repbs_dt' or 'repbs_multitensor' or 'ballstick' or 'wildbs_dt' or
            'bayesdirac' or 'bayesdirac_dt' or 'bedpostx_dyad' or 'bedpostx',
            nipy default value: dt)
    input model type
    argument: ``-inputmodel %s``
tracker: ('fact' or 'euler' or 'rk4', nipy default value: fact)
    The tracking algorithm controls streamlines are generated from the
    data. The choices are: - FACT, which follows the local fibre
    orientation in each voxel. No interpolation is used.- EULER, which
    uses a fixed step size along the local fibre orientation. With
    nearest-neighbour interpolation, this method may be very similar to
    FACT, except that the step size is fixed, whereas FACT steps extend
    to the boundary of the next voxel (distance variable depending on
    the entry and exit points to the voxel).- RK4: Fourth-order Runge-
    Kutta method. The step size is fixed, however the eventual direction
    of the step is determined by taking and averaging a series of
    partial steps.
    argument: ``-tracker %s``
interpolator: ('nn' or 'prob_nn' or 'linear')
    The interpolation algorithm determines how the fiber orientation(s)
    are defined at a given continuous point within the input image.
    Interpolators are only used when the tracking algorithm is not FACT.
    The choices are: - NN: Nearest-neighbour interpolation, just uses
    the local voxel data directly.- PROB_NN: Probabilistic nearest-
    neighbor interpolation, similar to the method pro- posed by Behrens
    et al [Magnetic Resonance in Medicine, 50:1077-1088, 2003]. The data
    is not interpolated, but at each point we randomly choose one of the
    8 voxels sur- rounding a point. The probability of choosing a
    particular voxel is based on how close the point is to the centre of
    that voxel.- LINEAR: Linear interpolation of the vector field
    containing the principal directions at each point.
    argument: ``-interpolator %s``
stepsize: (a float)
    Step size for EULER and RK4 tracking. The default is 1mm.
    argument: ``-stepsize %f``
    requires: tracker
inputdatatype: ('float' or 'double')
    input file type
    argument: ``-inputdatatype %s``
gzip: (a boolean)
    save the output image in gzip format
    argument: ``-gzip``
maxcomponents: (an integer (int or long))
    The maximum number of tensor components in a voxel. This determines
    the size of the input file and does not say anything about the voxel
    classification. The default is 2 if the input model is multitensor
    and 1 if the input model is dt.
    argument: ``-maxcomponents %d``
numpds: (an integer (int or long))
    The maximum number of PDs in a voxel for input models sfpeak and
    pico. The default is 3 for input model sfpeak and 1 for input model
    pico. This option determines the size of the voxels in the input
    file and does not affect tracking. For tensor data, use the
    -maxcomponents option.
    argument: ``-numpds %d``

```

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```

data_dims: (a list of from 3 to 3 items which are an integer (int or
            long))
            data dimensions in voxels
            argument: ``-datadims %s``
voxel_dims: (a list of from 3 to 3 items which are a float)
            voxel dimensions in mm
            argument: ``-voxeldims %s``
ipthresh: (a float)
            Curvature threshold for tracking, expressed as the minimum dot
            product between two streamline orientations calculated over the
            length of a voxel. If the dot product between the previous and
            current directions is less than this threshold, then the streamline
            terminates. The default setting will terminate fibres that curve by
            more than 80 degrees. Set this to -1.0 to disable curvature checking
            completely.
            argument: ``-ipthresh %f``
curvethresh: (a float)
            Curvature threshold for tracking, expressed as the maximum angle (in
            degrees) between between two streamline orientations calculated over
            the length of a voxel. If the angle is greater than this, then the
            streamline terminates.
            argument: ``-curvethresh %f``
curveinterval: (a float)
            Interval over which the curvature threshold should be evaluated, in
            mm. The default is 5mm. When using the default curvature threshold
            of 90 degrees, this means that streamlines will terminate if they
            curve by more than 90 degrees over a path length of 5mm.
            argument: ``-curveinterval %f``
            requires: curvethresh
anisthresh: (a float)
            Terminate fibres that enter a voxel with lower anisotropy than the
            threshold.
            argument: ``-anisthresh %f``
anisfile: (a pathlike object or string representing an existing file)
            File containing the anisotropy map. This is required to apply an
            anisotropy threshold with non tensor data. If the map issupplied it
            is always used, even in tensor data.
            argument: ``-anisfile %s``
outputtracts: ('float' or 'double' or 'oogl')
            output tract file type
            argument: ``-outputtracts %s``
out_file: (a pathlike object or string representing a file)
            output data file
            argument: ``-outputfile %s``, position: -1
output_root: (a pathlike object or string representing a file)
            root directory for output
            argument: ``-outputroot %s``, position: -1
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
            of class 'str' and with values which are a bytes or None or a
            value of class 'str', nipy default value: {})
            Environment variables

```

Outputs:

```
tracked: (a pathlike object or string representing an existing file)
         output file containing reconstructed tracts
```

55.4.16 TrackDT

[Link to code](#)

Wraps the executable command track.

Performs streamline tractography using tensor data

Example

```
>>> import nipy.interfaces.camino as cmon
>>> track = cmon.TrackDT()
>>> track.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> track.inputs.seed_file = 'seed_mask.nii'
>>> track.run() # doctest: +SKIP
```

Inputs:

```
[Optional]
in_file: (a pathlike object or string representing an existing file)
         input data file
         argument: ``-inputfile %s``, position: 1
seed_file: (a pathlike object or string representing an existing
            file)
            seed file
            argument: ``-seedfile %s``, position: 2
inputmodel: ('dt' or 'multitensor' or 'sfpeak' or 'pico' or
             'repbs_dt' or 'repbs_multitensor' or 'ballstick' or 'wildbs_dt' or
             'bayesdirac' or 'bayesdirac_dt' or 'bedpostx_dyad' or 'bedpostx',
             nipy default value: dt)
            input model type
            argument: ``-inputmodel %s``
tracker: ('fact' or 'euler' or 'rk4', nipy default value: fact)
         The tracking algorithm controls streamlines are generated from the
         data. The choices are: - FACT, which follows the local fibre
         orientation in each voxel. No interpolation is used.- EULER, which
         uses a fixed step size along the local fibre orientation. With
         nearest-neighbour interpolation, this method may be very similar to
         FACT, except that the step size is fixed, whereas FACT steps extend
         to the boundary of the next voxel (distance variable depending on
         the entry and exit points to the voxel).- RK4: Fourth-order Runge-
         Kutta method. The step size is fixed, however the eventual direction
         of the step is determined by taking and averaging a series of
         partial steps.
         argument: ``-tracker %s``
interpolator: ('nn' or 'prob_nn' or 'linear')
              The interpolation algorithm determines how the fiber orientation(s)
              are defined at a given continuous point within the input image.
              Interpolators are only used when the tracking algorithm is not FACT.
              The choices are: - NN: Nearest-neighbour interpolation, just uses
              the local voxel data directly.- PROB_NN: Probabilistic nearest-
              neighbor interpolation, similar to the method pro- posed by Behrens
              et al [Magnetic Resonance in Medicine, 50:1077-1088, 2003]. The data
              is not interpolated, but at each point we randomly choose one of the
              8 voxels sur- rounding a point. The probability of choosing a
```

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```

particular voxel is based on how close the point is to the centre of
that voxel.- LINEAR: Linear interpolation of the vector field
containing the principal directions at each point.
argument: ``-interpolator %s``
stepsize: (a float)
    Step size for EULER and RK4 tracking. The default is 1mm.
    argument: ``-stepsize %f``
    requires: tracker
inputdatatype: ('float' or 'double')
    input file type
    argument: ``-inputdatatype %s``
gzip: (a boolean)
    save the output image in gzip format
    argument: ``-gzip``
maxcomponents: (an integer (int or long))
    The maximum number of tensor components in a voxel. This determines
    the size of the input file and does not say anything about the voxel
    classification. The default is 2 if the input model is multitensor
    and 1 if the input model is dt.
    argument: ``-maxcomponents %d``
numpds: (an integer (int or long))
    The maximum number of PDs in a voxel for input models sfpeak and
    pico. The default is 3 for input model sfpeak and 1 for input model
    pico. This option determines the size of the voxels in the input
    file and does not affect tracking. For tensor data, use the
    -maxcomponents option.
    argument: ``-numpds %d``
data_dims: (a list of from 3 to 3 items which are an integer (int or
    long))
    data dimensions in voxels
    argument: ``-datadims %s``
voxel_dims: (a list of from 3 to 3 items which are a float)
    voxel dimensions in mm
    argument: ``-voxeldims %s``
ipthresh: (a float)
    Curvature threshold for tracking, expressed as the minimum dot
    product between two streamline orientations calculated over the
    length of a voxel. If the dot product between the previous and
    current directions is less than this threshold, then the streamline
    terminates. The default setting will terminate fibres that curve by
    more than 80 degrees. Set this to -1.0 to disable curvature checking
    completely.
    argument: ``-ipthresh %f``
curvethresh: (a float)
    Curvature threshold for tracking, expressed as the maximum angle (in
    degrees) between between two streamline orientations calculated over
    the length of a voxel. If the angle is greater than this, then the
    streamline terminates.
    argument: ``-curvethresh %f``
curveinterval: (a float)
    Interval over which the curvature threshold should be evaluated, in
    mm. The default is 5mm. When using the default curvature threshold
    of 90 degrees, this means that streamlines will terminate if they
    curve by more than 90 degrees over a path length of 5mm.
    argument: ``-curveinterval %f``
    requires: curvethresh
anisthresh: (a float)

```

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```

        Terminate fibres that enter a voxel with lower anisotropy than the
        threshold.
        argument: ``-anisthresh %f``
anisfile: (a pathlike object or string representing an existing file)
        File containing the anisotropy map. This is required to apply an
        anisotropy threshold with non tensor data. If the map is supplied it
        is always used, even in tensor data.
        argument: ``-anisfile %s``
outputtracts: ('float' or 'double' or 'oogl')
        output tract file type
        argument: ``-outputtracts %s``
out_file: (a pathlike object or string representing a file)
        output data file
        argument: ``-outputfile %s``, position: -1
output_root: (a pathlike object or string representing a file)
        root directory for output
        argument: ``-outputroot %s``, position: -1
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

tracked: (a pathlike object or string representing an existing file)
        output file containing reconstructed tracts

```

55.4.17 TrackPICO[Link to code](#)

Wraps the executable command track.

Performs streamline tractography using the Probabilistic Index of Connectivity (PICO) algorithm

Example

```

>>> import nipy.interfaces.camino as cmon
>>> track = cmon.TrackPICO()
>>> track.inputs.in_file = 'pdfs.Bfloat'
>>> track.inputs.seed_file = 'seed_mask.nii'
>>> track.run() # doctest: +SKIP

```

Inputs:

```

[Optional]
pdf: ('bingham' or 'watson' or 'acg')
        Specifies the model for PICO parameters. The default is "bingham.
        argument: ``-pdf %s``
iterations: (an integer (int or long))
        Number of streamlines to generate at each seed point. The default is
        5000.
        argument: ``-iterations %d``
in_file: (a pathlike object or string representing an existing file)
        input data file

```

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```

    argument: ``-inputfile %s``, position: 1
seed_file: (a pathlike object or string representing an existing
    file)
    seed file
    argument: ``-seedfile %s``, position: 2
inputmodel: ('dt' or 'multitensor' or 'sfpeak' or 'pico' or
    'repbs_dt' or 'repbs_multitensor' or 'ballstick' or 'wildbs_dt' or
    'bayesdirac' or 'bayesdirac_dt' or 'bedpostx_dyad' or 'bedpostx',
    nipy default value: dt)
    input model type
    argument: ``-inputmodel %s``
tracker: ('fact' or 'euler' or 'rk4', nipy default value: fact)
    The tracking algorithm controls streamlines are generated from the
    data. The choices are: - FACT, which follows the local fibre
    orientation in each voxel. No interpolation is used.- EULER, which
    uses a fixed step size along the local fibre orientation. With
    nearest-neighbour interpolation, this method may be very similar to
    FACT, except that the step size is fixed, whereas FACT steps extend
    to the boundary of the next voxel (distance variable depending on
    the entry and exit points to the voxel).- RK4: Fourth-order Runge-
    Kutta method. The step size is fixed, however the eventual direction
    of the step is determined by taking and averaging a series of
    partial steps.
    argument: ``-tracker %s``
interpolator: ('nn' or 'prob_nn' or 'linear')
    The interpolation algorithm determines how the fiber orientation(s)
    are defined at a given continuous point within the input image.
    Interpolators are only used when the tracking algorithm is not FACT.
    The choices are: - NN: Nearest-neighbour interpolation, just uses
    the local voxel data directly.- PROB_NN: Probabilistic nearest-
    neighbor interpolation, similar to the method pro- posed by Behrens
    et al [Magnetic Resonance in Medicine, 50:1077-1088, 2003]. The data
    is not interpolated, but at each point we randomly choose one of the
    8 voxels sur- rounding a point. The probability of choosing a
    particular voxel is based on how close the point is to the centre of
    that voxel.- LINEAR: Linear interpolation of the vector field
    containing the principal directions at each point.
    argument: ``-interpolator %s``
stepsize: (a float)
    Step size for EULER and RK4 tracking. The default is 1mm.
    argument: ``-stepsize %f``
    requires: tracker
inputdatatype: ('float' or 'double')
    input file type
    argument: ``-inputdatatype %s``
gzip: (a boolean)
    save the output image in gzip format
    argument: ``-gzip``
maxcomponents: (an integer (int or long))
    The maximum number of tensor components in a voxel. This determines
    the size of the input file and does not say anything about the voxel
    classification. The default is 2 if the input model is multitensor
    and 1 if the input model is dt.
    argument: ``-maxcomponents %d``
numpds: (an integer (int or long))
    The maximum number of PDs in a voxel for input models sfpeak and
    pico. The default is 3 for input model sfpeak and 1 for input model

```

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```

    pico. This option determines the size of the voxels in the input
    file and does not affect tracking. For tensor data, use the
    -maxcomponents option.
    argument: ``-numpds %d``
data_dims: (a list of from 3 to 3 items which are an integer (int or
    long))
    data dimensions in voxels
    argument: ``-datadims %s``
voxel_dims: (a list of from 3 to 3 items which are a float)
    voxel dimensions in mm
    argument: ``-voxeldims %s``
ipthresh: (a float)
    Curvature threshold for tracking, expressed as the minimum dot
    product between two streamline orientations calculated over the
    length of a voxel. If the dot product between the previous and
    current directions is less than this threshold, then the streamline
    terminates. The default setting will terminate fibres that curve by
    more than 80 degrees. Set this to -1.0 to disable curvature checking
    completely.
    argument: ``-ipthresh %f``
curvethresh: (a float)
    Curvature threshold for tracking, expressed as the maximum angle (in
    degrees) between two streamline orientations calculated over
    the length of a voxel. If the angle is greater than this, then the
    streamline terminates.
    argument: ``-curvethresh %f``
curveinterval: (a float)
    Interval over which the curvature threshold should be evaluated, in
    mm. The default is 5mm. When using the default curvature threshold
    of 90 degrees, this means that streamlines will terminate if they
    curve by more than 90 degrees over a path length of 5mm.
    argument: ``-curveinterval %f``
    requires: curvethresh
anisthresh: (a float)
    Terminate fibres that enter a voxel with lower anisotropy than the
    threshold.
    argument: ``-anisthresh %f``
anisfile: (a pathlike object or string representing an existing file)
    File containing the anisotropy map. This is required to apply an
    anisotropy threshold with non tensor data. If the map issupplied it
    is always used, even in tensor data.
    argument: ``-anisfile %s``
outputtracts: ('float' or 'double' or 'oogl')
    output tract file type
    argument: ``-outputtracts %s``
out_file: (a pathlike object or string representing a file)
    output data file
    argument: ``-outputfile %s``, position: -1
output_root: (a pathlike object or string representing a file)
    root directory for output
    argument: ``-outputroot %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})

```

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Environment variables

Outputs:

```
tracked: (a pathlike object or string representing an existing file)
         output file containing reconstructed tracts
```

55.5 interfaces.camino.odd

55.5.1 LinRecon

[Link to code](#)

Wraps the executable command `linrecon`.

Runs a linear transformation in each voxel.

Reads a linear transformation from the matrix file assuming the imaging scheme specified in the scheme file. Performs the linear transformation on the data in every voxel and outputs the result to the standard output. The output in every voxel is actually:

```
[exit code, ln(S(0)), p1, ..., pR]
```

where p_1, \dots, p_R are the parameters of the reconstruction. Possible exit codes are:

- 0. No problems.
- 6. Bad data replaced by substitution of zero.

The matrix must be R by $N+M$ where $N+M$ is the number of measurements and R is the number of parameters of the reconstruction. The matrix file contains binary double-precision floats. The matrix elements are stored row by row.

Example

First run `QBallMX` and create a linear transform matrix using Spherical Harmonics (`sh`).

```
>>> import nipy.interfaces.camino as cam
>>> qballmx = cam.QBallMX()
>>> qballmx.inputs.scheme_file = 'A.scheme'
>>> qballmx.inputs.basistype = 'sh'
>>> qballmx.inputs.order = 4
>>> qballmx.run() # doctest: +SKIP
```

Then run it over each voxel using `LinRecon`

```
>>> qballcoeffs = cam.LinRecon()
>>> qballcoeffs.inputs.in_file = 'SubjectA.Bfloat'
>>> qballcoeffs.inputs.scheme_file = 'A.scheme'
>>> qballcoeffs.inputs.qball_mat = 'A_qmat.Bdouble'
>>> qballcoeffs.inputs.normalize = True
>>> qballcoeffs.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         voxel-order data filename
         argument: ``%s``, position: 1
scheme_file: (a pathlike object or string representing an existing
             file)
             Specifies the scheme file for the diffusion MRI data
```

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```

        argument: ``%s``, position: 2
qball_mat: (a pathlike object or string representing an existing
            file)
            Linear transformation matrix.
            argument: ``%s``, position: 3

[Optional]
normalize: (a boolean)
            Normalize the measurements and discard the zero measurements before
            the linear transform.
            argument: ``-normalize``
log: (a boolean)
            Transform the log measurements rather than the measurements
            themselves
            argument: ``-log``
bgmask: (a pathlike object or string representing an existing file)
            background mask
            argument: ``-bgmask %s``
out_file: (a pathlike object or string representing a file)
            argument: ``> %s``, position: -1
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
            of class 'str' and with values which are a bytes or None or a
            value of class 'str', nipy default value: {})
            Environment variables

```

Outputs:

```

recon_data: (a pathlike object or string representing an existing
            file)
            Transformed data

```

55.5.2 MESD[Link to code](#)

Wraps the executable command `mesd`.

MESD is a general program for maximum entropy spherical deconvolution. It also runs PASMRI, which is a special case of spherical deconvolution. The input data must be in voxel order.

The format of the output in each voxel is: { exitcode, $\ln(A^{\star}(0))$, λ_0 , λ_1 , ..., λ_N }

The exitcode contains the results of three tests. The first test thresholds the maximum relative error between the numerical integrals computed at convergence and those computed using a larger test point set; if the error is greater than a threshold the exitcode is increased from zero to one as a warning; if it is greater than a larger threshold the exitcode is increased to two to suggest failure. The second test thresholds the predicted error in numerical integrals computed using the test point set; if the predicted error is greater than a threshold the exitcode is increased by 10. The third test thresholds the RMS error between the measurements and their predictions from the fitted deconvolution; if the errors are greater than a threshold, the exit code is increased by 100. An exitcode of 112 means that all three tests were failed and the result is likely to be unreliable. If all is well the exitcode is zero. Results are often still reliable even if one or two of the tests are failed.

Other possible exitcodes are:

- 5 - The optimization failed to converge
- -1 - Background
- -100 - Something wrong in the MRI data, e.g. negative or zero measurements, so that the optimization could not run.

The standard MESD implementation is computationally demanding, particularly as the number of measurements

increases (computation is approximately $O(N^2)$, where N is the number of measurements). There are two ways to obtain significant computational speed-up:

i) Turn off error checks and use a small point set for computing numerical integrals in the algorithm by adding the flag `-fastmesd`. Sakaie CDMRI 2008 shows that using the smallest point set (`-basepointset 0`) with no error checks usually has only a minor effect on the output of the algorithm, but provides a major reduction in computation time. You can increase the point set size using `-basepointset` with an argument higher than 0, which may produce better results in some voxels, but will increase computation time, which approximately doubles every time the point set index increases by 1.

ii) Reduce the complexity of the maximum entropy encoding using `-mepointset <X>`. By default $\langle X \rangle = N$, the number of measurements, and is the number of parameters in the max. ent. representation of the output function, ie the number of lambda parameters, as described in Jansons and Alexander Inverse Problems 2003. However, we can represent the function using less components and $\langle X \rangle$ here specifies the number of lambda parameters. To obtain speed-up, set $\langle X \rangle < N$; complexity become $O(\langle X \rangle^2)$ rather than $O(N^2)$. Note that $\langle X \rangle$ must be chosen so that the `camino/PointSets` directory contains a point set with that number of elements. When `-mepointset` decreases, the numerical integration checks make less and less of a difference and smaller point sets for numerical integration (see `-basepointset`) become adequate. So when $\langle X \rangle$ is low `-fastmesd` is worth using to get even more speed-up.

The choice of $\langle X \rangle$ is a parameter of the technique. Too low and you lose angular resolution; too high and you see no computational benefit and may even suffer from overfitting. Empirically, we have found that $\langle X \rangle = 16$ often gives good results and good speed up, but it is worth trying a few values a comparing performance. The reduced encoding is described in the following ISMRM abstract: Sweet and Alexander “Reduced Encoding Persistent Angular Structure” 572 ISMRM 2010.

Example

Run MESD on every voxel of the data file `SubjectA.Bfloat` using the PASMRI kernel.

```
>>> import nipy.interfaces.camino as cam
>>> mesd = cam.MESD()
>>> mesd.inputs.in_file = 'SubjectA.Bfloat'
>>> mesd.inputs.scheme_file = 'A.scheme'
>>> mesd.inputs.inverter = 'PAS'
>>> mesd.inputs.inverter_param = 1.4
>>> mesd.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         voxel-order data filename
         argument: ``-inputfile %s``, position: 1
inverter: ('SPIKE' or 'PAS')
         The inversion index specifies the type of inversion to perform on
         the data. The currently available choices are: Inverter name |
         Inverter parameters-----|-----SPIKE | bd
         (b-value x diffusivity along the fibre.) PAS | r
         argument: ``-filter %s``, position: 2
inverter_param: (a float)
         Parameter associated with the inverter. Cf. inverter description
         for more information.
         argument: ``%f``, position: 3
scheme_file: (a pathlike object or string representing an existing
             file)
             Specifies the scheme file for the diffusion MRI data
             argument: ``-scheme file %s``

[Optional]
```

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```

fastmesd: (a boolean)
    Turns off numerical integration checks and fixes the integration
    point set size at that of the index specified by -basepointset..
    argument: ``-fastmesd``
    requires: mepointset
mepointset: (an integer (int or long))
    Use a set of directions other than those in the scheme file for the
    deconvolution kernel. The number refers to the number of directions
    on the unit sphere. For example, "-mepointset 54" uses the
    directions in "camino/PointSets/Elec054.txt".
    argument: ``-mepointset %d``
bgmask: (a pathlike object or string representing an existing file)
    background mask
    argument: ``-bgmask %s``
inputdatatype: ('float' or 'char' or 'short' or 'int' or 'long' or
    'double')
    Specifies the data type of the input file: "char", "short", "int",
    "long", "float" or "double". The input file must have BIG-ENDIAN
    ordering. By default, the input type is "float".
    argument: ``-inputdatatype %s``
out_file: (a pathlike object or string representing a file)
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables

```

Outputs:

```

mesd_data: (a pathlike object or string representing an existing
    file)
    MESD data

```

55.5.3 QBallMX

[Link to code](#)

Wraps the executable command qballmx.

Generates a reconstruction matrix for Q-Ball. Used in LinRecon with the same scheme file to reconstruct data.

Example 1

To create a linear transform matrix using Spherical Harmonics (sh).

```

>>> import nipyne.interfaces.camino as cam
>>> qballmx = cam.QBallMX()
>>> qballmx.inputs.scheme_file = 'A.scheme'
>>> qballmx.inputs.basistype = 'sh'
>>> qballmx.inputs.order = 6
>>> qballmx.run() # doctest: +SKIP

```

Example 2

To create a linear transform matrix using Radial Basis Functions (rbf). This command uses the default setting of rbf sigma = 0.2618 (15 degrees), data smoothing sigma = 0.1309 (7.5 degrees), rbf pointset 246

```
>>> import nipy.interfaces.camino as cam
>>> qballmx = cam.QBallMX()
>>> qballmx.inputs.scheme_file = 'A.scheme'
>>> qballmx.run() # doctest: +SKIP
```

The linear transform matrix from any of these two examples can then be run over each voxel using LinRecon

```
>>> qballcoeffs = cam.LinRecon()
>>> qballcoeffs.inputs.in_file = 'SubjectA.Bfloat'
>>> qballcoeffs.inputs.scheme_file = 'A.scheme'
>>> qballcoeffs.inputs.qball_mat = 'A_qmat.Bdouble'
>>> qballcoeffs.inputs.normalize = True
>>> qballcoeffs.inputs.bgmask = 'brain_mask.nii'
>>> qballcoeffs.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
scheme_file: (a pathlike object or string representing an existing
             file)
             Specifies the scheme file for the diffusion MRI data
             argument: ``-schemefile %s``

[Optional]
basistype: ('rbf' or 'sh', nipy default value: rbf)
           Basis function type. "rbf" to use radial basis functions "sh" to use
           spherical harmonics
           argument: ``-basistype %s``
order: (an integer (int or long))
        Specific to sh. Maximum order of the spherical harmonic series.
        Default is 4.
        argument: ``-order %d``
rbfpointset: (an integer (int or long))
             Specific to rbf. Sets the number of radial basis functions to use.
             The value specified must be present in the Pointsets directory. The
             default value is 246.
             argument: ``-rbfpointset %d``
rbfsigma: (a float)
           Specific to rbf. Sets the width of the interpolating basis
           functions. The default value is 0.2618 (15 degrees).
           argument: ``-rbfsigma %f``
smoothing_sigma: (a float)
                 Specific to rbf. Sets the width of the smoothing basis functions.
                 The default value is 0.1309 (7.5 degrees).
                 argument: ``-smoothing_sigma %f``
out_file: (a pathlike object or string representing a file)
           argument: ``> %s``, position: -1
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
qmat: (a pathlike object or string representing an existing file)
       Q-Ball reconstruction matrix
```

55.5.4 SFPeaks

[Link to code](#)

Wraps the executable command `sfpeaks`.

Finds the peaks of spherical functions.

This utility reads coefficients of the spherical functions and outputs a list of peak directions of the function. It computes the value of the function at each of a set of sample points. Then it finds local maxima by finding all points at which the function is larger than for any other point within a fixed search radius (the default is 0.4). The utility then uses Powell's algorithm to optimize the position of each local maximum. Finally the utility removes duplicates and tiny peaks with function value smaller than some threshold, which is the mean of the function plus some number of standard deviations. By default the program checks for consistency with a second set of starting points, but skips the optimization step. To speed up execution, you can turn off the consistency check by setting the `noconsistencycheck` flag to `True`.

By default, the utility constructs a set of sample points by randomly rotating a unit icosahedron repeatedly (the default is 1000 times, which produces a set of 6000 points) and concatenating the lists of vertices. The `'pointset = <index>'` attribute can tell the utility to use an evenly distributed set of points (index 0 gives 1082 points, 1 gives 1922, 2 gives 4322, 3 gives 8672, 4 gives 15872, 5 gives 32762, 6 gives 72032), which is quicker, because you can get away with fewer points. We estimate that you can use a factor of 2.5 less evenly distributed points than randomly distributed points and still expect similar performance levels.

The output for each voxel is:

- `exitcode` (inherited from the input data).
- `ln(A(0))`
- number of peaks found.
- flag for consistency with a repeated run (number of directions is the same and the directions are the same to within a threshold.)
- `mean(f)`.
- `std(f)`.
- direction 1 (`x, y, z, f, H00, H01, H10, H11`).
- direction 2 (`x, y, z, f, H00, H01, H10, H11`).
- direction 3 (`x, y, z, f, H00, H01, H10, H11`).

`H` is the Hessian of `f` at the peak. It is the matrix:

```
[d^2f/ds^2 d^2f/dsdt]
[d^2f/dtds d^2f/dt^2]
= [H00 H01]
  [H10 H11]
```

where `s` and `t` are orthogonal coordinates local to the peak.

By default the maximum number of peak directions output in each voxel is three. If less than three directions are found, zeros are output for later directions. The peaks are ordered by the value of the function at the peak. If more than the maximum number of directions are found only the strongest ones are output. The maximum number can be changed setting the `'numpds'` attribute.

The utility can read various kinds of spherical function, but must be told what kind of function is input using the `'inputmodel'` attribute. The description of the `'inputmodel'` attribute lists additional information required by SFPeaks for each input model.

Example

First run QBallMX and create a linear transform matrix using Spherical Harmonics (`sh`).

```
>>> import nipy.interfaces.camino as cam
>>> sf_peaks = cam.SFPeaks()
>>> sf_peaks.inputs.in_file = 'A_recon_params.Bdouble'
>>> sf_peaks.inputs.inputmodel = 'sh'
>>> sf_peaks.inputs.order = 4
>>> sf_peaks.inputs.density = 100
```

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```
>>> sf_peaks.inputs.searchradius = 1.0
>>> sf_peaks.run()           # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        Voxel-order data of spherical functions
        argument: ``-inputfile %s``
inputmodel: ('sh' or 'maxent' or 'rbf')
        Type of functions input via in_file. Currently supported options
        are: sh - Spherical harmonic series. Specify the maximum order of
        the SH series with the "order" attribute if different from the
        default of 4. maxent - Maximum entropy representations output by
        MESD. The reconstruction directions input to MESD must be specified.
        By default this is the same set of gradient directions (excluding
        zero gradients) in the scheme file, so specify the "schemefile"
        attribute unless the "mepointset" attribute was set in MESD. rbf -
        Sums of radial basis functions. Specify the pointset with the
        attribute "rbfpointset" if different from the default. See QBallMX.
        argument: ``-inputmodel %s``

[Optional]
order: (an integer (int or long))
        Specific to sh. Maximum order of the spherical harmonic series.
        argument: ``-order %d``
scheme_file: (a pathlike object or string representing an existing
             file)
             Specific to maxent. Specifies the scheme file.
             argument: ``%s``
rbfpointset: (an integer (int or long))
             Specific to rbf. Sets the number of radial basis functions to use.
             The value specified must be present in the Pointsets directory. The
             default value is 246.
             argument: ``-rbfpointset %d``
mepointset: (an integer (int or long))
             Use a set of directions other than those in the scheme file for the
             deconvolution kernel. The number refers to the number of directions
             on the unit sphere. For example, "mepointset = 54" uses the
             directions in "camino/PointSets/Elec054.txt" Use this option only if
             you told MESD to use a custom set of directions with the same
             option. Otherwise, specify the scheme file with the "schemefile"
             attribute.
             argument: ``-mepointset %d``
numpds: (an integer (int or long))
             The largest number of peak directions to output in each voxel.
             argument: ``-numpds %d``
noconsistencycheck: (a boolean)
             Turns off the consistency check. The output shows all consistencies
             as true.
             argument: ``-noconsistencycheck``
searchradius: (a float)
             The search radius in the peak finding algorithm. The default is 0.4
             (cf. "density")
             argument: ``-searchradius %f``
density: (an integer (int or long))
             The number of randomly rotated icosahedra to use in constructing the
```

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```

    set of points for random sampling in the peak finding algorithm.
    Default is 1000, which works well for very spiky maxent functions.
    For other types of function, it is reasonable to set the density
    much lower and increase the search radius slightly, which speeds up
    the computation.
    argument: ``-density %d``
pointset: (an integer (int or long))
    To sample using an evenly distributed set of points instead. The
    integer can be 0, 1, ..., 7. Index 0 gives 1082 points, 1 gives
    1922, 2 gives 3002, 3 gives 4322, 4 gives 5882, 5 gives 8672, 6
    gives 12002, 7 gives 15872.
    argument: ``-pointset %d``
pdthresh: (a float)
    Base threshold on the actual peak direction strength divided by the
    mean of the function. The default is 1.0 (the peak must be equal or
    greater than the mean).
    argument: ``-pdthresh %f``
stdsfrommean: (a float)
    This is the number of standard deviations of the function to be
    added to the "pdthresh" attribute in the peak directions pruning.
    argument: ``-stdsfrommean %f``
out_file: (a pathlike object or string representing a file)
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

peaks: (a pathlike object or string representing an existing file)
    Peaks of the spherical functions.

```

55.6 interfaces.camino.utils

55.6.1 ImageStats

[Link to code](#)

Wraps the executable command imagestats.

This program computes voxelwise statistics on a series of 3D images. The images must be in the same space; the operation is performed voxelwise and one output is produced per voxel.

Examples

```

>>> import nipy.interfaces.camino as cam
>>> imstats = cam.ImageStats()
>>> imstats.inputs.in_files = ['im1.nii', 'im2.nii', 'im3.nii']
>>> imstats.inputs.stat = 'max'
>>> imstats.run()                                # doctest: +SKIP

```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
           representing an existing file)
           List of images to process. They must be in the same space and have
           the same dimensions.
           argument: ``-images %s``, position: -1
stat: ('min' or 'max' or 'mean' or 'median' or 'sum' or 'std' or
       'var')
       The statistic to compute.
       argument: ``-stat %s``
output_root: (a pathlike object or string representing a file)
             Filename root prepended onto the names of the output files. The
             extension will be determined from the input.
             argument: ``-outputroot %s``

[Optional]
out_type: ('float' or 'char' or 'short' or 'int' or 'long' or
           'double', nipyte default value: float)
           A Camino data type string, default is "float". Type must be signed.
           argument: ``-outputdatatype %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyte default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          Path of the file computed with the statistic chosen
```


56.1 interfaces.camino2trackvis.convert

56.1.1 Camino2Trackvis

[Link to code](#)

Wraps the executable command `camino_to_trackvis`.

Wraps `camino_to_trackvis` from Camino-Trackvis

Convert files from camino .Bfloat format to trackvis .trk format.

Example

```
>>> import nipy.interfaces.camino2trackvis as cam2trk
>>> c2t = cam2trk.Camino2Trackvis()
>>> c2t.inputs.in_file = 'data.Bfloat'
>>> c2t.inputs.out_file = 'streamlines.trk'
>>> c2t.inputs.min_length = 30
>>> c2t.inputs.data_dims = [128, 104, 64]
>>> c2t.inputs.voxel_dims = [2.0, 2.0, 2.0]
>>> c2t.inputs.voxel_order = 'LAS'
>>> c2t.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    The input .Bfloat (camino) file.
    argument: ``-i %s``, position: 1
data_dims: (a list of from 3 to 3 items which are an integer (int or
    long))
    Three comma-separated integers giving the number of voxels along
    each dimension of the source scans.
    argument: ``-d %s``, position: 4
voxel_dims: (a list of from 3 to 3 items which are a float)
    Three comma-separated numbers giving the size of each voxel in mm.
    argument: ``-x %s``, position: 5
voxel_order: (a pathlike object or string representing a file)
```

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```

    Set the order in which various directions were stored. Specify with
    three letters consisting of one each from the pairs LR, AP, and SI.
    These stand for Left-Right, Anterior-Posterior, and Superior-
    Inferior. Whichever is specified in each position will be the
    direction of increasing order. Read coordinate system from a NIfTI
    file.
    argument: ``--voxel-order %s``, position: 6

[Optional]
out_file: (a pathlike object or string representing a file)
    The filename to which to write the .trk (trackvis) file.
    argument: ``-o %s``, position: 2
min_length: (a float)
    The minimum length of tracts to output
    argument: ``-l %d``, position: 3
nifti_file: (a pathlike object or string representing an existing
    file)
    Read coordinate system from a NIfTI file.
    argument: ``--nifti %s``, position: 7
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

trackvis: (a pathlike object or string representing an existing file)
    The filename to which to write the .trk (trackvis) file.

```

56.1.2 Trackvis2Camino[Link to code](#)

Wraps the executable command trackvis_to_camino.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    The input .trk (trackvis) file.
    argument: ``-i %s``, position: 1

[Optional]
out_file: (a pathlike object or string representing a file)
    The filename to which to write the .Bfloat (camino).
    argument: ``-o %s``, position: 2
append_file: (a pathlike object or string representing an existing
    file)
    A file to which the append the .Bfloat data.
    argument: ``-a %s``, position: 2
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a

```

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```
value of class 'str', nipype default value: {}  
Environment variables
```

Outputs:

```
camino: (a pathlike object or string representing an existing file)  
The filename to which to write the .Bfloat (camino).
```


57.1 interfaces.cmtk.base

57.1.1 CFFBaseInterface

[Link to code](#)

Inputs:

None

Outputs:

None

57.2 interfaces.cmtk.cmtk

57.2.1 CreateMatrix

[Link to code](#)

Performs connectivity mapping and outputs the result as a NetworkX graph and a Matlab matrix

Example

```
>>> import nipy.interfaces.cmtk as cmtk
>>> conmap = cmtk.CreateMatrix()
>>> conmap.roi_file = 'fsLUT_aparc+aseg.nii'
>>> conmap.tract_file = 'fibers.trk'
>>> conmap.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
roi_file: (a pathlike object or string representing an existing file)
          Freesurfer aparc+aseg file
tract_file: (a pathlike object or string representing an existing
            file)
```

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```

    Trackvis tract file
resolution_network_file: (a pathlike object or string representing an
    existing file)
    Parcellation files from Connectome Mapping Toolkit

[Optional]
count_region_intersections: (a boolean, nipy default value: False)
    Counts all of the fiber-region traversals in the connectivity matrix
    (requires significantly more computational time)
out_matrix_file: (a pathlike object or string representing a file)
    NetworkX graph describing the connectivity
out_matrix_mat_file: (a pathlike object or string representing a
    file, nipy default value: cmatrix.mat)
    Matlab matrix describing the connectivity
out_mean_fiber_length_matrix_mat_file: (a pathlike object or string
    representing a file)
    Matlab matrix describing the mean fiber lengths between each node.
out_median_fiber_length_matrix_mat_file: (a pathlike object or string
    representing a file)
    Matlab matrix describing the mean fiber lengths between each node.
out_fiber_length_std_matrix_mat_file: (a pathlike object or string
    representing a file)
    Matlab matrix describing the deviation in fiber lengths connecting
    each node.
out_intersection_matrix_mat_file: (a pathlike object or string
    representing a file)
    Matlab connectivity matrix if all region/fiber intersections are
    counted.
out_endpoint_array_name: (a pathlike object or string representing a
    file)
    Name for the generated endpoint arrays

```

Outputs:

```

matrix_file: (a pathlike object or string representing an existing
    file)
    NetworkX graph describing the connectivity
intersection_matrix_file: (a pathlike object or string representing
    an existing file)
    NetworkX graph describing the connectivity
matrix_files: (a list of items which are a pathlike object or string
    representing an existing file)
matlab_matrix_files: (a list of items which are a pathlike object or
    string representing an existing file)
matrix_mat_file: (a pathlike object or string representing an
    existing file)
    Matlab matrix describing the connectivity
intersection_matrix_mat_file: (a pathlike object or string
    representing an existing file)
    Matlab matrix describing the mean fiber lengths between each node.
mean_fiber_length_matrix_mat_file: (a pathlike object or string
    representing an existing file)
    Matlab matrix describing the mean fiber lengths between each node.
median_fiber_length_matrix_mat_file: (a pathlike object or string
    representing an existing file)
    Matlab matrix describing the median fiber lengths between each node.
fiber_length_std_matrix_mat_file: (a pathlike object or string

```

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```

        representing an existing file)
        Matlab matrix describing the deviation in fiber lengths connecting
        each node.
    endpoint_file: (a pathlike object or string representing an existing
        file)
        Saved Numpy array with the endpoints of each fiber
    endpoint_file_mm: (a pathlike object or string representing an
        existing file)
        Saved Numpy array with the endpoints of each fiber (in millimeters)
    fiber_length_file: (a pathlike object or string representing an
        existing file)
        Saved Numpy array with the lengths of each fiber
    fiber_label_file: (a pathlike object or string representing an
        existing file)
        Saved Numpy array with the labels for each fiber
    fiber_labels_noorphans: (a pathlike object or string representing an
        existing file)
        Saved Numpy array with the labels for each non-orphan fiber
    filtered_tractography: (a pathlike object or string representing an
        existing file)
        TrackVis file containing only those fibers originate in one and
        terminate in another region
    filtered_tractography_by_intersections: (a pathlike object or string
        representing an existing file)
        TrackVis file containing all fibers which connect two regions
    filtered_tractographies: (a list of items which are a pathlike object
        or string representing an existing file)
    stats_file: (a pathlike object or string representing an existing
        file)
        Saved Matlab .mat file with the number of fibers saved at each stage

```

57.2.2 CreateNodes

[Link to code](#)

Generates a NetworkX graph containing nodes at the centroid of each region in the input ROI file. Node data is added from the resolution network file.

Example

```

>>> import nipyne.interfaces.cmtk as cmtk
>>> mknode = cmtk.CreateNodes()
>>> mknode.inputs.roi_file = 'ROI_scale500.nii.gz'
>>> mknode.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
roi_file: (a pathlike object or string representing an existing file)
        Region of interest file
resolution_network_file: (a pathlike object or string representing an
        existing file)
        Parcellation file from Connectome Mapping Toolkit

[Optional]
out_filename: (a pathlike object or string representing a file,

```

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```
nipy default value: nodenetwork.pck)
Output gpickled network with the nodes defined.
```

Outputs:

```
node_network: (a pathlike object or string representing a file)
Output gpickled network with the nodes defined.
```

57.2.3 ROI**Gen**

[Link to code](#)

Generates a ROI file for connectivity mapping and a dictionary file containing relevant node information

Example

```
>>> import nipy.interfaces.cmtk as cmtk
>>> rg = cmtk.ROIGen()
>>> rg.inputs.aparc_aseg_file = 'aparc+aseg.nii'
>>> rg.inputs.use_freesurfer_LUT = True
>>> rg.inputs.freesurfer_dir = '/usr/local/freesurfer'
>>> rg.run() # doctest: +SKIP
```

The label dictionary is written to disk using Pickle. Resulting data can be loaded using:

```
>>> file = open("FreeSurferColorLUT_adapted_aparc+aseg_out.pck", "r")
>>> file = open("fsLUT_aparc+aseg.pck", "r")
>>> labelDict = pickle.load(file) # doctest: +SKIP
>>> labelDict # doctest: +SKIP
```

Inputs:

```
[Mandatory]
aparc_aseg_file: (a pathlike object or string representing an
existing file)
Freesurfer aparc+aseg file

[Optional]
LUT_file: (a pathlike object or string representing an existing file)
Custom lookup table (cf. FreeSurferColorLUT.txt)
mutually_exclusive: use_freesurfer_LUT
use_freesurfer_LUT: (a boolean)
Boolean value; Set to True to use default Freesurfer LUT, False for
custom LUT
mutually_exclusive: LUT_file
freesurfer_dir: (a pathlike object or string representing a
directory)
Freesurfer main directory
requires: use_freesurfer_LUT
out_roi_file: (a pathlike object or string representing a file)
Region of Interest file for connectivity mapping
out_dict_file: (a pathlike object or string representing a file)
Label dictionary saved in Pickle format
```

Outputs:

```
roi_file: (a pathlike object or string representing a file)
Region of Interest file for connectivity mapping
```

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```
dict_file: (a pathlike object or string representing a file)
           Label dictionary saved in Pickle format
```

57.2.4 `cmat()`

[Link to code](#)

Create the connection matrix for each resolution using fibers and ROIs.

57.2.5 `create_allpoints_cmat()`

[Link to code](#)

Create the intersection arrays for each fiber

57.2.6 `create_endpoints_array()`

[Link to code](#)

Create the endpoints arrays for each fiber Parameters ~~~~~ fib: the fibers data voxelSize: 3-tuple containing the voxel size of the ROI image Returns ~~~~~ (endpoints: matrix of size [#fibers, 2, 3] containing for each fiber the index of its first and last point in the voxelSize volume endpointsmm) : endpoints in milimeter coordinates

57.2.7 `create_nodes()`

[Link to code](#)

57.2.8 `get_connectivity_matrix()`

[Link to code](#)

57.2.9 `get_rois_crossed()`

[Link to code](#)

57.2.10 `length()`

[Link to code](#)

Euclidean length of track line

Parameters

xyz [array-like shape (N,3)] array representing x,y,z of N points in a track

along [bool, optional] If True, return array giving cumulative length along track, otherwise (default) return scalar giving total length.

Returns

L [scalar or array shape (N-1,)] scalar in case of *along* == False, giving total length, array if *along* == True, giving cumulative lengths.

Examples

```

>>> xyz = np.array([[1,1,1],[2,3,4],[0,0,0]])
>>> expected_lens = np.sqrt([1+2**2+3**2, 2**2+3**2+4**2])
>>> length(xyz) == expected_lens.sum()
True
>>> len_along = length(xyz, along=True)
>>> np.allclose(len_along, expected_lens.cumsum())
True
>>> length([])
~
>>> length([[1, 2, 3]])
~
>>> length([], along=True)
array([0])

```

57.2.11 save_fibers()

[Link to code](#)

Stores a new trackvis file fname using only given indices

57.3 interfaces.cmtk.convert

57.3.1 CFFConverter

[Link to code](#)

Creates a Connectome File Format (CFF) file from input networks, surfaces, volumes, tracts, etcetera...

Example

```

>>> import nipy.interfaces.cmtk as cmtk
>>> cvt = cmtk.CFFConverter()
>>> cvt.inputs.title = 'subject 1'
>>> cvt.inputs.gifti_surfaces = ['lh.pial_converted.gii', 'rh.pial_converted.gii']
>>> cvt.inputs.tract_files = ['streamlines.trk']
>>> cvt.inputs.gpickled_networks = ['network0.gpickle']
>>> cvt.run()                                # doctest: +SKIP

```

Inputs:

```

[Optional]
graphml_networks: (a list of items which are a pathlike object or
    string representing an existing file)
    list of graphML networks
gpickled_networks: (a list of items which are a pathlike object or
    string representing an existing file)
    list of gpickled Networkx graphs
gifti_surfaces: (a list of items which are a pathlike object or
    string representing an existing file)
    list of GIFTI surfaces
gifti_labels: (a list of items which are a pathlike object or string
    representing an existing file)
    list of GIFTI labels
nifti_volumes: (a list of items which are a pathlike object or string
    representing an existing file)
    list of NIFTI volumes
tract_files: (a list of items which are a pathlike object or string

```

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```

        representing an existing file)
        list of Trackvis fiber files
timeseries_files: (a list of items which are a pathlike object or
        string representing an existing file)
        list of HDF5 timeseries files
script_files: (a list of items which are a pathlike object or string
        representing an existing file)
        list of script files to include
data_files: (a list of items which are a pathlike object or string
        representing an existing file)
        list of external data files (i.e. Numpy, HD5, XML)
title: (a unicode string)
        Connectome Title
creator: (a unicode string)
        Creator
email: (a unicode string)
        Email address
publisher: (a unicode string)
        Publisher
license: (a unicode string)
        License
rights: (a unicode string)
        Rights
references: (a unicode string)
        References
relation: (a unicode string)
        Relation
species: (a unicode string, nipyype default value: Homo sapiens)
        Species
description: (a unicode string, nipyype default value: Created with
        the Nipyype CFF converter)
        Description
out_file: (a pathlike object or string representing a file, nipyype
        default value: connectome.cff)
        Output connectome file

```

Outputs:

```

connectome_file: (a pathlike object or string representing an
        existing file)
        Output connectome file

```

57.3.2 MergeCNetworks

[Link to code](#)

Merges networks from multiple CFF files into one new CFF file.

Example

```

>>> import nipyype.interfaces.cmtk as cmtk
>>> mrg = cmtk.MergeCNetworks()
>>> mrg.inputs.in_files = ['subj1.cff', 'subj2.cff']
>>> mrg.run()                                # doctest: +SKIP

```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
           representing an existing file)
           List of CFF files to extract networks from

[Optional]
out_file: (a pathlike object or string representing a file, nipyype
           default value: merged_network_connectome.cff)
           Output CFF file with all the networks added
```

Outputs:

```
connectome_file: (a pathlike object or string representing an
                  existing file)
                  Output CFF file with all the networks added
```

57.4 interfaces.cmtk.nbs

57.4.1 NetworkBasedStatistic

[Link to code](#)

Calculates and outputs the average network given a set of input NetworkX gpickle files

For documentation of Network-based statistic parameters:

https://github.com/LTS5/connectomeviewer/blob/master/cviewer/libs/pyconto/groupstatistics/nbs/_nbs.py

Example

```
>>> import nipyype.interfaces.cmtk as cmtk
>>> nbs = cmtk.NetworkBasedStatistic()
>>> nbs.inputs.in_group1 = ['subj1.pck', 'subj2.pck'] # doctest: +SKIP
>>> nbs.inputs.in_group2 = ['pat1.pck', 'pat2.pck'] # doctest: +SKIP
>>> nbs.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_group1: (a list of items which are a pathlike object or string
            representing an existing file)
            Networks for the first group of subjects
in_group2: (a list of items which are a pathlike object or string
            representing an existing file)
            Networks for the second group of subjects

[Optional]
node_position_network: (a pathlike object or string representing a
                        file)
                        An optional network used to position the nodes for the output
                        networks
number_of_permutations: (an integer (int or long), nipyype default
                         value: 1000)
                         Number of permutations to perform
threshold: (a float, nipyype default value: 3)
            T-statistic threshold
t_tail: ('left' or 'right' or 'both', nipyype default value: left)
         Can be one of "left", "right", or "both"
```

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```

edge_key: (a unicode string, nipy default value: number_of_fibers)
    Usually "number_of_fibers", "fiber_length_mean", "fiber_length_std"
    for matrices made with CMTKSometimes "weight" or "value" for
    functional networks.
out_nbs_network: (a pathlike object or string representing a file)
    Output network with edges identified by the NBS
out_nbs_pval_network: (a pathlike object or string representing a
    file)
    Output network with p-values to weight the edges identified by the
    NBS

```

Outputs:

```

nbs_network: (a pathlike object or string representing an existing
    file)
    Output network with edges identified by the NBS
nbs_pval_network: (a pathlike object or string representing an
    existing file)
    Output network with p-values to weight the edges identified by the
    NBS
network_files: (a list of items which are a pathlike object or string
    representing an existing file)
    Output network with edges identified by the NBS

```

57.4.2 ntwks_to_matrices()[Link to code](#)**57.5 interfaces.cmtk.nx****57.5.1 AverageNetworks**[Link to code](#)

Calculates and outputs the average network given a set of input NetworkX gpickle files

This interface will only keep an edge in the averaged network if that edge is present in at least half of the input networks.

Example

```

>>> import nipy.interfaces.cmtk as cmtk
>>> avg = cmtk.AverageNetworks()
>>> avg.inputs.in_files = ['subj1.pck', 'subj2.pck']
>>> avg.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string
    representing an existing file)
    Networks for a group of subjects

[Optional]
resolution_network_file: (a pathlike object or string representing an
    existing file)
    Parcellation files from Connectome Mapping Toolkit. This is not

```

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```

        necessary, but if included, the interface will output the
        statistical maps as networkx graphs.
    group_id: (a unicode string, nipy default value: group1)
        ID for group
    out_gpickled_groupavg: (a pathlike object or string representing a
        file)
        Average network saved as a NetworkX .pck
    out_gexf_groupavg: (a pathlike object or string representing a file)
        Average network saved as a .gexf file

```

Outputs:

```

gpickled_groupavg: (a pathlike object or string representing a file)
    Average network saved as a NetworkX .pck
gexf_groupavg: (a pathlike object or string representing a file)
    Average network saved as a .gexf file
matlab_groupavgs: (a list of items which are a pathlike object or
    string representing a file)

```

57.5.2 NetworkXMetrics[Link to code](#)

Calculates and outputs NetworkX-based measures for an input network

Example

```

>>> import nipy.interfaces.cmtk as cmtk
>>> nxmetrics = cmtk.NetworkXMetrics()
>>> nxmetrics.inputs.in_file = 'subj1.pck'
>>> nxmetrics.run()                                # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Input network

[Optional]
out_k_core: (a pathlike object or string representing a file, nipy
    default value: k_core)
    Computed k-core network stored as a NetworkX pickle.
out_k_shell: (a pathlike object or string representing a file, nipy
    default value: k_shell)
    Computed k-shell network stored as a NetworkX pickle.
out_k_crust: (a pathlike object or string representing a file, nipy
    default value: k_crust)
    Computed k-crust network stored as a NetworkX pickle.
treat_as_weighted_graph: (a boolean, nipy default value: True)
    Some network metrics can be calculated while considering only a
    binarized version of the graph
compute_clique_related_measures: (a boolean, nipy default value:
    False)
    Computing clique-related measures (e.g. node clique number) can be
    very time consuming
out_global_metrics_matlab: (a pathlike object or string representing
    a file)

```

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```

    Output node metrics in MATLAB .mat format
out_node_metrics_matlab: (a pathlike object or string representing a
    file)
    Output node metrics in MATLAB .mat format
out_edge_metrics_matlab: (a pathlike object or string representing a
    file)
    Output edge metrics in MATLAB .mat format
out_pickled_extra_measures: (a pathlike object or string representing
    a file, nipyre default value: extra_measures)
    Network measures for group 1 that return dictionaries stored as a
    Pickle.

```

Outputs:

```

gpickled_network_files: (a list of items which are a pathlike object
    or string representing a file)
matlab_matrix_files: (a list of items which are a pathlike object or
    string representing a file)
global_measures_matlab: (a pathlike object or string representing a
    file)
    Output global metrics in MATLAB .mat format
node_measures_matlab: (a pathlike object or string representing a
    file)
    Output node metrics in MATLAB .mat format
edge_measures_matlab: (a pathlike object or string representing a
    file)
    Output edge metrics in MATLAB .mat format
node_measure_networks: (a list of items which are a pathlike object
    or string representing a file)
edge_measure_networks: (a list of items which are a pathlike object
    or string representing a file)
k_networks: (a list of items which are a pathlike object or string
    representing a file)
k_core: (a pathlike object or string representing a file)
    Computed k-core network stored as a NetworkX pickle.
k_shell: (a pathlike object or string representing a file)
    Computed k-shell network stored as a NetworkX pickle.
k_crust: (a pathlike object or string representing a file)
    Computed k-crust network stored as a NetworkX pickle.
pickled_extra_measures: (a pathlike object or string representing a
    file)
    Network measures for the group that return dictionaries, stored as a
    Pickle.
matlab_dict_measures: (a list of items which are a pathlike object or
    string representing a file)

```

57.5.3 add_dicts_by_key()[Link to code](#)

Combines two dictionaries and adds the values for those keys that are shared

57.5.4 add_edge_data()[Link to code](#)

57.5.5 `add_node_data()`

[Link to code](#)

57.5.6 `average_networks()`

[Link to code](#)

Sums the edges of input networks and divides by the number of networks. Writes the average network as .pck and .gexf and returns the name of the written networks.

57.5.7 `compute_dict_measures()`

[Link to code](#)

Returns a dictionary

57.5.8 `compute_edge_measures()`

[Link to code](#)

These return edge-based measures

57.5.9 `compute_network_measures()`

[Link to code](#)

57.5.10 `compute_node_measures()`

[Link to code](#)

These return node-based measures

57.5.11 `compute_singlevalued_measures()`

[Link to code](#)

Returns a single value per network

57.5.12 `fix_keys_for_gexf()`

[Link to code](#)

GEXF Networks can be read in Gephi, however, the keys for the node and edge IDs must be converted to strings

57.5.13 `read_unknown_ntwk()`

[Link to code](#)

57.5.14 `remove_all_edges()`

[Link to code](#)

57.6 `interfaces.cmtk.parcellation`

57.6.1 `Parcellate`

[Link to code](#)

Subdivides segmented ROI file into smaller subregions

This interface implements the same procedure as in the ConnectomeMapper's parcellation stage (`cmp/stages/parcellation/maskcreation.py`) for a single parcellation scheme (e.g. 'scale500').

Example

```
>>> import nipyne.interfaces.cmtk as cmtk
>>> parcellate = cmtk.Parcellate()
>>> parcellate.inputs.freesurfer_dir = '.'
>>> parcellate.inputs.subjects_dir = '.'
>>> parcellate.inputs.subject_id = 'subj1'
>>> parcellate.inputs.dilation = True
>>> parcellate.inputs.parcellation_name = 'scale500'
>>> parcellate.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
subject_id: (a string)
    Subject ID

[Optional]
parcellation_name: ('scale33' or 'scale60' or 'scale125' or
    'scale250' or 'scale500', nipyne default value: scale500)
freesurfer_dir: (a pathlike object or string representing an existing
    directory)
    Freesurfer main directory
subjects_dir: (a pathlike object or string representing an existing
    directory)
    Freesurfer subjects directory
out_roi_file: (a pathlike object or string representing a file)
    Region of Interest file for connectivity mapping
dilation: (a boolean, nipyne default value: False)
    Dilate cortical parcels? Useful for fMRI connectivity
```

Outputs:

```
roi_file: (a pathlike object or string representing an existing file)
    Region of Interest file for connectivity mapping
roiv_file: (a pathlike object or string representing a file)
    Region of Interest file for fMRI connectivity mapping
white_matter_mask_file: (a pathlike object or string representing an
    existing file)
    White matter mask file
cc_unknown_file: (a pathlike object or string representing an
    existing file)
    Image file with regions labelled as unknown cortical structures
ribbon_file: (a pathlike object or string representing an existing
    file)
    Image file detailing the cortical ribbon
aseg_file: (a pathlike object or string representing an existing
    file)
    Automated segmentation file converted from Freesurfer "subjects"
    directory
roi_file_in_structural_space: (a pathlike object or string
    representing an existing file)
    ROI image resliced to the dimensions of the original structural
    image
dilated_roi_file_in_structural_space: (a pathlike object or string
    representing a file)
    dilated ROI image resliced to the dimensions of the original
    structural image
```

57.6.2 `create_annot_label()`

[Link to code](#)

57.6.3 `create_roi()`

[Link to code](#)

Creates the ROI_%s.nii.gz files using the given parcellation information from networks. Iteratively create volume.

57.6.4 `create_wm_mask()`

[Link to code](#)

57.6.5 `crop_and_move_datasets()`

[Link to code](#)

57.6.6 `extract()`

[Link to code](#)

Extract voxel neighbourhood Parameters ~~~~~ Z: the original data shape: tuple containing neighbourhood dimensions position: tuple containing central point indexes fill: value for the padding of Z Returns ~~~~~ R: the neighbourhood of the specified point in Z

58.1 interfaces.diffusion_toolkit.dti

58.1.1 DTIRecon

[Link to code](#)

Wraps the executable command `dti_recon`.

Use `dti_recon` to generate tensors and other maps

Inputs:

```
[Mandatory]
DWI: (a pathlike object or string representing an existing file)
      Input diffusion volume
      argument: ``%s``, position: 1
bvecs: (a pathlike object or string representing an existing file)
        b vectors file
        argument: ``-gm %s``
bvals: (a pathlike object or string representing an existing file)
        b values file

[Optional]
out_prefix: (a unicode string, nipype default value: dti)
            Output file prefix
            argument: ``%s``, position: 2
output_type: ('nii' or 'analyze' or 'nii.gz', nipype default
              value: nii)
            output file type
            argument: ``-ot %s``
n_averages: (an integer (int or long))
            Number of averages
            argument: ``-nex %s``
image_orientation_vectors: (a list of from 6 to 6 items which are a
                             float)
                             specify image orientation vectors. if just one argument given,
                             will treat it as filename and read the orientation vectors from
                             the file. if 6 arguments are given, will treat them as 6 float
                             numbers and construct the 1st and 2nd vector and calculate the 3rd
```

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```

        one automatically.
        this information will be used to determine image orientation,
        as well as to adjust gradient vectors with oblique angle when
        argument: ``-iop %f``
oblique_correction: (a boolean)
    when oblique angle(s) applied, some SIEMENS dti protocols do not
    adjust gradient accordingly, thus it requires adjustment for
    correct
    diffusion tensor calculation
    argument: ``-oc``
b0_threshold: (a float)
    program will use b0 image with the given threshold to mask out high
    background of fa/adc maps. by default it will calculate threshold
    automatically. but if it failed, you need to set it manually.
    argument: ``-b0_th``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

ADC: (a pathlike object or string representing an existing file)
B0: (a pathlike object or string representing an existing file)
L1: (a pathlike object or string representing an existing file)
L2: (a pathlike object or string representing an existing file)
L3: (a pathlike object or string representing an existing file)
exp: (a pathlike object or string representing an existing file)
FA: (a pathlike object or string representing an existing file)
FA_color: (a pathlike object or string representing an existing file)
tensor: (a pathlike object or string representing an existing file)
V1: (a pathlike object or string representing an existing file)
V2: (a pathlike object or string representing an existing file)
V3: (a pathlike object or string representing an existing file)

```

58.1.2 DTITracker[Link to code](#)Wraps the executable command `dti_tracker`.**Inputs:**

```

[Mandatory]
mask1_file: (a pathlike object or string representing a file)
    first mask image
    argument: ``-m %s``, position: 2

[Optional]
tensor_file: (a pathlike object or string representing an existing
    file)
    reconstructed tensor file
input_type: ('nii' or 'analyze' or 'nii' or 'nii.gz')
    input and output file type. accepted values are:
    analyze -> analyze format 7.5

```

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```

    nil -> nifti format saved in seperate .hdr and .img file
    nii -> nifti format with one .nii file
    nii.gz -> nifti format with compression
    default type is 'nii'
    argument: ``-it %s``
tracking_method: ('fact' or 'rk2' or 'tl' or 'sl')
    fact -> use FACT method for tracking. this is the default method.
    rk2 -> use 2nd order runge-kutta method for tracking.
    tl -> use tensorline method for tracking.
    sl -> use interpolated streamline method with fixed step-length
    argument: ``-s %s``
step_length: (a float)
    set step length, in the unit of minimum voxel size.
    default value is 0.5 for interpolated streamline method
    and 0.1 for other methods
    argument: ``-l %f``
angle_threshold: (a float)
    set angle threshold. default value is 35 degree
    argument: ``-at %f``
angle_threshold_weight: (a float)
    set angle threshold weighting factor. weighting will be be applied
    on top of the angle_threshold
    argument: ``-atw %f``
random_seed: (an integer (int or long))
    use random location in a voxel instead of the center of the voxel to
    seed. can also define number of seed per voxel. default is 1
    argument: ``-rseed %d``
invert_x: (a boolean)
    invert x component of the vector
    argument: ``-ix``
invert_y: (a boolean)
    invert y component of the vector
    argument: ``-iy``
invert_z: (a boolean)
    invert z component of the vector
    argument: ``-iz``
swap_xy: (a boolean)
    swap x & y vectors while tracking
    argument: ``-sxy``
swap_yz: (a boolean)
    swap y & z vectors while tracking
    argument: ``-syz``
swap_zx: (a boolean)
    swap x & z vectors while tracking
    argument: ``-szx``
mask1_threshold: (a float)
    threshold value for the first mask image, if not given, the program
    will try automatically find the threshold
mask2_file: (a pathlike object or string representing a file)
    second mask image
    argument: ``-m2 %s``, position: 4
mask2_threshold: (a float)
    threshold value for the second mask image, if not given, the program
    will try automatically find the threshold
input_data_prefix: (a unicode string, nipy default value: dti)
    for internal naming use only
    argument: ``%s``, position: 0

```

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```

output_file: (a pathlike object or string representing an existing
              file, nipype default value: tracks.trk)
              argument: ``%s``, position: 1
output_mask: (a pathlike object or string representing a file)
              output a binary mask file in analyze format
              argument: ``-om %s``
primary_vector: ('v2' or 'v3')
               which vector to use for fibre tracking: v2 or v3. If not set use v1
               argument: ``-%s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables

```

Outputs:

```

track_file: (a pathlike object or string representing an existing
            file)
mask_file: (a pathlike object or string representing an existing
            file)

```

58.2 interfaces.diffusion_toolkit.odb

58.2.1 HARDIMat

[Link to code](#)

Wraps the executable command hardi_mat.

Use hardi_mat to calculate a reconstruction matrix from a gradient table

Inputs:

```

[Mandatory]
bvecs: (a pathlike object or string representing an existing file)
       b vectors file
       argument: ``%s``, position: 1
bvals: (a pathlike object or string representing an existing file)
       b values file

[Optional]
out_file: (a pathlike object or string representing a file, nipype
          default value: recon_mat.dat)
          output matrix file
          argument: ``%s``, position: 2
order: (an integer (int or long))
       maximum order of spherical harmonics. must be even number. default
       is 4
       argument: ``-order %s``
odf_file: (a pathlike object or string representing an existing file)
          filename that contains the reconstruction points on a HEMI-sphere.
          use the pre-set 181 points by default
          argument: ``-odf %s``
reference_file: (a pathlike object or string representing an existing
               file)

```

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```

provide a dicom or nifti image as the reference for the program to
figure out the image orientation information. if no such info was
found in the given image header, the next 5 options -info, etc.,
will be used if provided. if image orientation info can be found
in the given reference, all other 5 image orientation options will
be IGNORED
argument: ``-ref %s``
image_info: (a pathlike object or string representing an existing
file)
specify image information file. the image info file is generated
from original dicom image by diff_unpack program and contains image
orientation and other information needed for reconstruction and
tracking. by default will look into the image folder for .info file
argument: ``-info %s``
image_orientation_vectors: (a list of from 6 to 6 items which are a
float)
specify image orientation vectors. if just one argument given,
will treat it as filename and read the orientation vectors from
the file. if 6 arguments are given, will treat them as 6 float
numbers and construct the 1st and 2nd vector and calculate the 3rd
one automatically.
this information will be used to determine image orientation,
as well as to adjust gradient vectors with oblique angle when
argument: ``-iop %f``
oblique_correction: (a boolean)
when oblique angle(s) applied, some SIEMENS dti protocols do not
adjust gradient accordingly, thus it requires adjustment for
correct
diffusion tensor calculation
argument: ``-oc``
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipype default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
output matrix file

```

58.2.2 ODFRecon[Link to code](#)Wraps the executable command `odf_recon`.Use `odf_recon` to generate tensors and other maps**Inputs:**

```

[Mandatory]
DWI: (a pathlike object or string representing an existing file)
Input raw data
argument: ``%s``, position: 1
n_directions: (an integer (int or long))
Number of directions

```

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```

    argument: ``%s``, position: 2
n_output_directions: (an integer (int or long))
    Number of output directions
    argument: ``%s``, position: 3
matrix: (a pathlike object or string representing an existing file)
    use given file as reconstruction matrix.
    argument: ``-mat %s``
n_b0: (an integer (int or long))
    number of b0 scans. by default the program gets this information
    from the number of directions and number of volumes in
    the raw data. useful when dealing with incomplete raw
    data set or only using part of raw data set to reconstruct
    argument: ``-b0 %s``

[Optional]
out_prefix: (a unicode string, nipy default value: odf)
    Output file prefix
    argument: ``%s``, position: 4
output_type: ('nii' or 'analyze' or 'nii.gz', nipy default
    value: nii)
    output file type
    argument: ``-ot %s``
sharpness: (a float)
    smooth or sharpen the raw data. factor > 0 is smoothing.
    factor < 0 is sharpening. default value is 0
    NOTE: this option applies to DSI study only
    argument: ``-s %f``
filter: (a boolean)
    apply a filter (e.g. high pass) to the raw image
    argument: ``-f``
subtract_background: (a boolean)
    subtract the background value before reconstruction
    argument: ``-bg``
dsi: (a boolean)
    indicates that the data is dsi
    argument: ``-dsi``
output_entropy: (a boolean)
    output entropy map
    argument: ``-oe``
image_orientation_vectors: (a list of from 6 to 6 items which are a
    float)
    specify image orientation vectors. if just one argument given,
    will treat it as filename and read the orientation vectors from
    the file. if 6 arguments are given, will treat them as 6 float
    numbers and construct the 1st and 2nd vector and calculate the 3rd
    one automatically.
    this information will be used to determine image orientation,
    as well as to adjust gradient vectors with oblique angle when
    argument: ``-iop %f``
oblique_correction: (a boolean)
    when oblique angle(s) applied, some SIEMENS dti protocols do not
    adjust gradient accordingly, thus it requires adjustment for
    correct
    diffusion tensor calculation
    argument: ``-oc``
args: (a unicode string)
    Additional parameters to the command

```

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```

    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

B0: (a pathlike object or string representing an existing file)
DWI: (a pathlike object or string representing an existing file)
max: (a pathlike object or string representing an existing file)
ODF: (a pathlike object or string representing an existing file)
entropy: (a pathlike object or string representing a file)

```

58.2.3 ODFTracker[Link to code](#)Wraps the executable command `odf_tracker`.Use `odf_tracker` to generate track file**Inputs:**

```

[Mandatory]
max: (a pathlike object or string representing an existing file)
ODF: (a pathlike object or string representing an existing file)
mask1_file: (a pathlike object or string representing a file)
             first mask image
             argument: ``-m %s``, position: 2

[Optional]
input_data_prefix: (a unicode string, nipy default value: odf)
                   recon data prefix
                   argument: ``%s``, position: 0
out_file: (a pathlike object or string representing a file, nipy
           default value: tracks.trk)
           output track file
           argument: ``%s``, position: 1
input_output_type: ('nii' or 'analyze' or 'nii' or 'nii.gz', nipy
                   default value: nii)
                   input and output file type
                   argument: ``-it %s``
runge_kutta2: (a boolean)
              use 2nd order runge-kutta method for tracking.
              default tracking method is non-interpolate streamline
              argument: ``-rk2``
step_length: (a float)
             set step length, in the unit of minimum voxel size.
             default value is 0.1.
             argument: ``-l %f``
angle_threshold: (a float)
                set angle threshold. default value is 35 degree for
                default tracking method and 25 for rk2
                argument: ``-at %f``
random_seed: (an integer (int or long))
             use random location in a voxel instead of the center of the voxel
             to seed. can also define number of seed per voxel. default is 1
             argument: ``-rseed %s``

```

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```

invert_x: (a boolean)
    invert x component of the vector
    argument: ``-ix``
invert_y: (a boolean)
    invert y component of the vector
    argument: ``-iy``
invert_z: (a boolean)
    invert z component of the vector
    argument: ``-iz``
swap_xy: (a boolean)
    swap x and y vectors while tracking
    argument: ``-sxy``
swap_yz: (a boolean)
    swap y and z vectors while tracking
    argument: ``-syz``
swap_zx: (a boolean)
    swap x and z vectors while tracking
    argument: ``-szx``
disc: (a boolean)
    use disc tracking
    argument: ``-disc``
mask1_threshold: (a float)
    threshold value for the first mask image, if not given, the program
    will try automatically find the threshold
mask2_file: (a pathlike object or string representing a file)
    second mask image
    argument: ``-m2 %s``, position: 4
mask2_threshold: (a float)
    threshold value for the second mask image, if not given, the program
    will try automatically find the threshold
limit: (an integer (int or long))
    in some special case, such as heart data, some track may go into
    infinite circle and take long time to stop. this option allows
    setting a limit for the longest tracking steps (voxels)
    argument: ``-limit %d``
dsi: (a boolean)
    specify the input odf data is dsi. because dsi recon uses fixed
    pre-calculated matrix, some special orientation patch needs to
    be applied to keep dti/dsi/q-ball consistent.
    argument: ``-dsi``
image_orientation_vectors: (a list of from 6 to 6 items which are a
    float)
    specify image orientation vectors. if just one argument given,
    will treat it as filename and read the orientation vectors from
    the file. if 6 arguments are given, will treat them as 6 float
    numbers and construct the 1st and 2nd vector and calculate the 3rd
    one automatically.
    this information will be used to determine image orientation,
    as well as to adjust gradient vectors with oblique angle when
    argument: ``-iop %f``
slice_order: (an integer (int or long))
    set the slice order. 1 means normal, -1 means reversed. default
    value is 1
    argument: ``-sorder %d``
voxel_order: ('RAS' or 'RPS' or 'RAI' or 'RPI' or 'LAI' or 'LAS' or
    'LPS' or 'LPI')
    specify the voxel order in RL/AP/IS (human brain) reference. must be

```

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```

    3 letters with no space in between.
    for example, RAS means the voxel row is from L->R, the column
    is from P->A and the slice order is from I->S.
    by default voxel order is determined by the image orientation
    (but NOT guaranteed to be correct because of various standards).
    for example, siemens axial image is LPS, coronal image is LIP and
    sagittal image is PIL.
    this information also is NOT needed for tracking but will be saved
    in the track file and is essential for track display to map onto
    the right coordinates
    argument: ``-vorder %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

track_file: (a pathlike object or string representing an existing
    file)
    output track file

```

58.3 interfaces.diffusion_toolkit.postproc

58.3.1 SplineFilter

[Link to code](#)Wraps the executable command `spline_filter`.

Smooths TrackVis track files with a B-Spline filter.

Helps remove redundant track points and segments (thus reducing the size of the track file) and also make tracks nicely smoothed. It will NOT change the quality of the tracks or lose any original information.

Example

```

>>> import nipype.interfaces.diffusion_toolkit as dtk
>>> filt = dtk.SplineFilter()
>>> filt.inputs.track_file = 'tracks.trk'
>>> filt.inputs.step_length = 0.5
>>> filt.run()                                     # doctest: +SKIP

```

Inputs:

```

[Mandatory]
track_file: (a pathlike object or string representing an existing
    file)
    file containing tracks to be filtered
    argument: ``%s``, position: 0
step_length: (a float)
    in the unit of minimum voxel size
    argument: ``%f``, position: 1

[Optional]

```

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```

output_file: (a pathlike object or string representing a file, nipy
              default value: spline_tracks.trk)
              target file for smoothed tracks
              argument: ``%s``, position: 2
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

smoothed_track_file: (a pathlike object or string representing an
                     existing file)

```

58.3.2 TrackMerge[Link to code](#)

Wraps the executable command `track_merge`.

Merges several TrackVis track files into a single track file.

An id type property tag is added to each track in the newly merged file, with each unique id representing where the track was originally from. When the merged file is loaded in TrackVis, a property filter will show up in Track Property panel. Users can adjust that to distinguish and sub-group tracks by its id (origin).

Example

```

>>> import nipy.interfaces.diffusion_toolkit as dtk
>>> mrg = dtk.TrackMerge()
>>> mrg.inputs.track_files = ['track1.trk', 'track2.trk']
>>> mrg.run()                                     # doctest: +SKIP

```

Inputs:

```

[Mandatory]
track_files: (a list of items which are a pathlike object or string
              representing an existing file)
              file containing tracks to be filtered
              argument: ``%s...``, position: 0

[Optional]
output_file: (a pathlike object or string representing a file, nipy
              default value: merged_tracks.trk)
              target file for merged tracks
              argument: ``%s``, position: -1
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:


```
track_file: (a pathlike object or string representing an existing
            file)
```


59.1 interfaces.dipy.anisotropic_power

59.1.1 APMQball

[Link to code](#)

Calculates the anisotropic power map

Example

```
>>> import nipype.interfaces.dipy as dipy
>>> apm = dipy.APMQball()
>>> apm.inputs.in_file = 'diffusion.nii'
>>> apm.inputs.in_bvec = 'bvecs'
>>> apm.inputs.in_bval = 'bvals'
>>> apm.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input diffusion data
in_bval: (a pathlike object or string representing an existing file)
         input b-values table
in_bvec: (a pathlike object or string representing an existing file)
         input b-vectors table

[Optional]
mask_file: (a pathlike object or string representing an existing
           file)
           An optional brain mask
b0_thres: (an integer (int or long), nipype default value: 700)
           b0 threshold
out_prefix: (a unicode string)
            output prefix for file names
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

59.2 interfaces.dipy.base

59.2.1 DipyBaseInterface

[Link to code](#)

A base interface for py:mod:*dipy* computations

Inputs:

```
None
```

Outputs:

```
None
```

59.2.2 DipyDiffusionInterface

[Link to code](#)

A base interface for py:mod:*dipy* computations

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input diffusion data
in_bval: (a pathlike object or string representing an existing file)
         input b-values table
in_bvec: (a pathlike object or string representing an existing file)
         input b-vectors table

[Optional]
b0_thres: (an integer (int or long), nipype default value: 700)
         b0 threshold
out_prefix: (a unicode string)
            output prefix for file names
```

Outputs:

```
None
```

59.2.3 convert_to_traits_type()

[Link to code](#)

Convert DIPY type to Traits type.

59.2.4 create_interface_specs()

[Link to code](#)

Create IN/Out interface specifications dynamically.

Parameters

class_name: `str` The future class name(e.g, (MyClassInSpec))

params: `list of tuple` dipy argument list

BaseClass: `TraitedSpec object` parent class

Returns

newclass: **object** new nipy interface specification class

59.2.5 dipy_to_nipy_interface()

[Link to code](#)

Construct a class in order to respect nipy interface specifications.
This convenient class factory convert a DIPY Workflow to a nipy interface.

Parameters

cls_name: **string** new class name

dipy_flow: **Workflow class type.** It should be any children class of *dipy.workflows.workflow.Workflow*

BaseClass: **object** nipy instance object

Returns

newclass: **object** new nipy interface specification class

59.2.6 get_dipy_workflows()

[Link to code](#)

Search for DIPY workflow class.

Parameters

module [object] module object

Returns

l_wkflw [list of tuple] This a list of tuple containing 2 elements: Workflow name, Workflow class obj

Examples

```
>>> from dipy.workflows import align # doctest: +SKIP
>>> get_dipy_workflows(align) # doctest: +SKIP
```

59.3 interfaces.dipy.preprocess**59.3.1 Denoise**

[Link to code](#)

An interface to denoising diffusion datasets [Coupe2008]. See http://nipy.org/dipy/examples_built/denoise_nlmeans.html#example-denoise-nlmeans.

Example

```
>>> import nipy.interfaces.dipy as dipy
>>> denoise = dipy.Denoise()
>>> denoise.inputs.in_file = 'diffusion.nii'
>>> denoise.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    The input 4D diffusion-weighted image file
noise_model: ('rician' or 'gaussian', nipy default value: rician)
    noise distribution model

[Optional]
in_mask: (a pathlike object or string representing an existing file)
    brain mask
signal_mask: (a pathlike object or string representing an existing
    file)
    mask in which the mean signal will be computed
noise_mask: (a pathlike object or string representing an existing
    file)
    mask in which the standard deviation of noise will be computed
patch_radius: (an integer (int or long), nipy default value: 1)
    patch radius
block_radius: (an integer (int or long), nipy default value: 5)
    block_radius
snr: (a float)
    manually set an SNR
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

59.3.2 Resample

[Link to code](#)

An interface to reslicing diffusion datasets. See http://nipy.org/dipy/examples_built/reslice_datasets.html#example-reslice-datasets.

Example

```
>>> import nipy.interfaces.dipy as dipy
>>> reslice = dipy.Resample()
>>> reslice.inputs.in_file = 'diffusion.nii'
>>> reslice.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    The input 4D diffusion-weighted image file
interp: (an integer (int or long), nipy default value: 1)
    order of the interpolator (0 = nearest, 1 = linear, etc.)

[Optional]
vox_size: (a tuple of the form: (a float, a float, a float))
    specify the new voxel zooms. If no vox_size is set, then isotropic
    regridding will be performed, with spacing equal to the smallest
    current zoom.
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

59.3.3 nlmeans_proxy()

[Link to code](#)

Uses non-local means to denoise 4D datasets

59.3.4 resample_proxy()

[Link to code](#)

Performs regridding of an image to set isotropic voxel sizes using dipy.

59.4 interfaces.dipy.reconstruction

59.4.1 CSD

[Link to code](#)

Uses CSD [Tournier2007] to generate the fODF of DWIs. The interface uses dipy, as explained in dipy's CSD example.

Example

```
>>> from nipy.interfaces import dipy as ndp
>>> csd = ndp.CSD()
>>> csd.inputs.in_file = '4d_dwi.nii'
>>> csd.inputs.in_bval = 'bvals'
>>> csd.inputs.in_bvec = 'bvecs'
>>> res = csd.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input diffusion data
in_bval: (a pathlike object or string representing an existing file)
         input b-values table
in_bvec: (a pathlike object or string representing an existing file)
         input b-vectors table

[Optional]
in_mask: (a pathlike object or string representing an existing file)
         input mask in which compute tensors
response: (a pathlike object or string representing an existing file)
          single fiber estimated response
sh_order: (an integer (int or long), nipy default value: 8)
          maximal shperical harmonics order
save_fods: (a boolean, nipy default value: True)
           save fODFs in file
out_fods: (a pathlike object or string representing a file)
          fODFs output file name
b0_thres: (an integer (int or long), nipy default value: 700)
          b0 threshold
out_prefix: (a unicode string)
            output prefix for file names
```

Outputs:

```
model: (a pathlike object or string representing a file)
       Python pickled object of the CSD model fitted.
```

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```
out_fods: (a pathlike object or string representing a file)
          fODFs output file name
```

59.4.2 EstimateResponseSH

[Link to code](#)

Uses `dipy` to compute the single fiber response to be used in spherical deconvolution methods, in a similar way to MRTrix's command `estimate_response`.

Example

```
>>> from nipy.interfaces import dipy as ndp
>>> dti = ndp.EstimateResponseSH()
>>> dti.inputs.in_file = '4d_dwi.nii'
>>> dti.inputs.in_bval = 'bvals'
>>> dti.inputs.in_bvec = 'bvecs'
>>> dti.inputs.in_evals = 'dwi_evals.nii'
>>> res = dti.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_evals: (a pathlike object or string representing an existing file)
          input eigenvalues file
in_file: (a pathlike object or string representing an existing file)
          input diffusion data
in_bval: (a pathlike object or string representing an existing file)
          input b-values table
in_bvec: (a pathlike object or string representing an existing file)
          input b-vectors table

[Optional]
in_mask: (a pathlike object or string representing an existing file)
          input mask in which we find single fibers
fa_thresh: (a float, nipy default value: 0.7)
            FA threshold
roi_radius: (an integer (int or long), nipy default value: 10)
             ROI radius to be used in auto_response
auto: (a boolean)
       use the auto_response estimator from dipy
       mutually_exclusive: recursive
recursive: (a boolean)
            use the recursive response estimator from dipy
            mutually_exclusive: auto
response: (a pathlike object or string representing a file, nipy
           default value: response.txt)
           the output response file
out_mask: (a pathlike object or string representing a file, nipy
           default value: wm_mask.nii.gz)
           computed wm mask
b0_thres: (an integer (int or long), nipy default value: 700)
           b0 threshold
out_prefix: (a unicode string)
             output prefix for file names
```

Outputs:


```
response: (a pathlike object or string representing an existing file)
          the response file
out_mask: (a pathlike object or string representing an existing file)
          output wm mask
```

59.4.3 RESTORE

[Link to code](#)

Uses RESTORE [Chang2005] to perform DTI fitting with outlier detection. The interface uses dipy, as explained in dipy's documentation.

Example

```
>>> from nipy.interfaces import dipy as ndp
>>> dti = ndp.RESTORE()
>>> dti.inputs.in_file = '4d_dwi.nii'
>>> dti.inputs.in_bval = 'bvals'
>>> dti.inputs.in_bvec = 'bvecs'
>>> res = dti.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input diffusion data
in_bval: (a pathlike object or string representing an existing file)
         input b-values table
in_bvec: (a pathlike object or string representing an existing file)
         input b-vectors table

[Optional]
in_mask: (a pathlike object or string representing an existing file)
         input mask in which compute tensors
noise_mask: (a pathlike object or string representing an existing
            file)
            input mask in which compute noise variance
b0_thres: (an integer (int or long), nipy default value: 700)
         b0 threshold
out_prefix: (a unicode string)
            output prefix for file names
```

Outputs:

```
fa: (a pathlike object or string representing a file)
    output fractional anisotropy (FA) map computed from the fitted DTI
md: (a pathlike object or string representing a file)
    output mean diffusivity (MD) map computed from the fitted DTI
rd: (a pathlike object or string representing a file)
    output radial diffusivity (RD) map computed from the fitted DTI
mode: (a pathlike object or string representing a file)
    output mode (MO) map computed from the fitted DTI
trace: (a pathlike object or string representing a file)
    output the tensor trace map computed from the fitted DTI
evals: (a pathlike object or string representing a file)
    output the eigenvalues of the fitted DTI
evecs: (a pathlike object or string representing a file)
    output the eigenvectors of the fitted DTI
```

59.5 interfaces.dipy.simulate

59.5.1 SimulateMultiTensor

[Link to code](#)

Interface to MultiTensor model simulator in dipy http://nipy.org/dipy/examples_built/simulate_multi_tensor.html

Example

```
>>> import nipy.interfaces.dipy as dipy
>>> sim = dipy.SimulateMultiTensor()
>>> sim.inputs.in_dirs = ['fdir00.nii', 'fdir01.nii']
>>> sim.inputs.in_frac = ['ffra00.nii', 'ffra01.nii']
>>> sim.inputs.in_vfms = ['tpm_00.nii.gz', 'tpm_01.nii.gz',
...                       'tpm_02.nii.gz']
>>> sim.inputs.baseline = 'b0.nii'
>>> sim.inputs.in_bvec = 'bvecs'
>>> sim.inputs.in_bval = 'bvals'
>>> sim.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_dirs: (a list of items which are a pathlike object or string
          representing an existing file)
          list of fibers (principal directions)
in_frac: (a list of items which are a pathlike object or string
          representing an existing file)
          volume fraction of each fiber
in_vfms: (a list of items which are a pathlike object or string
          representing an existing file)
          volume fractions of isotropic compartments
baseline: (a pathlike object or string representing an existing file)
          baseline T2 signal

[Optional]
in_mask: (a pathlike object or string representing an existing file)
          mask to simulate data
diff_iso: (a list of items which are a float, nipy default value:
          [0.003, 0.00096, 0.00068])
          Diffusivity of isotropic compartments
diff_sf: (a tuple of the form: (a float, a float, a float), nipy
          default value: (0.0017, 0.0002, 0.0002))
          Single fiber tensor
n_proc: (an integer (int or long), nipy default value: 0)
          number of processes
gradients: (a pathlike object or string representing an existing
            file)
            gradients file
in_bvec: (a pathlike object or string representing an existing file)
          input bvecs file
in_bval: (a pathlike object or string representing an existing file)
          input bvals file
num_dirs: (an integer (int or long), nipy default value: 32)
          number of gradient directions (when table is automatically
          generated)
```

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```

bvalues: (a list of items which are an integer (int or long), nipy
         default value: [1000, 3000])
         list of b-values (when table is automatically generated)
out_file: (a pathlike object or string representing a file, nipy
         default value: sim_dwi.nii.gz)
         output file with fractions to be simulated
out_mask: (a pathlike object or string representing a file, nipy
         default value: sim_msk.nii.gz)
         file with the mask simulated
out_bvec: (a pathlike object or string representing a file, nipy
         default value: bvec.sim)
         simulated b vectors
out_bval: (a pathlike object or string representing a file, nipy
         default value: bval.sim)
         simulated b values
snr: (an integer (int or long), nipy default value: 0)
     signal-to-noise ratio (dB)

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
         simulated DWIs
out_mask: (a pathlike object or string representing an existing file)
         mask file
out_bvec: (a pathlike object or string representing an existing file)
         simulated b vectors
out_bval: (a pathlike object or string representing an existing file)
         simulated b values

```

59.6 interfaces.dipy.tensors

59.6.1 DTI

[Link to code](#)

Calculates the diffusion tensor model parameters

Example

```

>>> import nipy.interfaces.dipy as dipy
>>> dti = dipy.DTI()
>>> dti.inputs.in_file = 'diffusion.nii'
>>> dti.inputs.in_bvec = 'bvecs'
>>> dti.inputs.in_bval = 'bvals'
>>> dti.run()                                     # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input diffusion data
in_bval: (a pathlike object or string representing an existing file)
         input b-values table
in_bvec: (a pathlike object or string representing an existing file)
         input b-vectors table

```

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```
[Optional]
mask_file: (a pathlike object or string representing an existing
            file)
            An optional white matter mask
b0_thres: (an integer (int or long), nipy default value: 700)
            b0 threshold
out_prefix: (a unicode string)
            output prefix for file names
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
fa_file: (a pathlike object or string representing an existing file)
md_file: (a pathlike object or string representing an existing file)
rd_file: (a pathlike object or string representing an existing file)
ad_file: (a pathlike object or string representing an existing file)
color_fa_file: (a pathlike object or string representing an existing
                file)
```

59.6.2 TensorMode

[Link to code](#)

Creates a map of the mode of the diffusion tensors given a set of diffusion-weighted images, as well as their associated b-values and b-vectors. Fits the diffusion tensors and calculates tensor mode with Dipy.

Example

```
>>> import nipy.interfaces.dipy as dipy
>>> mode = dipy.TensorMode()
>>> mode.inputs.in_file = 'diffusion.nii'
>>> mode.inputs.in_bvec = 'bvecs'
>>> mode.inputs.in_bval = 'bvals'
>>> mode.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input diffusion data
in_bval: (a pathlike object or string representing an existing file)
         input b-values table
in_bvec: (a pathlike object or string representing an existing file)
         input b-vectors table

[Optional]
mask_file: (a pathlike object or string representing an existing
            file)
            An optional white matter mask
b0_thres: (an integer (int or long), nipy default value: 700)
            b0 threshold
out_prefix: (a unicode string)
            output prefix for file names
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

59.7 interfaces.dipy.tracks

59.7.1 StreamlineTractography

[Link to code](#)

Streamline tractography using EuDX [Garyfallidis12].

Example

```
>>> from nipy.interfaces import dipy as ndp
>>> track = ndp.StreamlineTractography()
>>> track.inputs.in_file = '4d_dwi.nii'
>>> track.inputs.in_model = 'model.pklz'
>>> track.inputs.tracking_mask = 'dilated_wm_mask.nii'
>>> res = track.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input diffusion data
gfa_thresh: (a float, nipy default value: 0.2)
            GFA threshold to compute tracking mask
peak_threshold: (a float, nipy default value: 0.5)
               threshold to consider peaks from model
min_angle: (a float, nipy default value: 25.0)
           minimum separation angle
multiprocess: (a boolean, nipy default value: True)
              use multiprocessing
save_seeds: (a boolean, nipy default value: False)
            save seeding voxels coordinates
num_seeds: (an integer (int or long), nipy default value: 10000)
           desired number of tracks in tractography

[Optional]
in_model: (a pathlike object or string representing an existing file)
          input f/d-ODF model extracted from.
tracking_mask: (a pathlike object or string representing an existing
               file)
               input mask within which perform tracking
seed_mask: (a pathlike object or string representing an existing
            file)
            input mask within which perform seeding
in_peaks: (a pathlike object or string representing an existing file)
           peaks computed from the odf
seed_coord: (a pathlike object or string representing an existing
             file)
             file containing the list of seed voxel coordinates (N,3)
out_prefix: (a unicode string)
            output prefix for file names
```

Outputs:

```
tracks: (a pathlike object or string representing a file)
        TrackVis file containing extracted streamlines
gfa: (a pathlike object or string representing a file)
     The resulting GFA (generalized FA) computed using the peaks of the
     ODF
```

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```
odf_peaks: (a pathlike object or string representing a file)
           peaks computed from the odf
out_seeds: (a pathlike object or string representing a file)
           file containing the (N,3) *voxel* coordinates used in seeding.
```

59.7.2 TrackDensityMap

[Link to code](#)

Creates a tract density image from a TrackVis track file using functions from dipy

Example

```
>>> import nipy.interfaces.dipy as dipy
>>> trk2tdi = dipy.TrackDensityMap()
>>> trk2tdi.inputs.in_file = 'converted.trk'
>>> trk2tdi.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         The input TrackVis track file

[Optional]
reference: (a pathlike object or string representing an existing
           file)
           A reference file to define RAS coordinates space
points_space: ('rasmm' or 'voxel' or None, nipy default value:
              rasmm)
              coordinates of trk file
voxel_dims: (a list of from 3 to 3 items which are a float)
             The size of each voxel in mm.
data_dims: (a list of from 3 to 3 items which are an integer (int or
              long))
            The size of the image in voxels.
out_filename: (a pathlike object or string representing a file,
              nipy default value: tdi.nii)
              The output filename for the tracks in TrackVis (.trk) format
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

60.1 interfaces.dtitk.base

60.1.1 CommandLineDtitk

[Link to code](#)

Inputs:

```
[Optional]
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

```
None
```

60.2 interfaces.dtitk.registration

60.2.1 AffScalarVol

[Link to code](#)

Wraps the executable command affineScalarVolume.

Applies affine transform to a scalar volume

Example

```
>>> from nipype.interfaces import dtitk
>>> node = dtitk.AffScalarVol()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.transform = 'im_affine.aff'
```

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```
>>> node.cmdline
'affineScalarVolume -in im1.nii -interp 0 -out im1_affxfmd.nii -trans
im_affine.aff'
>>> node.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        moving scalar volume
        argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output filename
        argument: ``-out %s``
transform: (a pathlike object or string representing an existing
        file)
        transform to apply: specify an input transformation file; parameters
        input will be ignored
        argument: ``-trans %s``
        mutually_exclusive: target, translation, euler, deformation
interpolation: ('trilinear' or 'NN', nipy default value: trilinear)
        trilinear or nearest neighbor interpolation
        argument: ``-interp %s``
target: (a pathlike object or string representing an existing file)
        output volume specification read from the target volume if specified
        argument: ``-target %s``
        mutually_exclusive: transform
translation: (a tuple of the form: (a float, a float, a float))
        translation (x,y,z) in mm
        argument: ``-translation %g %g %g``
        mutually_exclusive: transform
euler: (a tuple of the form: (a float, a float, a float))
        (theta, phi, psi) in degrees
        argument: ``-euler %g %g %g``
        mutually_exclusive: transform
deformation: (a tuple of the form: (a float, a float, a float, a
        float, a float, a float))
        (xx,yy,zz,xy,yz,xz)
        argument: ``-deformation %g %g %g %g %g %g``
        mutually_exclusive: transform
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
        moved volume
```

60.2.2 AffSymTensor3DVol[Link to code](#)

Wraps the executable command `affineSymTensor3DVolume`.
 Applies affine transform to a tensor volume

Example

```
>>> from nipy.interfaces import dtitk
>>> node = dtitk.AffSymTensor3DVol()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.transform = 'im_affine.aff'
>>> node.cmdline
'affineSymTensor3DVolume -in im1.nii -interp LEI -out im1_affxfmd.nii
-reorient PPD -trans im_affine.aff'
>>> node.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         moving tensor volume
         argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
         output filename
         argument: ``-out %s``
transform: (a pathlike object or string representing an existing
           file)
           transform to apply: specify an input transformation file; parameters
           input will be ignored
           argument: ``-trans %s``
           mutually_exclusive: target, translation, euler, deformation
interpolation: ('LEI' or 'EI', nipy default value: LEI)
               Log Euclidean/Euclidean Interpolation
               argument: ``-interp %s``
reorient: ('PPD' or 'NO' or 'FS', nipy default value: PPD)
           Reorientation strategy: preservation of principal direction, no
           reorientation, or finite strain
           argument: ``-reorient %s``
target: (a pathlike object or string representing an existing file)
        output volume specification read from the target volume if specified
        argument: ``-target %s``
        mutually_exclusive: transform
translation: (a tuple of the form: (a float, a float, a float))
             translation (x,y,z) in mm
             argument: ``-translation %g %g %g``
             mutually_exclusive: transform
euler: (a tuple of the form: (a float, a float, a float))
        (theta, phi, psi) in degrees
        argument: ``-euler %g %g %g``
        mutually_exclusive: transform
deformation: (a tuple of the form: (a float, a float, a float, a
                                     float, a float, a float))
              (xx,yy,zz,xy,yz,xz)
              argument: ``-deformation %g %g %g %g %g %g``
              mutually_exclusive: transform
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
```

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```
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipype default value: {})
Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

60.2.3 Affine

[Link to code](#)

Wraps the executable command dti_affine_reg.

Performs affine registration between two tensor volumes

Example

```
>>> from nipype.interfaces import dtitk
>>> node = dtitk.Affine()
>>> node.inputs.fixed_file = 'im1.nii'
>>> node.inputs.moving_file = 'im2.nii'
>>> node.inputs.similarity_metric = 'EDS'
>>> node.inputs.sampling_xyz = (4,4,4)
>>> node.inputs.ftol = 0.01
>>> node.inputs.initialize_xfm = 'im_affine.aff'
>>> node.cmdline
'dti_affine_reg im1.nii im2.nii EDS 4 4 4 0.01 im_affine.aff'
>>> node.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
fixed_file: (a pathlike object or string representing an existing
            file)
            fixed tensor volume
            argument: ``%s``, position: 0
moving_file: (a pathlike object or string representing an existing
            file)
            moving tensor volume
            argument: ``%s``, position: 1
similarity_metric: ('EDS' or 'GDS' or 'DDS' or 'NMI', nipype default
                  value: EDS)
                  similarity metric
                  argument: ``%s``, position: 2
sampling_xyz: (a tuple of the form: (a value of class 'int', a value
                  of class 'int', a value of class 'int'), nipype default value: (4,
                  4, 4))
                  dist between samp points (mm) (x,y,z)
                  argument: ``%g %g %g``, position: 3
ftol: (a float, nipype default value: 0.01)
      cost function tolerance
      argument: ``%g``, position: 4

[Optional]
initialize_xfm: (a pathlike object or string representing an existing
                file)
```

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```

        Initialize w/DTITK-FORMATAffine
        argument: ``%s``, position: 5
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
out_file_xfm: (a pathlike object or string representing an existing
              file)

```

60.2.4 AffineTask[Link to code](#)

Wraps the executable command dti_affine_reg.

Inputs:

```

[Mandatory]
fixed_file: (a pathlike object or string representing an existing
            file)
            fixed tensor volume
            argument: ``%s``, position: 0
moving_file: (a pathlike object or string representing an existing
             file)
             moving tensor volume
             argument: ``%s``, position: 1
similarity_metric: ('EDS' or 'GDS' or 'DDS' or 'NMI', nipy default
                  value: EDS)
                  similarity metric
                  argument: ``%s``, position: 2
sampling_xyz: (a tuple of the form: (a value of class 'int', a value
                  of class 'int', a value of class 'int'), nipy default value: (4,
                  4, 4))
                  dist between samp points (mm) (x,y,z)
                  argument: ``%g %g %g``, position: 3
ftol: (a float, nipy default value: 0.01)
      cost function tolerance
      argument: ``%g``, position: 4

```

```

[Optional]
initialize_xfm: (a pathlike object or string representing an existing
                file)
                Initialize w/DTITK-FORMATAffine
                argument: ``%s``, position: 5
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
out_file_xfm: (a pathlike object or string representing an existing
              file)
```

60.2.5 ComposeXfm

[Link to code](#)

Wraps the executable command `dfRightComposeAffine`.

Combines diffeomorphic and affine transforms

Example

```
>>> from nipy.interfaces import dtitk
>>> node = dtitk.ComposeXfm()
>>> node.inputs.in_df = 'im_warp.df.nii'
>>> node.inputs.in_aff= 'im_affine.aff'
>>> node.cmdline
'dfRightComposeAffine -aff im_affine.aff -df im_warp.df.nii -out
 im_warp_affdf.df.nii'
>>> node.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_df: (a pathlike object or string representing an existing file)
       diffeomorphic warp file
       argument: ``-df %s``
in_aff: (a pathlike object or string representing an existing file)
        affine transform file
        argument: ``-aff %s``

[Optional]
out_file: (a pathlike object or string representing a file)
          output path
          argument: ``-out %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

60.2.6 ComposeXfmTask

[Link to code](#)

Wraps the executable command `dfRightComposeAffine`.

Inputs:

```
[Mandatory]
in_df: (a pathlike object or string representing an existing file)
       diffeomorphic warp file
```

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```

        argument: ``-df %s``
in_aff: (a pathlike object or string representing an existing file)
        affine transform file
        argument: ``-aff %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output path
        argument: ``-out %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

60.2.7 Diffeo[Link to code](#)

Wraps the executable command `dti_diffeomorphic_reg`.
 Performs diffeomorphic registration between two tensor volumes

Example

```

>>> from nipy.interfaces import dtitk
>>> node = dtitk.Diffeo()
>>> node.inputs.fixed_file = 'im1.nii'
>>> node.inputs.moving_file = 'im2.nii'
>>> node.inputs.mask_file = 'mask.nii'
>>> node.inputs.legacy = 1
>>> node.inputs.n_iters = 6
>>> node.inputs.ftol = 0.002
>>> node.cmdline
'dti_diffeomorphic_reg im1.nii im2.nii mask.nii 1 6 0.002'
>>> node.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
legacy: (1, nipy default value: 1)
        legacy parameter; always set to 1
        argument: ``%d``, position: 3
n_iters: (an integer (int or long), nipy default value: 6)
        number of iterations
        argument: ``%d``, position: 4
ftol: (a float, nipy default value: 0.002)
        iteration for the optimization to stop
        argument: ``%g``, position: 5

[Optional]
fixed_file: (a pathlike object or string representing an existing

```

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```

        file)
        fixed tensor volume
        argument: ``%s``, position: 0
moving_file: (a pathlike object or string representing an existing
        file)
        moving tensor volume
        argument: ``%s``, position: 1
mask_file: (a pathlike object or string representing an existing
        file)
        mask
        argument: ``%s``, position: 2
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
out_file_xfm: (a pathlike object or string representing an existing
        file)

```

60.2.8 DiffeoScalarVol[Link to code](#)

Wraps the executable command deformationScalarVolume.

Applies diffeomorphic transform to a scalar volume

Example

```

>>> from nipy.interfaces import dtitk
>>> node = dtitk.DiffeoScalarVol()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.transform = 'im_warp.df.nii'
>>> node.cmdline
'deformationScalarVolume -in im1.nii -interp 0 -out im1_diffeoxfmd.nii
-trans im_warp.df.nii'
>>> node.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        moving scalar volume
        argument: ``-in %s``
transform: (a pathlike object or string representing an existing
        file)
        transform to apply
        argument: ``-trans %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output filename

```

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```

        argument: ``-out %s``
target: (a pathlike object or string representing an existing file)
        output volume specification read from the target volume if specified
        argument: ``-target %s``
        mutually_exclusive: voxel_size
voxel_size: (a tuple of the form: (a float, a float, a float))
        xyz voxel size (superseded by target)
        argument: ``-vsize %g %g %g``
        mutually_exclusive: target
flip: (a tuple of the form: (an integer (int or long), an integer
        (int or long), an integer (int or long)))
        argument: ``-flip %d %d %d``
resampling_type: ('backward' or 'forward')
        use backward or forward resampling
        argument: ``-type %s``
interpolation: ('trilinear' or 'NN', nipy default value: trilinear)
        trilinear, or nearest neighbor
        argument: ``-interp %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        moved volume

```

60.2.9 DiffeoSymTensor3DVol[Link to code](#)

Wraps the executable command deformationSymTensor3DVolume.

Applies diffeomorphic transform to a tensor volume

Example

```

>>> from nipy.interfaces import dtitk
>>> node = dtitk.DiffeoSymTensor3DVol()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.transform = 'im_warp.df.nii'
>>> node.cmdline
'deformationSymTensor3DVolume -df FD -in im1.nii -interp LEI -out
im1_diffeoxfmd.nii -reorient PPD -trans im_warp.df.nii'
>>> node.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        moving tensor volume
        argument: ``-in %s``
transform: (a pathlike object or string representing an existing
        file)

```

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```

        transform to apply
        argument: ``-trans %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output filename
        argument: ``-out %s``
df: (a unicode string, nipy default value: FD)
        argument: ``-df %s``
interpolation: ('LEI' or 'EI', nipy default value: LEI)
        Log Euclidean/Euclidean Interpolation
        argument: ``-interp %s``
reorient: ('PPD' or 'FS', nipy default value: PPD)
        Reorientation strategy: preservation of principal direction or
        finite strain
        argument: ``-reorient %s``
target: (a pathlike object or string representing an existing file)
        output volume specification read from the target volume if specified
        argument: ``-target %s``
        mutually_exclusive: voxel_size
voxel_size: (a tuple of the form: (a float, a float, a float))
        xyz voxel size (superseded by target)
        argument: ``-vsize %g %g %g``
        mutually_exclusive: target
flip: (a tuple of the form: (an integer (int or long), an integer
        (int or long), an integer (int or long)))
        argument: ``-flip %d %d %d``
resampling_type: ('backward' or 'forward')
        use backward or forward resampling
        argument: ``-type %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)

```

60.2.10 DiffeoTask[Link to code](#)Wraps the executable command `dti_diffeomorphic_reg`.**Inputs:**

```

[Mandatory]
legacy: (1, nipy default value: 1)
        legacy parameter; always set to 1
        argument: ``%d``, position: 3
n_iters: (an integer (int or long), nipy default value: 6)
        number of iterations
        argument: ``%d``, position: 4
ftol: (a float, nipy default value: 0.002)

```

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```

        iteration for the optimization to stop
        argument: ``%g``, position: 5

[Optional]
fixed_file: (a pathlike object or string representing an existing
            file)
            fixed tensor volume
            argument: ``%s``, position: 0
moving_file: (a pathlike object or string representing an existing
            file)
            moving tensor volume
            argument: ``%s``, position: 1
mask_file: (a pathlike object or string representing an existing
            file)
            mask
            argument: ``%s``, position: 2
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
out_file_xfm: (a pathlike object or string representing an existing
              file)

```

60.2.11 Rigid[Link to code](#)Wraps the executable command `dti_rigid_reg`.

Performs rigid registration between two tensor volumes

Example

```

>>> from nipy.interfaces import dtitk
>>> node = dtitk.Rigid()
>>> node.inputs.fixed_file = 'im1.nii'
>>> node.inputs.moving_file = 'im2.nii'
>>> node.inputs.similarity_metric = 'EDS'
>>> node.inputs.sampling_xyz = (4,4,4)
>>> node.inputs.ftol = 0.01
>>> node.cmdline
'dti_rigid_reg im1.nii im2.nii EDS 4 4 4 0.01'
>>> node.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
fixed_file: (a pathlike object or string representing an existing
            file)
            fixed tensor volume
            argument: ``%s``, position: 0

```

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```

moving_file: (a pathlike object or string representing an existing
              file)
              moving tensor volume
              argument: ``%s``, position: 1
similarity_metric: ('EDS' or 'GDS' or 'DDS' or 'NMI', nipy default
                   value: EDS)
                   similarity metric
                   argument: ``%s``, position: 2
sampling_xyz: (a tuple of the form: (a value of class 'int', a value
                                     of class 'int', a value of class 'int'), nipy default value: (4,
                                     4, 4))
               dist between samp points (mm) (x,y,z)
               argument: ``%g %g %g``, position: 3
ftol: (a float, nipy default value: 0.01)
      cost function tolerance
      argument: ``%g``, position: 4

[Optional]
initialize_xfm: (a pathlike object or string representing an existing
                file)
                Initialize w/DTITK-FORMATAffine
                argument: ``%s``, position: 5
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
out_file_xfm: (a pathlike object or string representing an existing
              file)

```

60.2.12 RigidTask[Link to code](#)Wraps the executable command `dti_rigid_reg`.**Inputs:**

```

[Mandatory]
fixed_file: (a pathlike object or string representing an existing
            file)
            fixed tensor volume
            argument: ``%s``, position: 0
moving_file: (a pathlike object or string representing an existing
             file)
             moving tensor volume
             argument: ``%s``, position: 1
similarity_metric: ('EDS' or 'GDS' or 'DDS' or 'NMI', nipy default
                   value: EDS)
                   similarity metric
                   argument: ``%s``, position: 2
sampling_xyz: (a tuple of the form: (a value of class 'int', a value

```

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```

        of class 'int', a value of class 'int'), nipy default value: (4,
        4, 4))
    dist between samp points (mm) (x,y,z)
    argument: ``%g %g %g``, position: 3
ftol: (a float, nipy default value: 0.01)
    cost function tolerance
    argument: ``%g``, position: 4

[Optional]
initialize_xfm: (a pathlike object or string representing an existing
    file)
    Initialize w/DTITK-FORMATAffine
    argument: ``%s``, position: 5
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
out_file_xfm: (a pathlike object or string representing an existing
    file)

```

60.2.13 affScalarVolTask[Link to code](#)

Wraps the executable command affineScalarVolume.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    moving scalar volume
    argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
    output filename
    argument: ``-out %s``
transform: (a pathlike object or string representing an existing
    file)
    transform to apply: specify an input transformation file; parameters
    input will be ignored
    argument: ``-trans %s``
    mutually_exclusive: target, translation, euler, deformation
interpolation: ('trilinear' or 'NN', nipy default value: trilinear)
    trilinear or nearest neighbor interpolation
    argument: ``-interp %s``
target: (a pathlike object or string representing an existing file)
    output volume specification read from the target volume if specified
    argument: ``-target %s``
    mutually_exclusive: transform
translation: (a tuple of the form: (a float, a float, a float))

```

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```

translation (x,y,z) in mm
argument: ``-translation %g %g %g``
mutually_exclusive: transform
euler: (a tuple of the form: (a float, a float, a float))
(theta, phi, psi) in degrees
argument: ``-euler %g %g %g``
mutually_exclusive: transform
deformation: (a tuple of the form: (a float, a float, a float, a
float, a float, a float))
(xx,yy,zz,xy,yz,xz)
argument: ``-deformation %g %g %g %g %g %g``
mutually_exclusive: transform
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
moved volume

```

60.2.14 affSymTensor3DVOLTask[Link to code](#)

Wraps the executable command affineSymTensor3DVolume.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
moving tensor volume
argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
output filename
argument: ``-out %s``
transform: (a pathlike object or string representing an existing
file)
transform to apply: specify an input transformation file; parameters
input will be ignored
argument: ``-trans %s``
mutually_exclusive: target, translation, euler, deformation
interpolation: ('LEI' or 'EI', nipy default value: LEI)
Log Euclidean/Euclidean Interpolation
argument: ``-interp %s``
reorient: ('PPD' or 'NO' or 'FS', nipy default value: PPD)
Reorientation strategy: preservation of principal direction, no
reorientation, or finite strain
argument: ``-reorient %s``
target: (a pathlike object or string representing an existing file)
output volume specification read from the target volume if specified
argument: ``-target %s``

```

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```

        mutually_exclusive: transform
translation: (a tuple of the form: (a float, a float, a float))
        translation (x,y,z) in mm
        argument: ``-translation %g %g %g``
        mutually_exclusive: transform
euler: (a tuple of the form: (a float, a float, a float))
        (theta, phi, psi) in degrees
        argument: ``-euler %g %g %g``
        mutually_exclusive: transform
deformation: (a tuple of the form: (a float, a float, a float, a
        float, a float, a float))
        (xx,yy,zz,xy,yz,xz)
        argument: ``-deformation %g %g %g %g %g %g``
        mutually_exclusive: transform
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

60.2.15 diffeoScalarVolTask[Link to code](#)

Wraps the executable command deformationScalarVolume.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        moving scalar volume
        argument: ``-in %s``
transform: (a pathlike object or string representing an existing
        file)
        transform to apply
        argument: ``-trans %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output filename
        argument: ``-out %s``
target: (a pathlike object or string representing an existing file)
        output volume specification read from the target volume if specified
        argument: ``-target %s``
        mutually_exclusive: voxel_size
voxel_size: (a tuple of the form: (a float, a float, a float))
        xyz voxel size (superseded by target)
        argument: ``-vsize %g %g %g``
        mutually_exclusive: target
flip: (a tuple of the form: (an integer (int or long), an integer
        (int or long), an integer (int or long)))
        argument: ``-flip %d %d %d``

```

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```

resampling_type: ('backward' or 'forward')
    use backward or forward resampling
    argument: ``-type %s``
interpolation: ('trilinear' or 'NN', nipy default value: trilinear)
    trilinear, or nearest neighbor
    argument: ``-interp %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    moved volume

```

60.2.16 diffeoSymTensor3DVOLTask[Link to code](#)

Wraps the executable command deformationSymTensor3DVolume.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    moving tensor volume
    argument: ``-in %s``
transform: (a pathlike object or string representing an existing
    file)
    transform to apply
    argument: ``-trans %s``

[Optional]
out_file: (a pathlike object or string representing a file)
    output filename
    argument: ``-out %s``
df: (a unicode string, nipy default value: FD)
    argument: ``-df %s``
interpolation: ('LEI' or 'EI', nipy default value: LEI)
    Log Euclidean/Euclidean Interpolation
    argument: ``-interp %s``
reorient: ('PPD' or 'FS', nipy default value: PPD)
    Reorientation strategy: preservation of principal direction or
    finite strain
    argument: ``-reorient %s``
target: (a pathlike object or string representing an existing file)
    output volume specification read from the target volume if specified
    argument: ``-target %s``
    mutually_exclusive: voxel_size
voxel_size: (a tuple of the form: (a float, a float, a float))
    xyz voxel size (superseded by target)
    argument: ``-vsize %g %g %g``
    mutually_exclusive: target
flip: (a tuple of the form: (an integer (int or long), an integer

```

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```

        (int or long), an integer (int or long))
        argument: ``-flip %d %d %d``
    resampling_type: ('backward' or 'forward')
        use backward or forward resampling
        argument: ``-type %s``
    args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
    environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipype default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)

```

60.3 interfaces.dtitk.utils

60.3.1 BinThresh

[Link to code](#)

Wraps the executable command BinaryThresholdImageFilter.

Binarizes an image

Example

```

>>> from nipype.interfaces import dtitk
>>> node = dtitk.BinThresh()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.lower_bound = 0
>>> node.inputs.upper_bound = 100
>>> node.inputs.inside_value = 1
>>> node.inputs.outside_value = 0
>>> node.cmdline
'BinaryThresholdImageFilter im1.nii im1_thrbin.nii 0 100 1 0'
>>> node.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Image to threshold/binarize
    argument: ``%s``, position: 0
lower_bound: (a float, nipype default value: 0.01)
    lower bound of binarization range
    argument: ``%g``, position: 2
upper_bound: (a float, nipype default value: 100)
    upper bound of binarization range
    argument: ``%g``, position: 3
inside_value: (a float, nipype default value: 1)
    value for voxels in binarization range
    argument: ``%g``, position: 4
outside_value: (a float, nipype default value: 0)
    value for voxelsoutside of binarization range

```

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```

        argument: ``%g``, position: 5

[Optional]
out_file: (a pathlike object or string representing a file)
        output path
        argument: ``%s``, position: 1
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)

```

60.3.2 BinThreshTask

[Link to code](#)

Wraps the executable command BinaryThresholdImageFilter.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        Image to threshold/binarize
        argument: ``%s``, position: 0
lower_bound: (a float, nipy default value: 0.01)
        lower bound of binarization range
        argument: ``%g``, position: 2
upper_bound: (a float, nipy default value: 100)
        upper bound of binarization range
        argument: ``%g``, position: 3
inside_value: (a float, nipy default value: 1)
        value for voxels in binarization range
        argument: ``%g``, position: 4
outside_value: (a float, nipy default value: 0)
        value for voxelsoutside of binarization range
        argument: ``%g``, position: 5

[Optional]
out_file: (a pathlike object or string representing a file)
        output path
        argument: ``%s``, position: 1
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)

```


60.3.3 SVAdjustVoxSp

[Link to code](#)

Wraps the executable command SVAdjustVoxelspace.

Adjusts the voxel space of a scalar volume

```
>>> from nipy.interfaces import dtitk
>>> node = dtitk.SVAdjustVoxSp()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.target_file = 'im2.nii'
>>> node.cmdline
'SVAdjustVoxelspace -in im1.nii -out im1_avs.nii -target im2.nii'
>>> node.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        scalar volume to modify
        argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output path
        argument: ``-out %s``
target_file: (a pathlike object or string representing a file)
        target volume to match
        argument: ``-target %s``
        mutually_exclusive: voxel_size, origin
voxel_size: (a tuple of the form: (a float, a float, a float))
        xyz voxel size (superseded by target)
        argument: ``-vsize %g %g %g``
        mutually_exclusive: target_file
origin: (a tuple of the form: (a float, a float, a float))
        xyz origin (superseded by target)
        argument: ``-origin %g %g %g``
        mutually_exclusive: target_file
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

60.3.4 SVAdjustVoxSpTask

[Link to code](#)

Wraps the executable command SVAdjustVoxelspace.

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        scalar volume to modify
```

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```

        argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output path
        argument: ``-out %s``
target_file: (a pathlike object or string representing a file)
        target volume to match
        argument: ``-target %s``
        mutually_exclusive: voxel_size, origin
voxel_size: (a tuple of the form: (a float, a float, a float))
        xyz voxel size (superseded by target)
        argument: ``-vsize %g %g %g``
        mutually_exclusive: target_file
origin: (a tuple of the form: (a float, a float, a float))
        xyz origin (superseded by target)
        argument: ``-origin %g %g %g``
        mutually_exclusive: target_file
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

60.3.5 SVResample

[Link to code](#)

Wraps the executable command SVResample.

Resamples a scalar volume

```

>>> from nipy.interfaces import dtitk
>>> node = dtitk.SVResample()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.target_file = 'im2.nii'
>>> node.cmdline
'SVResample -in im1.nii -out im1_resampled.nii -target im2.nii'
>>> node.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        image to resample
        argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output path
        argument: ``-out %s``
target_file: (a pathlike object or string representing a file)
        specs read from the target volume

```

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```

        argument: ``-target %s``
        mutually_exclusive: array_size, voxel_size, origin
align: ('center' or 'origin')
        how to align output volume to input volume
        argument: ``-align %s``
array_size: (a tuple of the form: (an integer (int or long), an
        integer (int or long), an integer (int or long)))
        resampled array size
        argument: ``-size %d %d %d``
        mutually_exclusive: target_file
voxel_size: (a tuple of the form: (a float, a float, a float))
        resampled voxel size
        argument: ``-vsize %g %g %g``
        mutually_exclusive: target_file
origin: (a tuple of the form: (a float, a float, a float))
        xyz origin
        argument: ``-origin %g %g %g``
        mutually_exclusive: target_file
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

60.3.6 SVResampleTask[Link to code](#)

Wraps the executable command SVResample.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        image to resample
        argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output path
        argument: ``-out %s``
target_file: (a pathlike object or string representing a file)
        specs read from the target volume
        argument: ``-target %s``
        mutually_exclusive: array_size, voxel_size, origin
align: ('center' or 'origin')
        how to align output volume to input volume
        argument: ``-align %s``
array_size: (a tuple of the form: (an integer (int or long), an
        integer (int or long), an integer (int or long)))
        resampled array size
        argument: ``-size %d %d %d``

```

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```

        mutually_exclusive: target_file
voxel_size: (a tuple of the form: (a float, a float, a float))
    resampled voxel size
    argument: ``-vsize %g %g %g``
    mutually_exclusive: target_file
origin: (a tuple of the form: (a float, a float, a float))
    xyz origin
    argument: ``-origin %g %g %g``
    mutually_exclusive: target_file
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)

```

60.3.7 TVAdjustOriginTask[Link to code](#)

Wraps the executable command TVAdjustVoxelspace.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    tensor volume to modify
    argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
    output path
    argument: ``-out %s``
target_file: (a pathlike object or string representing a file)
    target volume to match
    argument: ``-target %s``
    mutually_exclusive: voxel_size, origin
voxel_size: (a tuple of the form: (a float, a float, a float))
    xyz voxel size (superseded by target)
    argument: ``-vsize %g %g %g``
    mutually_exclusive: target_file
origin: (a tuple of the form: (a float, a float, a float))
    xyz origin (superseded by target)
    argument: ``-origin %g %g %g``
    mutually_exclusive: target_file
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

60.3.8 TVAdjustVoxSp

[Link to code](#)

Wraps the executable command TVAdjustVoxelspace.

Adjusts the voxel space of a tensor volume

Example

```
>>> from nipy.interfaces import dtitk
>>> node = dtitk.TVAdjustVoxSp()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.target_file = 'im2.nii'
>>> node.cmdline
'TVAdjustVoxelspace -in im1.nii -out im1_avs.nii -target im2.nii'
>>> node.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        tensor volume to modify
        argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output path
        argument: ``-out %s``
target_file: (a pathlike object or string representing a file)
        target volume to match
        argument: ``-target %s``
        mutually_exclusive: voxel_size, origin
voxel_size: (a tuple of the form: (a float, a float, a float))
        xyz voxel size (superseded by target)
        argument: ``-vsize %g %g %g``
        mutually_exclusive: target_file
origin: (a tuple of the form: (a float, a float, a float))
        xyz origin (superseded by target)
        argument: ``-origin %g %g %g``
        mutually_exclusive: target_file
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

60.3.9 TVAdjustVoxSpTask

[Link to code](#)

Wraps the executable command TVAdjustVoxelspace.

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        tensor volume to modify
        argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output path
        argument: ``-out %s``
target_file: (a pathlike object or string representing a file)
        target volume to match
        argument: ``-target %s``
        mutually_exclusive: voxel_size, origin
voxel_size: (a tuple of the form: (a float, a float, a float))
        xyz voxel size (superseded by target)
        argument: ``-vsize %g %g %g``
        mutually_exclusive: target_file
origin: (a tuple of the form: (a float, a float, a float))
        xyz origin (superseded by target)
        argument: ``-origin %g %g %g``
        mutually_exclusive: target_file
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

60.3.10 TVResample

[Link to code](#)

Wraps the executable command TVResample.

Resamples a tensor volume

```
>>> from nipy.interfaces import dtitk
>>> node = dtitk.TVResample()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.target_file = 'im2.nii'
>>> node.cmdline
'TVResample -in im1.nii -out im1_resampled.nii -target im2.nii'
>>> node.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        tensor volume to resample
        argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
```

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```

        output path
        argument: ``-out %s``
target_file: (a pathlike object or string representing a file)
        specs read from the target volume
        argument: ``-target %s``
        mutually_exclusive: array_size, voxel_size, origin
align: ('center' or 'origin')
        how to align output volume to input volume
        argument: ``-align %s``
interpolation: ('LEI' or 'EI')
        Log Euclidean Euclidean Interpolation
        argument: ``-interp %s``
array_size: (a tuple of the form: (an integer (int or long), an
        integer (int or long), an integer (int or long)))
        resampled array size
        argument: ``-size %d %d %d``
        mutually_exclusive: target_file
voxel_size: (a tuple of the form: (a float, a float, a float))
        resampled voxel size
        argument: ``-vsize %g %g %g``
        mutually_exclusive: target_file
origin: (a tuple of the form: (a float, a float, a float))
        xyz origin
        argument: ``-origin %g %g %g``
        mutually_exclusive: target_file
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)

```

60.3.11 TVResampleTask[Link to code](#)

Wraps the executable command TVResample.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        tensor volume to resample
        argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output path
        argument: ``-out %s``
target_file: (a pathlike object or string representing a file)
        specs read from the target volume
        argument: ``-target %s``
        mutually_exclusive: array_size, voxel_size, origin

```

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```

align: ('center' or 'origin')
    how to align output volume to input volume
    argument: ``-align %s``
interpolation: ('LEI' or 'EI')
    Log Euclidean Euclidean Interpolation
    argument: ``-interp %s``
array_size: (a tuple of the form: (an integer (int or long), an
    integer (int or long), an integer (int or long)))
    resampled array size
    argument: ``-size %d %d %d``
mutually_exclusive: target_file
voxel_size: (a tuple of the form: (a float, a float, a float))
    resampled voxel size
    argument: ``-vsize %g %g %g``
mutually_exclusive: target_file
origin: (a tuple of the form: (a float, a float, a float))
    xyz origin
    argument: ``-origin %g %g %g``
mutually_exclusive: target_file
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)

```

60.3.12 TVtool[Link to code](#)

Wraps the executable command TVtool.

Calculates a tensor metric volume from a tensor volume

```

>>> from nipy.interfaces import dtitk
>>> node = dtitk.TVtool()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.in_flag = 'fa'
>>> node.cmdline
'TVtool -in im1.nii -fa -out im1_fa.nii'
>>> node.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    scalar volume to resample
    argument: ``-in %s``

[Optional]
in_flag: ('fa' or 'tr' or 'ad' or 'rd' or 'pd' or 'rgb')
    argument: ``-%s``
out_file: (a pathlike object or string representing a file)
    argument: ``-out %s``

```

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```

args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)

```

60.3.13 TVtoolTask

[Link to code](#)

Wraps the executable command TVtool.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    scalar volume to resample
    argument: ``-in %s``

[Optional]
in_flag: ('fa' or 'tr' or 'ad' or 'rd' or 'pd' or 'rgb')
    argument: ``-%s``
out_file: (a pathlike object or string representing a file)
    argument: ``-out %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)

```


61.1 interfaces.elastix.registration

61.1.1 AnalyzeWarp

[Link to code](#)

Wraps the executable command `transformix`.

Use `transformix` to get details from the input transform (generate the corresponding deformation field, generate the determinant of the Jacobian map or the Jacobian map itself)

Example

```
>>> from nipy.interfaces.elastix import AnalyzeWarp
>>> reg = AnalyzeWarp()
>>> reg.inputs.transform_file = 'TransformParameters.0.txt'
>>> reg.cmdline
'transformix -def all -jac all -jacmat all -threads 1 -out ./ -tp_
↪TransformParameters.0.txt'
```

Inputs:

```
[Mandatory]
transform_file: (a pathlike object or string representing an existing
                file)
                transform-parameter file, only 1
                argument: ``-tp %s``
output_path: (a pathlike object or string representing an existing
              directory, nipy default value: ./)
              output directory
              argument: ``-out %s``

[Optional]
points: ('all', nipy default value: all)
        transform all points from the input-image, which effectively
        generates a deformation field.
        argument: ``-def %s``, position: 0
jac: ('all', nipy default value: all)
```

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```

        generate an image with the determinant of the spatial Jacobian
        argument: ``-jac %s``
jacmat: ('all', nipy default value: all)
        generate an image with the spatial Jacobian matrix at each voxel
        argument: ``-jacmat %s``
moving_image: (a pathlike object or string representing an existing
        file)
        input image to deform (not used)
        argument: ``-in %s``
num_threads: (an integer (int or long), nipy default value: 1)
        set the maximum number of threads of elastix
        argument: ``-threads %0ld``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

disp_field: (a pathlike object or string representing a file)
        displacements field
jacdet_map: (a pathlike object or string representing a file)
        det(Jacobian) map
jacmat_map: (a pathlike object or string representing a file)
        Jacobian matrix map

```

61.1.2 ApplyWarp

[Link to code](#)

Wraps the executable command transformix.

Use transformix to apply a transform on an input image. The transform is specified in the transform-parameter file.

Example

```

>>> from nipy.interfaces.elastix import ApplyWarp
>>> reg = ApplyWarp()
>>> reg.inputs.moving_image = 'moving1.nii'
>>> reg.inputs.transform_file = 'TransformParameters.0.txt'
>>> reg.cmdline
'transformix -in moving1.nii -threads 1 -out ./ -tp TransformParameters.0.txt'

```

Inputs:

```

[Mandatory]
transform_file: (a pathlike object or string representing an existing
        file)
        transform-parameter file, only 1
        argument: ``-tp %s``
moving_image: (a pathlike object or string representing an existing
        file)
        input image to deform
        argument: ``-in %s``

```

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```

output_path: (a pathlike object or string representing an existing
              directory, nipy default value: ./)
              output directory
              argument: ``-out %s``

[Optional]
num_threads: (an integer (int or long), nipy default value: 1)
              set the maximum number of threads of elastix
              argument: ``-threads %01d``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

warped_file: (a pathlike object or string representing a file)
              input moving image warped to fixed image

```

61.1.3 PointsWarp[Link to code](#)

Wraps the executable command transformix.

Use transformix to apply a transform on an input point set. The transform is specified in the transform-parameter file.

Example

```

>>> from nipy.interfaces.elastix import PointsWarp
>>> reg = PointsWarp()
>>> reg.inputs.points_file = 'surfl.vtk'
>>> reg.inputs.transform_file = 'TransformParameters.0.txt'
>>> reg.cmdline
'transformix -threads 1 -out ./ -def surfl.vtk -tp TransformParameters.0.txt'

```

Inputs:

```

[Mandatory]
points_file: (a pathlike object or string representing an existing
              file)
              input points (accepts .vtk triangular meshes).
              argument: ``-def %s``
transform_file: (a pathlike object or string representing an existing
                 file)
                 transform-parameter file, only 1
                 argument: ``-tp %s``
output_path: (a pathlike object or string representing an existing
              directory, nipy default value: ./)
              output directory
              argument: ``-out %s``

[Optional]
num_threads: (an integer (int or long), nipy default value: 1)

```

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```

        set the maximum number of threads of elastix
        argument: ``-threads %01d``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

warped_file: (a pathlike object or string representing a file)
             input points displaced in fixed image domain

```

61.1.4 Registration[Link to code](#)

Wraps the executable command elastix.

Elastix nonlinear registration interface

Example

```

>>> from nipy.interfaces.elastix import Registration
>>> reg = Registration()
>>> reg.inputs.fixed_image = 'fixed1.nii'
>>> reg.inputs.moving_image = 'moving1.nii'
>>> reg.inputs.parameters = ['elastix.txt']
>>> reg.cmdline
'elastix -f fixed1.nii -m moving1.nii -threads 1 -out ./ -p elastix.txt'

```

Inputs:

```

[Mandatory]
fixed_image: (a pathlike object or string representing an existing
              file)
              fixed image
              argument: ``-f %s``
moving_image: (a pathlike object or string representing an existing
               file)
               moving image
               argument: ``-m %s``
parameters: (a list of items which are a pathlike object or string
             representing an existing file)
             parameter file, elastix handles 1 or more -p
             argument: ``-p %s...``
output_path: (a pathlike object or string representing an existing
              directory, nipy default value: ./)
              output directory
              argument: ``-out %s``

[Optional]
fixed_mask: (a pathlike object or string representing an existing
             file)
             mask for fixed image
             argument: ``-fMask %s``

```

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```

moving_mask: (a pathlike object or string representing an existing
              file)
              mask for moving image
              argument: ``-mMask %s``
initial_transform: (a pathlike object or string representing an
                   existing file)
                   parameter file for initial transform
                   argument: ``-t0 %s``
num_threads: (an integer (int or long), nipyte default value: 1)
              set the maximum number of threads of elastix
              argument: ``-threads %01d``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyte default value: {})
          Environment variables

```

Outputs:

```

transform: (a list of items which are a pathlike object or string
            representing an existing file)
            output transform
warped_file: (a pathlike object or string representing a file)
             input moving image warped to fixed image
warped_files: (a list of items which are a pathlike object or string
               representing a file)
               input moving image warped to fixed image at each level
warped_files_flags: (a list of items which are a boolean)
                    flag indicating if warped image was generated

```

61.2 interfaces.elastix.utils

61.2.1 EditTransform

[Link to code](#)

Manipulates an existing transform file generated with elastix

Example

```

>>> from nipyte.interfaces.elastix import EditTransform
>>> tfm = EditTransform()
>>> tfm.inputs.transform_file = 'TransformParameters.0.txt' # doctest: +SKIP
>>> tfm.inputs.reference_image = 'fixed1.nii' # doctest: +SKIP
>>> tfm.inputs.output_type = 'unsigned char'
>>> tfm.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
transform_file: (a pathlike object or string representing an existing
                 file)
                 transform-parameter file, only 1

```

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```
[Optional]
reference_image: (a pathlike object or string representing an
                  existing file)
                  set a new reference image to change the target coordinate system.
interpolation: ('cubic' or 'linear' or 'nearest', nipy default
                value: cubic)
                set a new interpolator for transformation
                argument: ``FinalBSplineInterpolationOrder``
output_type: ('float' or 'unsigned char' or 'unsigned short' or
              'short' or 'unsigned long' or 'long' or 'double')
              set a new output pixel type for resampled images
              argument: ``ResultImagePixelType``
output_format: ('nii.gz' or 'nii' or 'mhd' or 'hdr' or 'vtk')
                set a new image format for resampled images
                argument: ``ResultImageFormat``
output_file: (a pathlike object or string representing a file)
              the filename for the resulting transform file
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
              file)
              output transform file
```


62.1 interfaces.freesurfer.longitudinal

62.1.1 FuseSegmentations

[Link to code](#)

Wraps the executable command `mri_fuse_segmentations`.
fuse segmentations together from multiple timepoints

Examples

```
>>> from nipy.interfaces.freesurfer import FuseSegmentations
>>> fuse = FuseSegmentations()
>>> fuse.inputs.subject_id = 'tp.long.A.template'
>>> fuse.inputs.timepoints = ['tp1', 'tp2']
>>> fuse.inputs.out_file = 'aseg.fused.mgz'
>>> fuse.inputs.in_segmentations = ['aseg.mgz', 'aseg.mgz']
>>> fuse.inputs.in_segmentations_noCC = ['aseg.mgz', 'aseg.mgz']
>>> fuse.inputs.in_norms = ['norm.mgz', 'norm.mgz', 'norm.mgz']
>>> fuse.cmdline
'mri_fuse_segmentations -n norm.mgz -a aseg.mgz -c aseg.mgz tp.long.A.template_
↪tp1 tp2'
```

Inputs:

```
[Mandatory]
timepoints: (a list of items which are a string)
             subject_ids or timepoints to be processed
             argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file)
           output fused segmentation file
in_segmentations: (a list of items which are a pathlike object or
                   string representing an existing file)
                   name of aseg file to use (default: aseg.mgz) must include the aseg
                   files for all the given timepoints
                   argument: ``-a %s``
in_segmentations_noCC: (a list of items which are a pathlike object
```

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```

        or string representing an existing file)
        name of aseg file w/o CC labels (default: aseg.auto_noCCseg.mgz)
        must include the corresponding file for all the given timepoints
        argument: ``-c %s``
in_norms: (a list of items which are a pathlike object or string
        representing an existing file)
        -n <filename> - name of norm file to use (default: norm.mgs) must
        include the corresponding norm file for all given timepoints as well
        as for the current subject
        argument: ``-n %s``

[Optional]
subject_id: (a string)
        subject_id being processed
        argument: ``%s``, position: -3
subjects_dir: (a pathlike object or string representing an existing
        directory)
        subjects directory
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
        output fused segmentation file

```

62.1.2 RobustTemplate[Link to code](#)

Wraps the executable command `mri_robust_template`.
construct an unbiased robust template for longitudinal volumes

Examples

```

>>> from nipy.interfaces.freesurfer import RobustTemplate
>>> template = RobustTemplate()
>>> template.inputs.in_files = ['structural.nii', 'functional.nii']
>>> template.inputs.auto_detect_sensitivity = True
>>> template.inputs.average_metric = 'mean'
>>> template.inputs.initial_timepoint = 1
>>> template.inputs.fixed_timepoint = True
>>> template.inputs.no_iteration = True
>>> template.inputs.subsample_threshold = 200
>>> template.cmdline #doctest:
'mri_robust_template --satit --average 0 --fixtp --mov structural.nii functional.
↪nii --inittp 1 --noit --template mri_robust_template_out.mgz --subsample 200'
>>> template.inputs.out_file = 'T1.nii'
>>> template.cmdline #doctest:
'mri_robust_template --satit --average 0 --fixtp --mov structural.nii functional.
↪nii --inittp 1 --noit --template T1.nii --subsample 200'

```

```
>>> template.inputs.transform_outputs = ['structural.lta',
...                                     'functional.lta']
>>> template.inputs.scaled_intensity_outputs = ['structural-iscale.txt',
...                                             'functional-iscale.txt']
>>> template.cmdline    #doctest: +ELLIPSIS
'mri_robust_template --satit --average 0 --fixtp --mov structural.nii functional.
↪nii --inittp 1 --noit --template T1.nii --iscaleout ../structural-iscale.txt ..
↪../functional-iscale.txt --subsample 200 --lta ../structural.lta ../functional.
↪lta'
```

```
>>> template.inputs.transform_outputs = True
>>> template.inputs.scaled_intensity_outputs = True
>>> template.cmdline    #doctest: +ELLIPSIS
'mri_robust_template --satit --average 0 --fixtp --mov structural.nii functional.
↪nii --inittp 1 --noit --template T1.nii --iscaleout ../is1.txt ../is2.txt --
↪subsample 200 --lta ../tp1.lta ../tp2.lta'
```

```
>>> template.run()    #doctest: +SKIP
```

References

[https://surfer.nmr.mgh.harvard.edu/fswiki/mri_robust_template]

Inputs:

[Mandatory]

in_files: (a list of items which are a pathlike object or string representing an existing file)
input movable volumes to be aligned to common mean/median template
argument: ``--mov %s``

out_file: (a pathlike object or string representing a file, nipy default value: `mri_robust_template_out.mgz`)
output template volume (final mean/median image)
argument: ``--template %s``

auto_detect_sensitivity: (a boolean)
auto-detect good sensitivity (recommended for head or full brain scans)
argument: ``--satit``
mutually_exclusive: `outlier_sensitivity`

outlier_sensitivity: (a float)
set outlier sensitivity manually (e.g. `--sat 4.685`). Higher values mean less sensitivity.
argument: ``--sat %.4f``
mutually_exclusive: `auto_detect_sensitivity`

[Optional]

transform_outputs: (a list of items which are a pathlike object or string representing a file or a boolean)
output xforms to template (for each input)
argument: ``--lta %s``

intensity_scaling: (a boolean)
allow also intensity scaling (default off)
argument: ``--iscale``

scaled_intensity_outputs: (a list of items which are a pathlike object or string representing a file or a boolean)
final intensity scales (will activate `--iscale`)
argument: ``--iscaleout %s``

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```

subsample_threshold: (an integer (int or long))
    subsample if dim > # on all axes (default no subs.)
    argument: ``--subsample %d``
average_metric: ('median' or 'mean')
    construct template from: 0 Mean, 1 Median (default)
    argument: ``--average %d``
initial_timepoint: (an integer (int or long))
    use TP# for spacial init (default random), 0: no init
    argument: ``--inittp %d``
fixed_timepoint: (a boolean)
    map everthing to init TP# (init TP is not resampled)
    argument: ``--fixtp``
no_iteration: (a boolean)
    do not iterate, just create first template
    argument: ``--noit``
initial_transforms: (a list of items which are a pathlike object or
    string representing an existing file)
    use initial transforms (lta) on source
    argument: ``--ixforms %s``
in_intensity_scales: (a list of items which are a pathlike object or
    string representing an existing file)
    use initial intensity scales
    argument: ``--iscalein %s``
num_threads: (an integer (int or long))
    allows for specifying more threads
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output template volume (final mean/median image)
transform_outputs: (a list of items which are a pathlike object or
    string representing an existing file)
    output xform files from moving to template
scaled_intensity_outputs: (a list of items which are a pathlike
    object or string representing an existing file)
    output final intensity scales

```

62.2 interfaces.freesurfer.model

62.2.1 Binarize

[Link to code](#)Wraps the executable command `mri_binarize`.Use FreeSurfer `mri_binarize` to threshold an input volume

Examples

```
>>> binvol = Binarize(in_file='structural.nii', min=10, binary_file='foo_out.nii')
>>> binvol.cmdline
'mri_binarize --o foo_out.nii --i structural.nii --min 10.000000'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input volume
         argument: ``--i %s``

[Optional]
min: (a float)
     min thresh
     argument: ``--min %f``
     mutually_exclusive: wm_ven_csf
max: (a float)
     max thresh
     argument: ``--max %f``
     mutually_exclusive: wm_ven_csf
rmin: (a float)
      compute min based on rmin*globalmean
      argument: ``--rmin %f``
rmax: (a float)
      compute max based on rmax*globalmean
      argument: ``--rmax %f``
match: (a list of items which are an integer (int or long))
       match instead of threshold
       argument: ``--match %d...``
wm: (a boolean)
    set match vals to 2 and 41 (aseg for cerebral WM)
    argument: ``--wm``
ventricles: (a boolean)
            set match vals those for aseg ventricles+choroid (not 4th)
            argument: ``--ventricles``
wm_ven_csf: (a boolean)
            WM and ventricular CSF, including choroid (not 4th)
            argument: ``--wm+vcsf``
            mutually_exclusive: min, max
binary_file: (a pathlike object or string representing a file)
             binary output volume
             argument: ``--o %s``
out_type: ('nii' or 'nii.gz' or 'mgz')
          output file type
count_file: (a boolean or a pathlike object or string representing a
            file)
            save number of hits in ascii file (hits, ntotvox, pct)
            argument: ``--count %s``
bin_val: (an integer (int or long))
         set vox within thresh to val (default is 1)
         argument: ``--binval %d``
bin_val_not: (an integer (int or long))
             set vox outside range to val (default is 0)
             argument: ``--binvalnot %d``
invert: (a boolean)
        set binval=0, binvalnot=1
```

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```

        argument: ``--inv``
frame_no: (an integer (int or long))
    use 0-based frame of input (default is 0)
    argument: ``--frame %s``
merge_file: (a pathlike object or string representing an existing
    file)
    merge with mergevol
    argument: ``--merge %s``
mask_file: (a pathlike object or string representing an existing
    file)
    must be within mask
    argument: ``--mask maskvol``
mask_thresh: (a float)
    set thresh for mask
    argument: ``--mask-thresh %f``
abs: (a boolean)
    take abs of invol first (ie, make unsigned)
    argument: ``--abs``
bin_col_num: (a boolean)
    set binarized voxel value to its column number
    argument: ``--bincol``
zero_edges: (a boolean)
    zero the edge voxels
    argument: ``--zero-edges``
zero_slice_edge: (a boolean)
    zero the edge slice voxels
    argument: ``--zero-slice-edges``
dilate: (an integer (int or long))
    niters: dilate binarization in 3D
    argument: ``--dilate %d``
erode: (an integer (int or long))
    nerode: erode binarization in 3D (after any dilation)
    argument: ``--erode %d``
erode2d: (an integer (int or long))
    nerode2d: erode binarization in 2D (after any 3D erosion)
    argument: ``--erode2d %d``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

binary_file: (a pathlike object or string representing an existing
    file)
    binarized output volume
count_file: (a pathlike object or string representing a file)
    ascii file containing number of hits

```

62.2.2 Concatenate

[Link to code](#)

Wraps the executable command `mri_concat`.

Use `Freesurfer mri_concat` to combine several input volumes into one output volume. Can concatenate by frames, or compute a variety of statistics on the input volumes.

Examples

Combine two input volumes into one volume with two frames

```
>>> concat = Concatenate()
>>> concat.inputs.in_files = ['cont1.nii', 'cont2.nii']
>>> concat.inputs.concatenated_file = 'bar.nii'
>>> concat.cmdline
'mri_concat --o bar.nii --i cont1.nii --i cont2.nii'
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
           representing an existing file)
           Individual volumes to be concatenated
           argument: ``--i %s...``

[Optional]
concatenated_file: (a pathlike object or string representing a file)
                   Output volume
                   argument: ``--o %s``
sign: ('abs' or 'pos' or 'neg')
      Take only pos or neg voxles from input, or take abs
      argument: ``--%s``
stats: ('sum' or 'var' or 'std' or 'max' or 'min' or 'mean')
       Compute the sum, var, std, max, min or mean of the input volumes
       argument: ``--%s``
paired_stats: ('sum' or 'avg' or 'diff' or 'diff-norm' or 'diff-
               norm1' or 'diff-norm2')
               Compute paired sum, avg, or diff
               argument: ``--paired-%s``
gmean: (an integer (int or long))
       create matrix to average Ng groups, Nper=Ntot/Ng
       argument: ``--gmean %d``
mean_div_n: (a boolean)
            compute mean/nframes (good for var)
            argument: ``--mean-div-n``
multiply_by: (a float)
            Multiply input volume by some amount
            argument: ``--mul %f``
add_val: (a float)
         Add some amount to the input volume
         argument: ``--add %f``
multiply_matrix_file: (a pathlike object or string representing an
                      existing file)
                      Multiply input by an ascii matrix in file
                      argument: ``--mtx %s``
combine: (a boolean)
         Combine non-zero values into single frame volume
         argument: ``--combine``
keep_dtype: (a boolean)
```

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```

        Keep voxelwise precision type (default is float
        argument: ``--keep-datatype``
max_bonfcor: (a boolean)
        Compute max and bonferroni correct (assumes -log10(ps))
        argument: ``--max-bonfcor``
max_index: (a boolean)
        Compute the index of max voxel in concatenated volumes
        argument: ``--max-index``
mask_file: (a pathlike object or string representing an existing
        file)
        Mask input with a volume
        argument: ``--mask %s``
vote: (a boolean)
        Most frequent value at each voxel and fraction of occurrences
        argument: ``--vote``
sort: (a boolean)
        Sort each voxel by ascending frame value
        argument: ``--sort``
subjects_dir: (a pathlike object or string representing an existing
        directory)
        subjects directory
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

concatenated_file: (a pathlike object or string representing an
        existing file)
        Path/name of the output volume

```

62.2.3 GLMFit[Link to code](#)Wraps the executable command `mri_glmfit`.Use FreeSurfer's `mri_glmfit` to specify and estimate a general linear model.**Examples**

```

>>> glmfit = GLMFit()
>>> glmfit.inputs.in_file = 'functional.nii'
>>> glmfit.inputs.one_sample = True
>>> glmfit.cmdline == 'mri_glmfit --glmdir %s --y functional.nii --osgm'%os.
↪getcwd()
True

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing a file)
        input 4D file
        argument: ``--y %s``

```

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```

[Optional]
glm_dir: (a unicode string)
    save outputs to dir
    argument: ``--glmdir %s``
fsgd: (a tuple of the form: (a pathlike object or string representing
    an existing file, 'doss' or 'dods'))
    freesurfer descriptor file
    argument: ``--fsgd %s %s``
    mutually_exclusive: fsgd, design, one_sample
design: (a pathlike object or string representing an existing file)
    design matrix file
    argument: ``--X %s``
    mutually_exclusive: fsgd, design, one_sample
contrast: (a list of items which are a pathlike object or string
    representing an existing file)
    contrast file
    argument: ``--C %s...``
one_sample: (a boolean)
    construct X and C as a one-sample group mean
    argument: ``--osgm``
    mutually_exclusive: one_sample, fsgd, design, contrast
no_contrast_ok: (a boolean)
    do not fail if no contrasts specified
    argument: ``--no-contrasts-ok``
per_voxel_reg: (a list of items which are a pathlike object or string
    representing an existing file)
    per-voxel regressors
    argument: ``--pvr %s...``
self_reg: (a tuple of the form: (an integer (int or long), an integer
    (int or long), an integer (int or long)))
    self-regressor from index col row slice
    argument: ``--selfreg %d %d %d``
weighted_ls: (a pathlike object or string representing an existing
    file)
    weighted least squares
    argument: ``--wls %s``
    mutually_exclusive: weight_file, weight_inv, weight_sqrt
fixed_fx_var: (a pathlike object or string representing an existing
    file)
    for fixed effects analysis
    argument: ``--yffxvar %s``
fixed_fx_dof: (an integer (int or long))
    dof for fixed effects analysis
    argument: ``--ffxdof %d``
    mutually_exclusive: fixed_fx_dof_file
fixed_fx_dof_file: (a pathlike object or string representing a file)
    text file with dof for fixed effects analysis
    argument: ``--ffxdofdat %d``
    mutually_exclusive: fixed_fx_dof
weight_file: (a pathlike object or string representing an existing
    file)
    weight for each input at each voxel
    mutually_exclusive: weighted_ls
weight_inv: (a boolean)
    invert weights
    argument: ``--w-inv``

```

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```

        mutually_exclusive: weighted_ls
weight_sqrt: (a boolean)
    sqrt of weights
    argument: ``--w-sqrt``
    mutually_exclusive: weighted_ls
fwhm: (a floating point number >= 0.0)
    smooth input by fwhm
    argument: ``--fwhm %f``
var_fwhm: (a floating point number >= 0.0)
    smooth variance by fwhm
    argument: ``--var-fwhm %f``
no_mask_smooth: (a boolean)
    do not mask when smoothing
    argument: ``--no-mask-smooth``
no_est_fwhm: (a boolean)
    turn off FWHM output estimation
    argument: ``--no-est-fwhm``
mask_file: (a pathlike object or string representing an existing
    file)
    binary mask
    argument: ``--mask %s``
label_file: (a pathlike object or string representing an existing
    file)
    use label as mask, surfaces only
    argument: ``--label %s``
    mutually_exclusive: cortex
cortex: (a boolean)
    use subjects ?h.cortex.label as label
    argument: ``--cortex``
    mutually_exclusive: label_file
invert_mask: (a boolean)
    invert mask
    argument: ``--mask-inv``
prune: (a boolean)
    remove voxels that do not have a non-zero value at each frame (def)
    argument: ``--prune``
no_prune: (a boolean)
    do not prune
    argument: ``--no-prune``
    mutually_exclusive: prunethresh
prune_thresh: (a float)
    prune threshold. Default is FLT_MIN
    argument: ``--prune_thr %f``
    mutually_exclusive: noprun
compute_log_y: (a boolean)
    compute natural log of y prior to analysis
    argument: ``--logy``
save_estimate: (a boolean)
    save signal estimate (yhat)
    argument: ``--yhat-save``
save_residual: (a boolean)
    save residual error (eres)
    argument: ``--eres-save``
save_res_corr_mtx: (a boolean)
    save residual error spatial correlation matrix (eres.scm). Big!
    argument: ``--eres-scm``
surf: (a boolean)

```

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```

        analysis is on a surface mesh
        argument: ``--surf %s %s %s``
        requires: subject_id, hemi
subject_id: (a unicode string)
        subject id for surface geometry
hemi: ('lh' or 'rh')
        surface hemisphere
surf_geo: (a unicode string, nipy default value: white)
        surface geometry name (e.g. white, pial)
simulation: (a tuple of the form: ('perm' or 'mc-full' or 'mc-z', an
        integer (int or long), a float, a unicode string))
        nulltype nsim thresh csdbasename
        argument: ``--sim %s %d %f %s``
sim_sign: ('abs' or 'pos' or 'neg')
        abs, pos, or neg
        argument: ``--sim-sign %s``
uniform: (a tuple of the form: (a float, a float))
        use uniform distribution instead of gaussian
        argument: ``--uniform %f %f``
pca: (a boolean)
        perform pca/svd analysis on residual
        argument: ``--pca``
calc_AR1: (a boolean)
        compute and save temporal AR1 of residual
        argument: ``--tar1``
save_cond: (a boolean)
        flag to save design matrix condition at each voxel
        argument: ``--save-cond``
vox_dump: (a tuple of the form: (an integer (int or long), an integer
        (int or long), an integer (int or long)))
        dump voxel GLM and exit
        argument: ``--voxdump %d %d %d``
seed: (an integer (int or long))
        used for synthesizing noise
        argument: ``--seed %d``
synth: (a boolean)
        replace input with gaussian
        argument: ``--synth``
resynth_test: (an integer (int or long))
        test GLM by resynthesis
        argument: ``--resynthtest %d``
profile: (an integer (int or long))
        niters : test speed
        argument: ``--profile %d``
force_perm: (a boolean)
        force permutation test, even when design matrix is not orthog
        argument: ``--perm-force``
diag: (an integer (int or long))
        Gdiag_no : set diagnositic level
        argument: ``--diag %d``
diag_cluster: (a boolean)
        save sig volume and exit from first sim loop
        argument: ``--diag-cluster``
debug: (a boolean)
        turn on debugging
        argument: ``--debug``
check_opts: (a boolean)

```

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```

        don't run anything, just check options and exit
        argument: ``--checkopts``
allow_repeated_subjects: (a boolean)
        allow subject names to repeat in the fsgd file (must appear before
        --fsgd
        argument: ``--allowsbjrep``
allow_ill_cond: (a boolean)
        allow ill-conditioned design matrices
        argument: ``--illcond``
sim_done_file: (a pathlike object or string representing a file)
        create file when simulation finished
        argument: ``--sim-done %s``
subjects_dir: (a pathlike object or string representing an existing
        directory)
        subjects directory
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipyre default value: {})
        Environment variables

```

Outputs:

```

glm_dir: (a pathlike object or string representing an existing
        directory)
        output directory
beta_file: (a pathlike object or string representing an existing
        file)
        map of regression coefficients
error_file: (a pathlike object or string representing a file)
        map of residual error
error_var_file: (a pathlike object or string representing a file)
        map of residual error variance
error_stddev_file: (a pathlike object or string representing a file)
        map of residual error standard deviation
estimate_file: (a pathlike object or string representing a file)
        map of the estimated Y values
mask_file: (a pathlike object or string representing a file)
        map of the mask used in the analysis
fwhm_file: (a pathlike object or string representing a file)
        text file with estimated smoothness
dof_file: (a pathlike object or string representing a file)
        text file with effective degrees-of-freedom for the analysis
gamma_file: (a list of items which are any value)
        map of contrast of regression coefficients
gamma_var_file: (a list of items which are any value)
        map of regression contrast variance
sig_file: (a list of items which are any value)
        map of F-test significance (in -log10p)
ftest_file: (a list of items which are any value)
        map of test statistic values
spatial_eigenvectors: (a pathlike object or string representing a
        file)
        map of spatial eigenvectors from residual PCA
frame_eigenvectors: (a pathlike object or string representing a file)

```

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```

    matrix of frame eigenvectors from residual PCA
singular_values: (a pathlike object or string representing a file)
    matrix singular values from residual PCA
svd_stats_file: (a pathlike object or string representing a file)
    text file summarizing the residual PCA

```

62.2.4 Label2Annot

[Link to code](#)

Wraps the executable command `mris_label2annot`.

Converts a set of surface labels to an annotation file

Examples

```

>>> from nipy.interfaces.freesurfer import Label2Annot
>>> l2a = Label2Annot()
>>> l2a.inputs.hemisphere = 'lh'
>>> l2a.inputs.subject_id = '10335'
>>> l2a.inputs.in_labels = ['lh.aparc.label']
>>> l2a.inputs.orig = 'lh.pial'
>>> l2a.inputs.out_annot = 'test'
>>> l2a.cmdline
'mris_label2annot --hemi lh --l lh.aparc.label --a test --s 10335'

```

Inputs:

```

[Mandatory]
hemisphere: ('lh' or 'rh')
    Input hemisphere
    argument: ``--hemi %s``
subject_id: (a string, nipy default value: subject_id)
    Subject name/ID
    argument: ``--s %s``
in_labels: (a list of items which are any value)
    List of input label files
    argument: ``--l %s...``
out_annot: (a string)
    Name of the annotation to create
    argument: ``--a %s``
orig: (a pathlike object or string representing an existing file)
    implicit {hemisphere}.orig

[Optional]
keep_max: (a boolean)
    Keep label with highest 'stat' value
    argument: ``--maxstatwinner``
verbose_off: (a boolean)
    Turn off overlap and stat override messages
    argument: ``--noverbose``
color_table: (a pathlike object or string representing an existing
    file)
    File that defines the structure names, their indices, and their
    color
    argument: ``--ctab %s``
copy_inputs: (a boolean)

```

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```

copy implicit inputs and create a temp subjects_dir
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          Output annotation file

```

62.2.5 Label2Label

[Link to code](#)

Wraps the executable command `mri_label2label`.

Converts a label in one subject's space to a label in another subject's space using either talairach or spherical as an intermediate registration space.

If a source mask is used, then the input label must have been created from a surface (ie, the vertex numbers are valid). The format can be anything supported by `mri_convert` or `curv` or `paint`. Vertices in the source label that do not meet threshold in the mask will be removed from the label.

Examples

```

>>> from nipy.interfaces.freesurfer import Label2Label
>>> l2l = Label2Label()
>>> l2l.inputs.hemisphere = 'lh'
>>> l2l.inputs.subject_id = '10335'
>>> l2l.inputs.sphere_reg = 'lh.pial'
>>> l2l.inputs.white = 'lh.pial'
>>> l2l.inputs.source_subject = 'fsaverage'
>>> l2l.inputs.source_label = 'lh-pial.stl'
>>> l2l.inputs.source_white = 'lh.pial'
>>> l2l.inputs.source_sphere_reg = 'lh.pial'
>>> l2l.cmdline
'mri_label2label --hemi lh --trglabel lh-pial_converted.stl --regmethod surface --
↪srclabel lh-pial.stl --srcsubject fsaverage --trgsubject 10335'

```

Inputs:

```

[Mandatory]
hemisphere: ('lh' or 'rh')
             Input hemisphere
             argument: ``--hemi %s``
subject_id: (a string, nipy default value: subject_id)
             Target subject
             argument: ``--trgsubject %s``
sphere_reg: (a pathlike object or string representing an existing
             file)
             Implicit input <hemisphere>.sphere.reg
white: (a pathlike object or string representing an existing file)

```

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```

        Implicit input <hemisphere>.white
source_sphere_reg: (a pathlike object or string representing an
                    existing file)
        Implicit input <hemisphere>.sphere.reg
source_white: (a pathlike object or string representing an existing
              file)
        Implicit input <hemisphere>.white
source_label: (a pathlike object or string representing an existing
              file)
        Source label
        argument: ``--srclabel %s``
source_subject: (a string)
        Source subject name
        argument: ``--srcsubject %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        Target label
        argument: ``--trglabel %s``
registration_method: ('surface' or 'volume', nipy default value:
                     surface)
        Registration method
        argument: ``--regmethod %s``
copy_inputs: (a boolean)
        If running as a node, set this to True. This will copy the input
        files to the node directory.
subjects_dir: (a pathlike object or string representing an existing
              directory)
        subjects directory
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        Output label

```

62.2.6 Label2Vol[Link to code](#)Wraps the executable command `mri_label2vol`.

Make a binary volume from a Freesurfer label

Examples

```

>>> binvol = Label2Vol(label_file='cortex.label', template_file='structural.nii',
↳ reg_file='register.dat', fill_thresh=0.5, vol_label_file='foo_out.nii')
>>> binvol.cmdline
'mri_label2vol --fillthresh 0.5 --label cortex.label --reg register.dat --temp_
↳ structural.nii --o foo_out.nii'

```

Inputs:

```
[Mandatory]
label_file: (a list of items which are a pathlike object or string
             representing an existing file)
             list of label files
             argument: ``--label %s...``
             mutually_exclusive: label_file, annot_file, seg_file, aparc_aseg
annot_file: (a pathlike object or string representing an existing
             file)
             surface annotation file
             argument: ``--annot %s``
             mutually_exclusive: label_file, annot_file, seg_file, aparc_aseg
             requires: subject_id, hemi
seg_file: (a pathlike object or string representing an existing file)
            segmentation file
            argument: ``--seg %s``
            mutually_exclusive: label_file, annot_file, seg_file, aparc_aseg
aparc_aseg: (a boolean)
            use aparc+aseg.mgz in subjectdir as seg
            argument: ``--aparc+aseg``
            mutually_exclusive: label_file, annot_file, seg_file, aparc_aseg
template_file: (a pathlike object or string representing an existing
                file)
                output template volume
                argument: ``--temp %s``

[Optional]
reg_file: (a pathlike object or string representing an existing file)
           tkregister style matrix VolXYZ = R*LabelXYZ
           argument: ``--reg %s``
           mutually_exclusive: reg_file, reg_header, identity
reg_header: (a pathlike object or string representing an existing
             file)
             label template volume
             argument: ``--regheader %s``
             mutually_exclusive: reg_file, reg_header, identity
identity: (a boolean)
           set R=I
           argument: ``--identity``
           mutually_exclusive: reg_file, reg_header, identity
invert_mtx: (a boolean)
            Invert the registration matrix
            argument: ``--invertmtx``
fill_thresh: (0.0 <= a floating point number <= 1.0)
             thresh : between 0 and 1
             argument: ``--fillthresh %g``
label_voxel_volume: (a float)
                    volume of each label point (def 1mm3)
                    argument: ``--labvoxvol %f``
proj: (a tuple of the form: ('abs' or 'frac', a float, a float, a
                             float))
       project along surface normal
       argument: ``--proj %s %f %f %f``
       requires: subject_id, hemi
subject_id: (a unicode string)
            subject id
            argument: ``--subject %s``
hemi: ('lh' or 'rh')
```

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```

        hemisphere to use lh or rh
        argument: ``--hemi %s``
surface: (a unicode string)
        use surface instead of white
        argument: ``--surf %s``
vol_label_file: (a pathlike object or string representing a file)
        output volume
        argument: ``--o %s``
label_hit_file: (a pathlike object or string representing a file)
        file with each frame is nhits for a label
        argument: ``--hits %s``
map_label_stat: (a pathlike object or string representing a file)
        map the label stats field into the vol
        argument: ``--label-stat %s``
native_vox2ras: (a boolean)
        use native vox2ras xform instead of tkregister-style
        argument: ``--native-vox2ras``
subjects_dir: (a pathlike object or string representing an existing
        directory)
        subjects directory
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipype default value: {})
        Environment variables

```

Outputs:

```

vol_label_file: (a pathlike object or string representing an existing
        file)
        output volume

```

62.2.7 MRISPreproc[Link to code](#)Wraps the executable command `mriss_preproc`.Use FreeSurfer `mriss_preproc` to prepare a group of contrasts for a second level analysis**Examples**

```

>>> preproc = MRISPreproc()
>>> preproc.inputs.target = 'fsaverage'
>>> preproc.inputs.hemi = 'lh'
>>> preproc.inputs.vol_measure_file = [('cont1.nii', 'register.dat'),
    ↪                                ('cont1a.nii', 'register.dat')]
>>> preproc.inputs.out_file = 'concatenated_file.mgz'
>>> preproc.cmdline
'mriss_preproc --hemi lh --out concatenated_file.mgz --target fsaverage --iv cont1.
    ↪nii register.dat --iv cont1a.nii register.dat'

```

Inputs:

```

[Mandatory]
target: (a unicode string)

```

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```

        target subject name
        argument: ``--target %s``
hemi: ('lh' or 'rh')
        hemisphere for source and target
        argument: ``--hemi %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        output filename
        argument: ``--out %s``
surf_measure: (a unicode string)
        Use subject/surf/hemi.surf_measure as input
        argument: ``--meas %s``
        mutually_exclusive: surf_measure, surf_measure_file, surf_area
surf_area: (a unicode string)
        Extract vertex area from subject/surf/hemi.surfname to use as input.
        argument: ``--area %s``
        mutually_exclusive: surf_measure, surf_measure_file, surf_area
subjects: (a list of items which are any value)
        subjects from who measures are calculated
        argument: ``--s %s...``
        mutually_exclusive: subjects, fsgd_file, subject_file
fsgd_file: (a pathlike object or string representing an existing
        file)
        specify subjects using fsgd file
        argument: ``--fsgd %s``
        mutually_exclusive: subjects, fsgd_file, subject_file
subject_file: (a pathlike object or string representing an existing
        file)
        file specifying subjects separated by white space
        argument: ``--f %s``
        mutually_exclusive: subjects, fsgd_file, subject_file
surf_measure_file: (a list of items which are a pathlike object or
        string representing an existing file)
        file alternative to surfmeas, still requires list of subjects
        argument: ``--is %s...``
        mutually_exclusive: surf_measure, surf_measure_file, surf_area
source_format: (a unicode string)
        source format
        argument: ``--srcfmt %s``
surf_dir: (a unicode string)
        alternative directory (instead of surf)
        argument: ``--surfdir %s``
vol_measure_file: (a list of items which are a tuple of the form: (a
        pathlike object or string representing an existing file, a
        pathlike object or string representing an existing file))
        list of volume measure and reg file tuples
        argument: ``--iv %s %s...``
proj_frac: (a float)
        projection fraction for vol2surf
        argument: ``--projfrac %s``
fwhm: (a float)
        smooth by fwhm mm on the target surface
        argument: ``--fwhm %f``
        mutually_exclusive: num_iters
num_iters: (an integer (int or long))
        niters : smooth by niters on the target surface

```

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```

        argument: ``--nitters %d``
        mutually_exclusive: fwhm
fwhm_source: (a float)
    smooth by fwhm mm on the source surface
    argument: ``--fwhm-src %f``
    mutually_exclusive: num_iters_source
num_iters_source: (an integer (int or long))
    nitters : smooth by nitters on the source surface
    argument: ``--nitterssrc %d``
    mutually_exclusive: fwhm_source
smooth_cortex_only: (a boolean)
    only smooth cortex (ie, exclude medial wall)
    argument: ``--smooth-cortex-only``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    preprocessed output file

```

62.2.8 MRISPreprocReconAll

[Link to code](#)Wraps the executable command `mris_preproc`.

Extends MRISPreproc to allow it to be used in a recon-all workflow

Examples

```

>>> preproc = MRISPreprocReconAll()
>>> preproc.inputs.target = 'fsaverage'
>>> preproc.inputs.hemi = 'lh'
>>> preproc.inputs.vol_measure_file = [('cont1.nii', 'register.dat'),
    ↪ ('cont1a.nii', 'register.dat')]
>>> preproc.inputs.out_file = 'concatenated_file.mgz'
>>> preproc.cmdline
'mris_preproc --hemi lh --out concatenated_file.mgz --s subject_id --target_
    ↪ fsaverage --iv cont1.nii register.dat --iv cont1a.nii register.dat'

```

Inputs:

```

[Mandatory]
target: (a unicode string)
    target subject name
    argument: ``--target %s``
hemi: ('lh' or 'rh')
    hemisphere for source and target
    argument: ``--hemi %s``

```

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```

[Optional]
surf_measure_file: (a pathlike object or string representing an
    existing file)
    file necessary for surfmeas
    argument: ``--meas %s``
    mutually_exclusive: surf_measure, surf_measure_file, surf_area
surfreg_files: (a list of items which are a pathlike object or string
    representing an existing file)
    lh and rh input surface registration files
    argument: ``--surfreg %s``
    requires: lh_surfreg_target, rh_surfreg_target
lh_surfreg_target: (a pathlike object or string representing a file)
    Implicit target surface registration file
    requires: surfreg_files
rh_surfreg_target: (a pathlike object or string representing a file)
    Implicit target surface registration file
    requires: surfreg_files
subject_id: (a string, nipy default value: subject_id)
    subject from whom measures are calculated
    argument: ``--s %s``
    mutually_exclusive: subjects, fsgd_file, subject_file, subject_id
copy_inputs: (a boolean)
    If running as a node, set this to True this will copy some implicit
    inputs to the node directory.
out_file: (a pathlike object or string representing a file)
    output filename
    argument: ``--out %s``
surf_measure: (a unicode string)
    Use subject/surf/hemi.surf_measure as input
    argument: ``--meas %s``
    mutually_exclusive: surf_measure, surf_measure_file, surf_area
surf_area: (a unicode string)
    Extract vertex area from subject/surf/hemi.surfname to use as input.
    argument: ``--area %s``
    mutually_exclusive: surf_measure, surf_measure_file, surf_area
subjects: (a list of items which are any value)
    subjects from who measures are calculated
    argument: ``--s %s...``
    mutually_exclusive: subjects, fsgd_file, subject_file
fsgd_file: (a pathlike object or string representing an existing
    file)
    specify subjects using fsgd file
    argument: ``--fsgd %s``
    mutually_exclusive: subjects, fsgd_file, subject_file
subject_file: (a pathlike object or string representing an existing
    file)
    file specifying subjects separated by white space
    argument: ``--f %s``
    mutually_exclusive: subjects, fsgd_file, subject_file
source_format: (a unicode string)
    source format
    argument: ``--srcfmt %s``
surf_dir: (a unicode string)
    alternative directory (instead of surf)
    argument: ``--surfdir %s``
vol_measure_file: (a list of items which are a tuple of the form: (a

```

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```

        pathlike object or string representing an existing file, a
        pathlike object or string representing an existing file))
    list of volume measure and reg file tuples
    argument: ``--iv %s %s...``
proj_frac: (a float)
    projection fraction for vol2surf
    argument: ``--projfrac %s``
fwhm: (a float)
    smooth by fwhm mm on the target surface
    argument: ``--fwhm %f``
    mutually_exclusive: num_iters
num_iters: (an integer (int or long))
    niters : smooth by niters on the target surface
    argument: ``--niters %d``
    mutually_exclusive: fwhm
fwhm_source: (a float)
    smooth by fwhm mm on the source surface
    argument: ``--fwhm-src %f``
    mutually_exclusive: num_iters_source
num_iters_source: (an integer (int or long))
    niters : smooth by niters on the source surface
    argument: ``--niterssrc %d``
    mutually_exclusive: fwhm_source
smooth_cortex_only: (a boolean)
    only smooth cortex (ie, exclude medial wall)
    argument: ``--smooth-cortex-only``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    preprocessed output file

```

62.2.9 MS_LDA[Link to code](#)Wraps the executable command `mri_ms_LDA`.

Perform LDA reduction on the intensity space of an arbitrary # of FLASH images

Examples

```

>>> grey_label = 2
>>> white_label = 3
>>> zero_value = 1
>>> optimalWeights = MS_LDA(lda_labels=[grey_label, white_label],
    ↪          label_file='label.mgz', weight_file='weights.txt',
    ↪          shift=zero_value, vol_synth_file='synth_out.mgz',
    ↪          conform=True, use_weights=True,
    ↪          images=['FLASH1.mgz', 'FLASH2.mgz', 'FLASH3.mgz'])

```

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```
>>> optimalWeights.cmdline
'mri_ms_LDA -conform -label label.mgz -lda 2 3 -shift 1 -W -synth synth_out.mgz -
↳weight weights.txt FLASH1.mgz FLASH2.mgz FLASH3.mgz'
```

Inputs:

```
[Mandatory]
lda_labels: (a list of from 2 to 2 items which are an integer (int or
            long))
            pair of class labels to optimize
            argument: ``-lda %s``
weight_file: (a pathlike object or string representing a file)
            filename for the LDA weights (input or output)
            argument: ``-weight %s``
vol_synth_file: (a pathlike object or string representing a file)
            filename for the synthesized output volume
            argument: ``-synth %s``
images: (a list of items which are a pathlike object or string
        representing an existing file)
        list of input FLASH images
        argument: ``%s``, position: -1

[Optional]
label_file: (a pathlike object or string representing an existing
            file)
            filename of the label volume
            argument: ``-label %s``
mask_file: (a pathlike object or string representing an existing
            file)
            filename of the brain mask volume
            argument: ``-mask %s``
shift: (an integer (int or long))
        shift all values equal to the given value to zero
        argument: ``-shift %d``
conform: (a boolean)
        Conform the input volumes (brain mask typically already conformed)
        argument: ``-conform``
use_weights: (a boolean)
        Use the weights from a previously generated weight file
        argument: ``-W``
subjects_dir: (a pathlike object or string representing an existing
              directory)
              subjects directory
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
weight_file: (a pathlike object or string representing an existing
            file)
vol_synth_file: (a pathlike object or string representing an existing
                file)
```

62.2.10 OneSampleTTest

[Link to code](#)

Wraps the executable command `mri_glmfit`.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing a file)
         input 4D file
         argument: ``--y %s``

[Optional]
glm_dir: (a unicode string)
         save outputs to dir
         argument: ``--glmdir %s``
fsgd: (a tuple of the form: (a pathlike object or string representing
        an existing file, 'doss' or 'dods'))
        freesurfer descriptor file
        argument: ``--fsgd %s %s``
        mutually_exclusive: fsgd, design, one_sample
design: (a pathlike object or string representing an existing file)
        design matrix file
        argument: ``--X %s``
        mutually_exclusive: fsgd, design, one_sample
contrast: (a list of items which are a pathlike object or string
            representing an existing file)
            contrast file
            argument: ``--C %s...``
one_sample: (a boolean)
            construct X and C as a one-sample group mean
            argument: ``--osgm``
            mutually_exclusive: one_sample, fsgd, design, contrast
no_contrast_ok: (a boolean)
            do not fail if no contrasts specified
            argument: ``--no-contrasts-ok``
per_voxel_reg: (a list of items which are a pathlike object or string
                representing an existing file)
                per-voxel regressors
                argument: ``--pvr %s...``
self_reg: (a tuple of the form: (an integer (int or long), an integer
        (int or long), an integer (int or long)))
        self-regressor from index col row slice
        argument: ``--selfreg %d %d %d``
weighted_ls: (a pathlike object or string representing an existing
            file)
            weighted least squares
            argument: ``--wls %s``
            mutually_exclusive: weight_file, weight_inv, weight_sqrt
fixed_fx_var: (a pathlike object or string representing an existing
            file)
            for fixed effects analysis
            argument: ``--yffxvar %s``
fixed_fx_dof: (an integer (int or long))
            dof for fixed effects analysis
            argument: ``--ffxdof %d``
            mutually_exclusive: fixed_fx_dof_file
fixed_fx_dof_file: (a pathlike object or string representing a file)
            text file with dof for fixed effects analysis

```

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```

        argument: ``--ffxdofdat %d``
        mutually_exclusive: fixed_fx_dof
weight_file: (a pathlike object or string representing an existing
              file)
              weight for each input at each voxel
              mutually_exclusive: weighted_ls
weight_inv: (a boolean)
            invert weights
            argument: ``--w-inv``
            mutually_exclusive: weighted_ls
weight_sqrt: (a boolean)
            sqrt of weights
            argument: ``--w-sqrt``
            mutually_exclusive: weighted_ls
fwhm: (a floating point number >= 0.0)
      smooth input by fwhm
      argument: ``--fwhm %f``
var_fwhm: (a floating point number >= 0.0)
          smooth variance by fwhm
          argument: ``--var-fwhm %f``
no_mask_smooth: (a boolean)
                do not mask when smoothing
                argument: ``--no-mask-smooth``
no_est_fwhm: (a boolean)
             turn off FWHM output estimation
             argument: ``--no-est-fwhm``
mask_file: (a pathlike object or string representing an existing
            file)
            binary mask
            argument: ``--mask %s``
label_file: (a pathlike object or string representing an existing
            file)
            use label as mask, surfaces only
            argument: ``--label %s``
            mutually_exclusive: cortex
cortex: (a boolean)
        use subjects ?h.cortex.label as label
        argument: ``--cortex``
        mutually_exclusive: label_file
invert_mask: (a boolean)
            invert mask
            argument: ``--mask-inv``
prune: (a boolean)
       remove voxels that do not have a non-zero value at each frame (def)
       argument: ``--prune``
no_prune: (a boolean)
          do not prune
          argument: ``--no-prune``
          mutually_exclusive: prunethresh
prune_thresh: (a float)
              prune threshold. Default is FLT_MIN
              argument: ``--prune_thr %f``
              mutually_exclusive: noprune
compute_log_y: (a boolean)
               compute natural log of y prior to analysis
               argument: ``--logy``
save_estimate: (a boolean)

```

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```

        save signal estimate (yhat)
        argument: ``--yhat-save``
save_residual: (a boolean)
        save residual error (eres)
        argument: ``--eres-save``
save_res_corr_mtx: (a boolean)
        save residual error spatial correlation matrix (eres.scm). Big!
        argument: ``--eres-scm``
surf: (a boolean)
        analysis is on a surface mesh
        argument: ``--surf %s %s %s``
        requires: subject_id, hemi
subject_id: (a unicode string)
        subject id for surface geometry
hemi: ('lh' or 'rh')
        surface hemisphere
surf_geo: (a unicode string, nipyne default value: white)
        surface geometry name (e.g. white, pial)
simulation: (a tuple of the form: ('perm' or 'mc-full' or 'mc-z', an
        integer (int or long), a float, a unicode string))
        nulltype nsim thresh csdbasename
        argument: ``--sim %s %d %f %s``
sim_sign: ('abs' or 'pos' or 'neg')
        abs, pos, or neg
        argument: ``--sim-sign %s``
uniform: (a tuple of the form: (a float, a float))
        use uniform distribution instead of gaussian
        argument: ``--uniform %f %f``
pca: (a boolean)
        perform pca/svd analysis on residual
        argument: ``--pca``
calc_AR1: (a boolean)
        compute and save temporal AR1 of residual
        argument: ``--tar1``
save_cond: (a boolean)
        flag to save design matrix condition at each voxel
        argument: ``--save-cond``
vox_dump: (a tuple of the form: (an integer (int or long), an integer
        (int or long), an integer (int or long)))
        dump voxel GLM and exit
        argument: ``--voxdump %d %d %d``
seed: (an integer (int or long))
        used for synthesizing noise
        argument: ``--seed %d``
synth: (a boolean)
        replace input with gaussian
        argument: ``--synth``
resynth_test: (an integer (int or long))
        test GLM by resynthesis
        argument: ``--resynthtest %d``
profile: (an integer (int or long))
        niters : test speed
        argument: ``--profile %d``
force_perm: (a boolean)
        force permutation test, even when design matrix is not orthog
        argument: ``--perm-force``
diag: (an integer (int or long))

```

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```

    Gdiag_no : set diagnositic level
    argument: ``--diag %d``
diag_cluster: (a boolean)
    save sig volume and exit from first sim loop
    argument: ``--diag-cluster``
debug: (a boolean)
    turn on debugging
    argument: ``--debug``
check_opts: (a boolean)
    don't run anything, just check options and exit
    argument: ``--checkopts``
allow_repeated_subjects: (a boolean)
    allow subject names to repeat in the fsgd file (must appear before
    --fsgd
    argument: ``--allowsubprep``
allow_ill_cond: (a boolean)
    allow ill-conditioned design matrices
    argument: ``--illcond``
sim_done_file: (a pathlike object or string representing a file)
    create file when simulation finished
    argument: ``--sim-done %s``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables

```

Outputs:

```

glm_dir: (a pathlike object or string representing an existing
    directory)
    output directory
beta_file: (a pathlike object or string representing an existing
    file)
    map of regression coefficients
error_file: (a pathlike object or string representing a file)
    map of residual error
error_var_file: (a pathlike object or string representing a file)
    map of residual error variance
error_stddev_file: (a pathlike object or string representing a file)
    map of residual error standard deviation
estimate_file: (a pathlike object or string representing a file)
    map of the estimated Y values
mask_file: (a pathlike object or string representing a file)
    map of the mask used in the analysis
fwhm_file: (a pathlike object or string representing a file)
    text file with estimated smoothness
dof_file: (a pathlike object or string representing a file)
    text file with effective degrees-of-freedom for the analysis
gamma_file: (a list of items which are any value)
    map of contrast of regression coefficients
gamma_var_file: (a list of items which are any value)

```

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```

    map of regression contrast variance
sig_file: (a list of items which are any value)
    map of F-test significance (in -log10p)
ftest_file: (a list of items which are any value)
    map of test statistic values
spatial_eigenvectors: (a pathlike object or string representing a
    file)
    map of spatial eigenvectors from residual PCA
frame_eigenvectors: (a pathlike object or string representing a file)
    matrix of frame eigenvectors from residual PCA
singular_values: (a pathlike object or string representing a file)
    matrix singular values from residual PCA
svd_stats_file: (a pathlike object or string representing a file)
    text file summarizing the residual PCA

```

62.2.11 SegStats

[Link to code](#)

Wraps the executable command `mri_segstats`.

Use FreeSurfer `mri_segstats` for ROI analysis

Examples

```

>>> import nipy.interfaces.freesurfer as fs
>>> ss = fs.SegStats()
>>> ss.inputs.annot = ('PWS04', 'lh', 'aparc')
>>> ss.inputs.in_file = 'functional.nii'
>>> ss.inputs.subjects_dir = '.'
>>> ss.inputs.avgwf_txt_file = 'avgwf.txt'
>>> ss.inputs.summary_file = 'summary.stats'
>>> ss.cmdline
'mri_segstats --annot PWS04 lh aparc --avgwf ./avgwf.txt --i functional.nii --sum_
↪ ./summary.stats'

```

Inputs:

```

[Mandatory]
segmentation_file: (a pathlike object or string representing an
    existing file)
    segmentation volume path
    argument: ``--seg %s``
    mutually_exclusive: segmentation_file, annot, surf_label
annot: (a tuple of the form: (a unicode string, 'lh' or 'rh', a
    unicode string))
    subject hemi parc : use surface parcellation
    argument: ``--annot %s %s %s``
    mutually_exclusive: segmentation_file, annot, surf_label
surf_label: (a tuple of the form: (a unicode string, 'lh' or 'rh', a
    unicode string))
    subject hemi label : use surface label
    argument: ``--slabel %s %s %s``
    mutually_exclusive: segmentation_file, annot, surf_label

[Optional]
summary_file: (a pathlike object or string representing a file)

```

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```

Segmentation stats summary table file
argument: ``--sum %s``, position: -1
partial_volume_file: (a pathlike object or string representing an
    existing file)
    Compensate for partial voluming
    argument: ``--pv %s``
in_file: (a pathlike object or string representing an existing file)
    Use the segmentation to report stats on this volume
    argument: ``--i %s``
frame: (an integer (int or long))
    Report stats on nth frame of input volume
    argument: ``--frame %d``
multiply: (a float)
    multiply input by val
    argument: ``--mul %f``
calc_snr: (a boolean)
    save mean/std as extra column in output table
    argument: ``--snr``
calc_power: ('sqr' or 'sqrt')
    Compute either the sqr or the sqrt of the input
    argument: ``--%s``
color_table_file: (a pathlike object or string representing an
    existing file)
    color table file with seg id names
    argument: ``--ctab %s``
    mutually_exclusive: color_table_file, default_color_table,
        gca_color_table
default_color_table: (a boolean)
    use $FREESURFER_HOME/FreeSurferColorLUT.txt
    argument: ``--ctab-default``
    mutually_exclusive: color_table_file, default_color_table,
        gca_color_table
gca_color_table: (a pathlike object or string representing an
    existing file)
    get color table from GCA (CMA)
    argument: ``--ctab-gca %s``
    mutually_exclusive: color_table_file, default_color_table,
        gca_color_table
segment_id: (a list of items which are any value)
    Manually specify segmentation ids
    argument: ``--id %s...``
exclude_id: (an integer (int or long))
    Exclude seg id from report
    argument: ``--excludeid %d``
exclude_ctx_gm_wm: (a boolean)
    exclude cortical gray and white matter
    argument: ``--excl-ctxgmwm``
wm_vol_from_surf: (a boolean)
    Compute wm volume from surf
    argument: ``--surf-wm-vol``
cortex_vol_from_surf: (a boolean)
    Compute cortex volume from surf
    argument: ``--surf-ctx-vol``
non_empty_only: (a boolean)
    Only report nonempty segmentations
    argument: ``--nonempty``
empty: (a boolean)

```

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```

        Report on segmentations listed in the color table
        argument: ``--empty``
mask_file: (a pathlike object or string representing an existing
            file)
            Mask volume (same size as seg
            argument: ``--mask %s``
mask_thresh: (a float)
            binarize mask with this threshold <0.5>
            argument: ``--maskthresh %f``
mask_sign: ('abs' or 'pos' or 'neg' or '--masksign %s')
            Sign for mask threshold: pos, neg, or abs
mask_frame: (an integer (int or long))
            Mask with this (0 based) frame of the mask volume
            requires: mask_file
mask_invert: (a boolean)
            Invert binarized mask volume
            argument: ``--maskinvert``
mask_erode: (an integer (int or long))
            Erode mask by some amount
            argument: ``--maskerode %d``
brain_vol: ('brain-vol-from-seg' or 'brainmask')
            Compute brain volume either with ``brainmask`` or ``brain-vol-from-
            seg``
            argument: ``--%s``
brainmask_file: (a pathlike object or string representing an existing
                file)
                Load brain mask and compute the volume of the brain as the non-zero
                voxels in this volume
                argument: ``--brainmask %s``
etiv: (a boolean)
            Compute ICV from talairach transform
            argument: ``--etiv``
etiv_only: ('etiv' or 'old-etiv' or '--%s-only')
            Compute etiv and exit. Use ``etiv`` or ``old-etiv``
avgwf_txt_file: (a boolean or a pathlike object or string
                representing a file)
                Save average waveform into file (bool or filename)
                argument: ``--avgwf %s``
avgwf_file: (a boolean or a pathlike object or string representing a
                file)
                Save as binary volume (bool or filename)
                argument: ``--avgwfvol %s``
sf_avg_file: (a boolean or a pathlike object or string representing a
                file)
                Save mean across space and time
                argument: ``--sfavg %s``
vox: (a list of items which are an integer (int or long))
            Replace seg with all 0s except at C R S (three int inputs)
            argument: ``--vox %s``
supratent: (a boolean)
            Undocumented input flag
            argument: ``--supratent``
subcort_gm: (a boolean)
            Compute volume of subcortical gray matter
            argument: ``--subcortgray``
total_gray: (a boolean)
            Compute volume of total gray matter

```

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```

        argument: ``--totalgray``
euler: (a boolean)
        Write out number of defect holes in orig.nofix based on the euler
        number
        argument: ``--euler``
in_intensity: (a pathlike object or string representing a file)
        Undocumented input norm.mgz file
        argument: ``--in %s --in-intensity-name %s``
intensity_units: ('MR')
        Intensity units
        argument: ``--in-intensity-units %s``
        requires: in_intensity
subjects_dir: (a pathlike object or string representing an existing
        directory)
        subjects directory
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

summary_file: (a pathlike object or string representing an existing
        file)
        Segmentation summary statistics table
avgwf_txt_file: (a pathlike object or string representing a file)
        Text file with functional statistics averaged over segs
avgwf_file: (a pathlike object or string representing a file)
        Volume with functional statistics averaged over segs
sf_avg_file: (a pathlike object or string representing a file)
        Text file with func statistics averaged over segs and framss

```

62.2.12 SegStatsReconAll[Link to code](#)Wraps the executable command `mri_segstats`.

This class inherits `SegStats` and modifies it for use in a recon-all workflow. This implementation mandates implicit inputs that `SegStats`. To ensure backwards compatability of `SegStats`, this class was created.

Examples

```

>>> from nipy.interfaces.freesurfer import SegStatsReconAll
>>> segstatsreconall = SegStatsReconAll()
>>> segstatsreconall.inputs.annot = ('PWS04', 'lh', 'aparc')
>>> segstatsreconall.inputs.avgwf_txt_file = 'avgwf.txt'
>>> segstatsreconall.inputs.summary_file = 'summary.stats'
>>> segstatsreconall.inputs.subject_id = '10335'
>>> segstatsreconall.inputs.ribbon = 'wm.mgz'
>>> segstatsreconall.inputs.transform = 'trans.mat'
>>> segstatsreconall.inputs.presurf_seg = 'wm.mgz'
>>> segstatsreconall.inputs.lh_orig_nofix = 'lh.pial'
>>> segstatsreconall.inputs.rh_orig_nofix = 'lh.pial'

```

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```

>>> segstatsreconall.inputs.lh_pial = 'lh.pial'
>>> segstatsreconall.inputs.rh_pial = 'lh.pial'
>>> segstatsreconall.inputs.lh_white = 'lh.pial'
>>> segstatsreconall.inputs.rh_white = 'lh.pial'
>>> segstatsreconall.inputs.empty = True
>>> segstatsreconall.inputs.brain_vol = 'brain-vol-from-seg'
>>> segstatsreconall.inputs.exclude_ctx_gm_wm = True
>>> segstatsreconall.inputs.supratent = True
>>> segstatsreconall.inputs.subcort_gm = True
>>> segstatsreconall.inputs.etiv = True
>>> segstatsreconall.inputs.wm_vol_from_surf = True
>>> segstatsreconall.inputs.cortex_vol_from_surf = True
>>> segstatsreconall.inputs.total_gray = True
>>> segstatsreconall.inputs.euler = True
>>> segstatsreconall.inputs.exclude_id = 0
>>> segstatsreconall.cmdline
'mri_segstats --annot PWS04 lh aparc --avgwf ./avgwf.txt --brain-vol-from-seg --
↪surf-ctx-vol --empty --etiv --euler --excl-ctxgmwm --excludeid 0 --subcortgray -
↪-subject 10335 --supratent --totalgray --surf-wm-vol --sum ./summary.stats'

```

Inputs:

```

[Mandatory]
subject_id: (a string, nipy default value: subject_id)
    Subject id being processed
    argument: ``--subject %s``
ribbon: (a pathlike object or string representing an existing file)
    Input file mri/ribbon.mgz
transform: (a pathlike object or string representing an existing
    file)
    Input transform file
lh_orig_nofix: (a pathlike object or string representing an existing
    file)
    Input lh.orig.nofix
rh_orig_nofix: (a pathlike object or string representing an existing
    file)
    Input rh.orig.nofix
lh_white: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/surf/lh.white
rh_white: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/surf/rh.white
lh_pial: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/surf/lh.pial
rh_pial: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/surf/rh.pial
segmentation_file: (a pathlike object or string representing an
    existing file)
    segmentation volume path
    argument: ``--seg %s``
    mutually_exclusive: segmentation_file, annot, surf_label
annot: (a tuple of the form: (a unicode string, 'lh' or 'rh', a
    unicode string))
    subject hemi parc : use surface parcellation
    argument: ``--annot %s %s %s``
    mutually_exclusive: segmentation_file, annot, surf_label
surf_label: (a tuple of the form: (a unicode string, 'lh' or 'rh', a
    unicode string))

```

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```

subject hemi label : use surface label
argument: ``--slabel %s %s %s``
mutually_exclusive: segmentation_file, annot, surf_label

[Optional]
presurf_seg: (a pathlike object or string representing an existing
             file)
             Input segmentation volume
aseg: (a pathlike object or string representing an existing file)
      Mandatory implicit input in 5.3
copy_inputs: (a boolean)
             If running as a node, set this to True otherwise, this will copy the
             implicit inputs to the node directory.
summary_file: (a pathlike object or string representing a file)
              Segmentation stats summary table file
              argument: ``--sum %s``, position: -1
partial_volume_file: (a pathlike object or string representing an
                     existing file)
                     Compensate for partial voluming
                     argument: ``--pv %s``
in_file: (a pathlike object or string representing an existing file)
         Use the segmentation to report stats on this volume
         argument: ``--i %s``
frame: (an integer (int or long))
       Report stats on nth frame of input volume
       argument: ``--frame %d``
multiply: (a float)
          multiply input by val
          argument: ``--mul %f``
calc_snr: (a boolean)
          save mean/std as extra column in output table
          argument: ``--snr``
calc_power: ('sqr' or 'sqrt')
            Compute either the sqr or the sqrt of the input
            argument: ``--%s``
color_table_file: (a pathlike object or string representing an
                  existing file)
                  color table file with seg id names
                  argument: ``--ctab %s``
                  mutually_exclusive: color_table_file, default_color_table,
                  gca_color_table
default_color_table: (a boolean)
                    use $FREESURFER_HOME/FreeSurferColorLUT.txt
                    argument: ``--ctab-default``
                    mutually_exclusive: color_table_file, default_color_table,
                    gca_color_table
gca_color_table: (a pathlike object or string representing an
                 existing file)
                 get color table from GCA (CMA)
                 argument: ``--ctab-gca %s``
                 mutually_exclusive: color_table_file, default_color_table,
                 gca_color_table
segment_id: (a list of items which are any value)
            Manually specify segmentation ids
            argument: ``--id %s...``
exclude_id: (an integer (int or long))
            Exclude seg id from report

```

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```

        argument: ``--excludeid %d``
exclude_ctx_gm_wm: (a boolean)
    exclude cortical gray and white matter
    argument: ``--excl-ctxgmwm``
wm_vol_from_surf: (a boolean)
    Compute wm volume from surf
    argument: ``--surf-wm-vol``
cortex_vol_from_surf: (a boolean)
    Compute cortex volume from surf
    argument: ``--surf-ctx-vol``
non_empty_only: (a boolean)
    Only report nonempty segmentations
    argument: ``--nonempty``
empty: (a boolean)
    Report on segmentations listed in the color table
    argument: ``--empty``
mask_file: (a pathlike object or string representing an existing
    file)
    Mask volume (same size as seg
    argument: ``--mask %s``
mask_thresh: (a float)
    binarize mask with this threshold <0.5>
    argument: ``--maskthresh %f``
mask_sign: ('abs' or 'pos' or 'neg' or '--masksign %s')
    Sign for mask threshold: pos, neg, or abs
mask_frame: (an integer (int or long))
    Mask with this (0 based) frame of the mask volume
    requires: mask_file
mask_invert: (a boolean)
    Invert binarized mask volume
    argument: ``--maskinvert``
mask_erode: (an integer (int or long))
    Erode mask by some amount
    argument: ``--maskerode %d``
brain_vol: ('brain-vol-from-seg' or 'brainmask')
    Compute brain volume either with ``brainmask`` or ``brain-vol-from-
    seg``
    argument: ``--%s``
brainmask_file: (a pathlike object or string representing an existing
    file)
    Load brain mask and compute the volume of the brain as the non-zero
    voxels in this volume
    argument: ``--brainmask %s``
etiv: (a boolean)
    Compute ICV from talairach transform
    argument: ``--etiv``
etiv_only: ('etiv' or 'old-etiv' or '--%s-only')
    Compute etiv and exit. Use ``etiv`` or ``old-etiv``
avgwf_txt_file: (a boolean or a pathlike object or string
    representing a file)
    Save average waveform into file (bool or filename)
    argument: ``--avgwf %s``
avgwf_file: (a boolean or a pathlike object or string representing a
    file)
    Save as binary volume (bool or filename)
    argument: ``--avgwfvol %s``
sf_avg_file: (a boolean or a pathlike object or string representing a

```

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```

        file)
        Save mean across space and time
        argument: ``--sfavg %s``
vox: (a list of items which are an integer (int or long))
        Replace seg with all 0s except at C R S (three int inputs)
        argument: ``--vox %s``
supratent: (a boolean)
        Undocumented input flag
        argument: ``--supratent``
subcort_gm: (a boolean)
        Compute volume of subcortical gray matter
        argument: ``--subcortgray``
total_gray: (a boolean)
        Compute volume of total gray matter
        argument: ``--totalgray``
euler: (a boolean)
        Write out number of defect holes in orig.nofix based on the euler
        number
        argument: ``--euler``
in_intensity: (a pathlike object or string representing a file)
        Undocumented input norm.mgz file
        argument: ``--in %s --in-intensity-name %s``
intensity_units: ('MR')
        Intensity units
        argument: ``--in-intensity-units %s``
        requires: in_intensity
subjects_dir: (a pathlike object or string representing an existing
        directory)
        subjects directory
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

summary_file: (a pathlike object or string representing an existing
        file)
        Segmentation summary statistics table
avgwf_txt_file: (a pathlike object or string representing a file)
        Text file with functional statistics averaged over segs
avgwf_file: (a pathlike object or string representing a file)
        Volume with functional statistics averaged over segs
sf_avg_file: (a pathlike object or string representing a file)
        Text file with func statistics averaged over segs and framss

```

62.2.13 SphericalAverage[Link to code](#)Wraps the executable command `mrissphericalaverage`.

This program will add a template into an average surface.

Examples

```
>>> from nipy.interfaces.freesurfer import SphericalAverage
>>> sphericalavg = SphericalAverage()
>>> sphericalavg.inputs.out_file = 'test.out'
>>> sphericalavg.inputs.in_average = '.'
>>> sphericalavg.inputs.in_surf = 'lh.pial'
>>> sphericalavg.inputs.hemisphere = 'lh'
>>> sphericalavg.inputs.fname = 'lh.entorhinal'
>>> sphericalavg.inputs.which = 'label'
>>> sphericalavg.inputs.subject_id = '10335'
>>> sphericalavg.inputs.erode = 2
>>> sphericalavg.inputs.threshold = 5
>>> sphericalavg.cmdline
'mris_spherical_average -erode 2 -o 10335 -t 5.0 label lh.entorhinal lh pial .
↳test.out'
```

Inputs:

```
[Mandatory]
in_surf: (a pathlike object or string representing an existing file)
    Input surface file
    argument: ``%s``, position: -3
hemisphere: ('lh' or 'rh')
    Input hemisphere
    argument: ``%s``, position: -4
fname: (a string)
    Filename from the average subject directory.
    Example: to use rh.entorhinal.label as the input label
    filename, set fname to 'rh.entorhinal' and which to
    'label'. The program will then search for
    '{in_average}/label/rh.entorhinal.label'
    argument: ``%s``, position: -5
which: ('coords' or 'label' or 'vals' or 'curv' or 'area')
    No documentation
    argument: ``%s``, position: -6
subject_id: (a string)
    Output subject id
    argument: ``-o %s``

[Optional]
out_file: (a pathlike object or string representing a file)
    Output filename
    argument: ``%s``, position: -1
in_average: (a pathlike object or string representing an existing
    directory)
    Average subject
    argument: ``%s``, position: -2
erode: (an integer (int or long))
    Undocumented
    argument: ``-erode %d``
in_orig: (a pathlike object or string representing an existing file)
    Original surface filename
    argument: ``-orig %s``
threshold: (a float)
    Undocumented
    argument: ``-t %.1f``
subjects_dir: (a pathlike object or string representing an existing
```

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```

        directory)
        subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    Output label

```

62.3 interfaces.freesurfer.preprocess

62.3.1 ApplyVolTransform

[Link to code](#)Wraps the executable command `mri_vol2vol`.Use FreeSurfer `mri_vol2vol` to apply a transform.**Examples**

```

>>> from nipy.interfaces.freesurfer import ApplyVolTransform
>>> applyreg = ApplyVolTransform()
>>> applyreg.inputs.source_file = 'structural.nii'
>>> applyreg.inputs.reg_file = 'register.dat'
>>> applyreg.inputs.transformed_file = 'struct_warped.nii'
>>> applyreg.inputs.fs_target = True
>>> applyreg.cmdline
'mri_vol2vol --fstarg --reg register.dat --mov structural.nii --o struct_warped.
↪nii'

```

Inputs:

```

[Mandatory]
source_file: (a pathlike object or string representing an existing
    file)
    Input volume you wish to transform
    argument: ``--mov %s``
target_file: (a pathlike object or string representing an existing
    file)
    Output template volume
    argument: ``--targ %s``
    mutually_exclusive: target_file, tal, fs_target
tal: (a boolean)
    map to a sub FOV of MNI305 (with --reg only)
    argument: ``--tal``
    mutually_exclusive: target_file, tal, fs_target
fs_target: (a boolean)
    use orig.mgz from subject in regfile as target
    argument: ``--fstarg``
    mutually_exclusive: target_file, tal, fs_target

```

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```

requires: reg_file
reg_file: (a pathlike object or string representing an existing file)
tkRAS-to-tkRAS matrix (tkregister2 format)
argument: ``--reg %s``
mutually_exclusive: reg_file, lta_file, lta_inv_file, fsl_reg_file,
                    xfm_reg_file, reg_header, mni_152_reg, subject
lta_file: (a pathlike object or string representing an existing file)
Linear Transform Array file
argument: ``--lta %s``
mutually_exclusive: reg_file, lta_file, lta_inv_file, fsl_reg_file,
                    xfm_reg_file, reg_header, mni_152_reg, subject
lta_inv_file: (a pathlike object or string representing an existing
file)
LTA, invert
argument: ``--lta-inv %s``
mutually_exclusive: reg_file, lta_file, lta_inv_file, fsl_reg_file,
                    xfm_reg_file, reg_header, mni_152_reg, subject
fsl_reg_file: (a pathlike object or string representing an existing
file)
fslRAS-to-fslRAS matrix (FSL format)
argument: ``--fsl %s``
mutually_exclusive: reg_file, lta_file, lta_inv_file, fsl_reg_file,
                    xfm_reg_file, reg_header, mni_152_reg, subject
xfm_reg_file: (a pathlike object or string representing an existing
file)
ScannerRAS-to-ScannerRAS matrix (MNI format)
argument: ``--xfm %s``
mutually_exclusive: reg_file, lta_file, lta_inv_file, fsl_reg_file,
                    xfm_reg_file, reg_header, mni_152_reg, subject
reg_header: (a boolean)
ScannerRAS-to-ScannerRAS matrix = identity
argument: ``--regheader``
mutually_exclusive: reg_file, lta_file, lta_inv_file, fsl_reg_file,
                    xfm_reg_file, reg_header, mni_152_reg, subject
mni_152_reg: (a boolean)
target MNI152 space
argument: ``--regheader``
mutually_exclusive: reg_file, lta_file, lta_inv_file, fsl_reg_file,
                    xfm_reg_file, reg_header, mni_152_reg, subject
subject: (a unicode string)
set matrix = identity and use subject for any templates
argument: ``--s %s``
mutually_exclusive: reg_file, lta_file, lta_inv_file, fsl_reg_file,
                    xfm_reg_file, reg_header, mni_152_reg, subject

[Optional]
transformed_file: (a pathlike object or string representing a file)
Output volume
argument: ``--o %s``
tal_resolution: (a float)
Resolution to sample when using tal
argument: ``--talres %.10f``
inverse: (a boolean)
sample from target to source
argument: ``--inv``
interp: ('trilin' or 'nearest' or 'cubic')
Interpolation method (<trilin> or nearest)

```

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```

        argument: ``--interp %s``
no_resample: (a boolean)
    Do not resample; just change vox2ras matrix
    argument: ``--no-resample``
m3z_file: (a pathlike object or string representing a file)
    This is the morph to be applied to the volume. Unless the morph is
    in mri/transforms (eg.: for talairach.m3z computed by reconall), you
    will need to specify the full path to this morph and use the
    --noDefM3zPath flag.
    argument: ``--m3z %s``
no_ded_m3z_path: (a boolean)
    To be used with the m3z flag. Instructs the code not to look for
    them3z morph in the default location
    (SUBJECTS_DIR/subj/mri/transforms), but instead just use the path
    indicated in --m3z.
    argument: ``--noDefM3zPath``
    requires: m3z_file
invert_morph: (a boolean)
    Compute and use the inverse of the non-linear morph to resample the
    input volume. To be used by --m3z.
    argument: ``--inv-morph``
    requires: m3z_file
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

transformed_file: (a pathlike object or string representing an
    existing file)
    Path to output file if used normally

```

62.3.2 BBRegister[Link to code](#)

Wraps the executable command bregister.

Use FreeSurfer bregister to register a volume to the FreeSurfer anatomical.

This program performs within-subject, cross-modal registration using a boundary-based cost function. It is required that you have an anatomical scan of the subject that has already been recon-all-ed using freesurfer.

Examples

```

>>> from nipy.interfaces.freesurfer import BBRegister
>>> bbreg = BBRegister(subject_id='me', source_file='structural.nii', init='header
↳', contrast_type='t2')
>>> bbreg.cmdline
'bbregister --t2 --init-header --reg structural_bbreg_me.dat --mov structural.nii_
↳--s me'

```

Inputs:

```

[Mandatory]
subject_id: (a unicode string)
    freesurfer subject id
    argument: ``--s %s``
source_file: (a pathlike object or string representing a file)
    source file to be registered
    argument: ``--mov %s``
contrast_type: ('t1' or 't2' or 'bold' or 'dti')
    contrast type of image
    argument: ``--%s``

[Optional]
init: ('coreg' or 'rr' or 'spm' or 'fsl' or 'header' or 'best')
    initialize registration with mri_coreg, spm, fsl, or header
    argument: ``--init-%s``
    mutually_exclusive: init_reg_file
init_reg_file: (a pathlike object or string representing an existing
    file)
    existing registration file
    argument: ``--init-reg %s``
    mutually_exclusive: init
intermediate_file: (a pathlike object or string representing an
    existing file)
    Intermediate image, e.g. in case of partial FOV
    argument: ``--int %s``
reg_frame: (an integer (int or long))
    0-based frame index for 4D source file
    argument: ``--frame %d``
    mutually_exclusive: reg_middle_frame
reg_middle_frame: (a boolean)
    Register middle frame of 4D source file
    argument: ``--mid-frame``
    mutually_exclusive: reg_frame
out_reg_file: (a pathlike object or string representing a file)
    output registration file
    argument: ``--reg %s``
spm_nifti: (a boolean)
    force use of nifti rather than analyze with SPM
    argument: ``--spm-nii``
epi_mask: (a boolean)
    mask out B0 regions in stages 1 and 2
    argument: ``--epi-mask``
dof: (6 or 9 or 12)
    number of transform degrees of freedom
    argument: ``--%d``
fsl dof: (an integer (int or long))
    degrees of freedom for initial registration (FSL)
    argument: ``--fsl-dof %d``
out_fsl_file: (a boolean or a pathlike object or string representing
    a file)
    write the transformation matrix in FSL FLIRT format
    argument: ``--fslmat %s``
out_lta_file: (a boolean or a pathlike object or string representing
    a file)
    write the transformation matrix in LTA format
    argument: ``--lta %s``
registered_file: (a boolean or a pathlike object or string

```

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```

        representing a file)
        output warped sourcefile either True or filename
        argument: ``--o %s``
init_cost_file: (a boolean or a pathlike object or string
        representing a file)
        output initial registration cost file
        argument: ``--initcost %s``
subjects_dir: (a pathlike object or string representing an existing
        directory)
        subjects directory
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_reg_file: (a pathlike object or string representing an existing
        file)
        Output registration file
out_fsl_file: (a pathlike object or string representing an existing
        file)
        Output FLIRT-style registration file
out_lta_file: (a pathlike object or string representing an existing
        file)
        Output LTA-style registration file
min_cost_file: (a pathlike object or string representing an existing
        file)
        Output registration minimum cost file
init_cost_file: (a pathlike object or string representing an existing
        file)
        Output initial registration cost file
registered_file: (a pathlike object or string representing an
        existing file)
        Registered and resampled source file

```

62.3.3 CAlabel****[Link to code](#)Wraps the executable command `mri_ca_label`.For complete details, see the [FS Documenta**tion**](#)**Examples**

```

>>> from nipy.interfaces import freesurfer
>>> ca_label = freesurfer.CAlabel()
>>> ca_label.inputs.in_file = "norm.mgz"
>>> ca_label.inputs.out_file = "out.mgz"
>>> ca_label.inputs.transform = "trans.mat"
>>> ca_label.inputs.template = "Template_6.nii" # in practice use .gcs extension
>>> ca_label.cmdline
'mri_ca_label norm.mgz trans.mat Template_6.nii out.mgz'

```

Inputs:


```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Input volume for CALabel
    argument: ``%s``, position: -4
out_file: (a pathlike object or string representing a file)
    Output file for CALabel
    argument: ``%s``, position: -1
transform: (a pathlike object or string representing an existing
    file)
    Input transform for CALabel
    argument: ``%s``, position: -3
template: (a pathlike object or string representing an existing file)
    Input template for CALabel
    argument: ``%s``, position: -2

[Optional]
in_vol: (a pathlike object or string representing an existing file)
    set input volume
    argument: ``-r %s``
intensities: (a pathlike object or string representing an existing
    file)
    input label intensities file(used in longitudinal processing)
    argument: ``-r %s``
no_big_ventricles: (a boolean)
    No big ventricles
    argument: ``-nobigventricles``
align: (a boolean)
    Align CALabel
    argument: ``-align``
prior: (a float)
    Prior for CALabel
    argument: ``-prior %.1f``
relabel_unlikely: (a tuple of the form: (an integer (int or long), a
    float))
    Reclassify voxels at least some std devs from the mean using some
    size Gaussian window
    argument: ``-relabel_unlikely %d %.1f``
label: (a pathlike object or string representing an existing file)
    Undocumented flag. Autorecon3 uses
    ../label/{hemisphere}.cortex.label as input file
    argument: ``-l %s``
aseg: (a pathlike object or string representing an existing file)
    Undocumented flag. Autorecon3 uses ../mri/aseg.presurf.mgz as input
    file
    argument: ``-aseg %s``
num_threads: (an integer (int or long))
    allows for specifying more threads
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing a file)
          Output volume from CALabel
```

62.3.4 CANormalize

[Link to code](#)

Wraps the executable command `mri_ca_normalize`.

This program creates a normalized volume using the brain volume and an input gca file.

For complete details, see the [FS Documentation](#)

Examples

```
>>> from nipy.interfaces import freesurfer
>>> ca_normalize = freesurfer.CANormalize()
>>> ca_normalize.inputs.in_file = "T1.mgz"
>>> ca_normalize.inputs.atlas = "atlas.nii.gz" # in practice use .gca atlases
>>> ca_normalize.inputs.transform = "trans.mat" # in practice use .lta transforms
>>> ca_normalize.cmdline
'mri_ca_normalize T1.mgz atlas.nii.gz trans.mat T1_norm.mgz'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         The input file for CANormalize
         argument: ``%s``, position: -4
atlas: (a pathlike object or string representing an existing file)
        The atlas file in gca format
        argument: ``%s``, position: -3
transform: (a pathlike object or string representing an existing
            file)
            The tranform file in lta format
            argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
          The output file for CANormalize
          argument: ``%s``, position: -1
mask: (a pathlike object or string representing an existing file)
       Specifies volume to use as mask
       argument: ``-mask %s``
control_points: (a pathlike object or string representing a file)
                File name for the output control points
                argument: ``-c %s``
long_file: (a pathlike object or string representing a file)
            undocumented flag used in longitudinal processing
            argument: ``-long %s``
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    The output file for Normalize
control_points: (a pathlike object or string representing a file)
    The output control points for Normalize

```

62.3.5 CARegister[Link to code](#)

Wraps the executable command `mri_ca_register`.

Generates a multi-dimensional talairach transform from a gca file and talairach.lta file

For complete details, see the [FS Documentation](#)

Examples

```

>>> from nipy.interfaces import freesurfer
>>> ca_register = freesurfer.CARegister()
>>> ca_register.inputs.in_file = "norm.mgz"
>>> ca_register.inputs.out_file = "talairach.m3z"
>>> ca_register.cmdline
'mri_ca_register norm.mgz talairach.m3z'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    The input volume for CARegister
    argument: ``%s``, position: -3

[Optional]
out_file: (a pathlike object or string representing a file)
    The output volume for CARegister
    argument: ``%s``, position: -1
template: (a pathlike object or string representing an existing file)
    The template file in gca format
    argument: ``%s``, position: -2
mask: (a pathlike object or string representing an existing file)
    Specifies volume to use as mask
    argument: ``-mask %s``
invert_and_save: (a boolean)
    Invert and save the .m3z multi-dimensional talaraich transform to x,
    y, and z .mgz files
    argument: ``-invert-and-save``, position: -4
no_big_ventricles: (a boolean)
    No big ventricles
    argument: ``-nobigventricles``
transform: (a pathlike object or string representing an existing
    file)
    Specifies transform in lta format
    argument: ``-T %s``
align: (a string)
    Specifies when to perform alignment
    argument: ``-align-%s``
levels: (an integer (int or long))
    defines how many surrounding voxels will be used in interpolations,
    default is 6

```

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```

        argument: ``-levels %d``
A: (an integer (int or long))
    undocumented flag used in longitudinal processing
    argument: ``-A %d``
l_files: (a list of items which are a pathlike object or string
    representing a file)
    undocumented flag used in longitudinal processing
    argument: ``-l %s``
num_threads: (an integer (int or long))
    allows for specifying more threads
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    The output file for CRegister

```

62.3.6 ConcatenateLTA

[Link to code](#)Wraps the executable command `mri_concatenate_lta`.

Concatenates two consecutive LTA transformations into one overall transformation

Out = LTA2*LTA1

Examples

```

>>> from nipyne.interfaces.freesurfer import ConcatenateLTA
>>> conc_lta = ConcatenateLTA()
>>> conc_lta.inputs.in_lta1 = 'lta1.lta'
>>> conc_lta.inputs.in_lta2 = 'lta2.lta'
>>> conc_lta.cmdline
'mri_concatenate_lta lta1.lta lta2.lta lta1_concat.lta'

```

You can use 'identity.nofile' as the filename for `in_lta2`, e.g.:

```

>>> conc_lta.inputs.in_lta2 = 'identity.nofile'
>>> conc_lta.inputs.invert_1 = True
>>> conc_lta.inputs.out_file = 'inv1.lta'
>>> conc_lta.cmdline
'mri_concatenate_lta -invert1 lta1.lta identity.nofile inv1.lta'

```

To create a RAS2RAS transform:

```

>>> conc_lta.inputs.out_type = 'RAS2RAS'
>>> conc_lta.cmdline
'mri_concatenate_lta -invert1 -out_type 1 lta1.lta identity.nofile inv1.lta'

```

Inputs:

```

[Mandatory]
in_lta1: (a pathlike object or string representing an existing file)
    maps some src1 to dst1
    argument: ``%s``, position: -3
in_lta2: (a pathlike object or string representing an existing file
    or 'identity.nofile')
    maps dst1(src2) to dst2
    argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
    the combined LTA maps: src1 to dst2 = LTA2*LTA1
    argument: ``%s``, position: -1
invert_1: (a boolean)
    invert in_lta1 before applying it
    argument: ``-invert1``
invert_2: (a boolean)
    invert in_lta2 before applying it
    argument: ``-invert2``
invert_out: (a boolean)
    invert output LTA
    argument: ``-invertout``
out_type: ('VOX2VOX' or 'RAS2RAS')
    set final LTA type
    argument: ``-out_type %d``
tal_source_file: (a pathlike object or string representing an
    existing file)
    if in_lta2 is talairach.xfm, specify source for talairach
    argument: ``-tal %s``, position: -5
    requires: tal_template_file
tal_template_file: (a pathlike object or string representing an
    existing file)
    if in_lta2 is talairach.xfm, specify template for talairach
    argument: ``%s``, position: -4
    requires: tal_source_file
subject: (a unicode string)
    set subject in output LTA
    argument: ``-subject %s``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    the combined LTA maps: src1 to dst2 = LTA2*LTA1

```

62.3.7 DICOMConvert[Link to code](#)Wraps the executable command `mri_convert`.

use `fs_mri_convert` to convert dicom files

Examples

```
>>> from nipy.interfaces.freesurfer import DICOMConvert
>>> cvt = DICOMConvert()
>>> cvt.inputs.dicom_dir = 'dicomdir'
>>> cvt.inputs.file_mapping = [('nifti', '*.nii'), ('info', 'dicom*.txt'), ('dti',
↪ '*dti.bv*')]
```

Inputs:

```
[Mandatory]
dicom_dir: (a pathlike object or string representing an existing
            directory)
            dicom directory from which to convert dicom files
base_output_dir: (a pathlike object or string representing a
                  directory)
                  directory in which subject directories are created

[Optional]
subject_dir_template: (a unicode string, nipy default value:
                       S.%04d)
                       template for subject directory name
subject_id: (any value)
             subject identifier to insert into template
file_mapping: (a list of items which are a tuple of the form: (a
                    unicode string, a unicode string))
              defines the output fields of interface
out_type: ('cor' or 'mgh' or 'mgz' or 'minc' or 'analyze' or
            'analyze4d' or 'spm' or 'afni' or 'brik' or 'bshort' or 'bfloat'
            or 'sdt' or 'outline' or 'otl' or 'gdf' or 'nifti1' or 'nii' or
            'niigz', nipy default value: niigz)
            defines the type of output file produced
dicom_info: (a pathlike object or string representing an existing
            file)
            File containing summary information from mri_parse_sdcmdir
seq_list: (a list of items which are a unicode string)
           list of pulse sequence names to be converted.
           requires: dicom_info
ignore_single_slice: (a boolean)
                     ignore volumes containing a single slice
                     requires: dicom_info
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

None

62.3.8 EditWMwithAseg

[Link to code](#)

Wraps the executable command `mri_edit_wm_with_aseg`.

Edits a wm file using a segmentation

Examples

```
>>> from nipy.interfaces.freesurfer import EditWMwithAseg
>>> editwm = EditWMwithAseg()
>>> editwm.inputs.in_file = "T1.mgz"
>>> editwm.inputs.brain_file = "norm.mgz"
>>> editwm.inputs.seg_file = "aseg.mgz"
>>> editwm.inputs.out_file = "wm.asegedit.mgz"
>>> editwm.inputs.keep_in = True
>>> editwm.cmdline
'mri_edit_wm_with_aseg -keep-in T1.mgz norm.mgz aseg.mgz wm.asegedit.mgz'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Input white matter segmentation file
    argument: ``%s``, position: -4
brain_file: (a pathlike object or string representing an existing
    file)
    Input brain/T1 file
    argument: ``%s``, position: -3
seg_file: (a pathlike object or string representing an existing file)
    Input presurf segmentation file
    argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file)
    File to be written as output
    argument: ``%s``, position: -1

[Optional]
keep_in: (a boolean)
    Keep edits as found in input volume
    argument: ``-keep-in``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
    Output edited WM file
```

62.3.9 FitMSParams

[Link to code](#)

Wraps the executable command `mri_ms_fitparms`.
Estimate tissue paramaters from a set of FLASH images.

Examples

```
>>> from nipy.interfaces.freesurfer import FitMSParams
>>> msfit = FitMSParams()
>>> msfit.inputs.in_files = ['flash_05.mgz', 'flash_30.mgz']
>>> msfit.inputs.out_dir = 'flash_parameters'
>>> msfit.cmdline
'mri_ms_fitparms flash_05.mgz flash_30.mgz flash_parameters'
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
          representing an existing file)
          list of FLASH images (must be in mgh format)
          argument: ``%s``, position: -2

[Optional]
tr_list: (a list of items which are an integer (int or long))
          list of TRs of the input files (in msec)
te_list: (a list of items which are a float)
          list of TEs of the input files (in msec)
flip_list: (a list of items which are an integer (int or long))
            list of flip angles of the input files
xfm_list: (a list of items which are a pathlike object or string
            representing an existing file)
            list of transform files to apply to each FLASH image
out_dir: (a pathlike object or string representing a directory)
          directory to store output in
          argument: ``%s``, position: -1
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
t1_image: (a pathlike object or string representing an existing file)
           image of estimated T1 relaxation values
pd_image: (a pathlike object or string representing an existing file)
           image of estimated proton density values
t2star_image: (a pathlike object or string representing an existing
               file)
               image of estimated T2* values
```

62.3.10 MNIBiasCorrection

[Link to code](#)

Wraps the executable command `mri_nu_correct.mni`.

Wrapper for `nu_correct`, a program from the Montreal Neurological Insitute (MNI) used for correcting intensity non-uniformity (ie, bias fields). You must have the MNI software installed on your system to run this. See [\[www.bic.mni.mcgill.ca/software/N3\]](http://www.bic.mni.mcgill.ca/software/N3) for more info.

`mri_nu_correct.mni` uses float internally instead of uchar. It also rescales the output so that the global mean is the same as that of the input. These two changes are linked and can be turned off with `--no-float`

Examples

```
>>> from nipy.interfaces.freesurfer import MNIBiasCorrection
>>> correct = MNIBiasCorrection()
>>> correct.inputs.in_file = "norm.mgz"
>>> correct.inputs.iterations = 6
>>> correct.inputs.protocol_iterations = 1000
>>> correct.inputs.distance = 50
>>> correct.cmdline
'mri_nu_correct.mni --distance 50 --i norm.mgz --n 6 --o norm_output.mgz --proto-
  iters 1000'
```

References:

[\[http://freesurfer.net/fswiki/mri_nu_correct.mni\]](http://freesurfer.net/fswiki/mri_nu_correct.mni) [\[http://www.bic.mni.mcgill.ca/software/N3\]](http://www.bic.mni.mcgill.ca/software/N3) [\[https://github.com/BIC-MNI/N3\]](https://github.com/BIC-MNI/N3)

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input volume. Input can be any format accepted by mri_convert.
         argument: ``--i %s``

[Optional]
out_file: (a pathlike object or string representing a file)
         output volume. Output can be any format accepted by mri_convert. If
         the output format is COR, then the directory must exist.
         argument: ``--o %s``

iterations: (an integer (int or long), nipy default value: 4)
         Number of iterations to run nu_correct. Default is 4. This is the
         number of times that nu_correct is repeated (ie, using the output
         from the previous run as the input for the next). This is different
         than the -iterations option to nu_correct.
         argument: ``--n %d``

protocol_iterations: (an integer (int or long))
         Passes Np as argument of the -iterations flag of nu_correct. This is
         different than the --n flag above. Default is not to pass nu_correct
         the -iterations flag.
         argument: ``--proto-iters %d``

distance: (an integer (int or long))
         N3 -distance option
         argument: ``--distance %d``

no_rescale: (a boolean)
         do not rescale so that global mean of output == input global mean
         argument: ``--no-rescale``

mask: (a pathlike object or string representing an existing file)
       brainmask volume. Input can be any format accepted by mri_convert.
       argument: ``--mask %s``

transform: (a pathlike object or string representing an existing
           file)
```

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```

    tal.xfm. Use mri_make_uchar instead of conforming
    argument: ``--uchar %s``
stop: (a float)
    Convergence threshold below which iteration stops (suggest 0.01 to
    0.0001)
    argument: ``--stop %f``
shrink: (an integer (int or long))
    Shrink parameter for finer sampling (default is 4)
    argument: ``--shrink %d``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output volume

```

62.3.11 MRIConvert[Link to code](#)Wraps the executable command `mri_convert`.use `fs mri_convert` to manipulate files**Note:** Adds `niigz` as an output type option**Examples**

```

>>> mc = MRIConvert()
>>> mc.inputs.in_file = 'structural.nii'
>>> mc.inputs.out_file = 'outfile.mgz'
>>> mc.inputs.out_type = 'mgz'
>>> mc.cmdline
'mri_convert --out_type mgz --input_volume structural.nii --output_volume outfile.
↳mgz'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    File to read/convert
    argument: ``--input_volume %s``, position: -2

[Optional]
read_only: (a boolean)
    read the input volume
    argument: ``--read_only``
no_write: (a boolean)

```

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```

do not write output
argument: ``--no_write``
in_info: (a boolean)
display input info
argument: ``--in_info``
out_info: (a boolean)
display output info
argument: ``--out_info``
in_stats: (a boolean)
display input stats
argument: ``--in_stats``
out_stats: (a boolean)
display output stats
argument: ``--out_stats``
in_matrix: (a boolean)
display input matrix
argument: ``--in_matrix``
out_matrix: (a boolean)
display output matrix
argument: ``--out_matrix``
in_i_size: (an integer (int or long))
input i size
argument: ``--in_i_size %d``
in_j_size: (an integer (int or long))
input j size
argument: ``--in_j_size %d``
in_k_size: (an integer (int or long))
input k size
argument: ``--in_k_size %d``
force_ras: (a boolean)
use default when orientation info absent
argument: ``--force_ras_good``
in_i_dir: (a tuple of the form: (a float, a float, a float))
<R direction> <A direction> <S direction>
argument: ``--in_i_direction %f %f %f``
in_j_dir: (a tuple of the form: (a float, a float, a float))
<R direction> <A direction> <S direction>
argument: ``--in_j_direction %f %f %f``
in_k_dir: (a tuple of the form: (a float, a float, a float))
<R direction> <A direction> <S direction>
argument: ``--in_k_direction %f %f %f``
in_orientation: ('LAI' or 'LIA' or 'ALI' or 'AIL' or 'ILA' or 'IAL'
or 'LAS' or 'LSA' or 'ALS' or 'ASL' or 'SLA' or 'SAL' or 'LPI' or
'LIP' or 'PLI' or 'PIL' or 'ILP' or 'IPL' or 'LPS' or 'LSP' or
'PLS' or 'PSL' or 'SLP' or 'SPL' or 'RAI' or 'RIA' or 'ARI' or
'AIR' or 'IRA' or 'IAR' or 'RAS' or 'RSA' or 'ARS' or 'ASR' or
'SRA' or 'SAR' or 'RPI' or 'RIP' or 'PRI' or 'PIR' or 'IRP' or
'IPR' or 'RPS' or 'RSP' or 'PRS' or 'PSR' or 'SRP' or 'SPR')
specify the input orientation
argument: ``--in_orientation %s``
in_center: (a list of at most 3 items which are a float)
<R coordinate> <A coordinate> <S coordinate>
argument: ``--in_center %s``
sphinx: (a boolean)
change orientation info to sphinx
argument: ``--sphinx``
out_i_count: (an integer (int or long))

```

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```

        some count ?? in i direction
        argument: ``--out_i_count %d``
out_j_count: (an integer (int or long))
        some count ?? in j direction
        argument: ``--out_j_count %d``
out_k_count: (an integer (int or long))
        some count ?? in k direction
        argument: ``--out_k_count %d``
vox_size: (a tuple of the form: (a float, a float, a float))
        <size_x> <size_y> <size_z> specify the size (mm) - useful for
        upsampling or downsampling
        argument: ``-voysize %f %f %f``
out_i_size: (an integer (int or long))
        output i size
        argument: ``--out_i_size %d``
out_j_size: (an integer (int or long))
        output j size
        argument: ``--out_j_size %d``
out_k_size: (an integer (int or long))
        output k size
        argument: ``--out_k_size %d``
out_i_dir: (a tuple of the form: (a float, a float, a float))
        <R direction> <A direction> <S direction>
        argument: ``--out_i_direction %f %f %f``
out_j_dir: (a tuple of the form: (a float, a float, a float))
        <R direction> <A direction> <S direction>
        argument: ``--out_j_direction %f %f %f``
out_k_dir: (a tuple of the form: (a float, a float, a float))
        <R direction> <A direction> <S direction>
        argument: ``--out_k_direction %f %f %f``
out_orientation: ('LAI' or 'LIA' or 'ALI' or 'AIL' or 'ILA' or 'IAL'
        or 'LAS' or 'LSA' or 'ALS' or 'ASL' or 'SLA' or 'SAL' or 'LPI' or
        'LIP' or 'PLI' or 'PIL' or 'ILP' or 'IPL' or 'LPS' or 'LSP' or
        'PLS' or 'PSL' or 'SLP' or 'SPL' or 'RAI' or 'RIA' or 'ARI' or
        'AIR' or 'IRA' or 'IAR' or 'RAS' or 'RSA' or 'ARS' or 'ASR' or
        'SRA' or 'SAR' or 'RPI' or 'RIP' or 'PRI' or 'PIR' or 'IRP' or
        'IPR' or 'RPS' or 'RSP' or 'PRS' or 'PSR' or 'SRP' or 'SPR')
        specify the output orientation
        argument: ``--out_orientation %s``
out_center: (a tuple of the form: (a float, a float, a float))
        <R coordinate> <A coordinate> <S coordinate>
        argument: ``--out_center %f %f %f``
out_datatype: ('uchar' or 'short' or 'int' or 'float')
        output data type <uchar|short|int|float>
        argument: ``--out_data_type %s``
resample_type: ('interpolate' or 'weighted' or 'nearest' or 'sinc' or
        'cubic')
        <interpolate|weighted|nearest|sinc|cubic> (default is interpolate)
        argument: ``--resample_type %s``
no_scale: (a boolean)
        dont rescale values for COR
        argument: ``--no_scale 1``
no_change: (a boolean)
        don't change type of input to that of template
        argument: ``--nochange``
tr: (an integer (int or long))
        TR in msec

```

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```

        argument: ``-tr %d``
te: (an integer (int or long))
    TE in msec
    argument: ``-te %d``
ti: (an integer (int or long))
    TI in msec (note upper case flag)
    argument: ``-ti %d``
autoalign_matrix: (a pathlike object or string representing an
    existing file)
    text file with autoalign matrix
    argument: ``--autoalign %s``
unwarp_gradient: (a boolean)
    unwarp gradient nonlinearity
    argument: ``--unwarp_gradient_nonlinearity``
apply_transform: (a pathlike object or string representing an
    existing file)
    apply xfm file
    argument: ``--apply_transform %s``
apply_inv_transform: (a pathlike object or string representing an
    existing file)
    apply inverse transformation xfm file
    argument: ``--apply_inverse_transform %s``
devolve_transform: (a unicode string)
    subject id
    argument: ``--devolvexfm %s``
crop_center: (a tuple of the form: (an integer (int or long), an
    integer (int or long), an integer (int or long)))
    <x> <y> <z> crop to 256 around center (x, y, z)
    argument: ``--crop %d %d %d``
crop_size: (a tuple of the form: (an integer (int or long), an
    integer (int or long), an integer (int or long)))
    <dx> <dy> <dz> crop to size <dx, dy, dz>
    argument: ``--cropsizes %d %d %d``
cut_ends: (an integer (int or long))
    remove ncut slices from the ends
    argument: ``--cutends %d``
slice_crop: (a tuple of the form: (an integer (int or long), an
    integer (int or long)))
    s_start s_end : keep slices s_start to s_end
    argument: ``--slice-crop %d %d``
slice_reverse: (a boolean)
    reverse order of slices, update vox2ras
    argument: ``--slice-reverse``
slice_bias: (a float)
    apply half-cosine bias field
    argument: ``--slice-bias %f``
fwhm: (a float)
    smooth input volume by fwhm mm
    argument: ``--fwhm %f``
in_type: ('cor' or 'mgh' or 'mgz' or 'minc' or 'analyze' or
    'analyze4d' or 'spm' or 'afni' or 'brik' or 'bshort' or 'bfloat'
    or 'sdt' or 'outline' or 'otl' or 'gdf' or 'nifti1' or 'nii' or
    'niigz' or 'ge' or 'gelx' or 'lx' or 'ximg' or 'siemens' or
    'dicom' or 'siemens_dicom')
    input file type
    argument: ``--in_type %s``
out_type: ('cor' or 'mgh' or 'mgz' or 'minc' or 'analyze' or

```

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```

        'analyze4d' or 'spm' or 'afni' or 'brik' or 'bshort' or 'bfloat'
        or 'sdt' or 'outline' or 'otl' or 'gdf' or 'nifti1' or 'nii' or
        'niigz')
    output file type
    argument: ``--out_type %s``
ascii: (a boolean)
    save output as ascii col>row>slice>frame
    argument: ``--ascii``
reorder: (a tuple of the form: (an integer (int or long), an integer
    (int or long), an integer (int or long)))
    olddim1 olddim2 olddim3
    argument: ``--reorder %d %d %d``
invert_contrast: (a float)
    threshold for inversting contrast
    argument: ``--invert_contrast %f``
out_file: (a pathlike object or string representing a file)
    output filename or True to generate one
    argument: ``--output_volume %s``, position: -1
conform: (a boolean)
    conform to 1mm voxel size in coronal slice direction with 256^3 or
    more
    argument: ``--conform``
conform_min: (a boolean)
    conform to smallest size
    argument: ``--conform_min``
conform_size: (a float)
    conform to size_in_mm
    argument: ``--conform_size %s``
cw256: (a boolean)
    confrom to dimensions of 256^3
    argument: ``--cw256``
parse_only: (a boolean)
    parse input only
    argument: ``--parse_only``
subject_name: (a unicode string)
    subject name ???
    argument: ``--subject_name %s``
reslice_like: (a pathlike object or string representing an existing
    file)
    reslice output to match file
    argument: ``--reslice_like %s``
template_type: ('cor' or 'mgh' or 'mgz' or 'minc' or 'analyze' or
    'analyze4d' or 'spm' or 'afni' or 'brik' or 'bshort' or 'bfloat'
    or 'sdt' or 'outline' or 'otl' or 'gdf' or 'nifti1' or 'nii' or
    'niigz' or 'ge' or 'gelx' or 'lx' or 'ximg' or 'siemens' or
    'dicom' or 'siemens_dicom')
    template file type
    argument: ``--template_type %s``
split: (a boolean)
    split output frames into separate output files.
    argument: ``--split``
frame: (an integer (int or long))
    keep only 0-based frame number
    argument: ``--frame %d``
midframe: (a boolean)
    keep only the middle frame
    argument: ``--mid-frame``

```

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```

skip_n: (an integer (int or long))
    skip the first n frames
    argument: ``--nskip %d``
drop_n: (an integer (int or long))
    drop the last n frames
    argument: ``--ndrop %d``
frame_subsample: (a tuple of the form: (an integer (int or long), an
    integer (int or long), an integer (int or long)))
    start delta end : frame subsampling (end = -1 for end)
    argument: ``--fsubsample %d %d %d``
in_scale: (a float)
    input intensity scale factor
    argument: ``--scale %f``
out_scale: (a float)
    output intensity scale factor
    argument: ``--out-scale %d``
in_like: (a pathlike object or string representing an existing file)
    input looks like
    argument: ``--in_like %s``
fill_parcellation: (a boolean)
    fill parcellation
    argument: ``--fill_parcellation``
smooth_parcellation: (a boolean)
    smooth parcellation
    argument: ``--smooth_parcellation``
zero_outlines: (a boolean)
    zero outlines
    argument: ``--zero_outlines``
color_file: (a pathlike object or string representing an existing
    file)
    color file
    argument: ``--color_file %s``
no_translate: (a boolean)
    ~~~
    argument: ``--no_translate``
status_file: (a pathlike object or string representing a file)
    status file for DICOM conversion
    argument: ``--status %s``
sdcm_list: (a pathlike object or string representing an existing
    file)
    list of DICOM files for conversion
    argument: ``--sdcm_list %s``
template_info: (a boolean)
    dump info about template
    argument: ``--template_info``
crop_gdf: (a boolean)
    apply GDF cropping
    argument: ``--crop_gdf``
zero_ge_z_offset: (a boolean)
    zero ge z offset ???
    argument: ``--zero_ge_z_offset``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``

```

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```
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a list of items which are a pathlike object or string
          representing an existing file)
          converted output file
```

62.3.12 MRIsCALabel[Link to code](#)

Wraps the executable command `mriscalabel`.

For a single subject, produces an annotation file, in which each cortical surface vertex is assigned a neuroanatomical label. This automatic procedure employs data from a previously-prepared atlas file. An atlas file is created from a training set, capturing region data manually drawn by neuroanatomists combined with statistics on variability correlated to geometric information derived from the cortical model (sulcus and curvature). Besides the atlases provided with FreeSurfer, new ones can be prepared using `mriscal_train`.

Examples

```
>>> from nipy.interfaces import freesurfer
>>> ca_label = freesurfer.MRIsCALabel()
>>> ca_label.inputs.subject_id = "test"
>>> ca_label.inputs.hemisphere = "lh"
>>> ca_label.inputs.canonsurf = "lh.pial"
>>> ca_label.inputs.curv = "lh.pial"
>>> ca_label.inputs.sulc = "lh.pial"
>>> ca_label.inputs.classifier = "iml.nii" # in practice, use .gcs extension
>>> ca_label.inputs.smoothwm = "lh.pial"
>>> ca_label.cmdline
'mriscalabel test lh lh.pial iml.nii lh.aparc.annot'
```

Inputs:

```
[Mandatory]
subject_id: (a string, nipy default value: subject_id)
            Subject name or ID
            argument: ``%s``, position: -5
hemisphere: ('lh' or 'rh')
            Hemisphere ('lh' or 'rh')
            argument: ``%s``, position: -4
canonsurf: (a pathlike object or string representing an existing
            file)
            Input canonical surface file
            argument: ``%s``, position: -3
classifier: (a pathlike object or string representing an existing
            file)
            Classifier array input file
            argument: ``%s``, position: -2
smoothwm: (a pathlike object or string representing an existing file)
            implicit input {hemisphere}.smoothwm
curv: (a pathlike object or string representing an existing file)
       implicit input {hemisphere}.curv
```

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```

sulc: (a pathlike object or string representing an existing file)
      implicit input {hemisphere}.sulc

[Optional]
out_file: (a pathlike object or string representing a file)
          Annotated surface output file
          argument: ``%s``, position: -1
label: (a pathlike object or string representing an existing file)
        Undocumented flag. Autorecon3 uses
        ../label/{hemisphere}.cortex.label as input file
        argument: ``-l %s``
aseg: (a pathlike object or string representing an existing file)
        Undocumented flag. Autorecon3 uses ../mri/aseg.presurf.mgz as input
        file
        argument: ``-aseg %s``
seed: (an integer (int or long))
        argument: ``-seed %d``
copy_inputs: (a boolean)
              Copies implicit inputs to node directory and creates a temp
              subjects_directory. Use this when running as a node
num_threads: (an integer (int or long))
              allows for specifying more threads
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
          Output volume from MRIsCLabel

```

62.3.13 Normalize[Link to code](#)

Wraps the executable command `mri_normalize`.

Normalize the white-matter, optionally based on control points. The input volume is converted into a new volume where white matter image values all range around 110.

Examples

```

>>> from nipy.interfaces import freesurfer
>>> normalize = freesurfer.Normalize()
>>> normalize.inputs.in_file = "T1.mgz"
>>> normalize.inputs.gradient = 1
>>> normalize.cmdline
'mri_normalize -g 1 T1.mgz T1_norm.mgz'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    The input file for Normalize
    argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
    The output file for Normalize
    argument: ``%s``, position: -1
gradient: (an integer (int or long))
    use max intensity/mm gradient g (default=1)
    argument: ``-g %d``
mask: (a pathlike object or string representing an existing file)
    The input mask file for Normalize
    argument: ``-mask %s``
segmentation: (a pathlike object or string representing an existing
    file)
    The input segmentation for Normalize
    argument: ``-aseg %s``
transform: (a pathlike object or string representing an existing
    file)
    Tranform file from the header of the input file
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    The output file for Normalize

```

62.3.14 ParseDICOMDir[Link to code](#)Wraps the executable command `mri_parse_sdcmdir`.Uses `mri_parse_sdcmdir` to get information from dicom directories**Examples**

```

>>> from nipy.interfaces.freesurfer import ParseDICOMDir
>>> dcminfo = ParseDICOMDir()
>>> dcminfo.inputs.dicom_dir = '.'
>>> dcminfo.inputs.sortbyrun = True
>>> dcminfo.inputs.summarize = True
>>> dcminfo.cmdline
'mri_parse_sdcmdir --d . --o dicominfo.txt --sortbyrun --summarize'

```

Inputs:

```
[Mandatory]
dicom_dir: (a pathlike object or string representing an existing
           directory)
           path to siemens dicom directory
           argument: ``--d %s``

[Optional]
dicom_info_file: (a pathlike object or string representing a file,
                 nipype default value: dicominfo.txt)
                 file to which results are written
                 argument: ``--o %s``
sortbyrun: (a boolean)
            assign run numbers
            argument: ``--sortbyrun``
summarize: (a boolean)
            only print out info for run leaders
            argument: ``--summarize``
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

```
dicom_info_file: (a pathlike object or string representing an
                 existing file)
                 text file containing dicom information
```

62.3.15 ReconAll

[Link to code](#)

Wraps the executable command recon-all.

Uses recon-all to generate surfaces and parcellations of structural data from anatomical images of a subject.

Examples

```
>>> from nipype.interfaces.freesurfer import ReconAll
>>> reconall = ReconAll()
>>> reconall.inputs.subject_id = 'foo'
>>> reconall.inputs.directive = 'all'
>>> reconall.inputs.subjects_dir = '.'
>>> reconall.inputs.T1_files = 'structural.nii'
>>> reconall.cmdline
'recon-all -all -i structural.nii -subjid foo -sd .'
>>> reconall.inputs.flags = "-qcachee"
>>> reconall.cmdline
'recon-all -all -i structural.nii -qcachee -subjid foo -sd .'
>>> reconall.inputs.flags = ["-cw256", "-qcachee"]
>>> reconall.cmdline
'recon-all -all -i structural.nii -cw256 -qcachee -subjid foo -sd .'
```

Hemisphere may be specified regardless of directive:

```
>>> reconall.inputs.flags = []
>>> reconall.inputs.hemi = 'lh'
>>> reconall.cmdline
'recon-all -all -i structural.nii -hemi lh -subjid foo -sd .'
```

-autorecon-hemi uses the -hemi input to specify the hemisphere to operate upon:

```
>>> reconall.inputs.directive = 'autorecon-hemi'
>>> reconall.cmdline
'recon-all -autorecon-hemi lh -i structural.nii -subjid foo -sd .'
```

Hippocampal subfields can accept T1 and T2 images:

```
>>> reconall_subfields = ReconAll()
>>> reconall_subfields.inputs.subject_id = 'foo'
>>> reconall_subfields.inputs.directive = 'all'
>>> reconall_subfields.inputs.subjects_dir = '.'
>>> reconall_subfields.inputs.T1_files = 'structural.nii'
>>> reconall_subfields.inputs.hippocampal_subfields_T1 = True
>>> reconall_subfields.cmdline
'recon-all -all -i structural.nii -hippocampal-subfields-T1 -subjid foo -sd .'
>>> reconall_subfields.inputs.hippocampal_subfields_T2 = (
... 'structural.nii', 'test')
>>> reconall_subfields.cmdline
'recon-all -all -i structural.nii -hippocampal-subfields-T1T2 structural.nii test_
↳-subjid foo -sd .'
>>> reconall_subfields.inputs.hippocampal_subfields_T1 = False
>>> reconall_subfields.cmdline
'recon-all -all -i structural.nii -hippocampal-subfields-T2 structural.nii test -
↳subjid foo -sd .'
```

Inputs:

```
[Optional]
subject_id: (a unicode string, nipy default value: recon_all)
    subject name
    argument: ``-subjid %s``
directive: ('all' or 'autorecon1' or 'autorecon2' or
    'autorecon2-volonly' or 'autorecon2-perhemi' or
    'autorecon2-inflate1' or 'autorecon2-cp' or 'autorecon2-wm' or
    'autorecon3' or 'autorecon3-T2pial' or 'autorecon-pial' or
    'autorecon-hemi' or 'localGI' or 'qcache', nipy default value:
    all)
    process directive
    argument: ``-%s``, position: 0
hemi: ('lh' or 'rh')
    hemisphere to process
    argument: ``-hemi %s``
T1_files: (a list of items which are a pathlike object or string
    representing an existing file)
    name of T1 file to process
    argument: ``-i %s...``
T2_file: (a pathlike object or string representing an existing file)
    Convert T2 image to orig directory
    argument: ``-T2 %s``
FLAIR_file: (a pathlike object or string representing an existing
    file)
    Convert FLAIR image to orig directory
```

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```

        argument: ``-FLAIR %s``
use_T2: (a boolean)
    Use T2 image to refine the pial surface
    argument: ``-T2pial``
    mutually_exclusive: use_FLAIR
use_FLAIR: (a boolean)
    Use FLAIR image to refine the pial surface
    argument: ``-FLAIRpial``
    mutually_exclusive: use_T2
openmp: (an integer (int or long))
    Number of processors to use in parallel
    argument: ``-openmp %d``
parallel: (a boolean)
    Enable parallel execution
    argument: ``-parallel``
hires: (a boolean)
    Conform to minimum voxel size (for voxels < 1mm)
    argument: ``-hires``
mprage: (a boolean)
    Assume scan parameters are MGH MP-RAGE protocol, which produces
    darker gray matter
    argument: ``-mprage``
big_ventricles: (a boolean)
    For use in subjects with enlarged ventricles
    argument: ``-bigventricles``
brainstem: (a boolean)
    Segment brainstem structures
    argument: ``-brainstem-structures``
hippocampal_subfields_T1: (a boolean)
    segment hippocampal subfields using input T1 scan
    argument: ``-hippocampal-subfields-T1``
hippocampal_subfields_T2: (a tuple of the form: (a pathlike object or
    string representing an existing file, a unicode string))
    segment hippocampal subfields using T2 scan, identified by ID (may
    be combined with hippocampal_subfields_T1)
    argument: ``-hippocampal-subfields-T2 %s %s``
expert: (a pathlike object or string representing an existing file)
    Set parameters using expert file
    argument: ``-expert %s``
xopts: ('use' or 'clean' or 'overwrite')
    Use, delete or overwrite existing expert options file
    argument: ``-xopts-%s``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    path to subjects directory
    argument: ``-sd %s``
flags: (a list of items which are a unicode string)
    additional parameters
    argument: ``%s``
talairach: (a unicode string)
    Flags to pass to talairach commands
    mutually_exclusive: expert
mri_normalize: (a unicode string)
    Flags to pass to mri_normalize commands
    mutually_exclusive: expert
mri_watershed: (a unicode string)
    Flags to pass to mri_watershed commands

```

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```
        mutually_exclusive: expert
mri_em_register: (a unicode string)
    Flags to pass to mri_em_register commands
    mutually_exclusive: expert
mri_ca_normalize: (a unicode string)
    Flags to pass to mri_ca_normalize commands
    mutually_exclusive: expert
mri_ca_register: (a unicode string)
    Flags to pass to mri_ca_register commands
    mutually_exclusive: expert
mri_remove_neck: (a unicode string)
    Flags to pass to mri_remove_neck commands
    mutually_exclusive: expert
mri_ca_label: (a unicode string)
    Flags to pass to mri_ca_label commands
    mutually_exclusive: expert
mri_segstats: (a unicode string)
    Flags to pass to mri_segstats commands
    mutually_exclusive: expert
mri_mask: (a unicode string)
    Flags to pass to mri_mask commands
    mutually_exclusive: expert
mri_segment: (a unicode string)
    Flags to pass to mri_segment commands
    mutually_exclusive: expert
mri_edit_wm_with_aseg: (a unicode string)
    Flags to pass to mri_edit_wm_with_aseg commands
    mutually_exclusive: expert
mri_preteess: (a unicode string)
    Flags to pass to mri_preteess commands
    mutually_exclusive: expert
mri_fill: (a unicode string)
    Flags to pass to mri_fill commands
    mutually_exclusive: expert
mri_tessellate: (a unicode string)
    Flags to pass to mri_tessellate commands
    mutually_exclusive: expert
mris_smooth: (a unicode string)
    Flags to pass to mris_smooth commands
    mutually_exclusive: expert
mris_inflate: (a unicode string)
    Flags to pass to mris_inflate commands
    mutually_exclusive: expert
mris_sphere: (a unicode string)
    Flags to pass to mris_sphere commands
    mutually_exclusive: expert
mris_fix_topology: (a unicode string)
    Flags to pass to mris_fix_topology commands
    mutually_exclusive: expert
mris_make_surfaces: (a unicode string)
    Flags to pass to mris_make_surfaces commands
    mutually_exclusive: expert
mris_surf2vol: (a unicode string)
    Flags to pass to mris_surf2vol commands
    mutually_exclusive: expert
mris_register: (a unicode string)
    Flags to pass to mris_register commands
```

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```

        mutually_exclusive: expert
mrisp_paint: (a unicode string)
    Flags to pass to mrisp_paint commands
    mutually_exclusive: expert
mris_ca_label: (a unicode string)
    Flags to pass to mris_ca_label commands
    mutually_exclusive: expert
mris_anatomical_stats: (a unicode string)
    Flags to pass to mris_anatomical_stats commands
    mutually_exclusive: expert
mri_aparc2aseg: (a unicode string)
    Flags to pass to mri_aparc2aseg commands
    mutually_exclusive: expert
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

subjects_dir: (a pathlike object or string representing an existing
    directory)
    Freesurfer subjects directory.
subject_id: (a unicode string)
    Subject name for whom to retrieve data
T1: (a pathlike object or string representing an existing file)
    Intensity normalized whole-head volume
aseg: (a pathlike object or string representing an existing file)
    Volumetric map of regions from automatic segmentation
brain: (a pathlike object or string representing an existing file)
    Intensity normalized brain-only volume
brainmask: (a pathlike object or string representing an existing
    file)
    Skull-stripped (brain-only) volume
filled: (a pathlike object or string representing an existing file)
    Subcortical mass volume
norm: (a pathlike object or string representing an existing file)
    Normalized skull-stripped volume
nu: (a pathlike object or string representing an existing file)
    Non-uniformity corrected whole-head volume
orig: (a pathlike object or string representing an existing file)
    Base image conformed to Freesurfer space
rawavg: (a pathlike object or string representing an existing file)
    Volume formed by averaging input images
ribbon: (a list of items which are a pathlike object or string
    representing an existing file)
    Volumetric maps of cortical ribbons
wm: (a pathlike object or string representing an existing file)
    Segmented white-matter volume
wmparc: (a pathlike object or string representing an existing file)
    Aparc parcellation projected into subcortical white matter
curv: (a list of items which are a pathlike object or string
    representing an existing file)
    Maps of surface curvature

```

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```
avg_curv: (a list of items which are a pathlike object or string
           representing an existing file)
           Average atlas curvature, sampled to subject
inflated: (a list of items which are a pathlike object or string
           representing an existing file)
           Inflated surface meshes
pial: (a list of items which are a pathlike object or string
       representing an existing file)
       Gray matter/pia mater surface meshes
area_pial: (a list of items which are a pathlike object or string
            representing an existing file)
            Mean area of triangles each vertex on the pial surface is associated
            with
curv_pial: (a list of items which are a pathlike object or string
            representing an existing file)
            Curvature of pial surface
smoothwm: (a list of items which are a pathlike object or string
            representing an existing file)
            Smoothed original surface meshes
sphere: (a list of items which are a pathlike object or string
          representing an existing file)
          Spherical surface meshes
sulc: (a list of items which are a pathlike object or string
        representing an existing file)
        Surface maps of sulcal depth
thickness: (a list of items which are a pathlike object or string
            representing an existing file)
            Surface maps of cortical thickness
volume: (a list of items which are a pathlike object or string
          representing an existing file)
          Surface maps of cortical volume
white: (a list of items which are a pathlike object or string
         representing an existing file)
         White/gray matter surface meshes
jacobian_white: (a list of items which are a pathlike object or
                 string representing an existing file)
                 Distortion required to register to spherical atlas
graymid: (a list of items which are a pathlike object or string
           representing an existing file)
           Graymid/midthickness surface meshes
label: (a list of items which are a pathlike object or string
         representing an existing file)
         Volume and surface label files
annot: (a list of items which are a pathlike object or string
        representing an existing file)
        Surface annotation files
aparc_aseg: (a list of items which are a pathlike object or string
             representing an existing file)
             Aparc parcellation projected into aseg volume
sphere_reg: (a list of items which are a pathlike object or string
             representing an existing file)
             Spherical registration file
aseg_stats: (a list of items which are a pathlike object or string
             representing an existing file)
             Automated segmentation statistics file
wmparc_stats: (a list of items which are a pathlike object or string
               representing an existing file)
```

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```

        White matter parcellation statistics file
    aparc_stats: (a list of items which are a pathlike object or string
                  representing an existing file)
                  Aparc parcellation statistics files
    BA_stats: (a list of items which are a pathlike object or string
              representing an existing file)
              Brodmann Area statistics files
    aparc_a2009s_stats: (a list of items which are a pathlike object or
                       string representing an existing file)
                       Aparc a2009s parcellation statistics files
    curv_stats: (a list of items which are a pathlike object or string
                representing an existing file)
                Curvature statistics files
    entorhinal_exvivo_stats: (a list of items which are a pathlike object
                             or string representing an existing file)
                             Entorhinal exvivo statistics files

```

62.3.16 Resample

[Link to code](#)

Wraps the executable command `mri_convert`.

Use FreeSurfer `mri_convert` to up or down-sample image files

Examples

```

>>> from nipy.interfaces import freesurfer
>>> resampler = freesurfer.Resample()
>>> resampler.inputs.in_file = 'structural.nii'
>>> resampler.inputs.resampled_file = 'resampled.nii'
>>> resampler.inputs.voxel_size = (2.1, 2.1, 2.1)
>>> resampler.cmdline
'mri_convert -vs 2.10 2.10 2.10 -i structural.nii -o resampled.nii'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         file to resample
         argument: ``-i %s``, position: -2
voxel_size: (a tuple of the form: (a float, a float, a float))
            triplet of output voxel sizes
            argument: ``-vs %.2f %.2f %.2f``

[Optional]
resampled_file: (a pathlike object or string representing a file)
               output filename
               argument: ``-o %s``, position: -1
subjects_dir: (a pathlike object or string representing an existing
              directory)
              subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a

```

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```
value of class 'str', nipy default value: {}
Environment variables
```

Outputs:

```
resampled_file: (a pathlike object or string representing an existing
                 file)
                 output filename
```

62.3.17 RobustRegister[Link to code](#)Wraps the executable command `mri_robust_register`.

Perform intramodal linear registration (translation and rotation) using robust statistics.

Examples

```
>>> from nipy.interfaces.freesurfer import RobustRegister
>>> reg = RobustRegister()
>>> reg.inputs.source_file = 'structural.nii'
>>> reg.inputs.target_file = 'T1.nii'
>>> reg.inputs.auto_sens = True
>>> reg.inputs.init_orient = True
>>> reg.cmdline # doctest: +ELLIPSIS
'mri_robust_register --satit --initorient --lta .../structural_robustreg.lta --
↪mov structural.nii --dst T1.nii'
```

References

Reuter, M, Rosas, HD, and Fischl, B, (2010). Highly Accurate Inverse Consistent Registration: A Robust Approach. Neuroimage 53(4) 1181-96.

Inputs:

```
[Mandatory]
source_file: (a pathlike object or string representing an existing
             file)
             volume to be registered
             argument: ``--mov %s``
target_file: (a pathlike object or string representing an existing
             file)
             target volume for the registration
             argument: ``--dst %s``
auto_sens: (a boolean)
            auto-detect good sensitivity
            argument: ``--satit``
            mutually_exclusive: outlier_sens
outlier_sens: (a float)
              set outlier sensitivity explicitly
              argument: ``--sat %.4f``
              mutually_exclusive: auto_sens

[Optional]
out_reg_file: (a bool or None or a pathlike object or string
              representing a file, nipy default value: True)
              registration file; either True or filename
```

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```

        argument: ``--lta %s``
registered_file: (a boolean or a pathlike object or string
    representing a file)
    registered image; either True or filename
    argument: ``--warp %s``
weights_file: (a boolean or a pathlike object or string representing
    a file)
    weights image to write; either True or filename
    argument: ``--weights %s``
est_int_scale: (a boolean)
    estimate intensity scale (recommended for unnormalized images)
    argument: ``--iscale``
trans_only: (a boolean)
    find 3 parameter translation only
    argument: ``--transonly``
in_xfm_file: (a pathlike object or string representing an existing
    file)
    use initial transform on source
    argument: ``--transform``
half_source: (a boolean or a pathlike object or string representing a
    file)
    write source volume mapped to halfway space
    argument: ``--halfmov %s``
half_targ: (a boolean or a pathlike object or string representing a
    file)
    write target volume mapped to halfway space
    argument: ``--halfdst %s``
half_weights: (a boolean or a pathlike object or string representing
    a file)
    write weights volume mapped to halfway space
    argument: ``--halfweights %s``
half_source_xfm: (a boolean or a pathlike object or string
    representing a file)
    write transform from source to halfway space
    argument: ``--halfmovlta %s``
half_targ_xfm: (a boolean or a pathlike object or string representing
    a file)
    write transform from target to halfway space
    argument: ``--halfdstlta %s``
least_squares: (a boolean)
    use least squares instead of robust estimator
    argument: ``--leastsquares``
no_init: (a boolean)
    skip transform init
    argument: ``--noinit``
init_orient: (a boolean)
    use moments for initial orient (recommended for stripped brains)
    argument: ``--initorient``
max_iterations: (an integer (int or long))
    maximum # of times on each resolution
    argument: ``--maxit %d``
high_iterations: (an integer (int or long))
    max # of times on highest resolution
    argument: ``--highit %d``
iteration_thresh: (a float)
    stop iterations when below threshold
    argument: ``--epsit %.3f``

```

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```

subsample_thresh: (an integer (int or long))
    subsample if dimension is above threshold size
    argument: ``--subsample %d``
outlier_limit: (a float)
    set maximal outlier limit in satit
    argument: ``--wlimit %.3f``
write_vo2vox: (a boolean)
    output vox2vox matrix (default is RAS2RAS)
    argument: ``--vox2vox``
no_multi: (a boolean)
    work on highest resolution
    argument: ``--nomulti``
mask_source: (a pathlike object or string representing an existing
    file)
    image to mask source volume with
    argument: ``--maskmov %s``
mask_target: (a pathlike object or string representing an existing
    file)
    image to mask target volume with
    argument: ``--maskdst %s``
force_double: (a boolean)
    use double-precision intensities
    argument: ``--doubleprec``
force_float: (a boolean)
    use float intensities
    argument: ``--floattype``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_reg_file: (a pathlike object or string representing an existing
    file)
    output registration file
registered_file: (a pathlike object or string representing an
    existing file)
    output image with registration applied
weights_file: (a pathlike object or string representing an existing
    file)
    image of weights used
half_source: (a pathlike object or string representing an existing
    file)
    source image mapped to halfway space
half_targ: (a pathlike object or string representing an existing
    file)
    target image mapped to halfway space
half_weights: (a pathlike object or string representing an existing
    file)
    weights image mapped to halfway space

```

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```

half_source_xfm: (a pathlike object or string representing an
                  existing file)
                  transform file to map source image to halfway space
half_targ_xfm: (a pathlike object or string representing an existing
               file)
               transform file to map target image to halfway space

```

62.3.18 SegmentCC

[Link to code](#)

Wraps the executable command `mri_cc`.

This program segments the corpus callosum into five separate labels in the subcortical segmentation volume 'aseg.mgz'. The divisions of the cc are equally spaced in terms of distance along the primary eigendirection (pretty much the long axis) of the cc. The lateral extent can be changed with the `-T <thickness>` parameter, where `<thickness>` is the distance off the midline (so `-T 1` would result in the who CC being 3mm thick). The default is 2 so it's 5mm thick. The `aseg.stats` values should be volume.

Examples

```

>>> from nipy.interfaces import freesurfer
>>> SegmentCC_node = freesurfer.SegmentCC()
>>> SegmentCC_node.inputs.in_file = "aseg.mgz"
>>> SegmentCC_node.inputs.in_norm = "norm.mgz"
>>> SegmentCC_node.inputs.out_rotation = "cc.lta"
>>> SegmentCC_node.inputs.subject_id = "test"
>>> SegmentCC_node.cmdline
'mri_cc -aseg aseg.mgz -o aseg.auto.mgz -lta cc.lta test'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         Input aseg file to read from subjects directory
         argument: ``-aseg %s``
in_norm: (a pathlike object or string representing an existing file)
         Required undocumented input {subject}/mri/norm.mgz
out_rotation: (a pathlike object or string representing a file)
              Global filepath for writing rotation lta
              argument: ``-lta %s``
subject_id: (a string, nipy default value: subject_id)
            Subject name
            argument: ``%s``, position: -1

[Optional]
out_file: (a pathlike object or string representing a file)
          Filename to write aseg including CC
          argument: ``-o %s``
copy_inputs: (a boolean)
             If running as a node, set this to True. This will copy the input
             files to the node directory.
subjects_dir: (a pathlike object or string representing an existing
              directory)
              subjects directory
args: (a unicode string)
      Additional parameters to the command

```

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```

        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
          Output segmentation uncluding corpus collosum
out_rotation: (a pathlike object or string representing a file)
              Output lta rotation file

```

62.3.19 SegmentWM

[Link to code](#)Wraps the executable command `mri_segment`.

This program segments white matter from the input volume. The input volume should be normalized such that white matter voxels are ~110-valued, and the volume is conformed to 256^3 .

Examples

```

>>> from nipy.interfaces import freesurfer
>>> SegmentWM_node = freesurfer.SegmentWM()
>>> SegmentWM_node.inputs.in_file = "norm.mgz"
>>> SegmentWM_node.inputs.out_file = "wm.seg.mgz"
>>> SegmentWM_node.cmdline
'mri_segment norm.mgz wm.seg.mgz'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
          Input file for SegmentWM
          argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file)
          File to be written as output for SegmentWM
          argument: ``%s``, position: -1

[Optional]
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
          Output white matter segmentation

```

62.3.20 Smooth

[Link to code](#)

Wraps the executable command `mriss_volsmooth`.

Use FreeSurfer `mriss_volsmooth` to smooth a volume

This function smoothes cortical regions on a surface and non-cortical regions in volume.

Note: Cortical voxels are mapped to the surface (3D->2D) and then the smoothed values from the surface are put back into the volume to fill the cortical ribbon. If data is smoothed with this algorithm, one has to be careful about how further processing is interpreted.

Examples

```
>>> from nipy.interfaces.freesurfer import Smooth
>>> smoothvol = Smooth(in_file='functional.nii', smoothed_file = 'foo_out.nii',
↳ reg_file='register.dat', surface_fwhm=10, vol_fwhm=6)
>>> smoothvol.cmdline
'mriss_volsmooth --i functional.nii --reg register.dat --o foo_out.nii --fwhm 10.
↳ 000000 --vol-fwhm 6.000000'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         source volume
         argument: ``--i %s``
reg_file: (a pathlike object or string representing an existing file)
         registers volume to surface anatomical
         argument: ``--reg %s``
surface_fwhm: (a floating point number >= 0.0)
              surface FWHM in mm
              argument: ``--fwhm %f``
mutually_exclusive: num_iters
requires: reg_file
num_iters: (a long integer >= 1)
           number of iterations instead of fwhm
           argument: ``--nitters %d``
mutually_exclusive: surface_fwhm

[Optional]
smoothed_file: (a pathlike object or string representing a file)
              output volume
              argument: ``--o %s``
proj_frac_avg: (a tuple of the form: (a float, a float, a float))
              average a long normal min max delta
              argument: ``--projfrac-avg %.2f %.2f %.2f``
mutually_exclusive: proj_frac
proj_frac: (a float)
           project frac of thickness a long surface normal
           argument: ``--projfrac %s``
mutually_exclusive: proj_frac_avg
vol_fwhm: (a floating point number >= 0.0)
          volume smoothing outside of surface
          argument: ``--vol-fwhm %f``
subjects_dir: (a pathlike object or string representing an existing
              directory)
```

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```

    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

smoothed_file: (a pathlike object or string representing an existing
    file)
    smoothed input volume

```

62.3.21 SynthesizeFLASH[Link to code](#)Wraps the executable command `mri_synthesize`.

Synthesize a FLASH acquisition from T1 and proton density maps.

Examples

```

>>> from nipy.interfaces.freesurfer import SynthesizeFLASH
>>> syn = SynthesizeFLASH(tr=20, te=3, flip_angle=30)
>>> syn.inputs.t1_image = 'T1.mgz'
>>> syn.inputs.pd_image = 'PD.mgz'
>>> syn.inputs.out_file = 'flash_30syn.mgz'
>>> syn.cmdline
'mri_synthesize 20.00 30.00 3.000 T1.mgz PD.mgz flash_30syn.mgz'

```

Inputs:

```

[Mandatory]
tr: (a float)
    repetition time (in msec)
    argument: ``%.2f``, position: 2
flip_angle: (a float)
    flip angle (in degrees)
    argument: ``%.2f``, position: 3
te: (a float)
    echo time (in msec)
    argument: ``%.3f``, position: 4
t1_image: (a pathlike object or string representing an existing file)
    image of T1 values
    argument: ``%s``, position: 5
pd_image: (a pathlike object or string representing an existing file)
    image of proton density values
    argument: ``%s``, position: 6

[Optional]
fixed_weighting: (a boolean)
    use a fixed weighting to generate optimal gray/white contrast
    argument: ``-w``, position: 1
out_file: (a pathlike object or string representing a file)
    image to write

```

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```

        argument: ``%s``
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          synthesized FLASH acquisition

```

62.3.22 UnpackSDICOMDir[Link to code](#)

Wraps the executable command unpacksdcmdir.

Use unpacksdcmdir to convert dicom files

Call unpacksdcmdir -help from the command line to see more information on using this command.

Examples

```

>>> from nipy.interfaces.freesurfer import UnpackSDICOMDir
>>> unpack = UnpackSDICOMDir()
>>> unpack.inputs.source_dir = '.'
>>> unpack.inputs.output_dir = '.'
>>> unpack.inputs.run_info = (5, 'mprage', 'nii', 'struct')
>>> unpack.inputs.dir_structure = 'generic'
>>> unpack.cmdline
'unpacksdcmdir -generic -targ . -run 5 mprage nii struct -src .'

```

Inputs:

```

[Mandatory]
source_dir: (a pathlike object or string representing an existing
            directory)
            directory with the DICOM files
            argument: ``-src %s``
run_info: (a tuple of the form: (an integer (int or long), a unicode
            string, a unicode string, a unicode string))
            runno subdir format name : spec unpacking rules on cmdline
            argument: ``-run %d %s %s %s``
            mutually_exclusive: run_info, config, seq_config
config: (a pathlike object or string representing an existing file)
        specify unpacking rules in file
        argument: ``-cfg %s``
        mutually_exclusive: run_info, config, seq_config
seq_config: (a pathlike object or string representing an existing
            file)
            specify unpacking rules based on sequence
            argument: ``-seqcfg %s``
            mutually_exclusive: run_info, config, seq_config

```

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```

[Optional]
output_dir: (a pathlike object or string representing a directory)
    top directory into which the files will be unpacked
    argument: ``-targ %s``
dir_structure: ('fsfast' or 'generic')
    unpack to specified directory structures
    argument: ``-%s``
no_info_dump: (a boolean)
    do not create infodump file
    argument: ``-noinfodump``
scan_only: (a pathlike object or string representing an existing
    file)
    only scan the directory and put result in file
    argument: ``-scanonly %s``
log_file: (a pathlike object or string representing an existing file)
    explicilty set log file
    argument: ``-log %s``
spm_zeropad: (an integer (int or long))
    set frame number zero padding width for SPM
    argument: ``-nspmzeropad %d``
no_unpack_err: (a boolean)
    do not try to unpack runs with errors
    argument: ``-no-unpackerr``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

None

62.3.23 WatershedSkullStrip

[Link to code](#)

Wraps the executable command `mri_watershed`.

This program strips skull and other outer non-brain tissue and produces the brain volume from T1 volume or the scanned volume.

The “watershed” segmentation algorithm was used to dertermine the intensity values for white matter, grey matter, and CSF. A force field was then used to fit a spherical surface to the brain. The shape of the surface fit was then evaluated against a previously derived template.

The default parameters are: `-w 0.82 -b 0.32 -h 10 -seedpt -ta -wta`
(Segonne 2004)

Examples

```

>>> from nipy.interfaces.freesurfer import WatershedSkullStrip
>>> skullstrip = WatershedSkullStrip()

```

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```

>>> skullstrip.inputs.in_file = "T1.mgz"
>>> skullstrip.inputs.t1 = True
>>> skullstrip.inputs.transform = "transforms/talairach_with_skull.lta"
>>> skullstrip.inputs.out_file = "brainmask.auto.mgz"
>>> skullstrip.cmdline
'mri_watershed -T1 transforms/talairach_with_skull.lta T1.mgz brainmask.auto.mgz'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input volume
         argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file, nipy
         default value: brainmask.auto.mgz)
         output volume
         argument: ``%s``, position: -1

[Optional]
t1: (a boolean)
    specify T1 input volume (T1 grey value = 110)
    argument: ``-T1``
brain_atlas: (a pathlike object or string representing an existing
            file)
            argument: ``-brain_atlas %s``, position: -4
transform: (a pathlike object or string representing a file)
            undocumented
            argument: ``%s``, position: -3
subjects_dir: (a pathlike object or string representing an existing
            directory)
            subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
          skull stripped brain volume

```

62.4 interfaces.freesurfer.registration

62.4.1 EMRegister

[Link to code](#)Wraps the executable command `mri_em_register`.

This program creates a tranform in lta format

Examples

```
>>> from nipy.interfaces.freesurfer import EMRegister
>>> register = EMRegister()
>>> register.inputs.in_file = 'norm.mgz'
>>> register.inputs.template = 'aseg.mgz'
>>> register.inputs.out_file = 'norm_transform.lta'
>>> register.inputs.skull = True
>>> register.inputs.nbrspacing = 9
>>> register.cmdline
'mri_em_register -uns 9 -skull norm.mgz aseg.mgz norm_transform.lta'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         in brain volume
         argument: ``%s``, position: -3
template: (a pathlike object or string representing an existing file)
          template gca
          argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
          output transform
          argument: ``%s``, position: -1
skull: (a boolean)
        align to atlas containing skull (uns=5)
        argument: ``-skull``
mask: (a pathlike object or string representing an existing file)
       use volume as a mask
       argument: ``-mask %s``
nbrspacing: (an integer (int or long))
            align to atlas containing skull setting unknown_nbr_spacing =
            nbrspacing
            argument: ``-uns %d``
transform: (a pathlike object or string representing an existing
            file)
            Previously computed transform
            argument: ``-t %s``
num_threads: (an integer (int or long))
             allows for specifying more threads
subjects_dir: (a pathlike object or string representing an existing
              directory)
              subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
          output transform
```

62.4.2 MPRtoMNI305

[Link to code](#)

Wraps the executable command `mpr2mni305`.
For complete details, see FreeSurfer documentation

Examples

```
>>> from nipy.interfaces.freesurfer import MPRTomNI305, Info
>>> mprtomni305 = MPRTomNI305()
>>> mprtomni305.inputs.target = 'structural.nii'
>>> mprtomni305.inputs.reference_dir = '.' # doctest: +SKIP
>>> mprtomni305.cmdline # doctest: +SKIP
'mpr2mni305 output'
>>> mprtomni305.inputs.out_file = 'struct_out' # doctest: +SKIP
>>> mprtomni305.cmdline # doctest: +SKIP
'mpr2mni305 struct_out' # doctest: +SKIP
>>> mprtomni305.inputs.environ['REFDIR'] == os.path.join(Info.home(), 'average')
↪ # doctest: +SKIP
True
>>> mprtomni305.inputs.environ['MPR2MNI305_TARGET'] # doctest: +SKIP
'structural'
>>> mprtomni305.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
reference_dir: (a pathlike object or string representing an existing
               directory, nipy default value: )
               TODO
target: (a string, nipy default value: )
        input atlas file

[Optional]
in_file: (a pathlike object or string representing a file, nipy
         default value: <undefined>)
         the input file prefix for MPRTomNI305
         argument: ``%s``
subjects_dir: (a pathlike object or string representing an existing
              directory)
              subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
          The output file '<in_file>_to_<target>_t4_vox2vox.txt'
log_file: (a pathlike object or string representing an existing file,
          nipy default value: output.nipy)
          The output log
```

62.4.3 MRICoreg

[Link to code](#)

Wraps the executable command `mri_coreg`.

This program registers one volume to another
 mri_coreg is a C reimplementation of spm_coreg in FreeSurfer

Examples

```
>>> from nipy.interfaces.freesurfer import MRICoreg
>>> coreg = MRICoreg()
>>> coreg.inputs.source_file = 'moving1.nii'
>>> coreg.inputs.reference_file = 'fixed1.nii'
>>> coreg.inputs.subjects_dir = '.'
>>> coreg.cmdline # doctest: +ELLIPSIS
'mri_coreg --lta .../registration.lta --ref fixed1.nii --mov moving1.nii --sd .'
```

If passing a subject ID, the reference mask may be disabled:

```
>>> coreg = MRICoreg()
>>> coreg.inputs.source_file = 'moving1.nii'
>>> coreg.inputs.subjects_dir = '.'
>>> coreg.inputs.subject_id = 'fsaverage'
>>> coreg.inputs.reference_mask = False
>>> coreg.cmdline # doctest: +ELLIPSIS
'mri_coreg --s fsaverage --no-ref-mask --lta .../registration.lta --mov moving1.
↪nii --sd .'
```

Spatial scales may be specified as a list of one or two separations:

```
>>> coreg.inputs.sep = [4]
>>> coreg.cmdline # doctest: +ELLIPSIS
'mri_coreg --s fsaverage --no-ref-mask --lta .../registration.lta --sep 4 --mov_
↪moving1.nii --sd .'
```

```
>>> coreg.inputs.sep = [4, 5]
>>> coreg.cmdline # doctest: +ELLIPSIS
'mri_coreg --s fsaverage --no-ref-mask --lta .../registration.lta --sep 4 --sep 5_
↪--mov moving1.nii --sd .'
```

Inputs:

```
[Mandatory]
source_file: (a pathlike object or string representing a file)
    source file to be registered
    argument: ``--mov %s``
reference_file: (a pathlike object or string representing a file)
    reference (target) file
    argument: ``--ref %s``
    mutually_exclusive: subject_id
subject_id: (a unicode string)
    freesurfer subject ID (implies ``reference_mask == aparc+aseg.mgz``
    unless otherwise specified)
    argument: ``--s %s``, position: 1
    mutually_exclusive: reference_file
    requires: subjects_dir

[Optional]
out_lta_file: (a bool or None or a pathlike object or string
    representing a file, nipy default value: True)
    output registration file (LTA format)
    argument: ``--lta %s``
```

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```

out_reg_file: (a bool or None or a pathlike object or string
               representing a file)
               output registration file (REG format)
               argument: ``--regdat %s``
out_params_file: (a bool or None or a pathlike object or string
                  representing a file)
                  output parameters file
                  argument: ``--params %s``
subjects_dir: (a pathlike object or string representing an existing
               directory)
               FreeSurfer SUBJECTS_DIR
               argument: ``--sd %s``
dof: (6 or 9 or 12)
      number of transform degrees of freedom
      argument: ``--dof %d``
reference_mask: (a bool or None or a unicode string)
                 mask reference volume with given mask, or None if ``False``
                 argument: ``--ref-mask %s``, position: 2
source_mask: (a unicode string)
              mask source file with given mask
              argument: ``--mov-mask``
num_threads: (an integer (int or long))
              number of OpenMP threads
              argument: ``--threads %d``
no_coord_dithering: (a boolean)
                     turn off coordinate dithering
                     argument: ``--no-coord-dither``
no_intensity_dithering: (a boolean)
                         turn off intensity dithering
                         argument: ``--no-intensity-dither``
sep: (a list of from 1 to 2 items which are any value)
      set spatial scales, in voxels (default [2, 4])
      argument: ``--sep %s...``
initial_translation: (a tuple of the form: (a float, a float, a
      float))
      initial translation in mm (implies no_cras0)
      argument: ``--trans %g %g %g``
initial_rotation: (a tuple of the form: (a float, a float, a float))
                  initial rotation in degrees
                  argument: ``--rot %g %g %g``
initial_scale: (a tuple of the form: (a float, a float, a float))
               initial scale
               argument: ``--scale %g %g %g``
initial_shear: (a tuple of the form: (a float, a float, a float))
               initial shear (Hxy, Hxz, Hyz)
               argument: ``--shear %g %g %g``
no_cras0: (a boolean)
           do not set translation parameters to align centers of source and
           reference files
           argument: ``--no-cras0``
max_iters: (a long integer >= 1)
            maximum iterations (default: 4)
            argument: ``--nittersmax %d``
ftol: (a float)
       floating-point tolerance (default=1e-7)
       argument: ``--ftol %e``
linmintol: (a float)

```

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```

        argument: ``--linmintol %e``
saturation_threshold: (0.0 <= a floating point number <= 100.0)
    saturation threshold (default=9.999)
    argument: ``--sat %g``
conform_reference: (a boolean)
    conform reference without rescaling
    argument: ``--conf-ref``
no_brute_force: (a boolean)
    do not brute force search
    argument: ``--no-bf``
brute_force_limit: (a float)
    constrain brute force search to +/- lim
    argument: ``--bf-lim %g``
    mutually_exclusive: no_brute_force
brute_force_samples: (an integer (int or long))
    number of samples in brute force search
    argument: ``--bf-nsamp %d``
    mutually_exclusive: no_brute_force
no_smooth: (a boolean)
    do not apply smoothing to either reference or source file
    argument: ``--no-smooth``
ref_fwhm: (a float)
    apply smoothing to reference file
    argument: ``--ref-fwhm``
source_oob: (a boolean)
    count source voxels that are out-of-bounds as 0
    argument: ``--mov-oob``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_reg_file: (a pathlike object or string representing an existing
    file)
    output registration file
out_lta_file: (a pathlike object or string representing an existing
    file)
    output LTA-style registration file
out_params_file: (a pathlike object or string representing an
    existing file)
    output parameters file

```

62.4.4 Paint[Link to code](#)

Wraps the executable command `mrisc_paint`.

This program is useful for extracting one of the arrays (“a variable”) from a surface-registration template file. The output is a file containing a surface-worth of per-vertex values, saved in “curvature” format. Because the template data is sampled to a particular surface mesh, this conjures the idea of “painting to a surface”.

Examples

```
>>> from nipy.interfaces.freesurfer import Paint
>>> paint = Paint()
>>> paint.inputs.in_surf = 'lh.pial'
>>> paint.inputs.template = 'aseg.mgz'
>>> paint.inputs.averages = 5
>>> paint.inputs.out_file = 'lh.avg_curv'
>>> paint.cmdline
'mrisp_paint -a 5 aseg.mgz lh.pial lh.avg_curv'
```

Inputs:

```
[Mandatory]
in_surf: (a pathlike object or string representing an existing file)
    Surface file with grid (vertices) onto which the template data is to
    be sampled or 'painted'
    argument: ``%s``, position: -2
template: (a pathlike object or string representing an existing file)
    Template file
    argument: ``%s``, position: -3

[Optional]
template_param: (an integer (int or long))
    Frame number of the input template
averages: (an integer (int or long))
    Average curvature patterns
    argument: ``-a %d``
out_file: (a pathlike object or string representing a file)
    File containing a surface-worth of per-vertex values, saved in
    'curvature' format.
    argument: ``%s``, position: -1
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
    File containing a surface-worth of per-vertex values, saved in
    'curvature' format.
```

62.4.5 Register

[Link to code](#)

Wraps the executable command `mris_register`.

This program registers a surface to an average surface template.

Examples

```
>>> from nipyne.interfaces.freesurfer import Register
>>> register = Register()
>>> register.inputs.in_surf = 'lh.pial'
>>> register.inputs.in_smoothwm = 'lh.pial'
>>> register.inputs.in_sulc = 'lh.pial'
>>> register.inputs.target = 'aseg.mgz'
>>> register.inputs.out_file = 'lh.pial.reg'
>>> register.inputs.curv = True
>>> register.cmdline
'mris_register -curv lh.pial aseg.mgz lh.pial.reg'
```

Inputs:

```
[Mandatory]
in_surf: (a pathlike object or string representing an existing file)
    Surface to register, often {hemi}.sphere
    argument: ``%s``, position: -3
target: (a pathlike object or string representing an existing file)
    The data to register to. In normal recon-all usage, this is a
    template file for average surface.
    argument: ``%s``, position: -2
in_sulc: (a pathlike object or string representing an existing file)
    Undocumented mandatory input file
    ${SUBJECTS_DIR}/surf/{hemisphere}.sulc

[Optional]
out_file: (a pathlike object or string representing a file)
    Output surface file to capture registration
    argument: ``%s``, position: -1
curv: (a boolean)
    Use smoothwm curvature for final alignment
    argument: ``-curv``
    requires: in_smoothwm
in_smoothwm: (a pathlike object or string representing an existing
    file)
    Undocumented input file ${SUBJECTS_DIR}/surf/{hemisphere}.smoothwm
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
    Output surface file to capture registration
```

62.4.6 RegisterAVItoTalairach

[Link to code](#)

Wraps the executable command `avi2talxfrm`.
converts the `vox2vox` from `talairach_avi` to a `talairach.xfm` file

This is a script that converts the vox2vox from talairach_avi to a talairach.xfm file. It is meant to replace the following cmd line:

```
tkregister2_cmdl -mov $InVol -targ $FREESURFER_HOME/average/mni305.cor.mgz
-xfmout ${XFM} -vox2vox talsrcimg_to_${target}_t4_vox2vox.txt -noedit -reg tal-
srcimg.reg.tmp.dat set targ = $FREESURFER_HOME/average/mni305.cor.mgz set subject
= mgh-02407836-v2 set InVol = $SUBJECTS_DIR/$subject/mri/orig.mgz set vox2vox =
$SUBJECTS_DIR/$subject/mri/transforms/talsrcimg_to_711-2C_as_mni_average_305_t4_vox2vox.txt
```

Examples

```
>>> from nipy.interfaces.freesurfer import RegisterAVItoTalairach
>>> register = RegisterAVItoTalairach()
>>> register.inputs.in_file = 'structural.mgz' # doctest:␣
↪+SKIP
>>> register.inputs.target = 'mni305.cor.mgz' # doctest:␣
↪+SKIP
>>> register.inputs.vox2vox = 'talsrcimg_to_structural_t4_vox2vox.txt' # doctest:␣
↪+SKIP
>>> register.cmdline # doctest:␣
↪+SKIP
'avi2talxfm structural.mgz mni305.cor.mgz talsrcimg_to_structural_t4_vox2vox.txt␣
↪talairach.auto.xfm'
```

```
>>> register.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    The input file
    argument: ``%s``, position: 0
target: (a pathlike object or string representing an existing file)
    The target file
    argument: ``%s``, position: 1
vox2vox: (a pathlike object or string representing an existing file)
    The vox2vox file
    argument: ``%s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file, nipy
    default value: talairach.auto.xfm)
    The transform output
    argument: ``%s``, position: 3
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
```

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```

    The output file for RegisterAVitoTalairach
log_file: (a pathlike object or string representing an existing file,
           nipype default value: output.nipype)
    The output log

```

62.5 interfaces.freesurfer.utils

62.5.1 AddXFormToHeader

[Link to code](#)

Wraps the executable command `mri_add_xform_to_header`.

Just adds specified xform to the volume header

(!) **WARNING:** transform input **MUST** be an absolute path to a DataSink'ed transform or the output will reference a transform in the workflow cache directory!

```

>>> from nipype.interfaces.freesurfer import AddXFormToHeader
>>> adder = AddXFormToHeader()
>>> adder.inputs.in_file = 'norm.mgz'
>>> adder.inputs.transform = 'trans.mat'
>>> adder.cmdline
'mri_add_xform_to_header trans.mat norm.mgz output.mgz'

```

```

>>> adder.inputs.copy_name = True
>>> adder.cmdline
'mri_add_xform_to_header -c trans.mat norm.mgz output.mgz'

```

```

>>> adder.run()    # doctest: +SKIP

```

References:

[https://surfer.nmr.mgh.harvard.edu/fswiki/mri_add_xform_to_header]

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input volume
         argument: ``%s``, position: -2
transform: (a pathlike object or string representing a file)
           xfm file
           argument: ``%s``, position: -3

[Optional]
out_file: (a pathlike object or string representing a file, nipype
          default value: output.mgz)
          output volume
          argument: ``%s``, position: -1
copy_name: (a boolean)
            do not try to load the xfmfile, just copy name
            argument: ``-c``
verbose: (a boolean)
          be verbose
          argument: ``-v``
subjects_dir: (a pathlike object or string representing an existing

```

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```

        directory)
        subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output volume

```

62.5.2 Aparc2Aseg

[Link to code](#)

Wraps the executable command `mri_aparc2aseg`.

Maps the cortical labels from the automatic cortical parcellation (aparc) to the automatic segmentation volume (aseg). The result can be used as the aseg would. The algorithm is to find each aseg voxel labeled as cortex (3 and 42) and assign it the label of the closest cortical vertex. If the voxel is not in the ribbon (as defined by `mri/ lh.ribbon` and `rh.ribbon`), then the voxel is marked as unknown (0). This can be turned off with `-noribbon`. The cortical parcellation is obtained from `subject/label/hemi.aparc.annot` which should be based on the curvature.buckner40.filled.desikan_killiany.gcs atlas. The aseg is obtained from `subject/mri/aseg.mgz` and should be based on the RB40_talairach_2005-07-20.gca atlas. If these atlases are used, then the segmentations can be viewed with `tkmedit` and the `FreeSurferColorLUT.txt` color table found in `$FREESURFER_HOME`. These are the default atlases used by `recon-all`.

Examples

```

>>> from nipype.interfaces.freesurfer import Aparc2Aseg
>>> aparc2aseg = Aparc2Aseg()
>>> aparc2aseg.inputs.lh_white = 'lh.pial'
>>> aparc2aseg.inputs.rh_white = 'lh.pial'
>>> aparc2aseg.inputs.lh_pial = 'lh.pial'
>>> aparc2aseg.inputs.rh_pial = 'lh.pial'
>>> aparc2aseg.inputs.lh_ribbon = 'label.mgz'
>>> aparc2aseg.inputs.rh_ribbon = 'label.mgz'
>>> aparc2aseg.inputs.ribbon = 'label.mgz'
>>> aparc2aseg.inputs.lh_annotation = 'lh.pial'
>>> aparc2aseg.inputs.rh_annotation = 'lh.pial'
>>> aparc2aseg.inputs.out_file = 'aparc+aseg.mgz'
>>> aparc2aseg.inputs.label_wm = True
>>> aparc2aseg.inputs.rip_unknown = True
>>> aparc2aseg.cmdline # doctest: +SKIP
'mri_aparc2aseg --labelwm --o aparc+aseg.mgz --rip-unknown --s subject_id'

```

Inputs:

```

[Mandatory]
subject_id: (a string, nipype default value: subject_id)
    Subject being processed
    argument: ``--s %s``
out_file: (a pathlike object or string representing a file)

```

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```

    Full path of file to save the output segmentation in
    argument: ``--o %s``
lh_white: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/surf/lh.white
rh_white: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/surf/rh.white
lh_pial: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/surf/lh.pial
rh_pial: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/surf/rh.pial
lh_ribbon: (a pathlike object or string representing an existing
    file)
    Input file must be <subject_id>/mri/lh.ribbon.mgz
rh_ribbon: (a pathlike object or string representing an existing
    file)
    Input file must be <subject_id>/mri/rh.ribbon.mgz
ribbon: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/mri/ribbon.mgz
lh_annotation: (a pathlike object or string representing an existing
    file)
    Input file must be <subject_id>/label/lh.aparc.annot
rh_annotation: (a pathlike object or string representing an existing
    file)
    Input file must be <subject_id>/label/rh.aparc.annot

[Optional]
filled: (a pathlike object or string representing an existing file)
    Implicit input filled file. Only required with FS v5.3.
aseg: (a pathlike object or string representing an existing file)
    Input aseg file
    argument: ``--aseg %s``
volmask: (a boolean)
    Volume mask flag
    argument: ``--volmask``
ctxseg: (a pathlike object or string representing an existing file)
    argument: ``--ctxseg %s``
label_wm: (a boolean)
    For each voxel labeled as white matter in the aseg, re-assign
    its label to be that of the closest cortical point if its
    distance is less than dmaxctx
    argument: ``--labelwm``
hypo_wm: (a boolean)
    Label hypointensities as WM
    argument: ``--hypo-as-wm``
rip_unknown: (a boolean)
    Do not label WM based on 'unknown' corical label
    argument: ``--rip-unknown``
a2009s: (a boolean)
    Using the a2009s atlas
    argument: ``--a2009s``
copy_inputs: (a boolean)
    If running as a node, set this to True.This will copy the input
    files to the node directory.
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)

```

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```

Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
          Output aseg file
          argument: ``%s``

```

62.5.3 Apas2Aseg[Link to code](#)Wraps the executable command `apas2aseg`.

Converts `aparc+aseg.mgz` into something like `aseg.mgz` by replacing the cortical segmentations 1000-1035 with 3 and 2000-2035 with 42. The advantage of this output is that the cortical label conforms to the actual surface (this is not the case with `aseg.mgz`).

Examples

```

>>> from nipy.interfaces.freesurfer import Apas2Aseg
>>> apas2aseg = Apas2Aseg()
>>> apas2aseg.inputs.in_file = 'aseg.mgz'
>>> apas2aseg.inputs.out_file = 'output.mgz'
>>> apas2aseg.cmdline
'apas2aseg --i aseg.mgz --o output.mgz'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
          Input aparc+aseg.mgz
          argument: ``--i %s``
out_file: (a pathlike object or string representing a file)
          Output aseg file
          argument: ``--o %s``

[Optional]
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
          Output aseg file
          argument: ``%s``

```

62.5.4 ApplyMask

[Link to code](#)

Wraps the executable command `mri_mask`.

Use Freesurfer's `mri_mask` to apply a mask to an image.

The mask file need not be binarized; it can be thresholded above a given value before application. It can also optionally be transformed into input space with an LTA matrix.

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input image (will be masked)
         argument: ``%s``, position: -3
mask_file: (a pathlike object or string representing an existing
            file)
            image defining mask space
            argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
          final image to write
          argument: ``%s``, position: -1
xfm_file: (a pathlike object or string representing an existing file)
          LTA-format transformation matrix to align mask with input
          argument: ``-xform %s``
invert_xfm: (a boolean)
            invert transformation
            argument: ``-invert``
xfm_source: (a pathlike object or string representing an existing
            file)
            image defining transform source space
            argument: ``-lta_src %s``
xfm_target: (a pathlike object or string representing an existing
            file)
            image defining transform target space
            argument: ``-lta_dst %s``
use_abs: (a boolean)
         take absolute value of mask before applying
         argument: ``-abs``
mask_thresh: (a float)
             threshold mask before applying
             argument: ``-T %.4f``
keep_mask_deletion_edits: (a boolean)
                          transfer voxel-deletion edits (voxels=1) from mask to out vol
                          argument: ``-keep_mask_deletion_edits``
transfer: (an integer (int or long))
          transfer only voxel value # from mask to out
          argument: ``-transfer %d``
subjects_dir: (a pathlike object or string representing an existing
              directory)
              subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```


Outputs:

```
out_file: (a pathlike object or string representing an existing file)
masked image
```

62.5.5 CheckTalairachAlignment

[Link to code](#)

Wraps the executable command `talairach_afd`.

This program detects Talairach alignment failures

Examples

```
>>> from nipy.interfaces.freesurfer import CheckTalairachAlignment
>>> checker = CheckTalairachAlignment()
```

```
>>> checker.inputs.in_file = 'trans.mat'
>>> checker.inputs.threshold = 0.005
>>> checker.cmdline
'talairach_afd -T 0.005 -xfm trans.mat'
```

```
>>> checker.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    specify the talairach.xfm file to check
    argument: ``-xfm %s``, position: -1
    mutually_exclusive: subject
subject: (a string)
    specify subject's name
    argument: ``-subj %s``, position: -1
    mutually_exclusive: in_file

[Optional]
threshold: (a float, nipy default value: 0.01)
    Talairach transforms for subjects with p-values <= T are considered
    as very unlikely default=0.010
    argument: ``-T %.3f``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
The input file for CheckTalairachAlignment
```

62.5.6 Contrast

[Link to code](#)

Wraps the executable command `pctsurfcon`.

Compute surface-wise gray/white contrast

Examples

```
>>> from nipy.interfaces.freesurfer import Contrast
>>> contrast = Contrast()
>>> contrast.inputs.subject_id = '10335'
>>> contrast.inputs.hemisphere = 'lh'
>>> contrast.inputs.white = 'lh.white' # doctest: +SKIP
>>> contrast.inputs.thickness = 'lh.thickness' # doctest: +SKIP
>>> contrast.inputs.annotation = '../label/lh.aparc.annot' # doctest: +SKIP
>>> contrast.inputs.cortex = '../label/lh.cortex.label' # doctest: +SKIP
>>> contrast.inputs.rawavg = '../mri/rawavg.mgz' # doctest: +SKIP
>>> contrast.inputs.orig = '../mri/orig.mgz' # doctest: +SKIP
>>> contrast.cmdline # doctest: +SKIP
'pctsurfcon --lh-only --s 10335'
```

Inputs:

```
[Mandatory]
subject_id: (a string, nipy default value: subject_id)
    Subject being processed
    argument: ``--s %s``
hemisphere: ('lh' or 'rh')
    Hemisphere being processed
    argument: ``--%s-only``
thickness: (a pathlike object or string representing an existing
    file)
    Input file must be <subject_id>/surf/?h.thickness
white: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/surf/<hemisphere>.white
annotation: (a pathlike object or string representing an existing
    file)
    Input annotation file must be
    <subject_id>/label/<hemisphere>.aparc.annot
cortex: (a pathlike object or string representing an existing file)
    Input cortex label must be
    <subject_id>/label/<hemisphere>.cortex.label
orig: (a pathlike object or string representing an existing file)
    Implicit input file mri/orig.mgz
rawavg: (a pathlike object or string representing an existing file)
    Implicit input file mri/rawavg.mgz

[Optional]
copy_inputs: (a boolean)
    If running as a node, set this to True. This will copy the input
    files to the node directory.
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
```

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```

of class 'str' and with values which are a bytes or None or a
value of class 'str', nipyne default value: {})
Environment variables

```

Outputs:

```

out_contrast: (a pathlike object or string representing a file)
               Output contrast file from Contrast
out_stats: (a pathlike object or string representing a file)
            Output stats file from Contrast
out_log: (a pathlike object or string representing an existing file)
          Output log from Contrast

```

62.5.7 Curvature

[Link to code](#)Wraps the executable command `mris_curvature`.

This program will compute the second fundamental form of a cortical surface. It will create two new files `<hemi>.<surface>.H` and `<hemi>.<surface>.K` with the mean and Gaussian curvature respectively.

Examples

```

>>> from nipyne.interfaces.freesurfer import Curvature
>>> curv = Curvature()
>>> curv.inputs.in_file = 'lh.pial'
>>> curv.inputs.save = True
>>> curv.cmdline
'mris_curvature -w lh.pial'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
          Input file for Curvature
          argument: ``%s``, position: -2

[Optional]
threshold: (a float)
            Undocumented input threshold
            argument: ``-thresh %.3f``
n: (a boolean)
   Undocumented boolean flag
   argument: ``-n``
averages: (an integer (int or long))
           Perform this number iterative averages of curvature measure before
           saving
           argument: ``-a %d``
save: (a boolean)
      Save curvature files (will only generate screen output without this
      option)
      argument: ``-w``
distances: (a tuple of the form: (an integer (int or long), an
            integer (int or long)))
            Undocumented input integer distances
            argument: ``-distances %d %d``
copy_input: (a boolean)

```

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```

    Copy input file to current directory
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables

```

Outputs:

```

out_mean: (a pathlike object or string representing a file)
    Mean curvature output file
out_gauss: (a pathlike object or string representing a file)
    Gaussian curvature output file

```

62.5.8 CurvatureStats

[Link to code](#)

Wraps the executable command `mris_curvature_stats`.

In its simplest usage, 'mris_curvature_stats' will compute a set of statistics on its input <curvFile>. These statistics are the mean and standard deviation of the particular curvature on the surface, as well as the results from several surface-based integrals.

Additionally, 'mris_curvature_stats' can report the max/min curvature values, and compute a simple histogram based on all curvature values.

Curvatures can also be normalised and constrained to a given range before computation.

Principal curvature (K, H, k1 and k2) calculations on a surface structure can also be performed, as well as several functions derived from k1 and k2.

Finally, all output to the console, as well as any new curvatures that result from the above calculations can be saved to a series of text and binary-curvature files.

Examples

```

>>> from nipyne.interfaces.freesurfer import CurvatureStats
>>> curvstats = CurvatureStats()
>>> curvstats.inputs.hemisphere = 'lh'
>>> curvstats.inputs.curvfile1 = 'lh.pial'
>>> curvstats.inputs.curvfile2 = 'lh.pial'
>>> curvstats.inputs.surface = 'lh.pial'
>>> curvstats.inputs.out_file = 'lh.curv.stats'
>>> curvstats.inputs.values = True
>>> curvstats.inputs.min_max = True
>>> curvstats.inputs.write = True
>>> curvstats.cmdline
'mris_curvature_stats -m -o lh.curv.stats -F pial -G --writeCurvatureFiles_
↳subject_id lh pial pial'

```

Inputs:

```

[Mandatory]
curvfile1: (a pathlike object or string representing an existing
    file)

```

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```

        Input file for CurvatureStats
        argument: ``%s``, position: -2
curvfile2: (a pathlike object or string representing an existing
            file)
        Input file for CurvatureStats
        argument: ``%s``, position: -1
hemisphere: ('lh' or 'rh')
            Hemisphere being processed
            argument: ``%s``, position: -3
subject_id: (a string, nipy default value: subject_id)
            Subject being processed
            argument: ``%s``, position: -4

[Optional]
surface: (a pathlike object or string representing an existing file)
        Specify surface file for CurvatureStats
        argument: ``-F %s``
out_file: (a pathlike object or string representing a file)
        Output curvature stats file
        argument: ``-o %s``
min_max: (a boolean)
        Output min / max information for the processed curvature.
        argument: ``-m``
values: (a boolean)
        Triggers a series of derived curvature values
        argument: ``-G``
write: (a boolean)
        Write curvature files
        argument: ``--writeCurvatureFiles``
copy_inputs: (a boolean)
        If running as a node, set this to True. This will copy the input
        files to the node directory.
subjects_dir: (a pathlike object or string representing an existing
              directory)
              subjects directory
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
        Output curvature stats file

```

62.5.9 EulerNumber[Link to code](#)Wraps the executable command `mrisc EulerNumber`.

This program computes EulerNumber for a cortical surface

Examples

```
>>> from nipy.interfaces.freesurfer import EulerNumber
>>> ft = EulerNumber()
>>> ft.inputs.in_file = 'lh.pial'
>>> ft.cmdline
'mris_euler_number lh.pial'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         Input file for EulerNumber
         argument: ``%s``, position: -1

[Optional]
subjects_dir: (a pathlike object or string representing an existing
              directory)
              subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
          Output file for EulerNumber
```

62.5.10 ExtractMainComponent

[Link to code](#)

Wraps the executable command `mris_extract_main_component`.

Extract the main component of a tesslated surface

Examples

```
>>> from nipy.interfaces.freesurfer import ExtractMainComponent
>>> mcmp = ExtractMainComponent(in_file='lh.pial')
>>> mcmp.cmdline
'mris_extract_main_component lh.pial lh.maincmp'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input surface file
         argument: ``%s``, position: 1

[Optional]
out_file: (a pathlike object or string representing a file)
          surface containing main component
          argument: ``%s``, position: 2
args: (a unicode string)
```

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```

Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipyne default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          surface containing main component

```

62.5.11 FixTopology

[Link to code](#)Wraps the executable command `mris_fix_topology`.

This program computes a mapping from the unit sphere onto the surface of the cortex from a previously generated approximation of the cortical surface, thus guaranteeing a topologically correct surface.

Examples

```

>>> from nipyne.interfaces.freesurfer import FixTopology
>>> ft = FixTopology()
>>> ft.inputs.in_orig = 'lh.orig' # doctest: +SKIP
>>> ft.inputs.in_inflated = 'lh.inflated' # doctest: +SKIP
>>> ft.inputs.sphere = 'lh.qsphere.nofix' # doctest: +SKIP
>>> ft.inputs.hemisphere = 'lh'
>>> ft.inputs.subject_id = '10335'
>>> ft.inputs.mgz = True
>>> ft.inputs.ga = True
>>> ft.cmdline # doctest: +SKIP
'mris_fix_topology -ga -mgz -sphere qsphere.nofix 10335 lh'

```

Inputs:

```

[Mandatory]
in_orig: (a pathlike object or string representing an existing file)
         Undocumented input file <hemisphere>.orig
in_inflated: (a pathlike object or string representing an existing
            file)
            Undocumented input file <hemisphere>.inflated
in_brain: (a pathlike object or string representing an existing file)
          Implicit input brain.mgz
in_wm: (a pathlike object or string representing an existing file)
       Implicit input wm.mgz
hemisphere: (a string)
            Hemisphere being processed
            argument: ``%s``, position: -1
subject_id: (a string, nipyne default value: subject_id)
            Subject being processed
            argument: ``%s``, position: -2
copy_inputs: (a boolean)
            If running as a node, set this to True otherwise, the topology
            fixing will be done in place.

[Optional]

```

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```

seed: (an integer (int or long))
    Seed for setting random number generator
    argument: ``-seed %d``
ga: (a boolean)
    No documentation. Direct questions to analysis-
    bugs@nmr.mgh.harvard.edu
    argument: ``-ga``
mgz: (a boolean)
    No documentation. Direct questions to analysis-
    bugs@nmr.mgh.harvard.edu
    argument: ``-mgz``
sphere: (a pathlike object or string representing a file)
    Sphere input file
    argument: ``-sphere %s``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    Output file for FixTopology

```

62.5.12 Jacobian

[Link to code](#)Wraps the executable command `mris_jacobian`.

This program computes the Jacobian of a surface mapping.

Examples

```

>>> from nipyne.interfaces.freesurfer import Jacobian
>>> jacobian = Jacobian()
>>> jacobian.inputs.in_origsurf = 'lh.pial'
>>> jacobian.inputs.in_mappedsurf = 'lh.pial'
>>> jacobian.cmdline
'mris_jacobian lh.pial lh.pial lh.jacobian'

```

Inputs:

```

[Mandatory]
in_origsurf: (a pathlike object or string representing an existing
    file)
    Original surface
    argument: ``%s``, position: -3
in_mappedsurf: (a pathlike object or string representing an existing
    file)
    Mapped surface
    argument: ``%s``, position: -2

```

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```
[Optional]
out_file: (a pathlike object or string representing a file)
    Output Jacobian of the surface mapping
    argument: ``%s``, position: -1
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
    Output Jacobian of the surface mapping
```

62.5.13 LTACovert[Link to code](#)

Wraps the executable command `lta_convert`.

Convert different transformation formats. Some formats may require you to pass an image if the geometry information is missing from the transform file format.

For complete details, see the [lta_convert documentation](#).

Inputs:

```
[Mandatory]
in_lta: (a pathlike object or string representing an existing file or
    'identity.noimage')
    input transform of LTA type
    argument: ``--inlta %s``
    mutually_exclusive: in_lta, in_fsl, in_mni, in_reg, in_niftyreg,
        in_itk
in_fsl: (a pathlike object or string representing an existing file)
    input transform of FSL type
    argument: ``--infs %s``
    mutually_exclusive: in_lta, in_fsl, in_mni, in_reg, in_niftyreg,
        in_itk
in_mni: (a pathlike object or string representing an existing file)
    input transform of MNI/XFM type
    argument: ``--inmni %s``
    mutually_exclusive: in_lta, in_fsl, in_mni, in_reg, in_niftyreg,
        in_itk
in_reg: (a pathlike object or string representing an existing file)
    input transform of TK REG type (deprecated format)
    argument: ``--inreg %s``
    mutually_exclusive: in_lta, in_fsl, in_mni, in_reg, in_niftyreg,
        in_itk
in_niftyreg: (a pathlike object or string representing an existing
    file)
    input transform of Nifty Reg type (inverse RAS2RAS)
    argument: ``--inniftyreg %s``
```

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```

        mutually_exclusive: in_lta, in_fsl, in_mni, in_reg, in_niftyreg,
            in_itk
in_itk: (a pathlike object or string representing an existing file)
        input transform of ITK type
        argument: ``--initk %s``
        mutually_exclusive: in_lta, in_fsl, in_mni, in_reg, in_niftyreg,
            in_itk

[Optional]
out_lta: (a boolean or a pathlike object or string representing a
        file)
        output linear transform (LTA Freesurfer format)
        argument: ``--outlta %s``
out_fsl: (a boolean or a pathlike object or string representing a
        file)
        output transform in FSL format
        argument: ``--outfsl %s``
out_mni: (a boolean or a pathlike object or string representing a
        file)
        output transform in MNI/XFM format
        argument: ``--outmni %s``
out_reg: (a boolean or a pathlike object or string representing a
        file)
        output transform in reg dat format
        argument: ``--outreg %s``
out_itk: (a boolean or a pathlike object or string representing a
        file)
        output transform in ITK format
        argument: ``--outitk %s``
invert: (a boolean)
        argument: ``--invert``
ltavox2vox: (a boolean)
        argument: ``--ltavox2vox``
        requires: out_lta
source_file: (a pathlike object or string representing an existing
        file)
        argument: ``--src %s``
target_file: (a pathlike object or string representing an existing
        file)
        argument: ``--trg %s``
target_conform: (a boolean)
        argument: ``--trgconform``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_lta: (a pathlike object or string representing an existing file)
        output linear transform (LTA Freesurfer format)
out_fsl: (a pathlike object or string representing an existing file)
        output transform in FSL format
out_mni: (a pathlike object or string representing an existing file)

```

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```

        output transform in MNI/XFM format
out_reg: (a pathlike object or string representing an existing file)
        output transform in reg dat format
out_itk: (a pathlike object or string representing an existing file)
        output transform in ITK format

```

62.5.14 MRIFill

[Link to code](#)

Wraps the executable command `mri_fill`.

This program creates hemispheric cutting planes and fills white matter with specific values for subsequent surface tessellation.

Examples

```

>>> from nipy.interfaces.freesurfer import MRIFill
>>> fill = MRIFill()
>>> fill.inputs.in_file = 'wm.mgz' # doctest: +SKIP
>>> fill.inputs.out_file = 'filled.mgz' # doctest: +SKIP
>>> fill.cmdline # doctest: +SKIP
'mri_fill wm.mgz filled.mgz'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        Input white matter file
        argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file)
        Output filled volume file name for MRIFill
        argument: ``%s``, position: -1

[Optional]
segmentation: (a pathlike object or string representing an existing
        file)
        Input segmentation file for MRIFill
        argument: ``-segmentation %s``
transform: (a pathlike object or string representing an existing
        file)
        Input transform file for MRIFill
        argument: ``-xform %s``
log_file: (a pathlike object or string representing a file)
        Output log file for MRIFill
        argument: ``-a %s``
subjects_dir: (a pathlike object or string representing an existing
        directory)
        subjects directory
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
          Output file from MRIFill
log_file: (a pathlike object or string representing a file)
          Output log file from MRIFill

```

62.5.15 MRIMarchingCubes

[Link to code](#)

Wraps the executable command `mri_mc`.

Uses Freesurfer's `mri_mc` to create surfaces by tessellating a given input volume

Example

```

>>> import nipy.interfaces.freesurfer as fs
>>> mc = fs.MRIMarchingCubes()
>>> mc.inputs.in_file = 'aseg.mgz'
>>> mc.inputs.label_value = 17
>>> mc.inputs.out_file = 'lh.hippocampus'
>>> mc.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
          Input volume to tessellate voxels from.
          argument: ``%s``, position: 1
label_value: (an integer (int or long))
              Label value which to tessellate from the input volume. (integer, if
              input is "filled.mgz" volume, 127 is rh, 255 is lh)
              argument: ``%d``, position: 2

[Optional]
connectivity_value: (an integer (int or long), nipy default value:
                    1)
                    Alter the marching cubes connectivity: 1=6+,2=18,3=6,4=26
                    (default=1)
                    argument: ``%d``, position: -1
out_file: (a pathlike object or string representing a file)
          output filename or True to generate one
          argument: ``./%s``, position: -2
subjects_dir: (a pathlike object or string representing an existing
              directory)
              subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

surface: (a pathlike object or string representing an existing file)
          binary surface of the tessellation

```

62.5.16 MRIPretess

[Link to code](#)

Wraps the executable command `mri_pretess`.

Uses Freesurfer's `mri_pretess` to prepare volumes to be tessellated.

Description

Changes white matter (WM) segmentation so that the neighbors of all voxels labeled as WM have a face in common - no edges or corners allowed.

Example

```

>>> import nipy.interfaces.freesurfer as fs
>>> pretess = fs.MRIPretess()
>>> pretess.inputs.in_filled = 'wm.mgz'
>>> pretess.inputs.in_norm = 'norm.mgz'
>>> pretess.inputs.nocorners = True
>>> pretess.cmdline
'mri_pretess -nocorners wm.mgz wm norm.mgz wm_pretesswm.mgz'
>>> pretess.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_filled: (a pathlike object or string representing an existing
            file)
            filled volume, usually wm.mgz
            argument: ``%s``, position: -4
label: (a unicode string or an integer (int or long), nipy default
        value: wm)
        label to be picked up, can be a Freesurfer's string like 'wm' or a
        label value (e.g. 127 for rh or 255 for lh)
        argument: ``%s``, position: -3
in_norm: (a pathlike object or string representing an existing file)
          the normalized, brain-extracted T1w image. Usually norm.mgz
          argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
          the output file after mri_pretess.
          argument: ``%s``, position: -1
nocorners: (a boolean)
            do not remove corner configurations in addition to edge ones.
            argument: ``-nocorners``
keep: (a boolean)
       keep WM edits
       argument: ``-keep``
test: (a boolean)
       adds a voxel that should be removed by mri_pretess. The value of the
       voxel is set to that of an ON-edited WM, so it should be kept with
       -keep. The output will NOT be saved.
       argument: ``-test``
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
       Additional parameters to the command

```

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```

        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          output file after mri_preteess

```

62.5.17 MRITessellate

[Link to code](#)Wraps the executable command `mri_tessellate`.Uses Freesurfer's `mri_tessellate` to create surfaces by tessellating a given input volume

Example

```

>>> import nipy.interfaces.freesurfer as fs
>>> tess = fs.MRITessellate()
>>> tess.inputs.in_file = 'aseg.mgz'
>>> tess.inputs.label_value = 17
>>> tess.inputs.out_file = 'lh.hippocampus'
>>> tess.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
          Input volume to tessellate voxels from.
          argument: ``%s``, position: -3
label_value: (an integer (int or long))
              Label value which to tessellate from the input volume. (integer, if
              input is "filled.mgz" volume, 127 is rh, 255 is lh)
              argument: ``%d``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
          output filename or True to generate one
          argument: ``%s``, position: -1
tessellate_all_voxels: (a boolean)
                       Tessellate the surface of all voxels with different labels
                       argument: ``-a``
use_real_RAS_coordinates: (a boolean)
                           Saves surface with real RAS coordinates where c_(r,a,s) != 0
                           argument: ``-n``
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a

```

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```
value of class 'str', nipy default value: {}
Environment variables
```

Outputs:

```
surface: (a pathlike object or string representing an existing file)
         binary surface of the tessellation
```

62.5.18 MRIsCalc[Link to code](#)

Wraps the executable command `mris_calc`.

'mris_calc' is a simple calculator that operates on FreeSurfer curvatures and volumes. In most cases, the calculator functions with three arguments: two inputs and an <ACTION> linking them. Some actions, however, operate with only one input <file1>. In all cases, the first input <file1> is the name of a FreeSurfer curvature overlay (e.g. rh.curv) or volume file (e.g. orig.mgz). For two inputs, the calculator first assumes that the second input is a file. If, however, this second input file doesn't exist, the calculator assumes it refers to a float number, which is then processed according to <ACTION>. Note: <file1> and <file2> should typically be generated on the same subject.

Examples

```
>>> from nipy.interfaces.freesurfer import MRIsCalc
>>> example = MRIsCalc()
>>> example.inputs.in_file1 = 'lh.area' # doctest: +SKIP
>>> example.inputs.in_file2 = 'lh.area.pial' # doctest: +SKIP
>>> example.inputs.action = 'add'
>>> example.inputs.out_file = 'area.mid'
>>> example.cmdline # doctest: +SKIP
'mris_calc -o lh.area.mid lh.area add lh.area.pial'
```

Inputs:

```
[Mandatory]
in_file1: (a pathlike object or string representing an existing file)
          Input file 1
          argument: ``%s``, position: -3
action: (a string)
        Action to perform on input file(s)
        argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file)
          Output file after calculation
          argument: ``-o %s``

[Optional]
in_file2: (a pathlike object or string representing an existing file)
          Input file 2
          argument: ``%s``, position: -1
          mutually_exclusive: in_float, in_int
in_float: (a float)
          Input float
          argument: ``%f``, position: -1
          mutually_exclusive: in_file2, in_int
in_int: (an integer (int or long))
        Input integer
```

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```

        argument: ``%d``, position: -1
        mutually_exclusive: in_file2, in_float
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
          Output file after calculation

```

62.5.19 MRIsCombine[Link to code](#)

Wraps the executable command `mris_convert`.

Uses Freesurfer's `mris_convert` to combine two surface files into one.

For complete details, see the [mris_convert Documentation](#).

If given an `out_file` that does not begin with `'lh.'` or `'rh.'`, `mris_convert` will prepend `'lh.'` to the file name. To avoid this behavior, consider setting `out_file = './<filename>'`, or leaving `out_file` blank.

In a Node/Workflow, `out_file` is interpreted literally.

Example

```

>>> import nipy.interfaces.freesurfer as fs
>>> mris = fs.MRIsCombine()
>>> mris.inputs.in_files = ['lh.pial', 'rh.pial']
>>> mris.inputs.out_file = 'bh.pial'
>>> mris.cmdline
'mris_convert --combinesurfs lh.pial rh.pial bh.pial'
>>> mris.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a list of from 2 to 2 items which are a pathlike object or
           string representing a file)
           Two surfaces to be combined.
           argument: ``--combinesurfs %s``, position: 1
out_file: (a pathlike object or string representing a file)
           Output filename. Combined surfaces from in_files.
           argument: ``%s``, position: -1

[Optional]
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)

```

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```

Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          Output filename. Combined surfaces from in_files.

```

62.5.20 MRIsConvert[Link to code](#)Wraps the executable command `mrisc`.Uses Freesurfer's `mrisc` to convert surface files to various formats**Example**

```

>>> import nipy.interfaces.freesurfer as fs
>>> mris = fs.MRIsConvert()
>>> mris.inputs.in_file = 'lh.pial'
>>> mris.inputs.out_datatype = 'gii'
>>> mris.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         File to read/convert
         argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file)
          output filename or True to generate one
          argument: ``%s``, position: -1
          mutually_exclusive: out_datatype
out_datatype: ('asc' or 'ico' or 'tri' or 'stl' or 'vtk' or 'gii' or
              'mgh' or 'mgz')
             These file formats are supported: ASCII: .ascICO: .ico, .tri GEO:
             .geo STL: .stl VTK: .vtk GIFTI: .gii MGH surface-encoded 'volume':
             .mgh, .mgz
             mutually_exclusive: out_file

[Optional]
annot_file: (a pathlike object or string representing an existing
            file)
            input is annotation or gifti label data
            argument: ``--annot %s``
parcstats_file: (a pathlike object or string representing an existing
                 file)
                 infile is name of text file containing label/val pairs
                 argument: ``--parcstats %s``
label_file: (a pathlike object or string representing an existing
             file)
             infile is .label file, label is name of this label
             argument: ``--label %s``

```

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```

scalarcurv_file: (a pathlike object or string representing an
    existing file)
    input is scalar curv overlay file (must still specify surface)
    argument: ``-c %s``
functional_file: (a pathlike object or string representing an
    existing file)
    input is functional time-series or other multi-frame data (must
    specify surface)
    argument: ``-f %s``
labelstats_outfile: (a pathlike object or string representing a file)
    outfile is name of gifti file to which label stats will be written
    argument: ``--labelstats %s``
patch: (a boolean)
    input is a patch, not a full surface
    argument: ``-p``
rescale: (a boolean)
    rescale vertex xyz so total area is same as group average
    argument: ``-r``
normal: (a boolean)
    output is an ascii file where vertex data
    argument: ``-n``
xyz_ascii: (a boolean)
    Print only surface xyz to ascii file
    argument: ``-a``
vertex: (a boolean)
    Writes out neighbors of a vertex in each row
    argument: ``-v``
scale: (a float)
    scale vertex xyz by scale
    argument: ``-s %.3f``
dataarray_num: (an integer (int or long))
    if input is gifti, 'num' specifies which data array to use
    argument: ``--da_num %d``
talairachxfm_subjid: (a string)
    apply talairach xfm of subject to vertex xyz
    argument: ``-t %s``
origname: (a string)
    read orig positions
    argument: ``-o %s``
to_scanner: (a boolean)
    convert coordinates from native FS (tkr) coords to scanner coords
    argument: ``--to-scanner``
to_tkr: (a boolean)
    convert coordinates from scanner coords to native FS (tkr) coords
    argument: ``--to-tkr``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```
converted: (a pathlike object or string representing an existing
           file)
           converted output surface
```

62.5.21 MRIsExpand

[Link to code](#)

Wraps the executable command `mris_expand`.

Expands a surface (typically `?h.white`) outwards while maintaining smoothness and self-intersection constraints.

Examples

```
>>> from nipy.interfaces.freesurfer import MRIsExpand
>>> mris_expand = MRIsExpand(thickness=True, distance=0.5)
>>> mris_expand.inputs.in_file = 'lh.white'
>>> mris_expand.cmdline
'mris_expand -thickness lh.white 0.5 expanded'
>>> mris_expand.inputs.out_name = 'graymid'
>>> mris_expand.cmdline
'mris_expand -thickness lh.white 0.5 graymid'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         Surface to expand
         argument: ``%s``, position: -3
distance: (a float)
          Distance in mm or fraction of cortical thickness
          argument: ``%g``, position: -2

[Optional]
out_name: (a unicode string, nipy default value: expanded)
          Output surface file
          If no path, uses directory of `in_file`
          If no path AND missing "lh." or "rh.", derive from `in_file`
          argument: ``%s``, position: -1
thickness: (a boolean)
           Expand by fraction of cortical thickness, not mm
           argument: ``-thickness``
thickness_name: (a unicode string)
               Name of thickness file (implicit: "thickness")
               If no path, uses directory of `in_file`
               If no path AND missing "lh." or "rh.", derive from `in_file`
               argument: ``-thickness_name %s``
pial: (a unicode string)
      Name of pial file (implicit: "pial")
      If no path, uses directory of `in_file`
      If no path AND missing "lh." or "rh.", derive from `in_file`
      argument: ``-pial %s``
sphere: (a unicode string, nipy default value: sphere)
        WARNING: Do not change this trait
spring: (a float)
        Spring term (implicit: 0.05)
        argument: ``-S %g``
dt: (a float)
```

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```

    dt (implicit: 0.25)
    argument: ``-T %g``
write_iterations: (an integer (int or long))
    Write snapshots of expansion every N iterations
    argument: ``-W %d``
smooth_averages: (an integer (int or long))
    Smooth surface with N iterations after expansion
    argument: ``-A %d``
nsurfaces: (an integer (int or long))
    Number of surfaces to write during expansion
    argument: ``-N %d``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    Output surface file

```

62.5.22 MRIsInflate[Link to code](#)Wraps the executable command `mris_inflate`.

This program will inflate a cortical surface.

Examples

```

>>> from nipy.interfaces.freesurfer import MRIsInflate
>>> inflate = MRIsInflate()
>>> inflate.inputs.in_file = 'lh.pial'
>>> inflate.inputs.no_save_sulc = True
>>> inflate.cmdline # doctest: +SKIP
'mris_inflate -no-save-sulc lh.pial lh.inflated'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Input file for MRIsInflate
    argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
    Output file for MRIsInflate
    argument: ``%s``, position: -1
out_sulc: (a pathlike object or string representing a file)
    Output sulc file
    mutually_exclusive: no_save_sulc

```

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```

no_save_sulc: (a boolean)
    Do not save sulc file as output
    argument: ``-no-save-sulc``
    mutually_exclusive: out_sulc
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    Output file for MRIsInflate
out_sulc: (a pathlike object or string representing a file)
    Output sulc file

```

62.5.23 MakeAverageSubject[Link to code](#)Wraps the executable command `make_average_subject`.

Make an average freesurfer subject

Examples

```

>>> from nipype.interfaces.freesurfer import MakeAverageSubject
>>> avg = MakeAverageSubject(subjects_ids=['s1', 's2'])
>>> avg.cmdline
'make_average_subject --out average --subjects s1 s2'

```

Inputs:

```

[Mandatory]
subjects_ids: (a list of items which are a unicode string)
    freesurfer subjects ids to average
    argument: ``--subjects %s``

[Optional]
out_name: (a pathlike object or string representing a file, nipype
    default value: average)
    name for the average subject
    argument: ``--out %s``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a

```

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```
value of class 'str', nipy default value: {}
Environment variables
```

Outputs:

```
average_subject_name: (a unicode string)
Output registration file
```

62.5.24 MakeSurfaces[Link to code](#)

Wraps the executable command `mris_make_surfaces`.

This program positions the tessellation of the cortical surface at the white matter surface, then the gray matter surface and generate surface files for these surfaces as well as a ‘curvature’ file for the cortical thickness, and a surface file which approximates layer IV of the cortical sheet.

Examples

```
>>> from nipy.interfaces.freesurfer import MakeSurfaces
>>> makesurfaces = MakeSurfaces()
>>> makesurfaces.inputs.hemisphere = 'lh'
>>> makesurfaces.inputs.subject_id = '10335'
>>> makesurfaces.inputs.in_orig = 'lh.pial'
>>> makesurfaces.inputs.in_wm = 'wm.mgz'
>>> makesurfaces.inputs.in_filled = 'norm.mgz'
>>> makesurfaces.inputs.in_label = 'aparc+aseg.nii'
>>> makesurfaces.inputs.in_T1 = 'T1.mgz'
>>> makesurfaces.inputs.orig_pial = 'lh.pial'
>>> makesurfaces.cmdline
'mris_make_surfaces -T1 T1.mgz -orig pial -orig_pial pial 10335 lh'
```

Inputs:

```
[Mandatory]
hemisphere: ('lh' or 'rh')
    Hemisphere being processed
    argument: ``%s``, position: -1
subject_id: (a string, nipy default value: subject_id)
    Subject being processed
    argument: ``%s``, position: -2
in_orig: (a pathlike object or string representing an existing file)
    Implicit input file <hemisphere>.orig
    argument: ``-orig %s``
in_wm: (a pathlike object or string representing an existing file)
    Implicit input file wm.mgz
in_filled: (a pathlike object or string representing an existing
    file)
    Implicit input file filled.mgz

[Optional]
in_white: (a pathlike object or string representing an existing file)
    Implicit input that is sometimes used
in_label: (a pathlike object or string representing an existing file)
    Implicit input label/<hemisphere>.aparc.annot
    mutually_exclusive: noaparc
orig_white: (a pathlike object or string representing an existing
```

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```

    file)
    Specify a white surface to start with
    argument: ``-orig_white %s``
orig_pial: (a pathlike object or string representing an existing
    file)
    Specify a pial surface to start with
    argument: ``-orig_pial %s``
    requires: in_label
fix_mtl: (a boolean)
    Undocumented flag
    argument: ``-fix_mtl``
no_white: (a boolean)
    Undocumented flag
    argument: ``-nowhite``
white_only: (a boolean)
    Undocumented flag
    argument: ``-whiteonly``
in_aseg: (a pathlike object or string representing an existing file)
    Input segmentation file
    argument: ``-aseg %s``
in_T1: (a pathlike object or string representing an existing file)
    Input brain or T1 file
    argument: ``-T1 %s``
mgz: (a boolean)
    No documentation. Direct questions to analysis-
    bugs@nmr.mgh.harvard.edu
    argument: ``-mgz``
noaparc: (a boolean)
    No documentation. Direct questions to analysis-
    bugs@nmr.mgh.harvard.edu
    argument: ``-noaparc``
    mutually_exclusive: in_label
maximum: (a float)
    No documentation (used for longitudinal processing)
    argument: ``-max %.1f``
longitudinal: (a boolean)
    No documentation (used for longitudinal processing)
    argument: ``-long``
white: (a string)
    White surface name
    argument: ``-white %s``
copy_inputs: (a boolean)
    If running as a node, set this to True. This will copy the input
    files to the node directory.
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_white: (a pathlike object or string representing a file)
    Output white matter hemisphere surface
out_curv: (a pathlike object or string representing a file)
    Output curv file for MakeSurfaces
out_area: (a pathlike object or string representing a file)
    Output area file for MakeSurfaces
out_cortex: (a pathlike object or string representing a file)
    Output cortex file for MakeSurfaces
out_pial: (a pathlike object or string representing a file)
    Output pial surface for MakeSurfaces
out_thickness: (a pathlike object or string representing a file)
    Output thickness file for MakeSurfaces

```

62.5.25 ParcellationStats

[Link to code](#)

Wraps the executable command `mris_anatomical_stats`.

This program computes a number of anatomical properties.

Examples

```

>>> from nipy.interfaces.freesurfer import ParcellationStats
>>> import os
>>> parcellationstats = ParcellationStats()
>>> parcellationstats.inputs.subject_id = '10335'
>>> parcellationstats.inputs.hemisphere = 'lh'
>>> parcellationstats.inputs.wm = '../mri/wm.mgz' # doctest: +SKIP
>>> parcellationstats.inputs.transform = '../mri/transforms/talairach.xfm' # doctest:
↳+SKIP
>>> parcellationstats.inputs.brainmask = '../mri/brainmask.mgz' # doctest: +SKIP
>>> parcellationstats.inputs.aseg = '../mri/aseg.presurf.mgz' # doctest: +SKIP
>>> parcellationstats.inputs.ribbon = '../mri/ribbon.mgz' # doctest: +SKIP
>>> parcellationstats.inputs.lh_pial = 'lh.pial' # doctest: +SKIP
>>> parcellationstats.inputs.rh_pial = 'rh.pial' # doctest: +SKIP
>>> parcellationstats.inputs.lh_white = 'lh.white' # doctest: +SKIP
>>> parcellationstats.inputs.rh_white = 'rh.white' # doctest: +SKIP
>>> parcellationstats.inputs.thickness = 'lh.thickness' # doctest: +SKIP
>>> parcellationstats.inputs.surface = 'white'
>>> parcellationstats.inputs.out_table = 'lh.test.stats'
>>> parcellationstats.inputs.out_color = 'test.ctab'
>>> parcellationstats.cmdline # doctest: +SKIP
'mris_anatomical_stats -c test.ctab -f lh.test.stats 10335 lh white'

```

Inputs:

```

[Mandatory]
subject_id: (a string, nipy default value: subject_id)
    Subject being processed
    argument: ``%s``, position: -3
hemisphere: ('lh' or 'rh')
    Hemisphere being processed
    argument: ``%s``, position: -2
wm: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/mri/wm.mgz
lh_white: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/surf/lh.white

```

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```

rh_white: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/surf/rh.white
lh_pial: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/surf/lh.pial
rh_pial: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/surf/rh.pial
transform: (a pathlike object or string representing an existing
    file)
    Input file must be <subject_id>/mri/transforms/talairach.xfm
thickness: (a pathlike object or string representing an existing
    file)
    Input file must be <subject_id>/surf/?h.thickness
brainmask: (a pathlike object or string representing an existing
    file)
    Input file must be <subject_id>/mri/brainmask.mgz
aseg: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/mri/aseg.presurf.mgz
ribbon: (a pathlike object or string representing an existing file)
    Input file must be <subject_id>/mri/ribbon.mgz

[Optional]
cortex_label: (a pathlike object or string representing an existing
    file)
    implicit input file {hemi}.cortex.label
surface: (a string)
    Input surface (e.g. 'white')
    argument: ``%s``, position: -1
mgz: (a boolean)
    Look for mgz files
    argument: ``-mgz``
in_cortex: (a pathlike object or string representing an existing
    file)
    Input cortex label
    argument: ``-cortex %s``
in_annotation: (a pathlike object or string representing an existing
    file)
    compute properties for each label in the annotation file separately
    argument: ``-a %s``
    mutually_exclusive: in_label
in_label: (a pathlike object or string representing an existing file)
    limit calculations to specified label
    argument: ``-l %s``
    mutually_exclusive: in_annotation, out_color
tabular_output: (a boolean)
    Tabular output
    argument: ``-b``
out_table: (a pathlike object or string representing a file)
    Table output to tablefile
    argument: ``-f %s``
    requires: tabular_output
out_color: (a pathlike object or string representing a file)
    Output annotation files's colortable to text file
    argument: ``-c %s``
    mutually_exclusive: in_label
copy_inputs: (a boolean)
    If running as a node, set this to True. This will copy the input
    files to the node directory.

```

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```

th3: (a boolean)
    turns on new vertex-wise volume calc for mris_anat_stats
    argument: ``-th3``
    requires: cortex_label
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_table: (a pathlike object or string representing a file)
    Table output to tablefile
out_color: (a pathlike object or string representing a file)
    Output annotation files's colortable to text file

```

62.5.26 RelabelHypointensities[Link to code](#)Wraps the executable command `mri_relabel_hypointensities`.

Relabel Hypointensities

Examples

```

>>> from nipy.interfaces.freesurfer import RelabelHypointensities
>>> relabelhypos = RelabelHypointensities()
>>> relabelhypos.inputs.lh_white = 'lh.pial'
>>> relabelhypos.inputs.rh_white = 'lh.pial'
>>> relabelhypos.inputs.surf_directory = '.'
>>> relabelhypos.inputs.aseg = 'aseg.mgz'
>>> relabelhypos.cmdline
'mri_relabel_hypointensities aseg.mgz . aseg.hypos.mgz'

```

Inputs:

```

[Mandatory]
lh_white: (a pathlike object or string representing an existing file)
    Implicit input file must be lh.white
rh_white: (a pathlike object or string representing an existing file)
    Implicit input file must be rh.white
aseg: (a pathlike object or string representing an existing file)
    Input aseg file
    argument: ``%s``, position: -3

[Optional]
surf_directory: (a pathlike object or string representing an existing
    directory, nipy default value: .)
    Directory containing lh.white and rh.white
    argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file)

```

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```

    Output aseg file
    argument: ``%s``, position: -1
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    Output aseg file
    argument: ``%s``

```

62.5.27 RemoveIntersection[Link to code](#)Wraps the executable command `mris_remove_intersection`.

This program removes the intersection of the given MRI

Examples

```

>>> from nipy.interfaces.freesurfer import RemoveIntersection
>>> ri = RemoveIntersection()
>>> ri.inputs.in_file = 'lh.pial'
>>> ri.cmdline
'mris_remove_intersection lh.pial lh.pial'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Input file for RemoveIntersection
    argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
    Output file for RemoveIntersection
    argument: ``%s``, position: -1
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing a file)
          Output file for RemoveIntersection
```

62.5.28 RemoveNeck

[Link to code](#)

Wraps the executable command `mri_remove_neck`.

Crops the neck out of the mri image

Examples

```
>>> from nipy.interfaces.freesurfer import TalairachQC
>>> remove_neck = RemoveNeck()
>>> remove_neck.inputs.in_file = 'norm.mgz'
>>> remove_neck.inputs.transform = 'trans.mat'
>>> remove_neck.inputs.template = 'trans.mat'
>>> remove_neck.cmdline
'mri_remove_neck norm.mgz trans.mat trans.mat norm_noneck.mgz'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         Input file for RemoveNeck
         argument: ``%s``, position: -4
transform: (a pathlike object or string representing an existing
           file)
           Input transform file for RemoveNeck
           argument: ``%s``, position: -3
template: (a pathlike object or string representing an existing file)
          Input template file for RemoveNeck
          argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
          Output file for RemoveNeck
          argument: ``%s``, position: -1
radius: (an integer (int or long))
        Radius
        argument: ``-radius %d``
subjects_dir: (a pathlike object or string representing an existing
              directory)
              subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
          Output file with neck removed
```

62.5.29 SampleToSurface

[Link to code](#)

Wraps the executable command `mri_vol2surf`.

Sample a volume to the cortical surface using Freesurfer's `mri_vol2surf`.

You must supply a sampling method, range, and units. You can project either a given distance (in mm) or a given fraction of the cortical thickness at that vertex along the surface normal from the target surface, and then set the value of that vertex to be either the value at that point or the average or maximum value found along the projection vector.

By default, the surface will be saved as a vector with a length equal to the number of vertices on the target surface. This is not a problem for Freesurfer programs, but if you intend to use the file with interfaces to another package, you must set the `reshape` input to `True`, which will factor the surface vector into a matrix with dimensions compatible with proper Nifti files.

Examples

```
>>> import nipy.interfaces.freesurfer as fs
>>> sampler = fs.SampleToSurface(hemi="lh")
>>> sampler.inputs.source_file = "copel.nii.gz"
>>> sampler.inputs.reg_file = "register.dat"
>>> sampler.inputs.sampling_method = "average"
>>> sampler.inputs.sampling_range = 1
>>> sampler.inputs.sampling_units = "frac"
>>> sampler.cmdline # doctest: +ELLIPSIS
'mri_vol2surf --hemi lh --o ...lh.copel.mgz --reg register.dat --projfrac-avg 1.
 000 --mov copel.nii.gz'
>>> res = sampler.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
source_file: (a pathlike object or string representing an existing
             file)
             volume to sample values from
             argument: ``--mov %s``
hemi: ('lh' or 'rh')
       target hemisphere
       argument: ``--hemi %s``
reg_file: (a pathlike object or string representing an existing file)
           source-to-reference registration file
           argument: ``--reg %s``
           mutually_exclusive: reg_file, reg_header, mni152reg
reg_header: (a boolean)
            register based on header geometry
            argument: ``--regheader %s``
            mutually_exclusive: reg_file, reg_header, mni152reg
            requires: subject_id
mni152reg: (a boolean)
           source volume is in MNI152 space
           argument: ``--mni152reg``
           mutually_exclusive: reg_file, reg_header, mni152reg
sampling_method: ('point' or 'max' or 'average')
                how to sample -- at a point or at the max or average over a range
                argument: ``%s``
                mutually_exclusive: projection_stem
                requires: sampling_range, sampling_units
projection_stem: (a string)
```

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```

        stem for precomputed linear estimates and volume fractions
        mutually_exclusive: sampling_method

[Optional]
reference_file: (a pathlike object or string representing an existing
                file)
                reference volume (default is orig.mgz)
                argument: ``--ref %s``
surface: (a string)
          target surface (default is white)
          argument: ``--surf %s``
apply_rot: (a tuple of the form: (a float, a float, a float))
            rotation angles (in degrees) to apply to reg matrix
            argument: ``--rot %.3f %.3f %.3f``
apply_trans: (a tuple of the form: (a float, a float, a float))
              translation (in mm) to apply to reg matrix
              argument: ``--trans %.3f %.3f %.3f``
override_reg_subj: (a boolean)
                   override the subject in the reg file header
                   argument: ``--srcsubject %s``
                   requires: subject_id
sampling_range: (a float or a tuple of the form: (a float, a float, a
            float))
                sampling range - a point or a tuple of (min, max, step)
sampling_units: ('mm' or 'frac')
                sampling range type -- either 'mm' or 'frac'
smooth_vol: (a float)
             smooth input volume (mm fwhm)
             argument: ``--fwhm %.3f``
smooth_surf: (a float)
              smooth output surface (mm fwhm)
              argument: ``--surf-fwhm %.3f``
interp_method: ('nearest' or 'trilinear')
                interpolation method
                argument: ``--interp %s``
cortex_mask: (a boolean)
              mask the target surface with hemi.cortex.label
              argument: ``--cortex``
              mutually_exclusive: mask_label
mask_label: (a pathlike object or string representing an existing
            file)
            label file to mask output with
            argument: ``--mask %s``
            mutually_exclusive: cortex_mask
float2int_method: ('round' or 'tkregister')
                  method to convert reg matrix values (default is round)
                  argument: ``--float2int %s``
fix_tk_reg: (a boolean)
             make reg matrix round-compatible
             argument: ``--fixtkreg``
subject_id: (a string)
            subject id
target_subject: (a string)
                sample to surface of different subject than source
                argument: ``--trgsobject %s``
surf_reg: (a boolean or a unicode string)
           use surface registration to target subject

```

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```

        argument: ``--surfreg %s``
        requires: target_subject
    ico_order: (an integer (int or long))
        icosahedron order when target_subject is 'ico'
        argument: ``--icoorder %d``
        requires: target_subject
    reshape: (a boolean)
        reshape surface vector to fit in non-mgh format
        argument: ``--reshape``
        mutually_exclusive: no_reshape
    no_reshape: (a boolean)
        do not reshape surface vector (default)
        argument: ``--noreshape``
        mutually_exclusive: reshape
    reshape_slices: (an integer (int or long))
        number of 'slices' for reshaping
        argument: ``--rf %d``
    scale_input: (a float)
        multiple all intensities by scale factor
        argument: ``--scale %.3f``
    frame: (an integer (int or long))
        save only one frame (0-based)
        argument: ``--frame %d``
    out_file: (a pathlike object or string representing a file)
        surface file to write
        argument: ``--o %s``
    out_type: ('cor' or 'mgh' or 'mgz' or 'minc' or 'analyze' or
        'analyze4d' or 'spm' or 'afni' or 'brik' or 'bshort' or 'bfloat'
        or 'sdt' or 'outline' or 'otl' or 'gdf' or 'nifti1' or 'nii' or
        'niigz' or 'gii')
        output file type
        argument: ``--out_type %s``
    hits_file: (a boolean or a pathlike object or string representing an
        existing file)
        save image with number of hits at each voxel
        argument: ``--srchit %s``
    hits_type: ('cor' or 'mgh' or 'mgz' or 'minc' or 'analyze' or
        'analyze4d' or 'spm' or 'afni' or 'brik' or 'bshort' or 'bfloat'
        or 'sdt' or 'outline' or 'otl' or 'gdf' or 'nifti1' or 'nii' or
        'niigz')
        hits file type
        argument: ``--srchit_type``
    vox_file: (a boolean or a pathlike object or string representing a
        file)
        text file with the number of voxels intersecting the surface
        argument: ``--nvox %s``
    subjects_dir: (a pathlike object or string representing an existing
        directory)
        subjects directory
    args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
    environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          surface file
hits_file: (a pathlike object or string representing an existing
           file)
           image with number of hits at each voxel
vox_file: (a pathlike object or string representing an existing file)
          text file with the number of voxels intersecting the surface

```

62.5.30 SmoothTessellation

[Link to code](#)

Wraps the executable command `mris_smooth`.

This program smooths the tessellation of a surface using ‘`mris_smooth`’

See also:

SurfaceSmooth() Interface For smoothing a scalar field along a surface manifold

Example

```

>>> import nipy.interfaces.freesurfer as fs
>>> smooth = fs.SmoothTessellation()
>>> smooth.inputs.in_file = 'lh.hippocampus.stl'
>>> smooth.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         Input volume to tessellate voxels from.
         argument: ``%s``, position: -2

[Optional]
curvature_averaging_iterations: (an integer (int or long))
                                Number of curvature averaging iterations (default=10)
                                argument: ``-a %d``
smoothing_iterations: (an integer (int or long))
                       Number of smoothing iterations (default=10)
                       argument: ``-n %d``
snapshot_writing_iterations: (an integer (int or long))
                              Write snapshot every "n" iterations
                              argument: ``-w %d``
use_gaussian_curvature_smoothing: (a boolean)
                                   Use Gaussian curvature smoothing
                                   argument: ``-g``
gaussian_curvature_norm_steps: (an integer (int or long))
                                Use Gaussian curvature smoothing
                                argument: ``%d``
gaussian_curvature_smoothing_steps: (an integer (int or long))
                                     Use Gaussian curvature smoothing
                                     argument: ``%d``
disable_estimates: (a boolean)
                   Disables the writing of curvature and area estimates
                   argument: ``-nw``
normalize_area: (a boolean)
                Normalizes the area after smoothing
                argument: ``-area``
use_momentum: (a boolean)

```

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```

    Uses momentum
    argument: ``-m``
out_file: (a pathlike object or string representing a file)
    output filename or True to generate one
    argument: ``%s``, position: -1
out_curvature_file: (a pathlike object or string representing a file)
    Write curvature to ?h.curvname (default "curv")
    argument: ``-c %s``
out_area_file: (a pathlike object or string representing a file)
    Write area to ?h.areaname (default "area")
    argument: ``-b %s``
seed: (an integer (int or long))
    Seed for setting random number generator
    argument: ``-seed %d``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables

```

Outputs:

```

surface: (a pathlike object or string representing an existing file)
    Smoothed surface file

```

62.5.31 Sphere

[Link to code](#)Wraps the executable command `mris_sphere`.

This program will add a template into an average surface

Examples

```

>>> from nipyne.interfaces.freesurfer import Sphere
>>> sphere = Sphere()
>>> sphere.inputs.in_file = 'lh.pial'
>>> sphere.cmdline
'mris_sphere lh.pial lh.sphere'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Input file for Sphere
    argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file)
    Output file for Sphere
    argument: ``%s``, position: -1
seed: (an integer (int or long))

```

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```

        Seed for setting random number generator
        argument: ``-seed %d``
magic: (a boolean)
        No documentation. Direct questions to analysis-
        bugs@nmr.mgh.harvard.edu
        argument: ``-q``
in_smoothwm: (a pathlike object or string representing an existing
        file)
        Input surface required when -q flag is not selected
num_threads: (an integer (int or long))
        allows for specifying more threads
subjects_dir: (a pathlike object or string representing an existing
        directory)
        subjects directory
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
        Output file for Sphere

```

62.5.32 Surface2VolTransform

[Link to code](#)Wraps the executable command `mri_surf2vol`.Use FreeSurfer `mri_surf2vol` to apply a transform.**Examples**

```

>>> from nipy.interfaces.freesurfer import Surface2VolTransform
>>> xfm2vol = Surface2VolTransform()
>>> xfm2vol.inputs.source_file = 'lh.copel.mgz'
>>> xfm2vol.inputs.reg_file = 'register.mat'
>>> xfm2vol.inputs.hemi = 'lh'
>>> xfm2vol.inputs.template_file = 'copel.nii.gz'
>>> xfm2vol.inputs.subjects_dir = '.'
>>> xfm2vol.cmdline
'mri_surf2vol --hemi lh --volreg register.mat --surfval lh.copel.mgz --sd . --
↳template copel.nii.gz --outvol lh.copel_asVol.nii --vtxvol lh.copel_asVol_
↳vertex.nii'
>>> res = xfm2vol.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
source_file: (a pathlike object or string representing an existing
        file)
        This is the source of the surface values
        argument: ``--surfval %s``
mutually_exclusive: mkmask

```

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```

hemi: (a unicode string)
    hemisphere of data
    argument: ``--hemi %s``
reg_file: (a pathlike object or string representing an existing file)
    tkRAS-to-tkRAS matrix (tkregister2 format)
    argument: ``--volreg %s``
    mutually_exclusive: subject_id

[Optional]
transformed_file: (a pathlike object or string representing a file)
    Output volume
    argument: ``--outvol %s``
template_file: (a pathlike object or string representing an existing
    file)
    Output template volume
    argument: ``--template %s``
mkmask: (a boolean)
    make a mask instead of loading surface values
    argument: ``--mkmask``
    mutually_exclusive: source_file
vertexvol_file: (a pathlike object or string representing a file)
    Path name of the vertex output volume, which is the same as output
    volume except that the value of each voxel is the vertex-id that is
    mapped to that voxel.
    argument: ``--vtxvol %s``
surf_name: (a unicode string)
    surfname (default is white)
    argument: ``--surf %s``
projfrac: (a float)
    thickness fraction
    argument: ``--projfrac %s``
subjects_dir: (a unicode string)
    freesurfer subjects directory defaults to $SUBJECTS_DIR
    argument: ``--sd %s``
subject_id: (a unicode string)
    subject id
    argument: ``--identity %s``
    mutually_exclusive: reg_file
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

transformed_file: (a pathlike object or string representing an
    existing file)
    Path to output file if used normally
vertexvol_file: (a pathlike object or string representing a file)
    vertex map volume path id. Optional

```

62.5.33 SurfaceSmooth[Link to code](#)

Wraps the executable command `mri_surf2surf`.

Smooth a surface image with `mri_surf2surf`.

The surface is smoothed by an iterative process of averaging the value at each vertex with those of its adjacent neighbors. You may supply either the number of iterations to run or a desired effective FWHM of the smoothing process. If the latter, the underlying program will calculate the correct number of iterations internally.

See also:

SmoothTessellation() Interface For smoothing a tessellated surface (e.g. in `gifti` or `.stl`)

Examples

```
>>> import nipyre.interfaces.freesurfer as fs
>>> smoother = fs.SurfaceSmooth()
>>> smoother.inputs.in_file = "lh.cope1.mgz"
>>> smoother.inputs.subject_id = "subj_1"
>>> smoother.inputs.hemi = "lh"
>>> smoother.inputs.fwhm = 5
>>> smoother.cmdline # doctest: +ELLIPSIS
'mri_surf2surf --cortex --fwhm 5.0000 --hemi lh --sval lh.cope1.mgz --tval ...lh.
  ↳ cope1_smooth5.mgz --s subj_1'
>>> smoother.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing a file)
    source surface file
    argument: ``--sval %s``
subject_id: (a string)
    subject id of surface file
    argument: ``--s %s``
hemi: ('lh' or 'rh')
    hemisphere to operate on
    argument: ``--hemi %s``

[Optional]
fwhm: (a float)
    effective FWHM of the smoothing process
    argument: ``--fwhm %.4f``
    mutually_exclusive: smooth_iters
smooth_iters: (an integer (int or long))
    iterations of the smoothing process
    argument: ``--smooth %d``
    mutually_exclusive: fwhm
cortex: (a boolean, nipyre default value: True)
    only smooth within $hemi.cortex.label
    argument: ``--cortex``
reshape: (a boolean)
    reshape surface vector to fit in non-mgh format
    argument: ``--reshape``
out_file: (a pathlike object or string representing a file)
    surface file to write
    argument: ``--tval %s``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
```

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```

argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          smoothed surface file

```

62.5.34 SurfaceSnapshots

[Link to code](#)

Wraps the executable command `tksurfer`.

Use `Tksurfer` to save pictures of the cortical surface.

By default, this takes snapshots of the lateral, medial, ventral, and dorsal surfaces. See the `six_images` option to add the anterior and posterior surfaces.

You may also supply your own tcl script (see the `Freesurfer` wiki for information on scripting `tksurfer`). The screenshot stem is set as the environment variable “`_SNAPSHOT_STEM`”, which you can use in your own scripts.

Note that this interface will not run if you do not have graphics enabled on your system.

Examples

```

>>> import nipy.interfaces.freesurfer as fs
>>> shots = fs.SurfaceSnapshots(subject_id="fsaverage", hemi="lh", surface="pial")
>>> shots.inputs.overlay = "zstat1.nii.gz"
>>> shots.inputs.overlay_range = (2.3, 6)
>>> shots.inputs.overlay_reg = "register.dat"
>>> res = shots.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
subject_id: (a string)
             subject to visualize
             argument: ``%s``, position: 1
hemi: ('lh' or 'rh')
       hemisphere to visualize
       argument: ``%s``, position: 2
surface: (a string)
          surface to visualize
          argument: ``%s``, position: 3

[Optional]
show_curv: (a boolean)
            show curvature
            argument: ``-curv``
            mutually_exclusive: show_gray_curv
show_gray_curv: (a boolean)
                 show curvature in gray
                 argument: ``-gray``
                 mutually_exclusive: show_curv
overlay: (a pathlike object or string representing an existing file)

```

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```

    load an overlay volume/surface
    argument: ``-overlay %s``
    requires: overlay_range
overlay_reg: (a pathlike object or string representing an existing
    file)
    registration matrix file to register overlay to surface
    argument: ``-overlay-reg %s``
    mutually_exclusive: overlay_reg, identity_reg, mni152_reg
identity_reg: (a boolean)
    use the identity matrix to register the overlay to the surface
    argument: ``-overlay-reg-identity``
    mutually_exclusive: overlay_reg, identity_reg, mni152_reg
mni152_reg: (a boolean)
    use to display a volume in MNI152 space on the average subject
    argument: ``-mni152reg``
    mutually_exclusive: overlay_reg, identity_reg, mni152_reg
overlay_range: (a float or a tuple of the form: (a float, a float) or
    a tuple of the form: (a float, a float, a float))
    overlay range--either min, (min, max) or (min, mid, max)
    argument: ``%s``
overlay_range_offset: (a float)
    overlay range will be symettric around offset value
    argument: ``-foffset %.3f``
truncate_overlay: (a boolean)
    truncate the overlay display
    argument: ``-truncphaseflag 1``
reverse_overlay: (a boolean)
    reverse the overlay display
    argument: ``-revphaseflag 1``
invert_overlay: (a boolean)
    invert the overlay display
    argument: ``-invphaseflag 1``
demean_overlay: (a boolean)
    remove mean from overlay
    argument: ``-zm``
annot_file: (a pathlike object or string representing an existing
    file)
    path to annotation file to display
    argument: ``-annotation %s``
    mutually_exclusive: annot_name
annot_name: (a string)
    name of annotation to display (must be in $subject/label directory
    argument: ``-annotation %s``
    mutually_exclusive: annot_file
label_file: (a pathlike object or string representing an existing
    file)
    path to label file to display
    argument: ``-label %s``
    mutually_exclusive: label_name
label_name: (a string)
    name of label to display (must be in $subject/label directory
    argument: ``-label %s``
    mutually_exclusive: label_file
colortable: (a pathlike object or string representing an existing
    file)
    load colortable file
    argument: ``-colortable %s``

```

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```

label_under: (a boolean)
    draw label/annotation under overlay
    argument: ``-labels-under``
label_outline: (a boolean)
    draw label/annotation as outline
    argument: ``-label-outline``
patch_file: (a pathlike object or string representing an existing
    file)
    load a patch
    argument: ``-patch %s``
orig_suffix: (a string)
    set the orig surface suffix string
    argument: ``-orig %s``
sphere_suffix: (a string)
    set the sphere.reg suffix string
    argument: ``-sphere %s``
show_color_scale: (a boolean)
    display the color scale bar
    argument: ``-colscalebarflag 1``
show_color_text: (a boolean)
    display text in the color scale bar
    argument: ``-colscaletext 1``
six_images: (a boolean)
    also take anterior and posterior snapshots
screenshot_stem: (a string)
    stem to use for screenshot file names
stem_template_args: (a list of items which are a string)
    input names to use as arguments for a string-formated stem template
    requires: screenshot_stem
tcl_script: (a pathlike object or string representing an existing
    file)
    override default screenshot script
    argument: ``%s``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

snapshots: (a list of items which are a pathlike object or string
    representing an existing file)
    tiff images of the surface from different perspectives

```

62.5.35 SurfaceTransform[Link to code](#)Wraps the executable command `mri_surf2surf`.

Transform a surface file from one subject to another via a spherical registration.

Both the source and target subject must reside in your Subjects Directory, and they must have been processed with recon-all, unless you are transforming to one of the icosahedron meshes.

Examples

```
>>> from nipyne.interfaces.freesurfer import SurfaceTransform
>>> sxfm = SurfaceTransform()
>>> sxfm.inputs.source_file = "lh.copel.nii.gz"
>>> sxfm.inputs.source_subject = "my_subject"
>>> sxfm.inputs.target_subject = "fsaverage"
>>> sxfm.inputs.hemi = "lh"
>>> sxfm.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
source_file: (a pathlike object or string representing an existing
             file)
             surface file with source values
             argument: ``--sval %s``
             mutually_exclusive: source_annot_file
source_annot_file: (a pathlike object or string representing an
                   existing file)
                   surface annotation file
                   argument: ``--sval-annot %s``
                   mutually_exclusive: source_file
source_subject: (a string)
                subject id for source surface
                argument: ``--srcsubject %s``
hemi: ('lh' or 'rh')
      hemisphere to transform
      argument: ``--hemi %s``
target_subject: (a string)
                subject id of target surface
                argument: ``--trgsubject %s``

[Optional]
target_ico_order: (1 or 2 or 3 or 4 or 5 or 6 or 7)
                  order of the icosahedron if target_subject is 'ico'
                  argument: ``--trgicoorder %d``
source_type: ('cor' or 'mgh' or 'mgz' or 'minc' or 'analyze' or
              'analyze4d' or 'spm' or 'afni' or 'brik' or 'bshort' or 'bfloat'
              or 'sdt' or 'outline' or 'otl' or 'gdf' or 'nifti1' or 'nii' or
              'niigz')
              source file format
              argument: ``--sfmt %s``
              requires: source_file
target_type: ('cor' or 'mgh' or 'mgz' or 'minc' or 'analyze' or
              'analyze4d' or 'spm' or 'afni' or 'brik' or 'bshort' or 'bfloat'
              or 'sdt' or 'outline' or 'otl' or 'gdf' or 'nifti1' or 'nii' or
              'niigz' or 'gii')
              output format
              argument: ``--tfmt %s``
reshape: (a boolean)
          reshape output surface to conform with Nifti
          argument: ``--reshape``
reshape_factor: (an integer (int or long))
                 number of slices in reshaped image
                 argument: ``--reshape-factor``
out_file: (a pathlike object or string representing a file)
           surface file to write
```

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```

        argument: ``--tval %s``
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          transformed surface file

```

62.5.36 TalairachAVI[Link to code](#)

Wraps the executable command `talairach_avi`.

Front-end for Avi Snyders image registration tool. Computes the talairach transform that maps the input volume to the MNI average_305. This does not add the xfm to the header of the input file. When called by recon-all, the xfm is added to the header after the transform is computed.

Examples

```

>>> from nipype.interfaces.freesurfer import TalairachAVI
>>> example = TalairachAVI()
>>> example.inputs.in_file = 'norm.mgz'
>>> example.inputs.out_file = 'trans.mat'
>>> example.cmdline
'talairach_avi --i norm.mgz --xfm trans.mat'

```

```

>>> example.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input volume
         argument: ``--i %s``
out_file: (a pathlike object or string representing a file)
          output xfm file
          argument: ``--xfm %s``

[Optional]
atlas: (a string)
       alternate target atlas (in freesurfer/average dir)
       argument: ``--atlas %s``
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
      Additional parameters to the command

```

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```

    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
           The output transform for TalairachAVI
out_log: (a pathlike object or string representing a file)
           The output log file for TalairachAVI
out_txt: (a pathlike object or string representing a file)
           The output text file for TaliarachAVI

```

62.5.37 TalairachQC[Link to code](#)

Wraps the executable command tal_QC_AZS.

Examples

```

>>> from nipy.interfaces.freesurfer import TalairachQC
>>> qc = TalairachQC()
>>> qc.inputs.log_file = 'dirs.txt'
>>> qc.cmdline
'tal_QC_AZS dirs.txt'

```

Inputs:

```

[Mandatory]
log_file: (a pathlike object or string representing an existing file)
           The log file for TalairachQC
           argument: ``%s``, position: 0

[Optional]
subjects_dir: (a pathlike object or string representing an existing
               directory)
               subjects directory
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

log_file: (a pathlike object or string representing an existing file,
           nipy default value: output.nipy)
           The output log

```

62.5.38 Tkregister2[Link to code](#)

Wraps the executable command tkregister2.

Examples

Get transform matrix between orig (*tkRAS*) and native (*scannerRAS*) coordinates in Freesurfer. Implements the first step of mapping surfaces to native space in [this guide](#).

```
>>> from nipy.interfaces.freesurfer import Tkregister2
>>> tk2 = Tkregister2(reg_file='T1_to_native.dat')
>>> tk2.inputs.moving_image = 'T1.mgz'
>>> tk2.inputs.target_image = 'structural.nii'
>>> tk2.inputs.reg_header = True
>>> tk2.cmdline
'tkregister2 --mov T1.mgz --noedit --reg T1_to_native.dat --regheader --targ_
↳ structural.nii'
>>> tk2.run() # doctest: +SKIP
```

The example below uses tkregister2 without the manual editing stage to convert FSL-style registration matrix (.mat) to FreeSurfer-style registration matrix (.dat)

```
>>> from nipy.interfaces.freesurfer import Tkregister2
>>> tk2 = Tkregister2()
>>> tk2.inputs.moving_image = 'epi.nii'
>>> tk2.inputs.fsl_in_matrix = 'flirt.mat'
>>> tk2.cmdline
'tkregister2 --fsl flirt.mat --mov epi.nii --noedit --reg register.dat'
>>> tk2.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
moving_image: (a pathlike object or string representing an existing
               file)
               moving volume
               argument: ``--mov %s``
reg_file: (a pathlike object or string representing a file, nipy
           default value: register.dat)
           freesurfer-style registration file
           argument: ``--reg %s``

[Optional]
target_image: (a pathlike object or string representing an existing
               file)
               target volume
               argument: ``--targ %s``
               mutually_exclusive: fstarg
fstarg: (a boolean)
         use subject's T1 as reference
         argument: ``--fstarg``
         mutually_exclusive: target_image
fsl_in_matrix: (a pathlike object or string representing an existing
                file)
                fsl-style registration input matrix
                argument: ``--fsl %s``
xfm: (a pathlike object or string representing an existing file)
      use a matrix in MNI coordinates as initial registration
      argument: ``--xfm %s``
lta_in: (a pathlike object or string representing an existing file)
        use a matrix in MNI coordinates as initial registration
        argument: ``--lta %s``
invert_lta_in: (a boolean)
```

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```

    Invert input LTA before applying
    requires: lta_in
fsl_out: (a bool or None or a pathlike object or string representing
    a file)
    compute an FSL-compatible resgitration matrix
    argument: ``--fslregout %s``
lta_out: (a bool or None or a pathlike object or string representing
    a file)
    output registration file (LTA format)
    argument: ``--ltaout %s``
invert_lta_out: (a boolean)
    Invert input LTA before applying
    argument: ``--ltaout-inv``
    requires: lta_in
subject_id: (a string)
    freesurfer subject ID
    argument: ``--s %s``
noedit: (a boolean, nipy default value: True)
    do not open edit window (exit)
    argument: ``--noedit``
reg_header: (a boolean)
    compute registration from headers
    argument: ``--regheader``
fstal: (a boolean)
    set mov to be tal and reg to be tal xfm
    argument: ``--fstal``
    mutually_exclusive: target_image, moving_image, reg_file
movscale: (a float)
    adjust registration matrix to scale mov
    argument: ``--movscale %f``
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

reg_file: (a pathlike object or string representing an existing file)
    freesurfer-style registration file
fsl_file: (a pathlike object or string representing a file)
    FSL-style registration file
lta_file: (a pathlike object or string representing a file)
    LTA-style registration file

```

62.5.39 VolumeMask[Link to code](#)

Wraps the executable command `mrisc_volmask`.

Computes a volume mask, at the same resolution as the `<subject>/mri/brain.mgz`. The volume mask contains 4 values: `LH_WM` (default 10), `LH_GM` (default 100), `RH_WM` (default 20), `RH_GM` (default 200). The algorithm uses the 4 surfaces situated in `<subject>/surf/ [lh|rh].[whitelpial]` and labels voxels based on the

signed-distance function from the surface.

Examples

```
>>> from nipyre.interfaces.freesurfer import VolumeMask
>>> volmask = VolumeMask()
>>> volmask.inputs.left_whitelabel = 2
>>> volmask.inputs.left_ribbonlabel = 3
>>> volmask.inputs.right_whitelabel = 41
>>> volmask.inputs.right_ribbonlabel = 42
>>> volmask.inputs.lh_pial = 'lh.pial'
>>> volmask.inputs.rh_pial = 'lh.pial'
>>> volmask.inputs.lh_white = 'lh.pial'
>>> volmask.inputs.rh_white = 'lh.pial'
>>> volmask.inputs.subject_id = '10335'
>>> volmask.inputs.save_ribbon = True
>>> volmask.cmdline
'mris_volmask --label_left_ribbon 3 --label_left_white 2 --label_right_ribbon 42 -
↪-label_right_white 41 --save_ribbon 10335'
```

Inputs:

```
[Mandatory]
left_whitelabel: (an integer (int or long))
    Left white matter label
    argument: ``--label_left_white %d``
left_ribbonlabel: (an integer (int or long))
    Left cortical ribbon label
    argument: ``--label_left_ribbon %d``
right_whitelabel: (an integer (int or long))
    Right white matter label
    argument: ``--label_right_white %d``
right_ribbonlabel: (an integer (int or long))
    Right cortical ribbon label
    argument: ``--label_right_ribbon %d``
lh_pial: (a pathlike object or string representing an existing file)
    Implicit input left pial surface
rh_pial: (a pathlike object or string representing an existing file)
    Implicit input right pial surface
lh_white: (a pathlike object or string representing an existing file)
    Implicit input left white matter surface
rh_white: (a pathlike object or string representing an existing file)
    Implicit input right white matter surface
subject_id: (a string, nipyre default value: subject_id)
    Subject being processed
    argument: ``%s``, position: -1

[Optional]
aseg: (a pathlike object or string representing an existing file)
    Implicit aseg.mgz segmentation. Specify a different aseg by using
    the 'in_aseg' input.
    mutually_exclusive: in_aseg
in_aseg: (a pathlike object or string representing an existing file)
    Input aseg file for VolumeMask
    argument: ``--aseg_name %s``
    mutually_exclusive: aseg
save_ribbon: (a boolean)
    option to save just the ribbon for the hemispheres in the format
```

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```
?h.ribbon.mgz
argument: ``--save_ribbon``
copy_inputs: (a boolean)
    If running as a node, set this to True. This will copy the implicit
    input files to the node directory.
subjects_dir: (a pathlike object or string representing an existing
    directory)
    subjects directory
args: (a unicode string)
    Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_ribbon: (a pathlike object or string representing a file)
    Output cortical ribbon mask
lh_ribbon: (a pathlike object or string representing a file)
    Output left cortical ribbon mask
rh_ribbon: (a pathlike object or string representing a file)
    Output right cortical ribbon mask
```

62.5.40 copy2subjdir()[Link to code](#)

Method to copy an input to the subjects directory

62.5.41 createoutputdirs()[Link to code](#)

create all output directories. If not created, some freesurfer interfaces fail

63.1 interfaces.fsl.aroma

63.1.1 ICA_AROMA

[Link to code](#)

Wraps the executable command `ICA_AROMA.py`.

Interface for the `ICA_AROMA.py` script.

ICA-AROMA (i.e. ‘ICA-based Automatic Removal Of Motion Artifacts’) concerns a data-driven method to identify and remove motion-related independent components from fMRI data. To that end it exploits a small, but robust set of theoretically motivated features, preventing the need for classifier re-training and therefore providing direct and easy applicability.

See link for further documentation: <https://github.com/rhr-pruim/ICA-AROMA>

Example

```
>>> from nipy.interfaces.fsl import ICA_AROMA
>>> from nipy.testing import example_data
>>> AROMA_obj = ICA_AROMA()
>>> AROMA_obj.inputs.in_file = 'functional.nii'
>>> AROMA_obj.inputs.mat_file = 'func_to_struct.mat'
>>> AROMA_obj.inputs.fnirt_warp_file = 'warpfield.nii'
>>> AROMA_obj.inputs.motion_parameters = 'fsl_mcflirt_movpar.txt'
>>> AROMA_obj.inputs.mask = 'mask.nii.gz'
>>> AROMA_obj.inputs.denoise_type = 'both'
>>> AROMA_obj.inputs.out_dir = 'ICA_testout'
>>> AROMA_obj.cmdline # doctest: +ELLIPSIS
'ICA_AROMA.py -den both -warp warpfield.nii -i functional.nii -m mask.nii.gz -
↪affmat func_to_struct.mat -mc fsl_mcflirt_movpar.txt -o ../ICA_testout'
```

Inputs:

```
[Mandatory]
feat_dir: (a pathlike object or string representing an existing
          directory)
          If a feat directory exists and temporal filtering has not been run
```

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```

yet, ICA_AROMA can use the files in this directory.
argument: ``-feat %s``
mutually_exclusive: in_file, mat_file, fnirt_warp_file,
    motion_parameters
in_file: (a pathlike object or string representing an existing file)
    volume to be denoised
argument: ``-i %s``
mutually_exclusive: feat_dir
out_dir: (a pathlike object or string representing a directory,
    nipy default value: out)
    output directory
argument: ``-o %s``
motion_parameters: (a pathlike object or string representing an
    existing file)
    motion parameters file
argument: ``-mc %s``
mutually_exclusive: feat_dir
denoise_type: ('nonaggr' or 'aggr' or 'both' or 'no', nipy default
    value: nonaggr)
    Type of denoising strategy:
    -no: only classification, no denoising
    -nonaggr (default): non-aggresssive denoising, i.e. partial
        component regression
    -aggr: aggressive denoising, i.e. full component regression
    -both: both aggressive and non-aggressive denoising (two outputs)
argument: ``-den %s``

[Optional]
mask: (a pathlike object or string representing an existing file)
    path/name volume mask
argument: ``-m %s``
mutually_exclusive: feat_dir
dim: (an integer (int or long))
    Dimensionality reduction when running MELODIC (default is automatic
    estimation)
argument: ``-dim %d``
TR: (a float)
    TR in seconds. If this is not specified the TR will be extracted
    from the header of the fMRI nifti file.
argument: ``-tr %.3f``
melodic_dir: (a pathlike object or string representing an existing
    directory)
    path to MELODIC directory if MELODIC has already been run
argument: ``-meldir %s``
mat_file: (a pathlike object or string representing an existing file)
    path/name of the mat-file describing the affine registration (e.g.
    FSL FLIRT) of the functional data to structural space (.mat file)
argument: ``-affmat %s``
mutually_exclusive: feat_dir
fnirt_warp_file: (a pathlike object or string representing an
    existing file)
    File name of the warp-file describing the non-linear registration
    (e.g. FSL FNIRT) of the structural data to MNI152 space (.nii.gz)
argument: ``-warp %s``
mutually_exclusive: feat_dir
args: (a unicode string)
    Additional parameters to the command

```

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```

argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyne default value: {})
Environment variables

```

Outputs:

```

aggr_denoised_file: (a pathlike object or string representing an
                    existing file)
                    if generated: aggressively denoised volume
nonaggr_denoised_file: (a pathlike object or string representing an
                       existing file)
                       if generated: non aggressively denoised volume
out_dir: (a pathlike object or string representing an existing
         directory)
         directory contains (in addition to the denoised files): melodic.ica
         + classified_motion_components + classification_overview +
         feature_scores + melodic_ic_mni)

```

63.2 interfaces.fsl.dti

63.2.1 BEDPOSTX5

[Link to code](#)

Wraps the executable command bedpostx.

BEDPOSTX stands for Bayesian Estimation of Diffusion Parameters Obtained using Sampling Techniques. The X stands for modelling Crossing Fibres. bedpostx runs Markov Chain Monte Carlo sampling to build up distributions on diffusion parameters at each voxel. It creates all the files necessary for running probabilistic tractography. For an overview of the modelling carried out within bedpostx see this [technical report](#).

Note: Consider using `nipyne.workflows.fsl.dmri.create_bedpostx_pipeline()` instead.

Example

```

>>> from nipyne.interfaces import fsl
>>> bedp = fsl.BEDPOSTX5(bvecs='bvecs', bvals='bvals', dwi='diffusion.nii',
...                      mask='mask.nii', n_fibres=1)
>>> bedp.cmdline
'bedpostx bedpostx -b 0 --burnin_noard=0 --forcedir -n 1 -j 5000 -s 1 --
↪updateproposalevery=40'

```

Inputs:

```

[Mandatory]
dwi: (a pathlike object or string representing an existing file)
     diffusion weighted image data file
mask: (a pathlike object or string representing an existing file)
      bet binary mask file
bvecs: (a pathlike object or string representing an existing file)
       b vectors file
bvals: (a pathlike object or string representing an existing file)
       b values file
n_fibres: (a long integer >= 1, nipyne default value: 2)

```

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```

Maximum number of fibres to fit in each voxel
argument: ``-n %d``
out_dir: (a pathlike object or string representing a directory,
         nipy default value: bedpostx)
         output directory
         argument: ``%s``, position: 1

[Optional]
logdir: (a pathlike object or string representing a directory)
        argument: ``--logdir=%s``
model: (1 or 2 or 3)
        use monoexponential (1, default, required for single-shell) or
        multiexponential (2, multi-shell) model
        argument: ``-model %d``
fudge: (an integer (int or long))
        ARD fudge factor
        argument: ``-w %d``
n_jumps: (an integer (int or long), nipy default value: 5000)
        Num of jumps to be made by MCMC
        argument: ``-j %d``
burn_in: (a long integer >= 0, nipy default value: 0)
        Total num of jumps at start of MCMC to be discarded
        argument: ``-b %d``
sample_every: (a long integer >= 0, nipy default value: 1)
        Num of jumps for each sample (MCMC)
        argument: ``-s %d``
gradnonlin: (a boolean)
        consider gradient nonlinearities, default off
        argument: ``-g``
grad_dev: (a pathlike object or string representing an existing file)
        grad_dev file, if gradnonlin, -g is True
use_gpu: (a boolean)
        Use the GPU version of bedpostx
burn_in_no_ard: (a long integer >= 0, nipy default value: 0)
        num of burnin jumps before the ard is imposed
        argument: ``--burnin_noard=%d``
update_proposal_every: (a long integer >= 1, nipy default value:
                        40)
        Num of jumps for each update to the proposal density std (MCMC)
        argument: ``--updateproposalevery=%d``
seed: (an integer (int or long))
        seed for pseudo random number generator
        argument: ``--seed=%d``
no_ard: (a boolean)
        Turn ARD off on all fibres
        argument: ``--noard``
        mutually_exclusive: no_ard, all_ard
all_ard: (a boolean)
        Turn ARD on on all fibres
        argument: ``--allard``
        mutually_exclusive: no_ard, all_ard
no_spat: (a boolean)
        Initialise with tensor, not spatially
        argument: ``--nospat``
        mutually_exclusive: no_spat, non_linear, cnlinear
non_linear: (a boolean)
        Initialise with nonlinear fitting

```

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```

        argument: ``--nonlinear``
        mutually_exclusive: no_spat, non_linear, cilinear
cilinear: (a boolean)
    Initialise with constrained nonlinear fitting
    argument: ``--cnonlinear``
    mutually_exclusive: no_spat, non_linear, cilinear
rician: (a boolean)
    use Rician noise modeling
    argument: ``--rician``
f0_noard: (a boolean)
    Noise floor model: add to the model an unattenuated signal
    compartment f0
    argument: ``--f0``
    mutually_exclusive: f0_noard, f0_ard
f0_ard: (a boolean)
    Noise floor model: add to the model an unattenuated signal
    compartment f0
    argument: ``--f0 --ardf0``
    mutually_exclusive: f0_noard, f0_ard, all_ard
force_dir: (a boolean, nipy default value: True)
    use the actual directory name given (do not add + to make a new
    directory)
    argument: ``--forcedir``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

mean_dsamples: (a pathlike object or string representing an existing
    file)
    Mean of distribution on diffusivity d
mean_fsamples: (a list of items which are a pathlike object or string
    representing an existing file)
    Mean of distribution on f anisotropy
mean_S0samples: (a pathlike object or string representing an existing
    file)
    Mean of distribution on T2wbaseline signal intensity S0
mean_phsamples: (a list of items which are a pathlike object or
    string representing an existing file)
    Mean of distribution on phi
mean_thsamples: (a list of items which are a pathlike object or
    string representing an existing file)
    Mean of distribution on theta
merged_thsamples: (a list of items which are a pathlike object or
    string representing an existing file)
    Samples from the distribution on theta
merged_phsamples: (a list of items which are a pathlike object or
    string representing an existing file)
    Samples from the distribution on phi

```

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```
merged_fsamples: (a list of items which are a pathlike object or
                  string representing an existing file)
                  Samples from the distribution on anisotropic volume fraction
dyads: (a list of items which are a pathlike object or string
        representing an existing file)
        Mean of PDD distribution in vector form.
dyads_dispersion: (a list of items which are a pathlike object or
                  string representing an existing file)
                  Dispersion
```

References:

None

63.2.2 DTIFit[Link to code](#)

Wraps the executable command dtifit.

Use FSL dtifit command for fitting a diffusion tensor model at each voxel

Example

```
>>> from nipy.interfaces import fsl
>>> dti = fsl.DTIFit()
>>> dti.inputs.dwi = 'diffusion.nii'
>>> dti.inputs.bvecs = 'bvecs'
>>> dti.inputs.bvals = 'bvals'
>>> dti.inputs.base_name = 'TP'
>>> dti.inputs.mask = 'mask.nii'
>>> dti.cmdline
'dtifit -k diffusion.nii -o TP -m mask.nii -r bvecs -b bvals'
```

Inputs:

```
[Mandatory]
dwi: (a pathlike object or string representing an existing file)
     diffusion weighted image data file
     argument: ``-k %s``, position: 0
mask: (a pathlike object or string representing an existing file)
      bet binary mask file
      argument: ``-m %s``, position: 2
bvecs: (a pathlike object or string representing an existing file)
       b vectors file
       argument: ``-r %s``, position: 3
bvals: (a pathlike object or string representing an existing file)
       b values file
       argument: ``-b %s``, position: 4

[Optional]
base_name: (a unicode string, nipy default value: dtifit_)
          base_name that all output files will start with
          argument: ``-o %s``, position: 1
min_z: (an integer (int or long))
       min z
       argument: ``-z %d``
```

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```

max_z: (an integer (int or long))
    max z
    argument: ``-Z %d``
min_y: (an integer (int or long))
    min y
    argument: ``-y %d``
max_y: (an integer (int or long))
    max y
    argument: ``-Y %d``
min_x: (an integer (int or long))
    min x
    argument: ``-x %d``
max_x: (an integer (int or long))
    max x
    argument: ``-X %d``
save_tensor: (a boolean)
    save the elements of the tensor
    argument: ``--save_tensor``
sse: (a boolean)
    output sum of squared errors
    argument: ``--sse``
cni: (a pathlike object or string representing an existing file)
    input counfound regressors
    argument: ``--cni=%s``
little_bit: (a boolean)
    only process small area of brain
    argument: ``--littlebit``
gradnonlin: (a pathlike object or string representing an existing
    file)
    gradient non linearities
    argument: ``--gradnonlin=%s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

V1: (a pathlike object or string representing an existing file)
    path/name of file with the 1st eigenvector
V2: (a pathlike object or string representing an existing file)
    path/name of file with the 2nd eigenvector
V3: (a pathlike object or string representing an existing file)
    path/name of file with the 3rd eigenvector
L1: (a pathlike object or string representing an existing file)
    path/name of file with the 1st eigenvalue
L2: (a pathlike object or string representing an existing file)
    path/name of file with the 2nd eigenvalue
L3: (a pathlike object or string representing an existing file)
    path/name of file with the 3rd eigenvalue
MD: (a pathlike object or string representing an existing file)

```

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```

    path/name of file with the mean diffusivity
FA: (a pathlike object or string representing an existing file)
    path/name of file with the fractional anisotropy
MO: (a pathlike object or string representing an existing file)
    path/name of file with the mode of anisotropy
S0: (a pathlike object or string representing an existing file)
    path/name of file with the raw T2 signal with no diffusion weighting
tensor: (a pathlike object or string representing an existing file)
    path/name of file with the 4D tensor volume
sse: (a pathlike object or string representing an existing file)
    path/name of file with the summed squared error

```

References:

None

63.2.3 DistanceMap[Link to code](#)Wraps the executable command `distancemap`.Use FSL's `distancemap` to generate a map of the distance to the nearest nonzero voxel.**Example**

```

>>> import nipy.interfaces.fsl as fsl
>>> mapper = fsl.DistanceMap()
>>> mapper.inputs.in_file = "skeleton_mask.nii.gz"
>>> mapper.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    image to calculate distance values for
    argument: ``--in=%s``

[Optional]
mask_file: (a pathlike object or string representing an existing
    file)
    binary mask to constrain calculations
    argument: ``--mask=%s``
invert_input: (a boolean)
    invert input image
    argument: ``--invert``
local_max_file: (a boolean or a pathlike object or string
    representing a file)
    write an image of the local maxima
    argument: ``--localmax=%s``
distance_map: (a pathlike object or string representing a file)
    distance map to write
    argument: ``--out=%s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)

```

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```

Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyre default value: {})
Environment variables

```

Outputs:

```

distance_map: (a pathlike object or string representing an existing
              file)
              value is distance to nearest nonzero voxels
local_max_file: (a pathlike object or string representing a file)
               image of local maxima

```

References:

None

63.2.4 FindTheBiggest[Link to code](#)Wraps the executable command `find_the_biggest`.Use FSL `find_the_biggest` for performing hard segmentation on the outputs of connectivity-based thresholding in probtrack. For complete details, see the [FDT Documentation](#).**Example**

```

>>> from nipyre.interfaces import fsl
>>> ldir = ['seeds_to_M1.nii', 'seeds_to_M2.nii']
>>> fBig = fsl.FindTheBiggest(in_files=ldir, out_file='biggestSegmentation')
>>> fBig.cmdline
'find_the_biggest seeds_to_M1.nii seeds_to_M2.nii biggestSegmentation'

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string
          representing an existing file)
          a list of input volumes or a singleMatrixFile
          argument: ``%s``, position: 0

[Optional]
out_file: (a pathlike object or string representing a file)
          file with the resulting segmentation
          argument: ``%s``, position: 2
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyre default value: {})
Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          output file indexed in order of input files
          argument: ``%s``
```

References:

None

63.2.5 MakeDyadicVectors

[Link to code](#)

Wraps the executable command `make_dyadic_vectors`.

Create vector volume representing mean principal diffusion direction and its uncertainty (dispersion)

Inputs:

```
[Mandatory]
theta_vol: (a pathlike object or string representing an existing
           file)
           argument: ``%s``, position: 0
phi_vol: (a pathlike object or string representing an existing file)
          argument: ``%s``, position: 1

[Optional]
mask: (a pathlike object or string representing an existing file)
      argument: ``%s``, position: 2
output: (a pathlike object or string representing a file, nipype
         default value: dyads)
         argument: ``%s``, position: 3
perc: (a float)
       the {perc}% angle of the output cone of uncertainty (output will be
       in degrees)
       argument: ``%f``, position: 4
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

```
dyads: (a pathlike object or string representing an existing file)
dispersion: (a pathlike object or string representing an existing
            file)
```

References:

None

63.2.6 ProbTrackX

[Link to code](#)

Wraps the executable command `probtrackx`.
 Use FSL `probtrackx` for tractography on `bedpostx` results

Examples

```
>>> from nipyre.interfaces import fsl
>>> pbx = fsl.ProbTrackX(samples_base_name='merged', mask='mask.nii', seed=
↳ 'MASK_average_thal_right.nii', mode='seedmask', xfm='trans.mat', n_
↳ samples=3, n_steps=10, force_dir=True, opd=True, os2t=True, target_masks = [
↳ 'targets_MASK1.nii', 'targets_MASK2.nii'], thsamples='merged_thsamples.nii',
↳ fsamples='merged_fsamples.nii', phsamples='merged_phsamples.nii', out_dir=
↳ '.')
>>> pbx.cmdline
'probtrackx --forcedir -m mask.nii --mode=seedmask --nsamples=3 --nsteps=10 --opd_
↳ --os2t --dir=. --samples=merged --seed=MASK_average_thal_right.nii --
↳ targetmasks=targets.txt --xfm=trans.mat'
```

Inputs:

```
[Mandatory]
thsamples: (a list of items which are a pathlike object or string
            representing an existing file)
phsamples: (a list of items which are a pathlike object or string
            representing an existing file)
fsamples: (a list of items which are a pathlike object or string
            representing an existing file)
mask: (a pathlike object or string representing an existing file)
      bet binary mask file in diffusion space
      argument: ``-m %s``
seed: (a pathlike object or string representing an existing file or a
      list of items which are a pathlike object or string representing
      an existing file or a list of items which are a list of from 3 to
      3 items which are an integer (int or long))
      seed volume(s), or voxel(s) or freesurfer label file
      argument: ``--seed=%s``

[Optional]
mode: ('simple' or 'two_mask_symm' or 'seedmask')
      options: simple (single seed voxel), seedmask (mask of seed voxels),
      twomask_symm (two bet binary masks)
      argument: ``--mode=%s``
mask2: (a pathlike object or string representing an existing file)
      second bet binary mask (in diffusion space) in twomask_symm mode
      argument: ``--mask2=%s``
mesh: (a pathlike object or string representing an existing file)
      Freesurfer-type surface descriptor (in ascii format)
      argument: ``--mesh=%s``
samples_base_name: (a unicode string, nipyre default value: merged)
      the rootname/base_name for samples files
      argument: ``--samples=%s``
target_masks: (a list of items which are a pathlike object or string
              representing a file)
              list of target masks - required for seeds_to_targets classification
              argument: ``--targetmasks=%s``
waypoints: (a pathlike object or string representing an existing
            file)
            waypoint mask or ascii list of waypoint masks - only keep paths
            going through ALL the masks
```

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```

        argument: ``--waypoints=%s``
network: (a boolean)
    activate network mode - only keep paths going through at least one
    seed mask (required if multiple seed masks)
    argument: ``--network``
seed_ref: (a pathlike object or string representing an existing file)
    reference vol to define seed space in simple mode - diffusion space
    assumed if absent
    argument: ``--seedref=%s``
out_dir: (a pathlike object or string representing an existing
    directory)
    directory to put the final volumes in
    argument: ``--dir=%s``
force_dir: (a boolean, nipy default value: True)
    use the actual directory name given - i.e. do not add + to make a
    new directory
    argument: ``--forcedir``
opd: (a boolean, nipy default value: True)
    outputs path distributions
    argument: ``--opd``
correct_path_distribution: (a boolean)
    correct path distribution for the length of the pathways
    argument: ``--pd``
os2t: (a boolean)
    Outputs seeds to targets
    argument: ``--os2t``
avoid_mp: (a pathlike object or string representing an existing file)
    reject pathways passing through locations given by this mask
    argument: ``--avoid=%s``
stop_mask: (a pathlike object or string representing an existing
    file)
    stop tracking at locations given by this mask file
    argument: ``--stop=%s``
xfm: (a pathlike object or string representing an existing file)
    transformation matrix taking seed space to DTI space (either FLIRT
    matrix or FNIRT warp_field) - default is identity
    argument: ``--xfm=%s``
inv_xfm: (a pathlike object or string representing a file)
    transformation matrix taking DTI space to seed space (compulsory
    when using a warp_field for seeds_to_dti)
    argument: ``--invxfm=%s``
n_samples: (an integer (int or long), nipy default value: 5000)
    number of samples - default=5000
    argument: ``--nsamples=%d``
n_steps: (an integer (int or long))
    number of steps per sample - default=2000
    argument: ``--nsteps=%d``
dist_thresh: (a float)
    discards samples shorter than this threshold (in mm - default=0)
    argument: ``--distthresh=%.3f``
c_thresh: (a float)
    curvature threshold - default=0.2
    argument: ``--cthr=%.3f``
sample_random_points: (a boolean)
    sample random points within seed voxels
    argument: ``--sampvox``
step_length: (a float)

```

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```

    step_length in mm - default=0.5
    argument: ``--steplength=%.3f``
loop_check: (a boolean)
    perform loop_checks on paths - slower, but allows lower curvature
    threshold
    argument: ``--loopcheck``
use_anisotropy: (a boolean)
    use anisotropy to constrain tracking
    argument: ``--usef``
rand_fib: (0 or 1 or 2 or 3)
    options: 0 - default, 1 - to randomly sample initial fibres (with f
    > fibthresh), 2 - to sample in proportion fibres (with f>fibthresh)
    to f, 3 - to sample ALL populations at random (even if f<fibthresh)
    argument: ``--randfib=%d``
fibst: (an integer (int or long))
    force a starting fibre for tracking - default=1, i.e. first fibre
    orientation. Only works if randfib==0
    argument: ``--fibst=%d``
mod_euler: (a boolean)
    use modified euler streamlining
    argument: ``--modeuler``
random_seed: (a boolean)
    random seed
    argument: ``--rseed``
s2tastext: (a boolean)
    output seed-to-target counts as a text file (useful when seeding
    from a mesh)
    argument: ``--s2tastext``
verbose: (0 or 1 or 2)
    Verbose level, [0-2]. Level 2 is required to output particle files.
    argument: ``--verbose=%d``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

log: (a pathlike object or string representing an existing file)
    path/name of a text record of the command that was run
fdt_paths: (a list of items which are a pathlike object or string
    representing an existing file)
    path/name of a 3D image file containing the output connectivity
    distribution to the seed mask
way_total: (a pathlike object or string representing an existing
    file)
    path/name of a text file containing a single number corresponding to
    the total number of generated tracts that have not been rejected by
    inclusion/exclusion mask criteria
targets: (a list of items which are a pathlike object or string
    representing an existing file)

```

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```

a list with all generated seeds_to_target files
particle_files: (a list of items which are a pathlike object or
    string representing an existing file)
    Files describing all of the tract samples. Generated only if verbose
    is set to 2

```

References:

None

63.2.7 ProbTrackX2[Link to code](#)

Wraps the executable command probtrackx2.

Use FSL probtrackx2 for tractography on bedpostx results

Examples

```

>>> from nipy.interfaces import fsl
>>> pbx2 = fsl.ProbTrackX2()
>>> pbx2.inputs.seed = 'seed_source.nii.gz'
>>> pbx2.inputs.thsamples = 'merged_thlsamples.nii.gz'
>>> pbx2.inputs.fsamples = 'merged_flsamples.nii.gz'
>>> pbx2.inputs.phsamples = 'merged_phlsamples.nii.gz'
>>> pbx2.inputs.mask = 'nodif_brain_mask.nii.gz'
>>> pbx2.inputs.out_dir = '.'
>>> pbx2.inputs.n_samples = 3
>>> pbx2.inputs.n_steps = 10
>>> pbx2.cmdline
'probtrackx2 --forcedir -m nodif_brain_mask.nii.gz --nsamples=3 --nsteps=10 --opd_
↪--dir=. --samples=merged --seed=seed_source.nii.gz'

```

Inputs:

```

[Mandatory]
thsamples: (a list of items which are a pathlike object or string
    representing an existing file)
phsamples: (a list of items which are a pathlike object or string
    representing an existing file)
fsamples: (a list of items which are a pathlike object or string
    representing an existing file)
mask: (a pathlike object or string representing an existing file)
    bet binary mask file in diffusion space
    argument: ``-m %s``
seed: (a pathlike object or string representing an existing file or a
    list of items which are a pathlike object or string representing
    an existing file or a list of items which are a list of from 3 to
    3 items which are an integer (int or long))
    seed volume(s), or voxel(s) or freesurfer label file
    argument: ``--seed=%s``

[Optional]
simple: (a boolean)
    rack from a list of voxels (seed must be a ASCII list of
    coordinates)

```

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```

        argument: ``--simple``
fopd: (a pathlike object or string representing an existing file)
    Other mask for binning tract distribution
    argument: ``--fopd=%s``
waycond: ('OR' or 'AND')
    Waypoint condition. Either "AND" (default) or "OR"
    argument: ``--waycond=%s``
wayorder: (a boolean)
    Reject streamlines that do not hit waypoints in given order. Only
    valid if waycond=AND
    argument: ``--wayorder``
onewaycondition: (a boolean)
    Apply waypoint conditions to each half tract separately
    argument: ``--onewaycondition``
omatrix1: (a boolean)
    Output matrix1 - SeedToSeed Connectivity
    argument: ``--omatrix1``
distthresh1: (a float)
    Discards samples (in matrix1) shorter than this threshold (in mm -
    default=0)
    argument: ``--distthresh1=%.3f``
omatrix2: (a boolean)
    Output matrix2 - SeedToLowResMask
    argument: ``--omatrix2``
    requires: target2
target2: (a pathlike object or string representing an existing file)
    Low resolution binary brain mask for storing connectivity
    distribution in matrix2 mode
    argument: ``--target2=%s``
omatrix3: (a boolean)
    Output matrix3 (NxN connectivity matrix)
    argument: ``--omatrix3``
    requires: target3, lrtarget3
target3: (a pathlike object or string representing an existing file)
    Mask used for NxN connectivity matrix (or NxN if lrtarget3 is set)
    argument: ``--target3=%s``
lrtarget3: (a pathlike object or string representing an existing
    file)
    Column-space mask used for NxN connectivity matrix
    argument: ``--lrtarget3=%s``
distthresh3: (a float)
    Discards samples (in matrix3) shorter than this threshold (in mm -
    default=0)
    argument: ``--distthresh3=%.3f``
omatrix4: (a boolean)
    Output matrix4 - DtiMaskToSeed (special Oxford Sparse Format)
    argument: ``--omatrix4``
colmask4: (a pathlike object or string representing an existing file)
    Mask for columns of matrix4 (default=seed mask)
    argument: ``--colmask4=%s``
target4: (a pathlike object or string representing an existing file)
    Brain mask in DTI space
    argument: ``--target4=%s``
meshspace: ('caret' or 'freesurfer' or 'first' or 'vox')
    Mesh reference space - either "caret" (default) or "freesurfer" or
    "first" or "vox"
    argument: ``--meshspace=%s``

```

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```

samples_base_name: (a unicode string, nipy default value: merged)
    the rootname/base_name for samples files
    argument: ``--samples=%s``
target_masks: (a list of items which are a pathlike object or string
    representing a file)
    list of target masks - required for seeds_to_targets classification
    argument: ``--targetmasks=%s``
waypoints: (a pathlike object or string representing an existing
    file)
    waypoint mask or ascii list of waypoint masks - only keep paths
    going through ALL the masks
    argument: ``--waypoints=%s``
network: (a boolean)
    activate network mode - only keep paths going through at least one
    seed mask (required if multiple seed masks)
    argument: ``--network``
seed_ref: (a pathlike object or string representing an existing file)
    reference vol to define seed space in simple mode - diffusion space
    assumed if absent
    argument: ``--seedref=%s``
out_dir: (a pathlike object or string representing an existing
    directory)
    directory to put the final volumes in
    argument: ``--dir=%s``
force_dir: (a boolean, nipy default value: True)
    use the actual directory name given - i.e. do not add + to make a
    new directory
    argument: ``--forcedir``
opd: (a boolean, nipy default value: True)
    outputs path distributions
    argument: ``--opd``
correct_path_distribution: (a boolean)
    correct path distribution for the length of the pathways
    argument: ``--pd``
os2t: (a boolean)
    Outputs seeds to targets
    argument: ``--os2t``
avoid_mp: (a pathlike object or string representing an existing file)
    reject pathways passing through locations given by this mask
    argument: ``--avoid=%s``
stop_mask: (a pathlike object or string representing an existing
    file)
    stop tracking at locations given by this mask file
    argument: ``--stop=%s``
xfm: (a pathlike object or string representing an existing file)
    transformation matrix taking seed space to DTI space (either FLIRT
    matrix or FNIRT warp_field) - default is identity
    argument: ``--xfm=%s``
inv_xfm: (a pathlike object or string representing a file)
    transformation matrix taking DTI space to seed space (compulsory
    when using a warp_field for seeds_to_dti)
    argument: ``--invxfm=%s``
n_samples: (an integer (int or long), nipy default value: 5000)
    number of samples - default=5000
    argument: ``--nsamples=%d``
n_steps: (an integer (int or long))
    number of steps per sample - default=2000

```

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```

        argument: ``--nsteps=%d``
dist_thresh: (a float)
    discards samples shorter than this threshold (in mm - default=0)
    argument: ``--distthresh=%.3f``
c_thresh: (a float)
    curvature threshold - default=0.2
    argument: ``--cthr=%.3f``
sample_random_points: (a boolean)
    sample random points within seed voxels
    argument: ``--sampvox``
step_length: (a float)
    step_length in mm - default=0.5
    argument: ``--steplength=%.3f``
loop_check: (a boolean)
    perform loop_checks on paths - slower, but allows lower curvature
    threshold
    argument: ``--loopcheck``
use_anisotropy: (a boolean)
    use anisotropy to constrain tracking
    argument: ``--usef``
rand_fib: (0 or 1 or 2 or 3)
    options: 0 - default, 1 - to randomly sample initial fibres (with f
    > fibthresh), 2 - to sample in proportion fibres (with f>fibthresh)
    to f, 3 - to sample ALL populations at random (even if f<fibthresh)
    argument: ``--randfib=%d``
fibst: (an integer (int or long))
    force a starting fibre for tracking - default=1, i.e. first fibre
    orientation. Only works if randfib==0
    argument: ``--fibst=%d``
mod_euler: (a boolean)
    use modified euler streamlining
    argument: ``--modeuler``
random_seed: (a boolean)
    random seed
    argument: ``--rseed``
s2tastext: (a boolean)
    output seed-to-target counts as a text file (useful when seeding
    from a mesh)
    argument: ``--s2tastext``
verbose: (0 or 1 or 2)
    Verbose level, [0-2]. Level 2 is required to output particle files.
    argument: ``--verbose=%d``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

network_matrix: (a pathlike object or string representing an existing
    file)

```

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```

    the network matrix generated by --omatrix1 option
matrix1_dot: (a pathlike object or string representing an existing
    file)
    Output matrix1.dot - SeedToSeed Connectivity
lookup_tractspace: (a pathlike object or string representing an
    existing file)
    lookup_tractspace generated by --omatrix2 option
matrix2_dot: (a pathlike object or string representing an existing
    file)
    Output matrix2.dot - SeedToLowResMask
matrix3_dot: (a pathlike object or string representing an existing
    file)
    Output matrix3 - NxN connectivity matrix
log: (a pathlike object or string representing an existing file)
    path/name of a text record of the command that was run
fdt_paths: (a list of items which are a pathlike object or string
    representing an existing file)
    path/name of a 3D image file containing the output connectivity
    distribution to the seed mask
way_total: (a pathlike object or string representing an existing
    file)
    path/name of a text file containing a single number corresponding to
    the total number of generated tracts that have not been rejected by
    inclusion/exclusion mask criteria
targets: (a list of items which are a pathlike object or string
    representing an existing file)
    a list with all generated seeds_to_target files
particle_files: (a list of items which are a pathlike object or
    string representing an existing file)
    Files describing all of the tract samples. Generated only if verbose
is set to 2

```

References:

None

63.2.8 ProjThresh[Link to code](#)

Wraps the executable command proj_thresh.

Use FSL proj_thresh for thresholding some outputs of probtrack For complete details, see the FDT Documenta**tion** <http://www.fmrib.ox.ac.uk/fsl/fdt/fdt_thresh.html>**Example**

```

>>> from nipy.interfaces import fsl
>>> ldir = ['seeds_to_M1.nii', 'seeds_to_M2.nii']
>>> pThresh = fsl.ProjThresh(in_files=ldir, threshold=3)
>>> pThresh.cmdline
'proj_thresh seeds_to_M1.nii seeds_to_M2.nii 3'

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string

```

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```

        representing an existing file)
        a list of input volumes
        argument: ``%s``, position: 0
threshold: (an integer (int or long))
        threshold indicating minimum number of seed voxels entering this
        mask region
        argument: ``%d``, position: 1

[Optional]
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
        FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_files: (a list of items which are a pathlike object or string
            representing an existing file)
            path/name of output volume after thresholding

```

References:

None

63.2.9 TractSkeleton[Link to code](#)

Wraps the executable command `tbss_skeleton`.

Use FSL's `tbss_skeleton` to skeletonise an FA image or project arbitrary values onto a skeleton.

There are two ways to use this interface. To create a skeleton from an FA image, just supply the `in_file` and set `skeleton_file` to `True` (or specify a skeleton filename. To project values onto a skeleton, you must set `project_data` to `True`, and then also supply values for `threshold`, `distance_map`, and `data_file`. The `search_mask_file` and `use_cingulum_mask` inputs are also used in data projection, but `use_cingulum_mask` is set to `True` by default. This mask controls where the projection algorithm searches within a circular space around a tract, rather than in a single perpendicular direction.

Example

```

>>> import nipy.interfaces.fsl as fsl
>>> skeleton = fsl.TractSkeleton()
>>> skeleton.inputs.in_file = "all_FA.nii.gz"
>>> skeleton.inputs.skeleton_file = True
>>> skeleton.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input image (typically mean FA volume)

```

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```

        argument: ``-i %s``

[Optional]
project_data: (a boolean)
    project data onto skeleton
    argument: ``-p %.3f %s %s %s %s``
    requires: threshold, distance_map, data_file
threshold: (a float)
    skeleton threshold value
distance_map: (a pathlike object or string representing an existing
    file)
    distance map image
search_mask_file: (a pathlike object or string representing an
    existing file)
    mask in which to use alternate search rule
    mutually_exclusive: use_cingulum_mask
use_cingulum_mask: (a boolean, nipy default value: True)
    perform alternate search using built-in cingulum mask
    mutually_exclusive: search_mask_file
data_file: (a pathlike object or string representing an existing
    file)
    4D data to project onto skeleton (usually FA)
alt_data_file: (a pathlike object or string representing an existing
    file)
    4D non-FA data to project onto skeleton
    argument: ``-a %s``
alt_skeleton: (a pathlike object or string representing an existing
    file)
    alternate skeleton to use
    argument: ``-s %s``
projected_data: (a pathlike object or string representing a file)
    input data projected onto skeleton
skeleton_file: (a boolean or a pathlike object or string representing
    a file)
    write out skeleton image
    argument: ``-o %s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

projected_data: (a pathlike object or string representing a file)
    input data projected onto skeleton
skeleton_file: (a pathlike object or string representing a file)
    tract skeleton image

```

References:

None

63.2.10 VecReg

[Link to code](#)

Wraps the executable command vecreg.

Use FSL vecreg for registering vector data For complete details, see the FDT Documentation <http://www.fmrib.ox.ac.uk/fsl/fdt/fdt_vecreg.html>

Example

```

>>> from nipy.interfaces import fsl
>>> vreg = fsl.VecReg(in_file='diffusion.nii',          affine_mat='trans.
↳mat',          ref_vol='mni.nii',          out_file='diffusion_
↳vreg.nii')
>>> vreg.cmdline
'vecreg -t trans.mat -i diffusion.nii -o diffusion_vreg.nii -r mni.nii'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         filename for input vector or tensor field
         argument: ``-i %s``
ref_vol: (a pathlike object or string representing an existing file)
         filename for reference (target) volume
         argument: ``-r %s``

[Optional]
out_file: (a pathlike object or string representing a file)
          filename for output registered vector or tensor field
          argument: ``-o %s``
affine_mat: (a pathlike object or string representing an existing
            file)
            filename for affine transformation matrix
            argument: ``-t %s``
warp_field: (a pathlike object or string representing an existing
            file)
            filename for 4D warp field for nonlinear registration
            argument: ``-w %s``
rotation_mat: (a pathlike object or string representing an existing
              file)
              filename for secondary affine matrix if set, this will be used for
              the rotation of the vector/tensor field
              argument: ``--rotmat=%s``
rotation_warp: (a pathlike object or string representing an existing
              file)
              filename for secondary warp field if set, this will be used for the
              rotation of the vector/tensor field
              argument: ``--rotwarp=%s``
interpolation: ('nearestneighbour' or 'trilinear' or 'sinc' or
               'spline')
               interpolation method : nearestneighbour, trilinear (default), sinc
               or spline
               argument: ``--interp=%s``
mask: (a pathlike object or string representing an existing file)
       brain mask in input space
       argument: ``-m %s``
ref_mask: (a pathlike object or string representing an existing file)
          brain mask in output space (useful for speed up of nonlinear reg)

```

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```

        argument: ``--refmask=%s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
            FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          path/name of filename for the registered vector or tensor field

```

References:

None

63.2.11 XFibres5[Link to code](#)Wraps the executable command `xfibres`.

Perform model parameters estimation for local (voxelwise) diffusion parameters

Inputs:

```

[Mandatory]
dwi: (a pathlike object or string representing an existing file)
      diffusion weighted image data file
      argument: ``--data=%s``
mask: (a pathlike object or string representing an existing file)
      brain binary mask file (i.e. from BET)
      argument: ``--mask=%s``
bvecs: (a pathlike object or string representing an existing file)
        b vectors file
        argument: ``--bvecs=%s``
bvals: (a pathlike object or string representing an existing file)
        b values file
        argument: ``--bvals=%s``
n_fibres: (a long integer >= 1, nipy default value: 2)
          Maximum number of fibres to fit in each voxel
          argument: ``--nfibres=%d``

[Optional]
gradnonlin: (a pathlike object or string representing an existing
            file)
            gradient file corresponding to slice
            argument: ``--gradnonlin=%s``
logdir: (a pathlike object or string representing a directory, nipy
        default value: .)
        argument: ``--logdir=%s``
model: (1 or 2 or 3)
        use monoexponential (1, default, required for single-shell) or
        multiexponential (2, multi-shell) model

```

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```

        argument: ``--model=%d``
fudge: (an integer (int or long))
        ARD fudge factor
        argument: ``--fudge=%d``
n_jumps: (an integer (int or long), nipyre default value: 5000)
        Num of jumps to be made by MCMC
        argument: ``--njumps=%d``
burn_in: (a long integer >= 0, nipyre default value: 0)
        Total num of jumps at start of MCMC to be discarded
        argument: ``--burnin=%d``
burn_in_no_ard: (a long integer >= 0, nipyre default value: 0)
        num of burnin jumps before the ard is imposed
        argument: ``--burnin_noard=%d``
sample_every: (a long integer >= 0, nipyre default value: 1)
        Num of jumps for each sample (MCMC)
        argument: ``--sampleevery=%d``
update_proposal_every: (a long integer >= 1, nipyre default value:
        40)
        Num of jumps for each update to the proposal density std (MCMC)
        argument: ``--updateproposalevery=%d``
seed: (an integer (int or long))
        seed for pseudo random number generator
        argument: ``--seed=%d``
no_ard: (a boolean)
        Turn ARD off on all fibres
        argument: ``--noard``
        mutually_exclusive: no_ard, all_ard
all_ard: (a boolean)
        Turn ARD on on all fibres
        argument: ``--allard``
        mutually_exclusive: no_ard, all_ard
no_spat: (a boolean)
        Initialise with tensor, not spatially
        argument: ``--nospat``
        mutually_exclusive: no_spat, non_linear, cilinear
non_linear: (a boolean)
        Initialise with nonlinear fitting
        argument: ``--nonlinear``
        mutually_exclusive: no_spat, non_linear, cilinear
cilinear: (a boolean)
        Initialise with constrained nonlinear fitting
        argument: ``--cnonlinear``
        mutually_exclusive: no_spat, non_linear, cilinear
rician: (a boolean)
        use Rician noise modeling
        argument: ``--rician``
f0_noard: (a boolean)
        Noise floor model: add to the model an unattenuated signal
        compartment f0
        argument: ``--f0``
        mutually_exclusive: f0_noard, f0_ard
f0_ard: (a boolean)
        Noise floor model: add to the model an unattenuated signal
        compartment f0
        argument: ``--f0 --ardf0``
        mutually_exclusive: f0_noard, f0_ard, all_ard
force_dir: (a boolean, nipyre default value: True)

```

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```

        use the actual directory name given (do not add + to make a new
        directory)
        argument: ``--forcedir``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
            FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
        Environment variables

```

Outputs:

```

dyads: (a list of items which are a pathlike object or string
        representing an existing file)
        Mean of PDD distribution in vector form.
fsamples: (a list of items which are a pathlike object or string
           representing an existing file)
           Samples from the distribution on f anisotropy
mean_dsamples: (a pathlike object or string representing an existing
               file)
               Mean of distribution on diffusivity d
mean_fsamples: (a list of items which are a pathlike object or string
               representing an existing file)
               Mean of distribution on f anisotropy
mean_S0samples: (a pathlike object or string representing an existing
                file)
                Mean of distribution on T2wbaseline signal intensity S0
mean_tausamples: (a pathlike object or string representing an
                 existing file)
                 Mean of distribution on tau samples (only with rician noise)
phsamples: (a list of items which are a pathlike object or string
            representing an existing file)
            phi samples, per fiber
thsamples: (a list of items which are a pathlike object or string
            representing an existing file)
            theta samples, per fiber

```

References:

None

63.3 interfaces.fsl.epi

63.3.1 ApplyTOPUP

[Link to code](#)Wraps the executable command `applytopup`.Interface for FSL topup, a tool for estimating and correcting susceptibility induced distortions. [General reference](#) and [use example](#).

Examples

```
>>> from nipy.interfaces.fsl import ApplyTOPUP
>>> applytopup = ApplyTOPUP()
>>> applytopup.inputs.in_files = ["epi.nii", "epi_rev.nii"]
>>> applytopup.inputs.encoding_file = "topup_encoding.txt"
>>> applytopup.inputs.in_topup_fieldcoef = "topup_fieldcoef.nii.gz"
>>> applytopup.inputs.in_topup_movpar = "topup_movpar.txt"
>>> applytopup.inputs.output_type = "NIFTI_GZ"
>>> applytopup.cmdline # doctest: +ELLIPSIS
'applytopup --datain=topup_encoding.txt --imain=epi.nii,epi_rev.nii --inindex=1,2,
↳--topup=topup --out=epi_corrected.nii.gz'
>>> res = applytopup.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
           representing an existing file)
           name of file with images
           argument: ``--imain=%s``
encoding_file: (a pathlike object or string representing an existing
                file)
                name of text file with PE directions/times
                argument: ``--datain=%s``

[Optional]
in_index: (a list of items which are an integer (int or long))
           comma separated list of indices corresponding to --datain
           argument: ``--inindex=%s``
in_topup_fieldcoef: (a pathlike object or string representing an
                    existing file)
                    topup file containing the field coefficients
                    argument: ``--topup=%s``
                    requires: in_topup_movpar
in_topup_movpar: (a pathlike object or string representing an
                 existing file)
                 topup movpar.txt file
                 requires: in_topup_fieldcoef
out_corrected: (a pathlike object or string representing a file)
               output (warped) image
               argument: ``--out=%s``
method: ('jac' or 'lsr')
        use jacobian modulation (jac) or least-squares resampling (lsr)
        argument: ``--method=%s``
interp: ('trilinear' or 'spline')
        interpolation method
        argument: ``--interp=%s``
datatype: ('char' or 'short' or 'int' or 'float' or 'double')
          force output data type
          argument: ``-d=%s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
            FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
```

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```

of class 'str' and with values which are a bytes or None or a
value of class 'str', nipype default value: {})
Environment variables

```

Outputs:

```

out_corrected: (a pathlike object or string representing an existing
file)
name of 4D image file with unwarped images

```

References:

None

63.3.2 EPIDeWarp[Link to code](#)Wraps the executable command `epidewarp.fsl`.Wraps the unwarping script `epidewarp.fsl`.

Warning: deprecated in FSL, please use `nipype.workflows.dmri.preprocess.epi.sdc_fmb()` instead.

Examples

```

>>> from nipype.interfaces.fsl import EPIDeWarp
>>> dewarp = EPIDeWarp()
>>> dewarp.inputs.epi_file = "functional.nii"
>>> dewarp.inputs.mag_file = "magnitude.nii"
>>> dewarp.inputs.dph_file = "phase.nii"
>>> dewarp.inputs.output_type = "NIFTI_GZ"
>>> dewarp.cmdline # doctest: +ELLIPSIS
'epidewarp.fsl --mag magnitude.nii --dph phase.nii --epi functional.nii --esp 0.
↪58 --exfdw .../exfdw.nii.gz --nocleanup --sigma 2 --tediff 2.46 --tmpdir .../
↪temp --vsm .../vsm.nii.gz'
>>> res = dewarp.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
mag_file: (a pathlike object or string representing an existing file)
          Magnitude file
          argument: '--mag %s', position: 0
dph_file: (a pathlike object or string representing an existing file)
          Phase file assumed to be scaled from 0 to 4095
          argument: '--dph %s'

[Optional]
exf_file: (a pathlike object or string representing an existing file)
          example func volume (or use epi)
          argument: '--exf %s'
epi_file: (a pathlike object or string representing an existing file)
          EPI volume to unwarp
          argument: '--epi %s'
tediff: (a float, nipype default value: 2.46)

```

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```

        difference in B0 field map TEs
        argument: ``--tediff %s``
esp: (a float, nipyte default value: 0.58)
    EPI echo spacing
    argument: ``--esp %s``
sigma: (an integer (int or long), nipyte default value: 2)
    2D spatial gaussing smoothing stdev (default = 2mm)
    argument: ``--sigma %s``
vsm: (a string)
    voxel shift map
    argument: ``--vsm %s``
exfdw: (a string)
    dewarped example func volume
    argument: ``--exfdw %s``
epidw: (a string)
    dewarped epi volume
    argument: ``--epidw %s``
tmpdir: (a string)
    tmpdir
    argument: ``--tmpdir %s``
nocleanup: (a boolean, nipyte default value: True)
    no cleanup
    argument: ``--nocleanup``
cleanup: (a boolean)
    cleanup
    argument: ``--cleanup``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables

```

Outputs:

```

unwarped_file: (a pathlike object or string representing a file)
    unwarped epi file
vsm_file: (a pathlike object or string representing a file)
    voxel shift map
exfdw: (a pathlike object or string representing a file)
    dewarped functional volume example
exf_mask: (a pathlike object or string representing a file)
    Mask from example functional volume

```

References:

None

63.3.3 Eddy[Link to code](#)

Wraps the executable command eddy_openmp.

Interface for FSL eddy, a tool for estimating and correcting eddy currents induced distortions. [User guide](#) and

more info regarding acqp file.

Examples

```
>>> from nipyype.interfaces.fsl import Eddy
>>> eddy = Eddy()
>>> eddy.inputs.in_file = 'epi.nii'
>>> eddy.inputs.in_mask = 'epi_mask.nii'
>>> eddy.inputs.in_index = 'epi_index.txt'
>>> eddy.inputs.in_acqp = 'epi_acqp.txt'
>>> eddy.inputs.in_bvec = 'bvecs.scheme'
>>> eddy.inputs.in_bval = 'bvals.scheme'
>>> eddy.inputs.use_cuda = True
>>> eddy.cmdline # doctest: +ELLIPSIS
'eddy_cuda --ff=10.0 --acqp=epi_acqp.txt --bvals=bvals.scheme --bvecs=bvecs.
↪scheme --imain=epi.nii --index=epi_index.txt --mask=epi_mask.nii --niter=5 --
↪nvoxhp=1000 --out=.../eddy_corrected'
>>> eddy.inputs.use_cuda = False
>>> eddy.cmdline # doctest: +ELLIPSIS
'eddy_openmp --ff=10.0 --acqp=epi_acqp.txt --bvals=bvals.scheme --bvecs=bvecs.
↪scheme --imain=epi.nii --index=epi_index.txt --mask=epi_mask.nii --niter=5 --
↪nvoxhp=1000 --out=.../eddy_corrected'
>>> res = eddy.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        File containing all the images to estimate distortions for
        argument: ``--imain=%s``
in_mask: (a pathlike object or string representing an existing file)
        Mask to indicate brain
        argument: ``--mask=%s``
in_index: (a pathlike object or string representing an existing file)
        File containing indices for all volumes in --imain into --acqp and
        --topup
        argument: ``--index=%s``
in_acqp: (a pathlike object or string representing an existing file)
        File containing acquisition parameters
        argument: ``--acqp=%s``
in_bvec: (a pathlike object or string representing an existing file)
        File containing the b-vectors for all volumes in --imain
        argument: ``--bvecs=%s``
in_bval: (a pathlike object or string representing an existing file)
        File containing the b-values for all volumes in --imain
        argument: ``--bvals=%s``

[Optional]
out_base: (a unicode string, nipyype default value: eddy_corrected)
        basename for output (warped) image
        argument: ``--out=%s``
session: (a pathlike object or string representing an existing file)
        File containing session indices for all volumes in --imain
        argument: ``--session=%s``
in_topup_fieldcoef: (a pathlike object or string representing an
                    existing file)
                    topup file containing the field coefficients
                    argument: ``--topup=%s``
```

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```

    requires: in_topup_movpar
in_topup_movpar: (a pathlike object or string representing an
    existing file)
    topup movpar.txt file
    requires: in_topup_fieldcoef
flm: ('linear' or 'quadratic' or 'cubic')
    First level EC model
    argument: ``--flm=%s``
slm: ('none' or 'linear' or 'quadratic')
    Second level EC model
    argument: ``--slm=%s``
fep: (a boolean)
    Fill empty planes in x- or y-directions
    argument: ``--fep``
interp: ('spline' or 'trilinear')
    Interpolation model for estimation step
    argument: ``--interp=%s``
nvoxhp: (an integer (int or long), nipy default value: 1000)
    # of voxels used to estimate the hyperparameters
    argument: ``--nvoxhp=%s``
fudge_factor: (a float, nipy default value: 10.0)
    Fudge factor for hyperparameter error variance
    argument: ``--ff=%s``
dont_sep_offs_move: (a boolean)
    Do NOT attempt to separate field offset from subject movement
    argument: ``--dont_sep_offs_move``
dont_peas: (a boolean)
    Do NOT perform a post-eddy alignment of shells
    argument: ``--dont_peas``
fwhm: (a float)
    FWHM for conditioning filter when estimating the parameters
    argument: ``--fwhm=%s``
niter: (an integer (int or long), nipy default value: 5)
    Number of iterations
    argument: ``--niter=%s``
method: ('jac' or 'lsr')
    Final resampling method (jacobian/least squares)
    argument: ``--resamp=%s``
repol: (a boolean)
    Detect and replace outlier slices
    argument: ``--repol``
num_threads: (an integer (int or long), nipy default value: 1)
    Number of openmp threads to use
is_shelled: (a boolean)
    Override internal check to ensure that data are acquired on a set of
    b-value shells
    argument: ``--data_is_shelled``
field: (a unicode string)
    NonTOPUP fieldmap scaled in Hz - filename has to be provided without
    an extension. TOPUP is strongly recommended
    argument: ``--field=%s``
field_mat: (a pathlike object or string representing an existing
    file)
    Matrix that specifies the relative locations of the field specified
    by --field and first volume in file --imain
    argument: ``--field_mat=%s``
use_cuda: (a boolean)

```

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```

    Run eddy using cuda gpu
cnr_maps: (a boolean)
    Output CNR-Maps
    argument: ``--cnr_maps``
residuals: (a boolean)
    Output Residuals
    argument: ``--residuals``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_corrected: (a pathlike object or string representing an existing
    file)
    4D image file containing all the corrected volumes
out_parameter: (a pathlike object or string representing an existing
    file)
    text file with parameters definining the field andmovement for each
    scan
out_rotated_bvecs: (a pathlike object or string representing an
    existing file)
    File containing rotated b-values for all volumes
out_movement_rms: (a pathlike object or string representing an
    existing file)
    Summary of the "total movement" in each volume
out_restricted_movement_rms: (a pathlike object or string
    representing an existing file)
    Summary of the "total movement" in each volume disregarding
    translation in the PE direction
out_shell_alignment_parameters: (a pathlike object or string
    representing an existing file)
    File containing rigid body movement parameters between the different
    shells as estimated by a post-hoc mutual information based
    registration
out_outlier_report: (a pathlike object or string representing an
    existing file)
    Text-file with a plain language report on what outlier slices eddy
    has found
out_cnr_maps: (a pathlike object or string representing an existing
    file)
    path/name of file with the cnr_maps
out_residuals: (a pathlike object or string representing an existing
    file)
    path/name of file with the residuals

```

References:

None

63.3.4 EddyCorrect

[Link to code](#)

Wraps the executable command `eddy_correct`.

Warning: Deprecated in FSL. Please use `nipyne.interfaces.fsl.epi.Eddy` instead

Example

```
>>> from nipyne.interfaces.fsl import EddyCorrect
>>> eddyc = EddyCorrect(in_file='diffusion.nii',
...                     out_file="diffusion_edc.nii", ref_num=0)
>>> eddyc.cmdline
'eddy_correct diffusion.nii diffusion_edc.nii 0'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         4D input file
         argument: ``%s``, position: 0
ref_num: (an integer (int or long), nipyne default value: 0)
         reference number
         argument: ``%d``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
         4D output file
         argument: ``%s``, position: 1
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
             FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyne default value: {})
          Environment variables
```

Outputs:

```
eddy_corrected: (a pathlike object or string representing an existing
                 file)
                 path/name of 4D eddy corrected output file
```

References:

None

63.3.5 EddyQuad

[Link to code](#)

Wraps the executable command `eddy_quad`.

Interface for FSL `eddy_quad`, a tool for generating single subject reports and storing the quality assessment indices for each subject. [User guide](#)

Examples

```

>>> from nipy.interfaces.fsl import EddyQuad
>>> quad = EddyQuad()
>>> quad.inputs.base_name = 'eddy_corrected'
>>> quad.inputs.idx_file = 'epi_index.txt'
>>> quad.inputs.param_file = 'epi_acqp.txt'
>>> quad.inputs.mask_file = 'epi_mask.nii'
>>> quad.inputs.bval_file = 'bvals.scheme'
>>> quad.inputs.bvec_file = 'bvecs.scheme'
>>> quad.inputs.output_dir = 'eddy_corrected.qc'
>>> quad.inputs.field = 'fieldmap_phase_fslprepared.nii'
>>> quad.inputs.verbose = True
>>> quad.cmdline
'eddy_quad eddy_corrected --bvals bvals.scheme --bvecs bvecs.scheme --field_
↪fieldmap_phase_fslprepared.nii --eddyIdx epi_index.txt --mask epi_mask.nii --
↪output-dir eddy_corrected.qc --eddyParams epi_acqp.txt --verbose'
>>> res = quad.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
idx_file: (a pathlike object or string representing an existing file)
    File containing indices for all volumes into acquisition parameters
    argument: ``--eddyIdx %s``
param_file: (a pathlike object or string representing an existing
    file)
    File containing acquisition parameters
    argument: ``--eddyParams %s``
mask_file: (a pathlike object or string representing an existing
    file)
    Binary mask file
    argument: ``--mask %s``
bval_file: (a pathlike object or string representing an existing
    file)
    b-values file
    argument: ``--bvals %s``

[Optional]
base_name: (a unicode string, nipy default value: eddy_corrected)
    Basename (including path) for EDDY output files, i.e., corrected
    images and QC files
    argument: ``%s``, position: 0
bvec_file: (a pathlike object or string representing an existing
    file)
    b-vectors file - only used when <base_name>.eddy_residuals file is
    present
    argument: ``--bvecs %s``
output_dir: (a unicode string)
    Output directory - default = '<base_name>.qc'
    argument: ``--output-dir %s``
field: (a pathlike object or string representing an existing file)
    TOPUP estimated field (in Hz)
    argument: ``--field %s``
slice_spec: (a pathlike object or string representing an existing
    file)
    Text file specifying slice/group acquisition
    argument: ``--slspec %s``

```

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```

verbose: (a boolean)
    Display debug messages
    argument: ``--verbose``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

qc_json: (a pathlike object or string representing an existing file)
    Single subject database containing quality metrics and data info.
qc_pdf: (a pathlike object or string representing an existing file)
    Single subject QC report.
avg_b_png: (a list of items which are a pathlike object or string
    representing an existing file)
    Image showing mid-sagittal, -coronal and -axial slices of each
    averaged b-shell volume.
avg_b0_pe_png: (a list of items which are a pathlike object or string
    representing an existing file)
    Image showing mid-sagittal, -coronal and -axial slices of each
    averaged pe-direction b0 volume. Generated when using the -f option.
cnr_png: (a list of items which are a pathlike object or string
    representing an existing file)
    Image showing mid-sagittal, -coronal and -axial slices of each
    b-shell CNR volume. Generated when CNR maps are available.
vdm_png: (a pathlike object or string representing an existing file)
    Image showing mid-sagittal, -coronal and -axial slices of the voxel
    displacement map. Generated when using the -f option.
residuals: (a pathlike object or string representing an existing
    file)
    Text file containing the volume-wise mask-averaged squared
    residuals. Generated when residual maps are available.
clean_volumes: (a pathlike object or string representing an existing
    file)
    Text file containing a list of clean volumes, based on the eddy
    squared residuals. To generate a version of the pre-processed
    dataset without outlier volumes, use: `fslselectvols -i
    <eddy_corrected_data> -o eddy_corrected_data_clean
    --vols=vols_no_outliers.txt`

```

References:

None

63.3.6 EpiReg[Link to code](#)Wraps the executable command `epi_reg`.Runs FSL `epi_reg` script for simultaneous coregistration and fieldmap unwarping.

Examples

```
>>> from nipy.interfaces.fsl import EpiReg
>>> epiereg = EpiReg()
>>> epiereg.inputs.epi='epi.nii'
>>> epiereg.inputs.t1_head='T1.nii'
>>> epiereg.inputs.t1_brain='T1_brain.nii'
>>> epiereg.inputs.out_base='epi2struct'
>>> epiereg.inputs.fmap='fieldmap_phase_fslprepared.nii'
>>> epiereg.inputs.fmapmag='fieldmap_mag.nii'
>>> epiereg.inputs.fmapmagbrain='fieldmap_mag_brain.nii'
>>> epiereg.inputs.echos pacing=0.00067
>>> epiereg.inputs.pedir='y'
>>> epiereg.cmdline # doctest: +ELLIPSIS
'epi_reg --echos pacing=0.000670 --fmap=fieldmap_phase_fslprepared.nii --
↪fmapmag=fieldmap_mag.nii --fmapmagbrain=fieldmap_mag_brain.nii --noclean --
↪pedir=y --epi=epi.nii --t1=T1.nii --t1brain=T1_brain.nii --out=epi2struct'
>>> epiereg.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
epi: (a pathlike object or string representing an existing file)
     EPI image
     argument: ``--epi=%s``, position: -4
t1_head: (a pathlike object or string representing an existing file)
         wholehead T1 image
         argument: ``--t1=%s``, position: -3
t1_brain: (a pathlike object or string representing an existing file)
         brain extracted T1 image
         argument: ``--t1brain=%s``, position: -2

[Optional]
out_base: (a string, nipy default value: epi2struct)
         output base name
         argument: ``--out=%s``, position: -1
fmap: (a pathlike object or string representing an existing file)
      fieldmap image (in rad/s)
      argument: ``--fmap=%s``
fmapmag: (a pathlike object or string representing an existing file)
         fieldmap magnitude image - wholehead
         argument: ``--fmapmag=%s``
fmapmagbrain: (a pathlike object or string representing an existing
              file)
              fieldmap magnitude image - brain extracted
              argument: ``--fmapmagbrain=%s``
wmseg: (a pathlike object or string representing an existing file)
       white matter segmentation of T1 image, has to be named like the
       t1brain and end on _wmseg
       argument: ``--wmseg=%s``
echos pacing: (a float)
              Effective EPI echo spacing (sometimes called dwell time) - in
              seconds
              argument: ``--echos pacing=%f``
pedir: ('x' or 'y' or 'z' or '-x' or '-y' or '-z')
       phase encoding direction, dir = x/y/z/-x/-y/-z
       argument: ``--pedir=%s``
weight_image: (a pathlike object or string representing an existing
```

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```

        file)
        weighting image (in T1 space)
        argument: ``--weight=%s``
no_fmapreg: (a boolean)
        do not perform registration of fmap to T1 (use if fmap already
        registered)
        argument: ``--nofmapreg``
no_clean: (a boolean, nipy default value: True)
        do not clean up intermediate files
        argument: ``--noclean``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
        'NIFTI_PAIR_GZ')
        FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        unwarped and coregistered epi input
out_1vol: (a pathlike object or string representing an existing file)
        unwarped and coregistered single volume
fmap2str_mat: (a pathlike object or string representing an existing
        file)
        rigid fieldmap-to-structural transform
fmap2epi_mat: (a pathlike object or string representing an existing
        file)
        rigid fieldmap-to-epi transform
fmap_epi: (a pathlike object or string representing an existing file)
        fieldmap in epi space
fmap_str: (a pathlike object or string representing an existing file)
        fieldmap in structural space
fmapmag_str: (a pathlike object or string representing an existing
        file)
        fieldmap magnitude image in structural space
epi2str_inv: (a pathlike object or string representing an existing
        file)
        rigid structural-to-epi transform
epi2str_mat: (a pathlike object or string representing an existing
        file)
        rigid epi-to-structural transform
shiftmap: (a pathlike object or string representing an existing file)
        shiftmap in epi space
fullwarp: (a pathlike object or string representing an existing file)
        warpfield to unwarp epi and transform into structural space
wmseg: (a pathlike object or string representing an existing file)
        white matter segmentation used in flirt bbr
seg: (a pathlike object or string representing an existing file)
        white matter, gray matter, csf segmentation
wmedge: (a pathlike object or string representing an existing file)
        white matter edges for visualization

```

References:

None

63.3.7 PrepareFieldmap[Link to code](#)Wraps the executable command `fsl_prepare_fieldmap`.Interface for the `fsl_prepare_fieldmap` script (FSL 5.0)

Prepares a fieldmap suitable for FEAT from SIEMENS data - saves output in rad/s format (e.g. ``fsl_prepare_fieldmap SIEMENS images_3_gre_field_mapping images_4_gre_field_mapping fmap_rads 2.65``).

Examples

```
>>> from nipy.interfaces.fsl import PrepareFieldmap
>>> prepare = PrepareFieldmap()
>>> prepare.inputs.in_phase = "phase.nii"
>>> prepare.inputs.in_magnitude = "magnitude.nii"
>>> prepare.inputs.output_type = "NIFTI_GZ"
>>> prepare.cmdline # doctest: +ELLIPSIS
'fsl_prepare_fieldmap SIEMENS phase.nii magnitude.nii .../phase_fslprepared.nii.
  ↪gz 2.460000'
>>> res = prepare.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_phase: (a pathlike object or string representing an existing file)
           Phase difference map, in SIEMENS format range from 0-4096 or 0-8192)
           argument: ``%s``, position: 2
in_magnitude: (a pathlike object or string representing an existing
               file)
               Magnitude difference map, brain extracted
               argument: ``%s``, position: 3
delta_TE: (a float, nipy default value: 2.46)
           echo time difference of the fieldmap sequence in ms. (usually 2.46ms
           in Siemens)
           argument: ``%f``, position: -2

[Optional]
scanner: (a string, nipy default value: SIEMENS)
          must be SIEMENS
          argument: ``%s``, position: 1
nocheck: (a boolean, nipy default value: False)
          do not perform sanity checks for image size/range/dimensions
          argument: ``--nocheck``, position: -1
out_fieldmap: (a pathlike object or string representing a file)
              output name for prepared fieldmap
              argument: ``%s``, position: 4
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
```

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```

of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_fieldmap: (a pathlike object or string representing an existing
               file)
               output name for prepared fieldmap

```

References:

None

63.3.8 SigLoss[Link to code](#)

Wraps the executable command sigloss.

Estimates signal loss from a field map (in rad/s)

Examples

```

>>> from nipy.interfaces.fsl import SigLoss
>>> sigloss = SigLoss()
>>> sigloss.inputs.in_file = "phase.nii"
>>> sigloss.inputs.echo_time = 0.03
>>> sigloss.inputs.output_type = "NIFTI_GZ"
>>> sigloss.cmdline # doctest: +ELLIPSIS
'sigloss --te=0.030000 -i phase.nii -s ../phase_sigloss.nii.gz'
>>> res = sigloss.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         b0 fieldmap file
         argument: ``-i %s``

[Optional]
out_file: (a pathlike object or string representing a file)
          output signal loss estimate file
          argument: ``-s %s``
mask_file: (a pathlike object or string representing an existing
            file)
            brain mask file
            argument: ``-m %s``
echo_time: (a float)
            echo time in seconds
            argument: ``--te=%f``
slice_direction: ('x' or 'y' or 'z')
                 slicing direction
                 argument: ``-d %s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)

```

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```

Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          signal loss estimate file

```

References:

None

63.3.9 TOPUP[Link to code](#)

Wraps the executable command topup.

Interface for FSL topup, a tool for estimating and correcting susceptibility induced distortions. See FSL documentation for [reference](#), [usage examples](#), and [exemplary config files](#).**Examples**

```

>>> from nipy.interfaces.fsl import TOPUP
>>> topup = TOPUP()
>>> topup.inputs.in_file = "b0_b0rev.nii"
>>> topup.inputs.encoding_file = "topup_encoding.txt"
>>> topup.inputs.output_type = "NIFTI_GZ"
>>> topup.cmdline # doctest: +ELLIPSIS
'topup --config=b02b0.cnf --datain=topup_encoding.txt --imain=b0_b0rev.nii --
↳out=b0_b0rev_base --iout=b0_b0rev_corrected.nii.gz --fout=b0_b0rev_field.nii.gz
↳--jacout=jac --logout=b0_b0rev_topup.log --rbmout=xfm --dfout=warpfield'
>>> res = topup.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         name of 4D file with images
         argument: ``--imain=%s``
encoding_file: (a pathlike object or string representing an existing
               file)
               name of text file with PE directions/times
               argument: ``--datain=%s``
               mutually_exclusive: encoding_direction
encoding_direction: (a list of items which are 'y' or 'x' or 'z' or
                    'x-' or 'y-' or 'z-')
                    encoding direction for automatic generation of encoding_file
                    argument: ``--datain=%s``
                    mutually_exclusive: encoding_file
requires: readout_times
readout_times: (a list of items which are a float)
               readout times (dwell times by # phase-encode steps minus 1)
               mutually_exclusive: encoding_file

```

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```

        requires: encoding_direction

[Optional]
out_base: (a pathlike object or string representing a file)
    base-name of output files (spline coefficients (Hz) and movement
    parameters)
    argument: ``--out=%s``
out_field: (a pathlike object or string representing a file)
    name of image file with field (Hz)
    argument: ``--fout=%s``
out_warp_prefix: (a unicode string, nipy default value: warpfield)
    prefix for the warpfield images (in mm)
    argument: ``--dfout=%s``
out_mat_prefix: (a unicode string, nipy default value: xfm)
    prefix for the realignment matrices
    argument: ``--rbmout=%s``
out_jac_prefix: (a unicode string, nipy default value: jac)
    prefix for the warpfield images
    argument: ``--jacout=%s``
out_corrected: (a pathlike object or string representing a file)
    name of 4D image file with unwarped images
    argument: ``--iout=%s``
out_logfile: (a pathlike object or string representing a file)
    name of log-file
    argument: ``--logout=%s``
warp_res: (a float)
    (approximate) resolution (in mm) of warp basis for the different
    sub-sampling levels
    argument: ``--warpres=%f``
subsamp: (an integer (int or long))
    sub-sampling scheme
    argument: ``--subsamp=%d``
fwhm: (a float)
    FWHM (in mm) of gaussian smoothing kernel
    argument: ``--fwhm=%f``
config: (a string, nipy default value: b02b0.cnf)
    Name of config file specifying command line arguments
    argument: ``--config=%s``
max_iter: (an integer (int or long))
    max # of non-linear iterations
    argument: ``--miter=%d``
reg_lambda: (a float)
    Weight of regularisation, default depending on --ssqlambda and
    --regmod switches.
    argument: ``--lambda=%0.f``
ssqlambda: (1 or 0)
    Weight lambda by the current value of the ssd. If used (=1), the
    effective weight of regularisation term becomes higher for the
    initial iterations, therefore initial steps are a little smoother
    than they would without weighting. This reduces the risk of finding
    a local minimum.
    argument: ``--ssqlambda=%d``
regmod: ('bending_energy' or 'membrane_energy')
    Regularisation term implementation. Defaults to bending_energy. Note
    that the two functions have vastly different scales. The membrane
    energy is based on the first derivatives and the bending energy on
    the second derivatives. The second derivatives will typically be

```

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```

much smaller than the first derivatives, so input lambda will have
to be larger for bending_energy to yield approximately the same
level of regularisation.
argument: ``--regmod=%s``
estmov: (1 or 0)
estimate movements if set
argument: ``--estmov=%d``
minmet: (0 or 1)
Minimisation method 0=Levenberg-Marquardt, 1=Scaled Conjugate
Gradient
argument: ``--minmet=%d``
splineorder: (an integer (int or long))
order of spline, 2->Quadratic spline, 3->Cubic spline
argument: ``--splineorder=%d``
numprec: ('double' or 'float')
Precision for representing Hessian, double or float.
argument: ``--numprec=%s``
interp: ('spline' or 'linear')
Image interpolation model, linear or spline.
argument: ``--interp=%s``
scale: (0 or 1)
If set (=1), the images are individually scaled to a common mean
argument: ``--scale=%d``
regrid: (1 or 0)
If set (=1), the calculations are done in a different grid
argument: ``--regrid=%d``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
'NIFTI_PAIR_GZ')
FSL output type
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_fieldcoef: (a pathlike object or string representing an existing
file)
file containing the field coefficients
out_movpar: (a pathlike object or string representing an existing
file)
movpar.txt output file
out_enc_file: (a pathlike object or string representing a file)
encoding directions file output for applytopup
out_field: (a pathlike object or string representing a file)
name of image file with field (Hz)
out_warps: (a list of items which are a pathlike object or string
representing an existing file)
warpfield images
out_jacs: (a list of items which are a pathlike object or string
representing an existing file)
Jacobian images
out_mats: (a list of items which are a pathlike object or string
representing an existing file)

```

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```

    realignment matrices
out_corrected: (a pathlike object or string representing a file)
    name of 4D image file with unwarped images
out_logfile: (a pathlike object or string representing a file)
    name of log-file

```

References:

None

63.4 interfaces.fsl.fix**63.4.1 Classifier**[Link to code](#)

Classify ICA components using a specific training dataset (<thresh> is in the range 0-100, typically 5-20).

Inputs:

```

[Mandatory]
trained_wts_file: (a pathlike object or string representing an
    existing file)
    trained-weights file
    argument: ``%s``, position: 2
thresh: (an integer (int or long))
    Threshold for cleanup.
    argument: ``%d``, position: -1

[Optional]
mel_ica: (a pathlike object or string representing an existing
    directory)
    Melodic output directory or directories
    argument: ``%s``, position: 1
artifacts_list_file: (a pathlike object or string representing a
    file)
    Text file listing which ICs are artifacts; can be the output from
    classification or can be created manually
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

artifacts_list_file: (a pathlike object or string representing a
    file)
    Text file listing which ICs are artifacts; can be the output from
classification or can be created manually

```

63.4.2 Cleaner[Link to code](#)

Extract features (for later training and/or classifying)

Inputs:

```
[Mandatory]
artifacts_list_file: (a pathlike object or string representing an
    existing file)
    Text file listing which ICs are artifacts; can be the output from
    classification or can be created manually
    argument: ``%s``, position: 1

[Optional]
cleanup_motion: (a boolean)
    cleanup motion confounds, looks for design.fsf for highpass filter
    cut-off
    argument: ``-m``, position: 2
highpass: (a float, nipyne default value: 100)
    cleanup motion confounds
    argument: ``-m -h %f``, position: 2
aggressive: (a boolean)
    Apply aggressive (full variance) cleanup, instead of the default
    less-aggressive (unique variance) cleanup.
    argument: ``-A``, position: 3
confound_file: (a pathlike object or string representing a file)
    Include additional confound file.
    argument: ``-x %s``, position: 4
confound_file_1: (a pathlike object or string representing a file)
    Include additional confound file.
    argument: ``-x %s``, position: 5
confound_file_2: (a pathlike object or string representing a file)
    Include additional confound file.
    argument: ``-x %s``, position: 6
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables
```

Outputs:

```
cleaned_functional_file: (a pathlike object or string representing an
    existing file)
    Cleaned session data
```

63.4.3 FeatureExtractor[Link to code](#)

Extract features (for later training and/or classifying)

Inputs:

```
[Optional]
mel_ica: (a pathlike object or string representing an existing
    directory)
    Melodic output directory or directories
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
```

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```

of class 'str' and with values which are a bytes or None or a
value of class 'str', nipyne default value: {})
Environment variables

```

Outputs:

```

mel_ica: (a pathlike object or string representing an existing
         directory)
         Melodic output directory or directories
         argument: ``%s``, position: -1

```

63.4.4 Training

[Link to code](#)

Train the classifier based on your own FEAT/MELODIC output directory.

Inputs:

```

[Optional]
mel_icas: (a list of items which are a pathlike object or string
           representing an existing directory)
           Melodic output directories
           argument: ``%s``, position: -1
trained_wts_filestem: (a unicode string)
                      trained-weights filestem, used for trained_wts_file and output
                      directories
                      argument: ``%s``, position: 1
loo: (a boolean)
     full leave-one-out test with classifier training
     argument: ``-l``, position: 2
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a value
          of class 'str', nipyne default value: {})
          Environment variables

```

Outputs:

```

trained_wts_file: (a pathlike object or string representing an
                  existing file)
                  Trained-weights file

```

63.4.5 TrainingSetCreator

[Link to code](#)

Goes through set of provided melodic output directories, to find all the ones that have a hand_labels_noise.txt file in them.

This is outsourced as a separate class, so that the pipeline is rerun everytime a handlabeled file has been changed, or a new one created.

Inputs:

```

[Optional]
mel_icas_in: (a list of items which are a pathlike object or string
              representing an existing directory)

```

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```
Melodic output directories
argument: ``%s``, position: -1
```

Outputs:

```
mel_icas_out: (a list of items which are a pathlike object or string
               representing an existing directory)
Hand labels for noise vs signal
argument: ``%s``, position: -1
```

63.5 interfaces.fsl.maths

63.5.1 AR1Image

[Link to code](#)

Wraps the executable command `fslmaths`.

Use `fslmaths` to generate an AR1 coefficient image across a given dimension. (Should use `-odt float` and probably `demean first`)

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         image to operate on
         argument: ``%s``, position: 2

[Optional]
dimension: ('T' or 'X' or 'Y' or 'Z', nipy default value: T)
           dimension to find AR(1) coefficient across
           argument: ``-%sar1``, position: 4
out_file: (a pathlike object or string representing a file)
          image to write
          argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                   or 'input')
                datatype to use for calculations (default is float)
                argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                 or 'input')
                datatype to use for output (default uses input type)
                argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
            change NaNs to zeros before doing anything
            argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
            FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          image written after calculations
```

References:

None

63.5.2 ApplyMask[Link to code](#)

Wraps the executable command fslmaths.

Use fslmaths to apply a binary mask to another image.

Inputs:

```
[Mandatory]
mask_file: (a pathlike object or string representing an existing
            file)
            binary image defining mask space
            argument: ``-mas %s``, position: 4
in_file: (a pathlike object or string representing an existing file)
          image to operate on
          argument: ``%s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
          image to write
          argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                    or 'input')
                  datatype to use for calculations (default is float)
                  argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                  or 'input')
                  datatype to use for output (default uses input type)
                  argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
            change NaNs to zeros before doing anything
            argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          image written after calculations
```

References:

None

63.5.3 BinaryMaths

[Link to code](#)

Wraps the executable command `fslmaths`.

Use `fslmaths` to perform mathematical operations using a second image or a numeric value.

Inputs:

```
[Mandatory]
operation: ('add' or 'sub' or 'mul' or 'div' or 'rem' or 'max' or
           'min')
           operation to perform
           argument: ``-s``, position: 4
operand_file: (a pathlike object or string representing an existing
              file)
              second image to perform operation with
              argument: ``%s``, position: 5
              mutually_exclusive: operand_value
operand_value: (a float)
               value to perform operation with
               argument: ``%.8f``, position: 5
               mutually_exclusive: operand_file
in_file: (a pathlike object or string representing an existing file)
         image to operate on
         argument: ``%s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
         image to write
         argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                   or 'input')
                   datatype to use for calculations (default is float)
                   argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                  or 'input')
                  datatype to use for output (default uses input type)
                  argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
           change NaNs to zeros before doing anything
           argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
         image written after calculations
```

References:

None

63.5.4 ChangeDataType

[Link to code](#)

Wraps the executable command `fslmaths`.

Use `fslmaths` to change the datatype of an image.

Inputs:

```
[Mandatory]
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                  or 'input')
                  output data type
                  argument: ``-odt %s``, position: -1
in_file: (a pathlike object or string representing an existing file)
          image to operate on
          argument: ``%s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
          image to write
          argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                    or 'input')
                    datatype to use for calculations (default is float)
                    argument: ``-dt %s``, position: 1
nan2zeros: (a boolean)
            change NaNs to zeros before doing anything
            argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          image written after calculations
```

References:

None

63.5.5 DilateImage

[Link to code](#)

Wraps the executable command `fslmaths`.

Use `fslmaths` to perform a spatial dilation of an image.

Inputs:

```
[Mandatory]
operation: ('mean' or 'modal' or 'max')
           filtering operation to perfoem in dilation
           argument: ``-dil%s``, position: 6
```

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```

in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``%s``, position: 2

[Optional]
kernel_shape: ('3D' or '2D' or 'box' or 'boxv' or 'gauss' or 'sphere'
    or 'file')
    kernel shape to use
    argument: ``-kernel %s``, position: 4
kernel_size: (a float)
    kernel size - voxels for box/boxv, mm for sphere, mm sigma for gauss
    argument: ``%.4f``, position: 5
    mutually_exclusive: kernel_file
kernel_file: (a pathlike object or string representing an existing
    file)
    use external file for kernel
    argument: ``%s``, position: 5
    mutually_exclusive: kernel_size
out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for calculations (default is float)
    argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for output (default uses input type)
    argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
    change NaNs to zeros before doing anything
    argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    image written after calculations

```

References:

None

63.5.6 ErodelImage[Link to code](#)Wraps the executable command `fslmaths`.Use `fslmaths` to perform a spatial erosion of an image.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        image to operate on
        argument: ``%s``, position: 2

[Optional]
minimum_filter: (a boolean, nipy default value: False)
                if true, minimum filter rather than erosion by zeroing-out
                argument: ``%s``, position: 6
kernel_shape: ('3D' or '2D' or 'box' or 'boxv' or 'gauss' or 'sphere'
               or 'file')
               kernel shape to use
               argument: ``-kernel %s``, position: 4
kernel_size: (a float)
              kernel size - voxels for box/boxv, mm for sphere, mm sigma for gauss
              argument: ``%.4f``, position: 5
              mutually_exclusive: kernel_file
kernel_file: (a pathlike object or string representing an existing
              file)
              use external file for kernel
              argument: ``%s``, position: 5
              mutually_exclusive: kernel_size
out_file: (a pathlike object or string representing a file)
           image to write
           argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                    or 'input')
                    datatype to use for calculations (default is float)
                    argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                  or 'input')
                  datatype to use for output (default uses input type)
                  argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
            change NaNs to zeros before doing anything
            argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          image written after calculations

```

References:

None

63.5.7 IsotropicSmooth

[Link to code](#)

Wraps the executable command `fslmaths`.

Use `fslmaths` to spatially smooth an image with a gaussian kernel.

Inputs:

```
[Mandatory]
fwhm: (a float)
    fwhm of smoothing kernel [mm]
    argument: ``-s %.5f``, position: 4
    mutually_exclusive: sigma
sigma: (a float)
    sigma of smoothing kernel [mm]
    argument: ``-s %.5f``, position: 4
    mutually_exclusive: fwhm
in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``%s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for calculations (default is float)
    argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for output (default uses input type)
    argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
    change NaNs to zeros before doing anything
    argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
    image written after calculations
```

References:

None

63.5.8 MathsCommand

[Link to code](#)

Wraps the executable command `fslmaths`.

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         image to operate on
         argument: ``%s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
         image to write
         argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                    or 'input')
         datatype to use for calculations (default is float)
         argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                  or 'input')
         datatype to use for output (default uses input type)
         argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
         change NaNs to zeros before doing anything
         argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
         FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
         image written after calculations
```

References:

None

63.5.9 MaxImage

[Link to code](#)

Wraps the executable command fslmaths.

Use fslmaths to generate a max image across a given dimension.

Examples

```
>>> from nipy.interfaces.fsl.maths import MaxImage
>>> maxer = MaxImage()
>>> maxer.inputs.in_file = "functional.nii" # doctest: +SKIP
>>> maxer.dimension = "T"
>>> maxer.cmdline # doctest: +SKIP
'fslmaths functional.nii -Tmax functional_max.nii'
```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        image to operate on
        argument: ``%s``, position: 2

[Optional]
dimension: ('T' or 'X' or 'Y' or 'Z', nipy default value: T)
          dimension to max across
          argument: ``-smax``, position: 4
out_file: (a pathlike object or string representing a file)
          image to write
          argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                   or 'input')
                 datatype to use for calculations (default is float)
                 argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                 or 'input')
                 datatype to use for output (default uses input type)
                 argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
            change NaNs to zeros before doing anything
            argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
            FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          image written after calculations

```

References:

None

63.5.10 MaxnImage

[Link to code](#)

Wraps the executable command `fslmaths`.

Use `fslmaths` to generate an image of index of max across a given dimension.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        image to operate on
        argument: ``%s``, position: 2

[Optional]
dimension: ('T' or 'X' or 'Y' or 'Z', nipy default value: T)

```

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```

        dimension to index max across
        argument: ``-%smaxn``, position: 4
out_file: (a pathlike object or string representing a file)
        image to write
        argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
        or 'input')
        datatype to use for calculations (default is float)
        argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
        or 'input')
        datatype to use for output (default uses input type)
        argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
        argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
        'NIFTI_PAIR_GZ')
        FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipype default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        image written after calculations

```

References:

None

63.5.11 MeanImage[Link to code](#)Wraps the executable command `fslmaths`.Use `fslmaths` to generate a mean image across a given dimension.**Inputs:**

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        image to operate on
        argument: ``%s``, position: 2

[Optional]
dimension: ('T' or 'X' or 'Y' or 'Z', nipype default value: T)
        dimension to mean across
        argument: ``-%smean``, position: 4
out_file: (a pathlike object or string representing a file)
        image to write
        argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'

```

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```

    or 'input')
    datatype to use for calculations (default is float)
    argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for output (default uses input type)
    argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
    change NaNs to zeros before doing anything
    argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    image written after calculations

```

References:

None

63.5.12 MedianImage[Link to code](#)Wraps the executable command `fslmaths`.Use `fslmaths` to generate a median image across a given dimension.**Inputs:**

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``%s``, position: 2

[Optional]
dimension: ('T' or 'X' or 'Y' or 'Z', nipy default value: T)
    dimension to median across
    argument: ``-%smedian``, position: 4
out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for calculations (default is float)
    argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for output (default uses input type)

```

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```

        argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
    change NaNs to zeros before doing anything
    argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    image written after calculations

```

References:

None

63.5.13 MinImage[Link to code](#)Wraps the executable command `fslmaths`.Use `fslmaths` to generate a minimum image across a given dimension.**Inputs:**

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``%s``, position: 2

[Optional]
dimension: ('T' or 'X' or 'Y' or 'Z', nipype default value: T)
    dimension to min across
    argument: ``-%smin``, position: 4
out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for calculations (default is float)
    argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for output (default uses input type)
    argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
    change NaNs to zeros before doing anything
    argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')

```

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```

    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    image written after calculations

```

References:

None

63.5.14 MultiImageMaths[Link to code](#)Wraps the executable command `fslmaths`.Use `fslmaths` to perform a sequence of mathematical operations.**Examples**

```

>>> from nipy.interfaces.fsl import MultiImageMaths
>>> maths = MultiImageMaths()
>>> maths.inputs.in_file = "functional.nii"
>>> maths.inputs.op_string = "-add %s -mul -1 -div %s"
>>> maths.inputs.operand_files = ["functional2.nii", "functional3.nii"]
>>> maths.inputs.out_file = "functional4.nii"
>>> maths.cmdline
'fslmaths functional.nii -add functional2.nii -mul -1 -div functional3.nii_
↪functional4.nii'

```

Inputs:

```

[Mandatory]
op_string: (a string)
    python formatted string of operations to perform
    argument: ``%s``, position: 4
operand_files: (a list of items which are a pathlike object or string
    representing an existing file)
    list of file names to plug into op string
in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``%s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for calculations (default is float)

```

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```

        argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                  or 'input')
        datatype to use for output (default uses input type)
        argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
        argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
        FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          image written after calculations

```

References:

None

63.5.15 PercentileImage[Link to code](#)Wraps the executable command `fslmaths`.Use `fslmaths` to generate a percentile image across a given dimension.**Examples**

```

>>> from nipy.interfaces.fsl.maths import MaxImage
>>> percer = PercentileImage()
>>> percer.inputs.in_file = "functional.nii" # doctest: +SKIP
>>> percer.dimension = "T"
>>> percer.perc = 90
>>> percer.cmdline # doctest: +SKIP
'fslmaths functional.nii -Tperc 90 functional_perc.nii'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        image to operate on
        argument: ``%s``, position: 2

[Optional]
dimension: ('T' or 'X' or 'Y' or 'Z', nipy default value: T)
        dimension to percentile across
        argument: ``-%sperc``, position: 4
perc: (0 <= a long integer <= 100)

```

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```

    nth percentile (0-100) of FULL RANGE across dimension
    argument: ``%f``, position: 5
out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for calculations (default is float)
    argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for output (default uses input type)
    argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
    change NaNs to zeros before doing anything
    argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    image written after calculations

```

References:

None

63.5.16 SpatialFilter[Link to code](#)Wraps the executable command `fslmaths`.Use `fslmaths` to spatially filter an image.**Inputs:**

```

[Mandatory]
operation: ('mean' or 'median' or 'meanu')
    operation to filter with
    argument: ``-f%s``, position: 6
in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``%s``, position: 2

[Optional]
kernel_shape: ('3D' or '2D' or 'box' or 'boxv' or 'gauss' or 'sphere'
    or 'file')
    kernel shape to use
    argument: ``-kernel %s``, position: 4

```

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```

kernel_size: (a float)
    kernel size - voxels for box/boxv, mm for sphere, mm sigma for gauss
    argument: ``%.4f``, position: 5
    mutually_exclusive: kernel_file
kernel_file: (a pathlike object or string representing an existing
    file)
    use external file for kernel
    argument: ``%s``, position: 5
    mutually_exclusive: kernel_size
out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for calculations (default is float)
    argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for output (default uses input type)
    argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
    change NaNs to zeros before doing anything
    argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    image written after calculations

```

References:

None

63.5.17 StdImage[Link to code](#)Wraps the executable command `fslmaths`.Use `fslmaths` to generate a standard deviation in an image across a given dimension.**Inputs:**

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``%s``, position: 2

[Optional]

```

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```

dimension: ('T' or 'X' or 'Y' or 'Z', nipy default value: T)
    dimension to standard deviate across
    argument: ``-sstd``, position: 4
out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for calculations (default is float)
    argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for output (default uses input type)
    argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
    change NaNs to zeros before doing anything
    argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    image written after calculations

```

References:

None

63.5.18 TemporalFilter[Link to code](#)Wraps the executable command `fslmaths`.Use `fslmaths` to apply a low, high, or bandpass temporal filter to a timeseries.**Inputs:**

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``%s``, position: 2

[Optional]
lowpass_sigma: (a float, nipy default value: -1)
    lowpass filter sigma (in volumes)
    argument: ``%.6f``, position: 5
highpass_sigma: (a float, nipy default value: -1)
    highpass filter sigma (in volumes)
    argument: ``-bptf %.6f``, position: 4

```

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```

out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for calculations (default is float)
    argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for output (default uses input type)
    argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
    change NaNs to zeros before doing anything
    argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    image written after calculations

```

References:

None

63.5.19 Threshold[Link to code](#)

Wraps the executable command fslmaths.

Use fslmaths to apply a threshold to an image in a variety of ways.

Inputs:

```

[Mandatory]
thresh: (a float)
    threshold value
    argument: ``%s``, position: 4
in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``%s``, position: 2

[Optional]
direction: ('below' or 'above', nipy default value: below)
    zero-out either below or above thresh value
use_robust_range: (a boolean)
    interpret thresh as percentage (0-100) of robust range
use_nonzero_voxels: (a boolean)
    use nonzero voxels to calculate robust range

```

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```

    requires: use_robust_range
out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for calculations (default is float)
    argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for output (default uses input type)
    argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
    change NaNs to zeros before doing anything
    argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    image written after calculations

```

References:

None

63.5.20 UnaryMaths[Link to code](#)Wraps the executable command `fslmaths`.Use `fslmaths` to perform a variety of mathematical operations on an image.**Inputs:**

```

[Mandatory]
operation: ('exp' or 'log' or 'sin' or 'cos' or 'tan' or 'asin' or
    'acos' or 'atan' or 'sqr' or 'sqrt' or 'recip' or 'abs' or 'bin'
    or 'binv' or 'fillh' or 'fillh26' or 'index' or 'edge' or 'nan' or
    'nanm' or 'rand' or 'randn' or 'range')
    operation to perform
    argument: ``-%s``, position: 4
in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``%s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
    image to write

```

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```

        argument: ``%s``, position: -2
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                    or 'input')
                    datatype to use for calculations (default is float)
        argument: ``-dt %s``, position: 1
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                  or 'input')
                  datatype to use for output (default uses input type)
        argument: ``-odt %s``, position: -1
nan2zeros: (a boolean)
            change NaNs to zeros before doing anything
        argument: ``-nan``, position: 3
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          image written after calculations

```

References:

None

63.6 interfaces.fsl.model

63.6.1 Cluster

[Link to code](#)

Wraps the executable command cluster.

Uses FSL cluster to perform clustering on statistical output

Examples

```

>>> cl = Cluster()
>>> cl.inputs.threshold = 2.3
>>> cl.inputs.in_file = 'zstat1.nii.gz'
>>> cl.inputs.out_localmax_txt_file = 'stats.txt'
>>> cl.inputs.use_mm = True
>>> cl.cmdline
'cluster --in=zstat1.nii.gz --olmax=stats.txt --thresh=2.3000000000 --mm'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input volume

```

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```

        argument: ``--in=%s``
threshold: (a float)
    threshold for input volume
    argument: ``--thresh=%.10f``

[Optional]
out_index_file: (a boolean or a pathlike object or string
    representing a file)
    output of cluster index (in size order)
    argument: ``--oindex=%s``
out_threshold_file: (a boolean or a pathlike object or string
    representing a file)
    thresholded image
    argument: ``--othresh=%s``
out_localmax_txt_file: (a boolean or a pathlike object or string
    representing a file)
    local maxima text file
    argument: ``--olmax=%s``
out_localmax_vol_file: (a boolean or a pathlike object or string
    representing a file)
    output of local maxima volume
    argument: ``--olmaxim=%s``
out_size_file: (a boolean or a pathlike object or string representing
    a file)
    filename for output of size image
    argument: ``--osize=%s``
out_max_file: (a boolean or a pathlike object or string representing
    a file)
    filename for output of max image
    argument: ``--omax=%s``
out_mean_file: (a boolean or a pathlike object or string representing
    a file)
    filename for output of mean image
    argument: ``--omean=%s``
out_pval_file: (a boolean or a pathlike object or string representing
    a file)
    filename for image output of log pvals
    argument: ``--opvals=%s``
pthreshold: (a float)
    p-threshold for clusters
    argument: ``--pthresh=%.10f``
    requires: dlh, volume
peak_distance: (a float)
    minimum distance between local maxima/minima, in mm (default 0)
    argument: ``--peakdist=%.10f``
cope_file: (a pathlike object or string representing a file)
    cope volume
    argument: ``--cope=%s``
volume: (an integer (int or long))
    number of voxels in the mask
    argument: ``--volume=%d``
dlh: (a float)
    smoothness estimate = sqrt(det(Lambda))
    argument: ``--dlh=%.10f``
fractional: (a boolean, nipy default value: False)
    interprets the threshold as a fraction of the robust range
    argument: ``--fractional``

```

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```

connectivity: (an integer (int or long))
    the connectivity of voxels (default 26)
    argument: ``--connectivity=%d``
use_mm: (a boolean, nipy default value: False)
    use mm, not voxel, coordinates
    argument: ``--mm``
find_min: (a boolean, nipy default value: False)
    find minima instead of maxima
    argument: ``--min``
no_table: (a boolean, nipy default value: False)
    suppresses printing of the table info
    argument: ``--no_table``
minclustersize: (a boolean, nipy default value: False)
    prints out minimum significant cluster size
    argument: ``--minclustersize``
xfm_file: (a pathlike object or string representing a file)
    filename for Linear: input->standard-space transform. Non-linear:
    input->highres transform
    argument: ``--xfm=%s``
std_space_file: (a pathlike object or string representing a file)
    filename for standard-space volume
    argument: ``--stdvol=%s``
num_maxima: (an integer (int or long))
    no of local maxima to report
    argument: ``--num=%d``
warpfield_file: (a pathlike object or string representing a file)
    file containing warpfield
    argument: ``--warpvol=%s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

index_file: (a pathlike object or string representing a file)
    output of cluster index (in size order)
threshold_file: (a pathlike object or string representing a file)
    thresholded image
localmax_txt_file: (a pathlike object or string representing a file)
    local maxima text file
localmax_vol_file: (a pathlike object or string representing a file)
    output of local maxima volume
size_file: (a pathlike object or string representing a file)
    filename for output of size image
max_file: (a pathlike object or string representing a file)
    filename for output of max image
mean_file: (a pathlike object or string representing a file)
    filename for output of mean image
pval_file: (a pathlike object or string representing a file)
    filename for image output of log pvals

```

References:

None

63.6.2 ContrastMgr[Link to code](#)Wraps the executable command `contrast_mgr`.Use FSL `contrast_mgr` command to evaluate contrasts

In interface mode this file assumes that all the required inputs are in the same location. This has deprecated for FSL versions 5.0.7+ as the necessary corrections file is no longer generated by FILMGLS.

Inputs:

```
[Mandatory]
tcon_file: (a pathlike object or string representing an existing
            file)
            contrast file containing T-contrasts
            argument: ``%s``, position: -1
param_estimates: (a list of items which are a pathlike object or
                  string representing an existing file)
                  Parameter estimates for each column of the design matrix
corrections: (a pathlike object or string representing an existing
              file)
              statistical corrections used within FILM modelling
dof_file: (a pathlike object or string representing an existing file)
           degrees of freedom
sigmasquareds: (a pathlike object or string representing an existing
                file)
                summary of residuals, See Woolrich, et. al., 2001

[Optional]
fcon_file: (a pathlike object or string representing an existing
            file)
            contrast file containing F-contrasts
            argument: ``-f %s``
contrast_num: (a long integer >= 1)
               contrast number to start labeling copes from
               argument: ``-cope``
suffix: (a unicode string)
         suffix to put on the end of the cope filename before the contrast
         number, default is nothing
         argument: ``-suffix %s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
copes: (a list of items which are a pathlike object or string
        representing an existing file)
        Contrast estimates for each contrast
```

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```

varcopes: (a list of items which are a pathlike object or string
           representing an existing file)
           Variance estimates for each contrast
zstats: (a list of items which are a pathlike object or string
         representing an existing file)
         z-stat file for each contrast
tstats: (a list of items which are a pathlike object or string
         representing an existing file)
         t-stat file for each contrast
fstats: (a list of items which are a pathlike object or string
         representing an existing file)
         f-stat file for each contrast
zfstats: (a list of items which are a pathlike object or string
          representing an existing file)
          z-stat file for each F contrast
neffs: (a list of items which are a pathlike object or string
        representing an existing file)
        neff file ?? for each contrast

```

References:

None

63.6.3 DualRegression[Link to code](#)Wraps the executable command `dual_regression`.

Wrapper Script for Dual Regression Workflow

Examples

```

>>> dual_regression = DualRegression()
>>> dual_regression.inputs.in_files = ["functional.nii", "functional2.nii",
↪ "functional3.nii"]
>>> dual_regression.inputs.group_IC_maps_4D = "allFA.nii"
>>> dual_regression.inputs.des_norm = False
>>> dual_regression.inputs.one_sample_group_mean = True
>>> dual_regression.inputs.n_perm = 10
>>> dual_regression.inputs.out_dir = "my_output_directory"
>>> dual_regression.cmdline
'dual_regression allFA.nii 0 -1 10 my_output_directory functional.nii functional2.
↪ nii functional3.nii'
>>> dual_regression.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string
          representing an existing file)
          List all subjects' preprocessed, standard-space 4D datasets
          argument: ``%s``, position: -1
group_IC_maps_4D: (a pathlike object or string representing an
                  existing file)
                  4D image containing spatial IC maps (melodic_IC) from the whole-
                  group ICA analysis

```

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```

        argument: ``%s``, position: 1
n_perm: (an integer (int or long))
        Number of permutations for randomise; set to 1 for just raw tstat
        output, set to 0 to not run randomise at all.
        argument: ``%i``, position: 5

[Optional]
des_norm: (a boolean, nipy default value: True)
        Whether to variance-normalise the timecourses used as the stage-2
        regressors; True is default and recommended
        argument: ``%i``, position: 2
one_sample_group_mean: (a boolean)
        perform 1-sample group-mean test instead of generic permutation test
        argument: ``-1``, position: 3
design_file: (a pathlike object or string representing an existing
        file)
        Design matrix for final cross-subject modelling with randomise
        argument: ``%s``, position: 3
con_file: (a pathlike object or string representing an existing file)
        Design contrasts for final cross-subject modelling with randomise
        argument: ``%s``, position: 4
out_dir: (a pathlike object or string representing a directory,
        nipy default value: output)
        This directory will be created to hold all output and logfiles
        argument: ``%s``, position: 6
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
        'NIFTI_PAIR_GZ')
        FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_dir: (a pathlike object or string representing an existing
        directory)

```

References:

None

63.6.4 FEAT[Link to code](#)

Wraps the executable command feat.

Uses FSL feat to calculate first level stats

Inputs:

```

[Mandatory]
fsf_file: (a pathlike object or string representing an existing file)
        File specifying the feat design spec file
        argument: ``%s``, position: 0

```

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```
[Optional]
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

```
feat_dir: (a pathlike object or string representing an existing
           directory)
```

References:

None

63.6.5 FEATModel[Link to code](#)

Wraps the executable command feat_model.

Uses FSL feat_model to generate design.mat files

Inputs:

```
[Mandatory]
fsf_file: (a pathlike object or string representing an existing file)
           File specifying the feat design spec file
           argument: ``%s``, position: 0
ev_files: (a list of items which are a pathlike object or string
           representing an existing file)
           Event spec files generated by level1design
           argument: ``%s``, position: 1

[Optional]
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

```
design_file: (a pathlike object or string representing an existing
             file)
             Mat file containing ascii matrix for design
design_image: (a pathlike object or string representing an existing
              file)
```

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```

    Graphical representation of design matrix
design_cov: (a pathlike object or string representing an existing
            file)
    Graphical representation of design covariance
con_file: (a pathlike object or string representing an existing file)
    Contrast file containing contrast vectors
fcon_file: (a pathlike object or string representing a file)
    Contrast file containing contrast vectors

```

References:

None

63.6.6 FEATRegister[Link to code](#)

Register feat directories to a specific standard

Inputs:

```

[Mandatory]
feat_dirs: (a list of items which are a pathlike object or string
            representing an existing directory)
            Lower level feat dirs
reg_image: (a pathlike object or string representing an existing
            file)
            image to register to (will be treated as standard)

[Optional]
reg_dof: (an integer (int or long), nipy default value: 12)
         registration degrees of freedom

```

Outputs:

```

fsf_file: (a pathlike object or string representing an existing file)
          FSL feat specification file

```

63.6.7 FILMGLS[Link to code](#)

Wraps the executable command film_gls.

Use FSL film_gls command to fit a design matrix to voxel timeseries

Examples

Initialize with no options, assigning them when calling run:

```

>>> from nipy.interfaces import fsl
>>> fgls = fsl.FILMGLS()
>>> res = fgls.run('in_file', 'design_file', 'thresh', rn='stats') #doctest: +SKIP

```

Assign options through the inputs attribute:

```

>>> fgls = fsl.FILMGLS()
>>> fgls.inputs.in_file = 'functional.nii'
>>> fgls.inputs.design_file = 'design.mat'
>>> fgls.inputs.threshold = 10

```

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```
>>> fgls.inputs.results_dir = 'stats'
>>> res = fgls.run() #doctest: +SKIP
```

Specify options when creating an instance:

```
>>> fgls = fsl.FILMGLS(in_file='functional.nii', design_file='design.mat',
↳ threshold=10, results_dir='stats')
>>> res = fgls.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input data file
        argument: ``%s``, position: -3

[Optional]
design_file: (a pathlike object or string representing an existing
            file)
            design matrix file
            argument: ``%s``, position: -2
threshold: (a floating point number >= 0.0, nipy default value:
            1000.0)
            threshold
            argument: ``%f``, position: -1
smooth_autocorr: (a boolean)
                 Smooth auto corr estimates
                 argument: ``-sa``
mask_size: (an integer (int or long))
            susan mask size
            argument: ``-ms %d``
brightness_threshold: (a long integer >= 0)
                      susan brightness threshold, otherwise it is estimated
                      argument: ``-epith %d``
full_data: (a boolean)
            output full data
            argument: ``-v``
autocorr_estimate_only: (a boolean)
                        perform autocorrelation estimation only
                        argument: ``-ac``
                        mutually_exclusive: autocorr_estimate_only, fit_armodel,
                        tukey_window, multitaper_product, use_pava, autocorr_noestimate
fit_armodel: (a boolean)
             fits autoregressive model - default is to use tukey with
             M=sqrt(numvols)
             argument: ``-ar``
             mutually_exclusive: autocorr_estimate_only, fit_armodel,
             tukey_window, multitaper_product, use_pava, autocorr_noestimate
tukey_window: (an integer (int or long))
              tukey window size to estimate autocorr
              argument: ``-tukey %d``
              mutually_exclusive: autocorr_estimate_only, fit_armodel,
              tukey_window, multitaper_product, use_pava, autocorr_noestimate
multitaper_product: (an integer (int or long))
                    multitapering with slepian tapers and num is the time-bandwidth
                    product
                    argument: ``-mt %d``
                    mutually_exclusive: autocorr_estimate_only, fit_armodel,
```

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```

        tukey_window, multitaper_product, use_pava, autocorr_noestimate
use_pava: (a boolean)
    estimates autocorr using PAVA
    argument: ``-pava``
autocorr_noestimate: (a boolean)
    do not estimate autocorrs
    argument: ``-noest``
    mutually_exclusive: autocorr_estimate_only, fit_armodel,
        tukey_window, multitaper_product, use_pava, autocorr_noestimate
output_pwdata: (a boolean)
    output prewhitened data and average design matrix
    argument: ``-output_pwdata``
results_dir: (a pathlike object or string representing a directory,
    nipy default value: results)
    directory to store results in
    argument: ``-rn %s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

param_estimates: (a list of items which are a pathlike object or
    string representing an existing file)
    Parameter estimates for each column of the design matrix
residual4d: (a pathlike object or string representing an existing
    file)
    Model fit residual mean-squared error for each time point
dof_file: (a pathlike object or string representing an existing file)
    degrees of freedom
sigmasquareds: (a pathlike object or string representing an existing
    file)
    summary of residuals, See Woolrich, et. al., 2001
results_dir: (a pathlike object or string representing an existing
    directory)
    directory storing model estimation output
corrections: (a pathlike object or string representing an existing
    file)
    statistical corrections used within FILM modeling
thresholdac: (a pathlike object or string representing an existing
    file)
    The FILM autocorrelation parameters
logfile: (a pathlike object or string representing an existing file)
    FILM run logfile

```

References:

None

63.6.8 FLAMEO

[Link to code](#)

Wraps the executable command flameo.

Use FSL flameo command to perform higher level model fits

Examples

Initialize FLAMEO with no options, assigning them when calling run:

```
>>> from nipy.interfaces import fsl
>>> flameo = fsl.FLAMEO()
>>> flameo.inputs.cope_file = 'cope.nii.gz'
>>> flameo.inputs.var_cope_file = 'varcope.nii.gz'
>>> flameo.inputs.cov_split_file = 'cov_split.mat'
>>> flameo.inputs.design_file = 'design.mat'
>>> flameo.inputs.t_con_file = 'design.con'
>>> flameo.inputs.mask_file = 'mask.nii'
>>> flameo.inputs.run_mode = 'fe'
>>> flameo.cmdline
'flameo --copefile=cope.nii.gz --covsplitfile=cov_split.mat --designfile=design.
↪mat --ld=stats --maskfile=mask.nii --runmode=fe --tcontrastsfile=design.con --
↪varcopefile=varcope.nii.gz'
```

Inputs:

```
[Mandatory]
cope_file: (a pathlike object or string representing an existing
            file)
            cope regressor data file
            argument: ``--copefile=%s``
mask_file: (a pathlike object or string representing an existing
            file)
            mask file
            argument: ``--maskfile=%s``
design_file: (a pathlike object or string representing an existing
            file)
            design matrix file
            argument: ``--designfile=%s``
t_con_file: (a pathlike object or string representing an existing
            file)
            ascii matrix specifying t-contrasts
            argument: ``--tcontrastsfile=%s``
cov_split_file: (a pathlike object or string representing an existing
            file)
            ascii matrix specifying the groups the covariance is split into
            argument: ``--covsplitfile=%s``
run_mode: ('fe' or 'ols' or 'flame1' or 'flame12')
            inference to perform
            argument: ``--runmode=%s``

[Optional]
var_cope_file: (a pathlike object or string representing an existing
            file)
            varcope weightings data file
            argument: ``--varcopefile=%s``
dof_var_cope_file: (a pathlike object or string representing an
            existing file)
            dof data file for varcope data
```

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```

        argument: ``--dofvarcopefile=%s``
f_con_file: (a pathlike object or string representing an existing
            file)
            ascii matrix specifying f-contrasts
            argument: ``--fcontrastsfile=%s``
n_jumps: (an integer (int or long))
            number of jumps made by mcmc
            argument: ``--njumps=%d``
burnin: (an integer (int or long))
            number of jumps at start of mcmc to be discarded
            argument: ``--burnin=%d``
sample_every: (an integer (int or long))
            number of jumps for each sample
            argument: ``--sampleevery=%d``
fix_mean: (a boolean)
            fix mean for tfit
            argument: ``--fixmean``
infer_outliers: (a boolean)
            infer outliers - not for fe
            argument: ``--inferoutliers``
no_pe_outputs: (a boolean)
            do not output pe files
            argument: ``--nopeoutput``
sigma_dofs: (an integer (int or long))
            sigma (in mm) to use for Gaussian smoothing the DOFs in FLAME 2.
            Default is 1mm, -1 indicates no smoothing
            argument: ``--sigma_dofs=%d``
outlier_iter: (an integer (int or long))
            Number of max iterations to use when inferring outliers. Default is
            12.
            argument: ``--ioni=%d``
log_dir: (a pathlike object or string representing a directory,
            nipy default value: stats)
            argument: ``--ld=%s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
            'NIFTI_PAIR_GZ')
            FSL output type
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
            of class 'str' and with values which are a bytes or None or a
            value of class 'str', nipy default value: {})
            Environment variables

```

Outputs:

```

pes: (a list of items which are a pathlike object or string
            representing an existing file)
            Parameter estimates for each column of the design matrix for each
            voxel
res4d: (a list of items which are a pathlike object or string
            representing an existing file)
            Model fit residual mean-squared error for each time point
copes: (a list of items which are a pathlike object or string
            representing an existing file)
            Contrast estimates for each contrast

```

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```

var_copes: (a list of items which are a pathlike object or string
            representing an existing file)
            Variance estimates for each contrast
zstats: (a list of items which are a pathlike object or string
         representing an existing file)
         z-stat file for each contrast
tstats: (a list of items which are a pathlike object or string
         representing an existing file)
         t-stat file for each contrast
zfstats: (a list of items which are a pathlike object or string
          representing an existing file)
          z stat file for each f contrast
fstats: (a list of items which are a pathlike object or string
         representing an existing file)
         f-stat file for each contrast
mrefvars: (a list of items which are a pathlike object or string
           representing an existing file)
           mean random effect variances for each contrast
tdof: (a list of items which are a pathlike object or string
       representing an existing file)
       temporal dof file for each contrast
weights: (a list of items which are a pathlike object or string
          representing an existing file)
          weights file for each contrast
stats_dir: (a pathlike object or string representing a directory)
            directory storing model estimation output

```

References:

None None

63.6.9 GLM[Link to code](#)Wraps the executable command `fsl_glm`.

FSL GLM:

Example

```

>>> import nipy.interfaces.fsl as fsl
>>> glm = fsl.GLM(in_file='functional.nii', design='maps.nii', output_type='NIFTI
↪')
>>> glm.cmdline
'fsl_glm -i functional.nii -d maps.nii -o functional_glm.nii'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file name (text matrix or 3D/4D image file)
         argument: ``-i %s``, position: 1
design: (a pathlike object or string representing an existing file)
        file name of the GLM design matrix (text time courses for temporal
        regression or an image file for spatial regression)
        argument: ``-d %s``, position: 2

```

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```

[Optional]
out_file: (a pathlike object or string representing a file)
    filename for GLM parameter estimates (GLM betas)
    argument: ``-o %s``, position: 3
contrasts: (a pathlike object or string representing an existing
    file)
    matrix of t-statics contrasts
    argument: ``-c %s``
mask: (a pathlike object or string representing an existing file)
    mask image file name if input is image
    argument: ``-m %s``
dof: (an integer (int or long))
    set degrees of freedom explicitly
    argument: ``--dof=%d``
des_norm: (a boolean)
    switch on normalization of the design matrix columns to unit std
    deviation
    argument: ``--des_norm``
dat_norm: (a boolean)
    switch on normalization of the data time series to unit std
    deviation
    argument: ``--dat_norm``
var_norm: (a boolean)
    perform MELODIC variance-normalisation on data
    argument: ``--vn``
demean: (a boolean)
    switch on demeaning of design and data
    argument: ``--demean``
out_cope: (a pathlike object or string representing a file)
    output file name for COPE (either as txt or image)
    argument: ``--out_cope=%s``
out_z_name: (a pathlike object or string representing a file)
    output file name for Z-stats (either as txt or image)
    argument: ``--out_z=%s``
out_t_name: (a pathlike object or string representing a file)
    output file name for t-stats (either as txt or image)
    argument: ``--out_t=%s``
out_p_name: (a pathlike object or string representing a file)
    output file name for p-values of Z-stats (either as text file or
    image)
    argument: ``--out_p=%s``
out_f_name: (a pathlike object or string representing a file)
    output file name for F-value of full model fit
    argument: ``--out_f=%s``
out_pf_name: (a pathlike object or string representing a file)
    output file name for p-value for full model fit
    argument: ``--out_pf=%s``
out_res_name: (a pathlike object or string representing a file)
    output file name for residuals
    argument: ``--out_res=%s``
out_varcb_name: (a pathlike object or string representing a file)
    output file name for variance of COPEs
    argument: ``--out_varcb=%s``
out_sigsq_name: (a pathlike object or string representing a file)
    output file name for residual noise variance sigma-square
    argument: ``--out_sigsq=%s``

```

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```

out_data_name: (a pathlike object or string representing a file)
    output file name for pre-processed data
    argument: ``--out_data=%s``
out_vnscales_name: (a pathlike object or string representing a file)
    output file name for scaling factors for variance normalisation
    argument: ``--out_vnscales=%s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    file name of GLM parameters (if generated)
out_cope: (a list of items which are a pathlike object or string
    representing an existing file)
    output file name for COPEs (either as text file or image)
out_z: (a list of items which are a pathlike object or string
    representing an existing file)
    output file name for COPEs (either as text file or image)
out_t: (a list of items which are a pathlike object or string
    representing an existing file)
    output file name for t-stats (either as text file or image)
out_p: (a list of items which are a pathlike object or string
    representing an existing file)
    output file name for p-values of Z-stats (either as text file or
    image)
out_f: (a list of items which are a pathlike object or string
    representing an existing file)
    output file name for F-value of full model fit
out_pf: (a list of items which are a pathlike object or string
    representing an existing file)
    output file name for p-value for full model fit
out_res: (a list of items which are a pathlike object or string
    representing an existing file)
    output file name for residuals
out_varcb: (a list of items which are a pathlike object or string
    representing an existing file)
    output file name for variance of COPEs
out_sigsq: (a list of items which are a pathlike object or string
    representing an existing file)
    output file name for residual noise variance sigma-square
out_data: (a list of items which are a pathlike object or string
    representing an existing file)
    output file for preprocessed data
out_vnscales: (a list of items which are a pathlike object or string
    representing an existing file)
    output file name for scaling factors for variance normalisation

```

References:

None

63.6.10 L2Model

[Link to code](#)

Generate subject specific second level model

Examples

```
>>> from nipyne.interfaces.fsl import L2Model
>>> model = L2Model(num_copes=3) # 3 sessions
```

Inputs:

```
[Mandatory]
num_copes: (a long integer >= 1)
           number of copes to be combined
```

Outputs:

```
design_mat: (a pathlike object or string representing an existing
            file)
            design matrix file
design_con: (a pathlike object or string representing an existing
            file)
            design contrast file
design_grp: (a pathlike object or string representing an existing
            file)
            design group file
```

63.6.11 Level1Design

[Link to code](#)

Generate FEAT specific files

Examples

```
>>> level1design = Level1Design()
>>> level1design.inputs.interscan_interval = 2.5
>>> level1design.inputs.bases = {'dgamma':{'derivs': False}}
>>> level1design.inputs.session_info = 'session_info.npz'
>>> level1design.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
interscan_interval: (a float)
                   Interscan interval (in secs)
session_info: (any value)
              Session specific information generated by ``modelgen.SpecifyModel``
bases: (a dictionary with keys which are 'dgamma' and with values
       which are a dictionary with keys which are 'derivs' and with
       values which are a boolean or a dictionary with keys which are
       'gamma' and with values which are a dictionary with keys which are
       'derivs' or 'gammasigma' or 'gammadelay' and with values which are
```

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```

any value or a dictionary with keys which are 'custom' and with
values which are a dictionary with keys which are 'bfcustompath'
and with values which are a unicode string or a dictionary with
keys which are 'none' and with values which are a dictionary with
keys which are any value and with values which are any value or a
dictionary with keys which are 'none' and with values which are
None)
name of basis function and options e.g., {'dgamma': {'derivs':
True}}
model_serial_correlations: (a boolean)
    Option to model serial correlations using an autoregressive
    estimator (order 1). Setting this option is only useful in the
    context of the fsf file. If you set this to False, you need to
    repeat this option for FILMGLS by setting autocorr_noestimate to
    True

[Optional]
orthogonalization: (a dictionary with keys which are an integer (int
    or long) and with values which are a dictionary with keys which
    are an integer (int or long) and with values which are a boolean
    or an integer (int or long), nipy default value: {})
    which regressors to make orthogonal e.g., {1: {0:0,1:0,2:0}, 2:
    {0:1,1:1,2:0}} to make the second regressor in a 2-regressor model
    orthogonal to the first.
contrasts: (a list of items which are a tuple of the form: (a unicode
    string, 'T', a list of items which are a unicode string, a list of
    items which are a float) or a tuple of the form: (a unicode
    string, 'T', a list of items which are a unicode string, a list of
    items which are a float, a list of items which are a float) or a
    tuple of the form: (a unicode string, 'F', a list of items which
    are a tuple of the form: (a unicode string, 'T', a list of items
    which are a unicode string, a list of items which are a float) or
    a tuple of the form: (a unicode string, 'T', a list of items which
    are a unicode string, a list of items which are a float, a list of
    items which are a float)))
    List of contrasts with each contrast being a list of the form -
    [('name', 'stat', [condition list], [weight list], [session list])].
    if session list is None or not provided, all sessions are used. For
    F contrasts, the condition list should contain previously defined
    T-contrasts.

```

Outputs:

```

fsf_files: (a list of items which are a pathlike object or string
    representing an existing file)
    FSL feat specification files
ev_files: (a list of items which are a list of items which are a
    pathlike object or string representing an existing file)
    condition information files

```

63.6.12 MELODIC[Link to code](#)Wraps the executable command `melodic`.

Multivariate Exploratory Linear Optimised Decomposition into Independent Components

Examples

```
>>> melodic_setup = MELODIC()
>>> melodic_setup.inputs.approach = 'tica'
>>> melodic_setup.inputs.in_files = ['functional.nii', 'functional2.nii',
↳ 'functional3.nii']
>>> melodic_setup.inputs.no_bet = True
>>> melodic_setup.inputs.bg_threshold = 10
>>> melodic_setup.inputs.tr_sec = 1.5
>>> melodic_setup.inputs.mm_thresh = 0.5
>>> melodic_setup.inputs.out_stats = True
>>> melodic_setup.inputs.t_des = 'timeDesign.mat'
>>> melodic_setup.inputs.t_con = 'timeDesign.con'
>>> melodic_setup.inputs.s_des = 'subjectDesign.mat'
>>> melodic_setup.inputs.s_con = 'subjectDesign.con'
>>> melodic_setup.inputs.out_dir = 'groupICA.out'
>>> melodic_setup.cmdline
'melodic -i functional.nii,functional2.nii,functional3.nii -a tica --
↳ bgthreshold=10.000000 --mmthresh=0.500000 --nobet -o groupICA.out --Ostats --
↳ Scon=subjectDesign.con --Sdes=subjectDesign.mat --Tcon=timeDesign.con --
↳ Tdes=timeDesign.mat --tr=1.500000'
>>> melodic_setup.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
          representing an existing file)
          input file names (either single file name or a list)
          argument: ``-i %s``, position: 0

[Optional]
out_dir: (a pathlike object or string representing a directory)
          output directory name
          argument: ``-o %s``
mask: (a pathlike object or string representing an existing file)
       file name of mask for thresholding
       argument: ``-m %s``
no_mask: (a boolean)
          switch off masking
          argument: ``--nomask``
update_mask: (a boolean)
              switch off mask updating
              argument: ``--update_mask``
no_bet: (a boolean)
         switch off BET
         argument: ``--nobet``
bg_threshold: (a float)
               brain/non-brain threshold used to mask non-brain voxels, as a
               percentage (only if --nobet selected)
               argument: ``--bgthreshold=%f``
dim: (an integer (int or long))
      dimensionality reduction into #num dimensions (default: automatic
      estimation)
      argument: ``-d %d``
dim_est: (a unicode string)
          use specific dim. estimation technique: lap, bic, mdl, aic, mean
          (default: lap)
```

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```

        argument: ``--dimest=%s``
sep_whiten: (a boolean)
    switch on separate whitening
    argument: ``--sep_whiten``
sep_vn: (a boolean)
    switch off joined variance normalization
    argument: ``--sep_vn``
migp: (a boolean)
    switch on MIGP data reduction
    argument: ``--migp``
migpN: (an integer (int or long))
    number of internal Eigenmaps
    argument: ``--migpN %d``
migp_shuffle: (a boolean)
    randomise MIGP file order (default: TRUE)
    argument: ``--migp_shuffle``
migp_factor: (an integer (int or long))
    Internal Factor of mem-threshold relative to number of Eigenmaps
    (default: 2)
    argument: ``--migp_factor %d``
num_ICs: (an integer (int or long))
    number of IC's to extract (for deflation approach)
    argument: ``-n %d``
approach: (a unicode string)
    approach for decomposition, 2D: defl, symm (default), 3D: tica
    (default), concat
    argument: ``-a %s``
non_linearity: (a unicode string)
    nonlinearity: gauss, tanh, pow3, pow4
    argument: ``--nl=%s``
var_norm: (a boolean)
    switch off variance normalization
    argument: ``--vn``
pbsc: (a boolean)
    switch off conversion to percent BOLD signal change
    argument: ``--pbsc``
cov_weight: (a float)
    voxel-wise weights for the covariance matrix (e.g. segmentation
    information)
    argument: ``--covarweight=%f``
epsilon: (a float)
    minimum error change
    argument: ``--eps=%f``
epsilonS: (a float)
    minimum error change for rank-1 approximation in TICA
    argument: ``--epsS=%f``
maxit: (an integer (int or long))
    maximum number of iterations before restart
    argument: ``--maxit=%d``
max_restart: (an integer (int or long))
    maximum number of restarts
    argument: ``--maxrestart=%d``
mm_thresh: (a float)
    threshold for Mixture Model based inference
    argument: ``--mmthresh=%f``
no_mm: (a boolean)
    switch off mixture modelling on IC maps

```

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```

        argument: ``--no_mm``
ICs: (a pathlike object or string representing an existing file)
      filename of the IC components file for mixture modelling
      argument: ``--ICs=%s``
mix: (a pathlike object or string representing an existing file)
     mixing matrix for mixture modelling / filtering
     argument: ``--mix=%s``
smode: (a pathlike object or string representing an existing file)
       matrix of session modes for report generation
       argument: ``--smode=%s``
rem_cmp: (a list of items which are an integer (int or long))
         component numbers to remove
         argument: ``-f %d``
report: (a boolean)
        generate Melodic web report
        argument: ``--report``
bg_image: (a pathlike object or string representing an existing file)
          specify background image for report (default: mean image)
          argument: ``--bgimage=%s``
tr_sec: (a float)
        TR in seconds
        argument: ``--tr=%f``
log_power: (a boolean)
          calculate log of power for frequency spectrum
          argument: ``--logPower``
t_des: (a pathlike object or string representing an existing file)
       design matrix across time-domain
       argument: ``--Tdes=%s``
t_con: (a pathlike object or string representing an existing file)
       t-contrast matrix across time-domain
       argument: ``--Tcon=%s``
s_des: (a pathlike object or string representing an existing file)
       design matrix across subject-domain
       argument: ``--Sdes=%s``
s_con: (a pathlike object or string representing an existing file)
       t-contrast matrix across subject-domain
       argument: ``--Scon=%s``
out_all: (a boolean)
        output everything
        argument: ``--Oall``
out_unmix: (a boolean)
          output unmixing matrix
          argument: ``--Ounmix``
out_stats: (a boolean)
          output thresholded maps and probability maps
          argument: ``--Ostats``
out_pca: (a boolean)
          output PCA results
          argument: ``--Opca``
out_white: (a boolean)
          output whitening/dewhitening matrices
          argument: ``--Owhite``
out_orig: (a boolean)
          output the original ICs
          argument: ``--Oorig``
out_mean: (a boolean)
          output mean volume

```

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```

        argument: ``--Omean``
report_maps: (a unicode string)
    control string for spatial map images (see slicer)
    argument: ``--report_maps=%s``
remove_deriv: (a boolean)
    removes every second entry in paradigm file (EV derivatives)
    argument: ``--remove_deriv``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_dir: (a pathlike object or string representing an existing
    directory)
report_dir: (a pathlike object or string representing an existing
    directory)

```

References:

None

63.6.13 MultipleRegressDesign[Link to code](#)

Generate multiple regression design

Note: FSL does not demean columns for higher level analysis.Please see [FSL documentation](#) for more details on model specification for higher level analysis.**Examples**

```

>>> from nipy.interfaces.fsl import MultipleRegressDesign
>>> model = MultipleRegressDesign()
>>> model.inputs.contrasts = [['group mean', 'T', ['reg1'], [1]]]
>>> model.inputs.regressors = dict(reg1=[1, 1, 1], reg2=[2., -4, 3])
>>> model.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
contrasts: (a list of items which are a tuple of the form: (a unicode
    string, 'T', a list of items which are a unicode string, a list of
    items which are a float) or a tuple of the form: (a unicode
    string, 'F', a list of items which are a tuple of the form: (a
    unicode string, 'T', a list of items which are a unicode string, a
    list of items which are a float)))
    List of contrasts with each contrast being a list of the form -

```

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```
[('name', 'stat', [condition list], [weight list])]. if session list
is None or not provided, all sessions are used. For F contrasts, the
condition list should contain previously defined T-contrasts without
any weight list.
regressors: (a dictionary with keys which are a unicode string and
with values which are a list of items which are a float)
dictionary containing named lists of regressors

[Optional]
groups: (a list of items which are an integer (int or long))
list of group identifiers (defaults to single group)
```

Outputs:

```
design_mat: (a pathlike object or string representing an existing
file)
design matrix file
design_con: (a pathlike object or string representing an existing
file)
design t-contrast file
design_fts: (a pathlike object or string representing an existing
file)
design f-contrast file
design_grp: (a pathlike object or string representing an existing
file)
design group file
```

63.6.14 Randomise[Link to code](#)

Wraps the executable command randomise.

FSL Randomise: feeds the 4D projected FA data into GLM modelling and thresholding in order to find voxels which correlate with your model

Example

```
>>> import nipy.interfaces.fsl as fsl
>>> rand = fsl.Randomise(in_file='allFA.nii', mask = 'mask.nii', tcon='design.con
↪', design_mat='design.mat')
>>> rand.cmdline
'randomise -i allFA.nii -o "randomise" -d design.mat -t design.con -m mask.nii'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
4D input file
argument: ``-i %s``, position: 0

[Optional]
base_name: (a unicode string, nipy default value: randomise)
the rootname that all generated files will have
argument: ``-o "%s"`, position: 1
design_mat: (a pathlike object or string representing an existing
file)
design matrix file
```

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```

        argument: ``-d %s``, position: 2
tcon: (a pathlike object or string representing an existing file)
      t contrasts file
      argument: ``-t %s``, position: 3
fcon: (a pathlike object or string representing an existing file)
      f contrasts file
      argument: ``-f %s``
mask: (a pathlike object or string representing an existing file)
      mask image
      argument: ``-m %s``
x_block_labels: (a pathlike object or string representing an existing
                 file)
                 exchangeability block labels file
                 argument: ``-e %s``
demean: (a boolean)
          demean data temporally before model fitting
          argument: ``-D``
one_sample_group_mean: (a boolean)
                        perform 1-sample group-mean test instead of generic permutation test
                        argument: ``-1``
show_total_perms: (a boolean)
                  print out how many unique permutations would be generated and exit
                  argument: ``-q``
show_info_parallel_mode: (a boolean)
                          print out information required for parallel mode and exit
                          argument: ``-Q``
vox_p_values: (a boolean)
               output voxelwise (corrected and uncorrected) p-value images
               argument: ``-x``
tfce: (a boolean)
       carry out Threshold-Free Cluster Enhancement
       argument: ``-T``
tfce2D: (a boolean)
         carry out Threshold-Free Cluster Enhancement with 2D optimisation
         argument: ``--T2``
f_only: (a boolean)
         calculate f-statistics only
         argument: ``--f_only``
raw_stats_imgs: (a boolean)
                 output raw ( unpermuted ) statistic images
                 argument: ``-R``
p_vec_n_dist_files: (a boolean)
                     output permutation vector and null distribution text files
                     argument: ``-P``
num_perm: (an integer (int or long))
           number of permutations (default 5000, set to 0 for exhaustive)
           argument: ``-n %d``
seed: (an integer (int or long))
       specific integer seed for random number generator
       argument: ``--seed=%d``
var_smooth: (an integer (int or long))
             use variance smoothing (std is in mm)
             argument: ``-v %d``
c_thresh: (a float)
           carry out cluster-based thresholding
           argument: ``-c %.1f``
cm_thresh: (a float)

```

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```

        carry out cluster-mass-based thresholding
        argument: ``-C %.1f``
f_c_thresh: (a float)
        carry out f cluster thresholding
        argument: ``-F %.2f``
f_cm_thresh: (a float)
        carry out f cluster-mass thresholding
        argument: ``-S %.2f``
tfce_H: (a float)
        TFCE height parameter (default=2)
        argument: ``--tfce_H=%.2f``
tfce_E: (a float)
        TFCE extent parameter (default=0.5)
        argument: ``--tfce_E=%.2f``
tfce_C: (a float)
        TFCE connectivity (6 or 26; default=6)
        argument: ``--tfce_C=%.2f``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
        FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

tstat_files: (a list of items which are a pathlike object or string
              representing an existing file)
        t contrast raw statistic
fstat_files: (a list of items which are a pathlike object or string
              representing an existing file)
        f contrast raw statistic
t_p_files: (a list of items which are a pathlike object or string
            representing an existing file)
        f contrast uncorrected p values files
f_p_files: (a list of items which are a pathlike object or string
            representing an existing file)
        f contrast uncorrected p values files
t_corrected_p_files: (a list of items which are a pathlike object or
                     string representing an existing file)
        t contrast FWE (Family-wise error) corrected p values files
f_corrected_p_files: (a list of items which are a pathlike object or
                     string representing an existing file)
        f contrast FWE (Family-wise error) corrected p values files

```

References:

None

63.6.15 SMM[Link to code](#)Wraps the executable command `mm --ld=logdir`.

Spatial Mixture Modelling. For more detail on the spatial mixture modelling see Mixture Models with Adaptive Spatial Regularisation for Segmentation with an Application to FMRI Data; Woolrich, M., Behrens, T., Beckmann, C., and Smith, S.; IEEE Trans. Medical Imaging, 24(1):1-11, 2005.

Inputs:

```
[Mandatory]
spatial_data_file: (a pathlike object or string representing an
                    existing file)
                    statistics spatial map
                    argument: ``--sdf="%s"`, position: 0
mask: (a pathlike object or string representing an existing file)
      mask file
      argument: ``--mask="%s"`, position: 1

[Optional]
no_deactivation_class: (a boolean)
                      enforces no deactivation class
                      argument: ``--zfstatmode`, position: 2
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s`
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
null_p_map: (a pathlike object or string representing an existing
             file)
activation_p_map: (a pathlike object or string representing an
                  existing file)
deactivation_p_map: (a pathlike object or string representing an
                    existing file)
```

References:

None

63.6.16 SmoothEstimate

[Link to code](#)

Wraps the executable command `smoothest`.

Estimates the smoothness of an image

Examples

```
>>> est = SmoothEstimate()
>>> est.inputs.zstat_file = 'zstat1.nii.gz'
>>> est.inputs.mask_file = 'mask.nii'
>>> est.cmdline
'smoothest --mask=mask.nii --zstat=zstat1.nii.gz'
```

Inputs:

```
[Mandatory]
dof: (an integer (int or long))
    number of degrees of freedom
    argument: ``--dof=%d``
    mutually_exclusive: zstat_file
mask_file: (a pathlike object or string representing an existing
    file)
    brain mask volume
    argument: ``--mask=%s``

[Optional]
residual_fit_file: (a pathlike object or string representing an
    existing file)
    residual-fit image file
    argument: ``--res=%s``
    requires: dof
zstat_file: (a pathlike object or string representing an existing
    file)
    zstat image file
    argument: ``--zstat=%s``
    mutually_exclusive: dof
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
dlh: (a float)
    smoothness estimate sqrt(det(Lambda))
volume: (an integer (int or long))
    number of voxels in mask
resels: (a float)
    number of resels
```

References:

None

63.6.17 load_template()

[Link to code](#)

Load a template from the model_templates directory

Parameters

name [str] The name of the file to load

Returns

template : string.Template

63.7 interfaces.fsl.possum

63.7.1 B0Calc

[Link to code](#)

Wraps the executable command `b0calc`.

B0 inhomogeneities occur at interfaces of materials with different magnetic susceptibilities, such as tissue-air interfaces. These differences lead to distortion in the local magnetic field, as Maxwell's equations need to be satisfied. An example of B0 inhomogeneity is the first volume of the 4D volume ``$FSLDIR/data/possum/b0_ppm.nii.gz``.

Examples

```
>>> from nipy.interfaces.fsl import B0Calc
>>> b0calc = B0Calc()
>>> b0calc.inputs.in_file = 'tissue+air_map.nii'
>>> b0calc.inputs.z_b0 = 3.0
>>> b0calc.inputs.output_type = "NIFTI_GZ"
>>> b0calc.cmdline
'b0calc -i tissue+air_map.nii -o tissue+air_map_b0field.nii.gz --chi0=4.000000e-
↪07 -d -9.450000e-06 --extendboundary=1.00 --b0x=0.00 --gx=0.0000 --b0y=0.00 --
↪gy=0.0000 --b0=3.00 --gz=0.0000'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         filename of input image (usually a tissue/air segmentation)
         argument: ``-i %s``, position: 0

[Optional]
out_file: (a pathlike object or string representing a file)
         filename of B0 output volume
         argument: ``-o %s``, position: 1
x_grad: (a float, nipy default value: 0.0)
         Value for zeroth-order x-gradient field (per mm)
         argument: ``--gx=%0.4f``
y_grad: (a float, nipy default value: 0.0)
         Value for zeroth-order y-gradient field (per mm)
         argument: ``--gy=%0.4f``
z_grad: (a float, nipy default value: 0.0)
         Value for zeroth-order z-gradient field (per mm)
         argument: ``--gz=%0.4f``
x_b0: (a float, nipy default value: 0.0)
         Value for zeroth-order b0 field (x-component), in Tesla
         argument: ``--b0x=%0.2f``
         mutually_exclusive: xyz_b0
y_b0: (a float, nipy default value: 0.0)
         Value for zeroth-order b0 field (y-component), in Tesla
         argument: ``--b0y=%0.2f``
         mutually_exclusive: xyz_b0
z_b0: (a float, nipy default value: 1.0)
         Value for zeroth-order b0 field (z-component), in Tesla
         argument: ``--b0=%0.2f``
         mutually_exclusive: xyz_b0
xyz_b0: (a tuple of the form: (a float, a float, a float))
         Zeroth-order B0 field in Tesla
```

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```

        argument: ``--b0x=%0.2f --b0y=%0.2f --b0=%0.2f``
        mutually_exclusive: x_b0, y_b0, z_b0
    delta: (a float, nipy default value: -9.45e-06)
        Delta value (chi_tissue - chi_air)
        argument: ``-d %e``
    chi_air: (a float, nipy default value: 4e-07)
        susceptibility of air
        argument: ``--chi0=%e``
    compute_xyz: (a boolean, nipy default value: False)
        calculate and save all 3 field components (i.e. x,y,z)
        argument: ``--xyz``
    extendboundary: (a float, nipy default value: 1.0)
        Relative proportion to extend voxels at boundary
        argument: ``--extendboundary=%0.2f``
    directconv: (a boolean, nipy default value: False)
        use direct (image space) convolution, not FFT
        argument: ``--directconv``
    output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
        'NIFTI_PAIR_GZ')
        FSL output type
    args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
    environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        filename of B0 output volume

```

References:

None

63.8 interfaces.fsl.preprocess

63.8.1 ApplyWarp

[Link to code](#)

Wraps the executable command applywarp.

FSL's applywarp wrapper to apply the results of a FNIRT registration

Examples

```

>>> from nipy.interfaces import fsl
>>> from nipy.testing import example_data
>>> aw = fsl.ApplyWarp()
>>> aw.inputs.in_file = example_data('structural.nii')
>>> aw.inputs.ref_file = example_data('mni.nii')
>>> aw.inputs.field_file = 'my_coefficients_files.nii' #doctest: +SKIP
>>> res = aw.run() #doctest: +SKIP

```

Inputs:


```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        image to be warped
        argument: ``--in=%s``, position: 0
ref_file: (a pathlike object or string representing an existing file)
        reference image
        argument: ``--ref=%s``, position: 1

[Optional]
out_file: (a pathlike object or string representing a file)
        output filename
        argument: ``--out=%s``, position: 2
field_file: (a pathlike object or string representing an existing
            file)
            file containing warp field
            argument: ``--warp=%s``
abswarp: (a boolean)
        treat warp field as absolute:  $x' = w(x)$ 
        argument: ``--abs``
        mutually_exclusive: relwarp
relwarp: (a boolean)
        treat warp field as relative:  $x' = x + w(x)$ 
        argument: ``--rel``, position: -1
        mutually_exclusive: abswarp
datatype: ('char' or 'short' or 'int' or 'float' or 'double')
        Force output data type [char short int float double].
        argument: ``--datatype=%s``
supersample: (a boolean)
        intermediary supersampling of output, default is off
        argument: ``--super``
superlevel: ('a' or an integer (int or long))
        level of intermediary supersampling, a for 'automatic' or integer
        level. Default = 2
        argument: ``--superlevel=%s``
premat: (a pathlike object or string representing an existing file)
        filename for pre-transform (affine matrix)
        argument: ``--premat=%s``
postmat: (a pathlike object or string representing an existing file)
        filename for post-transform (affine matrix)
        argument: ``--postmat=%s``
mask_file: (a pathlike object or string representing an existing
            file)
            filename for mask image (in reference space)
            argument: ``--mask=%s``
interp: ('nn' or 'trilinear' or 'sinc' or 'spline')
        interpolation method
        argument: ``--interp=%s``, position: -2
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
             'NIFTI_PAIR_GZ')
        FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          Warped output file
```

References:

None

63.8.2 ApplyXFM[Link to code](#)

Wraps the executable command flirt.

Currently just a light wrapper around FLIRT, with no modifications

ApplyXFM is used to apply an existing transform to an image

Examples

```
>>> import nipy.interfaces.fsl as fsl
>>> from nipy.testing import example_data
>>> applyxfm = fsl.preprocess.ApplyXFM()
>>> applyxfm.inputs.in_file = example_data('structural.nii')
>>> applyxfm.inputs.in_matrix_file = example_data('trans.mat')
>>> applyxfm.inputs.out_file = 'newfile.nii'
>>> applyxfm.inputs.reference = example_data('mni.nii')
>>> applyxfm.inputs.apply_xfm = True
>>> result = applyxfm.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file
         argument: ``-in %s``, position: 0
reference: (a pathlike object or string representing an existing
           file)
           reference file
           argument: ``-ref %s``, position: 1

[Optional]
apply_xfm: (a boolean, nipy default value: True)
           apply transformation supplied by in_matrix_file or uses_qform to use
           the affine matrix stored in the reference header
           argument: ``-applyxfm``
out_file: (a pathlike object or string representing a file)
          registered output file
          argument: ``-out %s``, position: 2
out_matrix_file: (a pathlike object or string representing a file)
                 output affine matrix in 4x4 asiii format
                 argument: ``-omat %s``, position: 3
out_log: (a pathlike object or string representing a file)
         output log
         requires: save_log
in_matrix_file: (a pathlike object or string representing a file)
                input 4x4 affine matrix
                argument: ``-init %s``
apply_isoxfm: (a float)
              as applyxfm but forces isotropic resampling
```

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```

        argument: ``-applyisoxfm %f``
        mutually_exclusive: apply_xfm
datatype: ('char' or 'short' or 'int' or 'float' or 'double')
        force output data type
        argument: ``-datatype %s``
cost: ('mutualinfo' or 'corratio' or 'normcorr' or 'normmi' or
       'leastsq' or 'labeldiff' or 'bbr')
        cost function
        argument: ``-cost %s``
cost_func: ('mutualinfo' or 'corratio' or 'normcorr' or 'normmi' or
            'leastsq' or 'labeldiff' or 'bbr')
        cost function
        argument: ``-searchcost %s``
uses_qform: (a boolean)
        initialize using sform or qform
        argument: ``-usesqform``
display_init: (a boolean)
        display initial matrix
        argument: ``-displayinit``
angle_rep: ('quaternion' or 'euler')
        representation of rotation angles
        argument: ``-anglerep %s``
interp: ('trilinear' or 'nearestneighbour' or 'sinc' or 'spline')
        final interpolation method used in reslicing
        argument: ``-interp %s``
sinc_width: (an integer (int or long))
        full-width in voxels
        argument: ``-sincwidth %d``
sinc_window: ('rectangular' or 'hanning' or 'blackman')
        sinc window
        argument: ``-sincwindow %s``
bins: (an integer (int or long))
        number of histogram bins
        argument: ``-bins %d``
dof: (an integer (int or long))
        number of transform degrees of freedom
        argument: ``-dof %d``
no_resample: (a boolean)
        do not change input sampling
        argument: ``-noresample``
force_scaling: (a boolean)
        force rescaling even for low-res images
        argument: ``-forcescaling``
min_sampling: (a float)
        set minimum voxel dimension for sampling
        argument: ``-minsampling %f``
padding_size: (an integer (int or long))
        for applyxfm: interpolates outside image by size
        argument: ``-paddingsize %d``
searchr_x: (a list of from 2 to 2 items which are an integer (int or
            long))
        search angles along x-axis, in degrees
        argument: ``-searchrx %s``
searchr_y: (a list of from 2 to 2 items which are an integer (int or
            long))
        search angles along y-axis, in degrees
        argument: ``-searchry %s``

```

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```

searchr_z: (a list of from 2 to 2 items which are an integer (int or
            long))
            search angles along z-axis, in degrees
            argument: ``-searchrz %s``
no_search: (a boolean)
            set all angular searches to ranges 0 to 0
            argument: ``-nosearch``
coarse_search: (an integer (int or long))
            coarse search delta angle
            argument: ``-coarsesearch %d``
fine_search: (an integer (int or long))
            fine search delta angle
            argument: ``-finesearch %d``
schedule: (a pathlike object or string representing an existing file)
            replaces default schedule
            argument: ``-schedule %s``
ref_weight: (a pathlike object or string representing an existing
            file)
            File for reference weighting volume
            argument: ``-refweight %s``
in_weight: (a pathlike object or string representing an existing
            file)
            File for input weighting volume
            argument: ``-inweight %s``
no_clamp: (a boolean)
            do not use intensity clamping
            argument: ``-noclamp``
no_resample_blur: (a boolean)
            do not use blurring on downsampling
            argument: ``-noresampblur``
rigid2D: (a boolean)
            use 2D rigid body mode - ignores dof
            argument: ``-2D``
save_log: (a boolean)
            save to log file
verbose: (an integer (int or long))
            verbose mode, 0 is least
            argument: ``-verbose %d``
bgvalue: (a float)
            use specified background value for points outside FOV
            argument: ``-setbackground %f``
wm_seg: (a pathlike object or string representing a file)
            white matter segmentation volume needed by BBR cost function
            argument: ``-wmseg %s``
wmcoords: (a pathlike object or string representing a file)
            white matter boundary coordinates for BBR cost function
            argument: ``-wmcoords %s``
wmnorms: (a pathlike object or string representing a file)
            white matter boundary normals for BBR cost function
            argument: ``-wmnorms %s``
fieldmap: (a pathlike object or string representing a file)
            fieldmap image in rads/s - must be already registered to the
            reference image
            argument: ``-fieldmap %s``
fieldmapmask: (a pathlike object or string representing a file)
            mask for fieldmap image
            argument: ``-fieldmapmask %s``

```

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```

pedir: (an integer (int or long))
    phase encode direction of EPI - 1/2/3=x/y/z & -1/-2/-3=-x/-y/-z
    argument: ``-pedir %d``
echospacing: (a float)
    value of EPI echo spacing - units of seconds
    argument: ``-echospacing %f``
bbrtype: ('signed' or 'global_abs' or 'local_abs')
    type of bbr cost function: signed [default], global_abs, local_abs
    argument: ``-bbrtype %s``
bbrslope: (a float)
    value of bbr slope
    argument: ``-bbrslope %f``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyype default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    path/name of registered file (if generated)
out_matrix_file: (a pathlike object or string representing an
    existing file)
    path/name of calculated affine transform (if generated)
out_log: (a pathlike object or string representing a file)
    path/name of output log (if generated)

```

References:

None

63.8.3 BET[Link to code](#)

Wraps the executable command bet.

FSL BET wrapper for skull stripping

For complete details, see the [BET Documentation](#).**Examples**

```

>>> from nipyype.interfaces import fsl
>>> btr = fsl.BET()
>>> btr.inputs.in_file = 'structural.nii'
>>> btr.inputs.frac = 0.7
>>> btr.inputs.out_file = 'brain_anat.nii'
>>> btr.cmdline
'bet structural.nii brain_anat.nii -f 0.70'
>>> res = btr.run() # doctest: +SKIP

```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to skull strip
         argument: ``%s``, position: 0

[Optional]
out_file: (a pathlike object or string representing a file)
         name of output skull stripped image
         argument: ``%s``, position: 1
outline: (a boolean)
         create surface outline image
         argument: ``-o``
mask: (a boolean)
      create binary mask image
      argument: ``-m``
skull: (a boolean)
      create skull image
      argument: ``-s``
no_output: (a boolean)
          Don't generate segmented output
          argument: ``-n``
frac: (a float)
      fractional intensity threshold
      argument: ``-f %.2f``
vertical_gradient: (a float)
                  vertical gradient in fractional intensity threshold (-1, 1)
                  argument: ``-g %.2f``
radius: (an integer (int or long))
        head radius
        argument: ``-r %d``
center: (a list of at most 3 items which are an integer (int or
        long))
        center of gravity in voxels
        argument: ``-c %s``
threshold: (a boolean)
          apply thresholding to segmented brain image and mask
          argument: ``-t``
mesh: (a boolean)
      generate a vtk mesh brain surface
      argument: ``-e``
robust: (a boolean)
      robust brain centre estimation (iterates BET several times)
      argument: ``-R``
      mutually_exclusive: functional, reduce_bias, robust, padding,
                          remove_eyes, surfaces, t2_guided
padding: (a boolean)
      improve BET if FOV is very small in Z (by temporarily padding end
      slices)
      argument: ``-Z``
      mutually_exclusive: functional, reduce_bias, robust, padding,
                          remove_eyes, surfaces, t2_guided
remove_eyes: (a boolean)
            eye & optic nerve cleanup (can be useful in SIENA)
            argument: ``-S``
            mutually_exclusive: functional, reduce_bias, robust, padding,
                                remove_eyes, surfaces, t2_guided
surfaces: (a boolean)
```

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```

run bet2 and then betsurf to get additional skull and scalp surfaces
(includes registrations)
argument: ``-A``
mutually_exclusive: functional, reduce_bias, robust, padding,
    remove_eyes, surfaces, t2_guided
t2_guided: (a pathlike object or string representing a file)
    as with creating surfaces, when also feeding in non-brain-extracted
    T2 (includes registrations)
argument: ``-A2 %s``
mutually_exclusive: functional, reduce_bias, robust, padding,
    remove_eyes, surfaces, t2_guided
functional: (a boolean)
    apply to 4D fMRI data
argument: ``-F``
mutually_exclusive: functional, reduce_bias, robust, padding,
    remove_eyes, surfaces, t2_guided
reduce_bias: (a boolean)
    bias field and neck cleanup
argument: ``-B``
mutually_exclusive: functional, reduce_bias, robust, padding,
    remove_eyes, surfaces, t2_guided
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    path/name of skullstripped file (if generated)
mask_file: (a pathlike object or string representing a file)
    path/name of binary brain mask (if generated)
outline_file: (a pathlike object or string representing a file)
    path/name of outline file (if generated)
meshfile: (a pathlike object or string representing a file)
    path/name of vtk mesh file (if generated)
inskull_mask_file: (a pathlike object or string representing a file)
    path/name of inskull mask (if generated)
inskull_mesh_file: (a pathlike object or string representing a file)
    path/name of inskull mesh outline (if generated)
outskull_mask_file: (a pathlike object or string representing a file)
    path/name of outskull mask (if generated)
outskull_mesh_file: (a pathlike object or string representing a file)
    path/name of outskull mesh outline (if generated)
outskin_mask_file: (a pathlike object or string representing a file)
    path/name of outskin mask (if generated)
outskin_mesh_file: (a pathlike object or string representing a file)
    path/name of outskin mesh outline (if generated)
skull_mask_file: (a pathlike object or string representing a file)
    path/name of skull mask (if generated)

```

References:

None

63.8.4 FAST[Link to code](#)

Wraps the executable command fast.

FSL FAST wrapper for segmentation and bias correction

For complete details, see the [FAST Documenta  on](#).**Examples**

```
>>> from nipy.interfaces import fsl
>>> fastr = fsl.FAST()
>>> fastr.inputs.in_files = 'structural.nii'
>>> fastr.inputs.out_basename = 'fast_'
>>> fastr.cmdline
'fast -o fast_ -S 1 structural.nii'
>>> out = fastr.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
           representing an existing file)
           image, or multi-channel set of images, to be segmented
           argument: ``%s``, position: -1

[Optional]
out_basename: (a pathlike object or string representing a file)
               base name of output files
               argument: ``-o %s``
number_classes: (1 <= a long integer <= 10)
                 number of tissue-type classes
                 argument: ``-n %d``
output_biasfield: (a boolean)
                  output estimated bias field
                  argument: ``-b``
output_biascorrected: (a boolean)
                      output restored image (bias-corrected image)
                      argument: ``-B``
img_type: (1 or 2 or 3)
           int specifying type of image: (1 = T1, 2 = T2, 3 = PD)
           argument: ``-t %d``
bias_iters: (1 <= a long integer <= 10)
             number of main-loop iterations during bias-field removal
             argument: ``-I %d``
bias_lowpass: (4 <= a long integer <= 40)
              bias field smoothing extent (FWHM) in mm
              argument: ``-l %d``
init_seg_smooth: (0.0001 <= a floating point number <= 0.1)
                  initial segmentation spatial smoothness (during bias field
                  estimation)
                  argument: ``-f %.3f``
segments: (a boolean)
           outputs a separate binary image for each tissue type
```

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```

        argument: ``-g``
init_transform: (a pathlike object or string representing an existing
                 file)
                 <standard2input.mat> initialise using priors
                 argument: ``-a %s``
other_priors: (a list of from 3 to 3 items which are a pathlike
              object or string representing a file)
              alternative prior images
              argument: ``-A %s``
no_pve: (a boolean)
        turn off PVE (partial volume estimation)
        argument: ``--nopve``
no_bias: (a boolean)
        do not remove bias field
        argument: ``-N``
use_priors: (a boolean)
        use priors throughout
        argument: ``-P``
segment_iters: (1 <= a long integer <= 50)
               number of segmentation-initialisation iterations
               argument: ``-W %d``
mixel_smooth: (0.0 <= a floating point number <= 1.0)
              spatial smoothness for mixeltype
              argument: ``-R %.2f``
iters_afterbias: (1 <= a long integer <= 20)
                number of main-loop iterations after bias-field removal
                argument: ``-O %d``
hyper: (0.0 <= a floating point number <= 1.0)
       segmentation spatial smoothness
       argument: ``-H %.2f``
verbose: (a boolean)
        switch on diagnostic messages
        argument: ``-v``
manual_seg: (a pathlike object or string representing an existing
            file)
            Filename containing intensities
            argument: ``-s %s``
probability_maps: (a boolean)
                 outputs individual probability maps
                 argument: ``-p``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
             'NIFTI_PAIR_GZ')
             FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipype default value: {})
         Environment variables

```

Outputs:

```

tissue_class_map: (a pathlike object or string representing an
                  existing file)
                  path/name of binary segmented volume file one val for each class
                  _seg

```

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```
tissue_class_files: (a list of items which are a pathlike object or
    string representing a file)
restored_image: (a list of items which are a pathlike object or
    string representing a file)
mixeltype: (a pathlike object or string representing a file)
    path/name of mixeltype volume file _mixeltype
partial_volume_map: (a pathlike object or string representing a file)
    path/name of partial volume file _pveseg
partial_volume_files: (a list of items which are a pathlike object or
    string representing a file)
bias_field: (a list of items which are a pathlike object or string
    representing a file)
probability_maps: (a list of items which are a pathlike object or
    string representing a file)
```

References:

None

63.8.5 FIRST[Link to code](#)Wraps the executable command `run_first_all`.FSL `run_first_all` wrapper for segmentation of subcortical volumes<http://www.fmrib.ox.ac.uk/fsl/first/index.html>**Examples**

```
>>> from nipy.interfaces import fsl
>>> first = fsl.FIRST()
>>> first.inputs.in_file = 'structural.nii'
>>> first.inputs.out_file = 'segmented.nii'
>>> res = first.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    input data file
    argument: ``-i %s``, position: -2
out_file: (a pathlike object or string representing a file, nipy
    default value: segmented)
    output data file
    argument: ``-o %s``, position: -1

[Optional]
verbose: (a boolean)
    Use verbose logging.
    argument: ``-v``, position: 1
brain_extracted: (a boolean)
    Input structural image is already brain-extracted
    argument: ``-b``, position: 2
no_cleanup: (a boolean)
    Input structural image is already brain-extracted
    argument: ``-d``, position: 3
```

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```

method: ('auto' or 'fast' or 'none', nipyre default value: auto)
    Method must be one of auto, fast, none, or it can be entered using
    the 'method_as_numerical_threshold' input
    argument: ``-m %s``, position: 4
    mutually_exclusive: method_as_numerical_threshold
method_as_numerical_threshold: (a float)
    Specify a numerical threshold value or use the 'method' input to
    choose auto, fast, or none
    argument: ``-m %.4f``, position: 4
list_of_specific_structures: (a list of at least 1 items which are a
    unicode string)
    Runs only on the specified structures (e.g. L_Hipp, R_HippL_Accu,
    R_Accu, L_Amyg, R_AmygL_Caud, R_Caud, L_Pall, R_PallL_Puta, R_Puta,
    L_Thal, R_Thal, BrStem
    argument: ``-s %s``, position: 5
affine_file: (a pathlike object or string representing an existing
    file)
    Affine matrix to use (e.g. img2std.mat) (does not re-run
    registration)
    argument: ``-a %s``, position: 6
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyre default value: {})
    Environment variables

```

Outputs:

```

vtk_surfaces: (a list of items which are a pathlike object or string
    representing an existing file)
    VTK format meshes for each subcortical region
bvars: (a list of items which are a pathlike object or string
    representing an existing file)
    bvars for each subcortical region
original_segmentations: (a pathlike object or string representing an
    existing file)
    3D image file containing the segmented regions as integer values.
    Uses CMA labelling
segmentation_file: (a pathlike object or string representing an
    existing file)
    4D image file containing a single volume per segmented region

```

References:

None

63.8.6 FLIRT[Link to code](#)

Wraps the executable command flirt.

FSL FLIRT wrapper for coregistration

For complete details, see the [FLIRT Documentation](#).

To print out the command line help, use: `fsl.FLIRT().inputs_help()`

Examples

```
>>> from nipyype.interfaces import fsl
>>> from nipyype.testing import example_data
>>> flt = fsl.FLIRT(bins=640, cost_func='mutualinfo')
>>> flt.inputs.in_file = 'structural.nii'
>>> flt.inputs.reference = 'mni.nii'
>>> flt.inputs.output_type = "NIFTI_GZ"
>>> flt.cmdline # doctest: +ELLIPSIS
'flirt -in structural.nii -ref mni.nii -out structural_flirt.nii.gz -omat_
↳ structural_flirt.mat -bins 640 -searchcost mutualinfo'
>>> res = flt.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file
         argument: ``-in %s``, position: 0
reference: (a pathlike object or string representing an existing
           file)
           reference file
           argument: ``-ref %s``, position: 1

[Optional]
out_file: (a pathlike object or string representing a file)
          registered output file
          argument: ``-out %s``, position: 2
out_matrix_file: (a pathlike object or string representing a file)
                 output affine matrix in 4x4 asciiii format
                 argument: ``-omat %s``, position: 3
out_log: (a pathlike object or string representing a file)
          output log
          requires: save_log
in_matrix_file: (a pathlike object or string representing a file)
                 input 4x4 affine matrix
                 argument: ``-init %s``
apply_xfm: (a boolean)
            apply transformation supplied by in_matrix_file or uses_qform to use
            the affine matrix stored in the reference header
            argument: ``-applyxfm``
apply_isoxfm: (a float)
              as applyxfm but forces isotropic resampling
              argument: ``-applyisoxfm %f``
              mutually_exclusive: apply_xfm
datatype: ('char' or 'short' or 'int' or 'float' or 'double')
           force output data type
           argument: ``-datatype %s``
cost: ('mutualinfo' or 'corratio' or 'normcorr' or 'normmi' or
       'leastsq' or 'labeldiff' or 'bbr')
      cost function
      argument: ``-cost %s``
cost_func: ('mutualinfo' or 'corratio' or 'normcorr' or 'normmi' or
            'leastsq' or 'labeldiff' or 'bbr')
           cost function
           argument: ``-searchcost %s``
```

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```

uses_qform: (a boolean)
    initialize using sform or qform
    argument: ``-usesqform``
display_init: (a boolean)
    display initial matrix
    argument: ``-displayinit``
angle_rep: ('quaternion' or 'euler')
    representation of rotation angles
    argument: ``-anglerep %s``
interp: ('trilinear' or 'nearestneighbour' or 'sinc' or 'spline')
    final interpolation method used in reslicing
    argument: ``-interp %s``
sinc_width: (an integer (int or long))
    full-width in voxels
    argument: ``-sincwidth %d``
sinc_window: ('rectangular' or 'hanning' or 'blackman')
    sinc window
    argument: ``-sincwindow %s``
bins: (an integer (int or long))
    number of histogram bins
    argument: ``-bins %d``
dof: (an integer (int or long))
    number of transform degrees of freedom
    argument: ``-dof %d``
no_resample: (a boolean)
    do not change input sampling
    argument: ``-noresample``
force_scaling: (a boolean)
    force rescaling even for low-res images
    argument: ``-forcescaling``
min_sampling: (a float)
    set minimum voxel dimension for sampling
    argument: ``-minsampling %f``
padding_size: (an integer (int or long))
    for applyxfm: interpolates outside image by size
    argument: ``-paddingsize %d``
searchr_x: (a list of from 2 to 2 items which are an integer (int or
    long))
    search angles along x-axis, in degrees
    argument: ``-searchrx %s``
searchr_y: (a list of from 2 to 2 items which are an integer (int or
    long))
    search angles along y-axis, in degrees
    argument: ``-searchry %s``
searchr_z: (a list of from 2 to 2 items which are an integer (int or
    long))
    search angles along z-axis, in degrees
    argument: ``-searchrz %s``
no_search: (a boolean)
    set all angular searches to ranges 0 to 0
    argument: ``-nosearch``
coarse_search: (an integer (int or long))
    coarse search delta angle
    argument: ``-coarsesearch %d``
fine_search: (an integer (int or long))
    fine search delta angle
    argument: ``-finesearch %d``

```

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```

schedule: (a pathlike object or string representing an existing file)
    replaces default schedule
    argument: ``-schedule %s``
ref_weight: (a pathlike object or string representing an existing
    file)
    File for reference weighting volume
    argument: ``-refweight %s``
in_weight: (a pathlike object or string representing an existing
    file)
    File for input weighting volume
    argument: ``-inweight %s``
no_clamp: (a boolean)
    do not use intensity clamping
    argument: ``-noclamp``
no_resample_blur: (a boolean)
    do not use blurring on downsampling
    argument: ``-noresampblur``
rigid2D: (a boolean)
    use 2D rigid body mode - ignores dof
    argument: ``-2D``
save_log: (a boolean)
    save to log file
verbose: (an integer (int or long))
    verbose mode, 0 is least
    argument: ``-verbose %d``
bgvalue: (a float)
    use specified background value for points outside FOV
    argument: ``-setbackground %f``
wm_seg: (a pathlike object or string representing a file)
    white matter segmentation volume needed by BBR cost function
    argument: ``-wmseg %s``
wmcoords: (a pathlike object or string representing a file)
    white matter boundary coordinates for BBR cost function
    argument: ``-wmcoords %s``
wmnorms: (a pathlike object or string representing a file)
    white matter boundary normals for BBR cost function
    argument: ``-wmnorms %s``
fieldmap: (a pathlike object or string representing a file)
    fieldmap image in rads/s - must be already registered to the
    reference image
    argument: ``-fieldmap %s``
fieldmapmask: (a pathlike object or string representing a file)
    mask for fieldmap image
    argument: ``-fieldmapmask %s``
pedir: (an integer (int or long))
    phase encode direction of EPI - 1/2/3=x/y/z & -1/-2/-3=-x/-y/-z
    argument: ``-pedir %d``
echospacing: (a float)
    value of EPI echo spacing - units of seconds
    argument: ``-echospacing %f``
bbrtype: ('signed' or 'global_abs' or 'local_abs')
    type of bbr cost function: signed [default], global_abs, local_abs
    argument: ``-bbrtype %s``
bbrslope: (a float)
    value of bbr slope
    argument: ``-bbrslope %f``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or

```

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```

        'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    path/name of registered file (if generated)
out_matrix_file: (a pathlike object or string representing an
    existing file)
    path/name of calculated affine transform (if generated)
out_log: (a pathlike object or string representing a file)
    path/name of output log (if generated)

```

References:

None

63.8.7 FNIRT[Link to code](#)

Wraps the executable command fnirt.

FSL FNIRT wrapper for non-linear registration

For complete details, see the [FNIRT Documentation](#).**Examples**

```

>>> from nipyne.interfaces import fsl
>>> from nipyne.testing import example_data
>>> fnt = fsl.FNIRT(affine_file=example_data('trans.mat'))
>>> res = fnt.run(ref_file=example_data('mni.nii', in_file=example_data(
↪ 'structural.nii')) #doctest: +SKIP

```

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```

>>> from nipyne.interfaces import fsl
>>> fnirt_mprage = fsl.FNIRT()
>>> fnirt_mprage.inputs.in_fwhm = [8, 4, 2, 2]
>>> fnirt_mprage.inputs.subsampling_scheme = [4, 2, 1, 1]

```

Specify the resolution of the warps

```

>>> fnirt_mprage.inputs.warp_resolution = (6, 6, 6)
>>> res = fnirt_mprage.run(in_file='structural.nii', ref_file='mni.nii', warped_
↪ file='warped.nii', fieldcoeff_file='fieldcoeff.nii') #doctest: +SKIP

```

We can check the command line and confirm that it's what we expect.

```

>>> fnirt_mprage.cmdline #doctest: +SKIP
'fnirt --cout=fieldcoeff.nii --in=structural.nii --in_fwhm=8,4,2,2 --ref=mni.nii --
↪ subsamp=4,2,1,1 --warpres=6,6,6 --iout=warped.nii'

```

Inputs:

```
[Mandatory]
ref_file: (a pathlike object or string representing an existing file)
    name of reference image
    argument: ``--ref=%s``
in_file: (a pathlike object or string representing an existing file)
    name of input image
    argument: ``--in=%s``

[Optional]
affine_file: (a pathlike object or string representing an existing
    file)
    name of file containing affine transform
    argument: ``--aff=%s``
inwarp_file: (a pathlike object or string representing an existing
    file)
    name of file containing initial non-linear warps
    argument: ``--inwarp=%s``
in_intensitymap_file: (a list of from 1 to 2 items which are a
    pathlike object or string representing an existing file)
    name of file/files containing initial intensity mapping usually
    generated by previous fnirt run
    argument: ``--intin=%s``
fieldcoeff_file: (a boolean or a pathlike object or string
    representing a file)
    name of output file with field coefficients or true
    argument: ``--cout=%s``
warped_file: (a pathlike object or string representing a file)
    name of output image
    argument: ``--iout=%s``
field_file: (a boolean or a pathlike object or string representing a
    file)
    name of output file with field or true
    argument: ``--fout=%s``
jacobian_file: (a boolean or a pathlike object or string representing
    a file)
    name of file for writing out the Jacobian of the field (for
    diagnostic or VBM purposes)
    argument: ``--jout=%s``
modulatedref_file: (a boolean or a pathlike object or string
    representing a file)
    name of file for writing out intensity modulated --ref (for
    diagnostic purposes)
    argument: ``--refout=%s``
out_intensitymap_file: (a boolean or a pathlike object or string
    representing a file)
    name of files for writing information pertaining to intensity
    mapping
    argument: ``--intout=%s``
log_file: (a pathlike object or string representing a file)
    Name of log-file
    argument: ``--logout=%s``
config_file: ('T1_2_MNI152_2mm' or 'FA_2_FMRIB58_1mm' or a pathlike
    object or string representing an existing file)
    Name of config file specifying command line arguments
    argument: ``--config=%s``
refmask_file: (a pathlike object or string representing an existing
```

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```

    file)
    name of file with mask in reference space
    argument: ``--refmask=%s``
inmask_file: (a pathlike object or string representing an existing
    file)
    name of file with mask in input image space
    argument: ``--inmask=%s``
skip_refmask: (a boolean)
    Skip specified refmask if set, default false
    argument: ``--applyrefmask=0``
    mutually_exclusive: apply_refmask
skip_inmask: (a boolean)
    skip specified inmask if set, default false
    argument: ``--applyinmask=0``
    mutually_exclusive: apply_inmask
apply_refmask: (a list of items which are 0 or 1)
    list of iterations to use reference mask on (1 to use, 0 to skip)
    argument: ``--applyrefmask=%s``
    mutually_exclusive: skip_refmask
apply_inmask: (a list of items which are 0 or 1)
    list of iterations to use input mask on (1 to use, 0 to skip)
    argument: ``--applyinmask=%s``
    mutually_exclusive: skip_inmask
skip_implicit_ref_masking: (a boolean)
    skip implicit masking based on value in --ref image. Default = 0
    argument: ``--imprefm=0``
skip_implicit_in_masking: (a boolean)
    skip implicit masking based on value in --in image. Default = 0
    argument: ``--impinm=0``
refmask_val: (a float)
    Value to mask out in --ref image. Default =0.0
    argument: ``--imprefval=%f``
inmask_val: (a float)
    Value to mask out in --in image. Default =0.0
    argument: ``--impinval=%f``
max_nonlin_iter: (a list of items which are an integer (int or long))
    Max # of non-linear iterations list, default [5, 5, 5, 5]
    argument: ``--miter=%s``
subsampling_scheme: (a list of items which are an integer (int or
    long))
    sub-sampling scheme, list, default [4, 2, 1, 1]
    argument: ``--subsamp=%s``
warp_resolution: (a tuple of the form: (an integer (int or long), an
    integer (int or long), an integer (int or long)))
    (approximate) resolution (in mm) of warp basis in x-, y- and
    z-direction, default 10, 10, 10
    argument: ``--warpres=%d,%d,%d``
spline_order: (an integer (int or long))
    Order of spline, 2->Quadratic spline, 3->Cubic spline. Default=3
    argument: ``--splineorder=%d``
in_fwhm: (a list of items which are an integer (int or long))
    FWHM (in mm) of gaussian smoothing kernel for input volume, default
    [6, 4, 2, 2]
    argument: ``--infwhm=%s``
ref_fwhm: (a list of items which are an integer (int or long))
    FWHM (in mm) of gaussian smoothing kernel for ref volume, default
    [4, 2, 0, 0]

```

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```

        argument: ``--reffwhm=%s``
regularization_model: ('membrane_energy' or 'bending_energy')
    Model for regularisation of warp-field [membrane_energy
    bending_energy], default bending_energy
    argument: ``--regmod=%s``
regularization_lambda: (a list of items which are a float)
    Weight of regularisation, default depending on --ssqlambda and
    --regmod switches. See user documetation.
    argument: ``--lambda=%s``
skip_lambda_ssq: (a boolean)
    If true, lambda is not weighted by current ssq, default false
    argument: ``--ssqlambda=0``
jacobian_range: (a tuple of the form: (a float, a float))
    Allowed range of Jacobian determinants, default 0.01, 100.0
    argument: ``--jacrange=%f,%f``
derive_from_ref: (a boolean)
    If true, ref image is used to calculate derivatives. Default false
    argument: ``--refderiv``
intensity_mapping_model: ('none' or 'global_linear' or
    'global_non_linear' or 'local_linear' or
    'global_non_linear_with_bias' or 'local_non_linear')
    Model for intensity-mapping
    argument: ``--intmod=%s``
intensity_mapping_order: (an integer (int or long))
    Order of poynomial for mapping intensities, default 5
    argument: ``--intorder=%d``
biasfield_resolution: (a tuple of the form: (an integer (int or
    long), an integer (int or long), an integer (int or long)))
    Resolution (in mm) of bias-field modelling local intensities,
    default 50, 50, 50
    argument: ``--biasres=%d,%d,%d``
bias_regularization_lambda: (a float)
    Weight of regularisation for bias-field, default 10000
    argument: ``--biaslambda=%f``
skip_intensity_mapping: (a boolean)
    Skip estimate intensity-mapping default false
    argument: ``--estint=0``
    mutually_exclusive: apply_intensity_mapping
apply_intensity_mapping: (a list of items which are 0 or 1)
    List of subsampling levels to apply intensity mapping for (0 to
    skip, 1 to apply)
    argument: ``--estint=%s``
    mutually_exclusive: skip_intensity_mapping
hessian_precision: ('double' or 'float')
    Precision for representing Hessian, double or float. Default double
    argument: ``--numprec=%s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

fieldcoeff_file: (a pathlike object or string representing an
                  existing file)
                  file with field coefficients
warped_file: (a pathlike object or string representing an existing
              file)
              warped image
field_file: (a pathlike object or string representing a file)
            file with warp field
jacobian_file: (a pathlike object or string representing a file)
               file containing Jacobian of the field
modulatedref_file: (a pathlike object or string representing a file)
                   file containing intensity modulated --ref
out_intensitymap_file: (a list of from 2 to 2 items which are a
                       pathlike object or string representing a file)
                       files containing info pertaining to intensity mapping
log_file: (a pathlike object or string representing a file)
          Name of log-file

```

References:

None

63.8.8 FUGUE

[Link to code](#)

Wraps the executable command `fugue`.

FSL FUGUE set of tools for EPI distortion correction

FUGUE is, most generally, a set of tools for EPI distortion correction.

Distortions may be corrected for

1. improving registration with non-distorted images (e.g. structurals), or
2. dealing with motion-dependent changes.

FUGUE is designed to deal only with the first case - improving registration.

Examples

Unwarping an input image (shift map is known):

```

>>> from nipy.interfaces.fsl.preprocess import FUGUE
>>> fugue = FUGUE()
>>> fugue.inputs.in_file = 'epi.nii'
>>> fugue.inputs.mask_file = 'epi_mask.nii'
>>> fugue.inputs.shift_in_file = 'vsm.nii' # Previously computed with fugue as_
↪well
>>> fugue.inputs.unwarp_direction = 'y'
>>> fugue.inputs.output_type = "NIFTI_GZ"
>>> fugue.cmdline # doctest: +ELLIPSIS
'fugue --in=epi.nii --mask=epi_mask.nii --loadshift=vsm.nii --unwarmdir=y --
↪unwarp=epi_unwarped.nii.gz'
>>> fugue.run() #doctest: +SKIP

```

Warping an input image (shift map is known):

```

>>> from nipy.interfaces.fsl.preprocess import FUGUE
>>> fugue = FUGUE()
>>> fugue.inputs.in_file = 'epi.nii'
>>> fugue.inputs.forward_warping = True
>>> fugue.inputs.mask_file = 'epi_mask.nii'

```

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```
>>> fugue.inputs.shift_in_file = 'vsm.nii' # Previously computed with fugue as
↳well
>>> fugue.inputs.unwarp_direction = 'y'
>>> fugue.inputs.output_type = "NIFTI_GZ"
>>> fugue.cmdline # doctest: +ELLIPSIS
'fugue --in=epi.nii --mask=epi_mask.nii --loadshift=vsm.nii --unwarmdir=y --
↳warp=epi_warped.nii.gz'
>>> fugue.run() #doctest: +SKIP
```

Computing the vsm (unwrapped phase map is known):

```
>>> from nipy.interfaces.fsl.preprocess import FUGUE
>>> fugue = FUGUE()
>>> fugue.inputs.phasemap_in_file = 'epi_phasediff.nii'
>>> fugue.inputs.mask_file = 'epi_mask.nii'
>>> fugue.inputs.dwell_to_asym_ratio = (0.77e-3 * 3) / 2.46e-3
>>> fugue.inputs.unwarp_direction = 'y'
>>> fugue.inputs.save_shift = True
>>> fugue.inputs.output_type = "NIFTI_GZ"
>>> fugue.cmdline # doctest: +ELLIPSIS
'fugue --dwelltoasym=0.9390243902 --mask=epi_mask.nii --phasemap=epi_phasediff.
↳nii --saveshift=epi_phasediff_vsm.nii.gz --unwarmdir=y'
>>> fugue.run() #doctest: +SKIP
```

Inputs:

```
[Optional]
in_file: (a pathlike object or string representing an existing file)
    filename of input volume
    argument: ``--in=%s``
shift_in_file: (a pathlike object or string representing an existing
    file)
    filename for reading pixel shift volume
    argument: ``--loadshift=%s``
phasemap_in_file: (a pathlike object or string representing an
    existing file)
    filename for input phase image
    argument: ``--phasemap=%s``
fmap_in_file: (a pathlike object or string representing an existing
    file)
    filename for loading fieldmap (rad/s)
    argument: ``--loadfmap=%s``
unwarped_file: (a pathlike object or string representing a file)
    apply unwarping and save as filename
    argument: ``--unwarp=%s``
    mutually_exclusive: warped_file
    requires: in_file
warped_file: (a pathlike object or string representing a file)
    apply forward warping and save as filename
    argument: ``--warp=%s``
    mutually_exclusive: unwarped_file
    requires: in_file
forward_warping: (a boolean, nipy default value: False)
    apply forward warping instead of unwarping
dwell_to_asym_ratio: (a float)
    set the dwell to asym time ratio
    argument: ``--dwelltoasym=%.10f``
dwell_time: (a float)
```

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```

        set the EPI dwell time per phase-encode line - same as echo spacing
        - (sec)
        argument: ``--dwell=%.10f``
    asym_se_time: (a float)
        set the fieldmap asymmetric spin echo time (sec)
        argument: ``--asym=%.10f``
    median_2dfilter: (a boolean)
        apply 2D median filtering
        argument: ``--median``
    despike_2dfilter: (a boolean)
        apply a 2D de-spiking filter
        argument: ``--despike``
    no_gap_fill: (a boolean)
        do not apply gap-filling measure to the fieldmap
        argument: ``--nofill``
    no_extend: (a boolean)
        do not apply rigid-body extrapolation to the fieldmap
        argument: ``--noextend``
    smooth2d: (a float)
        apply 2D Gaussian smoothing of sigma N (in mm)
        argument: ``--smooth2=%.2f``
    smooth3d: (a float)
        apply 3D Gaussian smoothing of sigma N (in mm)
        argument: ``--smooth3=%.2f``
    poly_order: (an integer (int or long))
        apply polynomial fitting of order N
        argument: ``--poly=%d``
    fourier_order: (an integer (int or long))
        apply Fourier (sinusoidal) fitting of order N
        argument: ``--fourier=%d``
    pava: (a boolean)
        apply monotonic enforcement via PAVA
        argument: ``--pava``
    despike_threshold: (a float)
        specify the threshold for de-spiking (default=3.0)
        argument: ``--despikethreshold=%s``
    unwarped_direction: ('x' or 'y' or 'z' or 'x-' or 'y-' or 'z-')
        specifies direction of warping (default y)
        argument: ``--unwarpedir=%s``
    phase_conjugate: (a boolean)
        apply phase conjugate method of unwarping
        argument: ``--phaseconj``
    icorr: (a boolean)
        apply intensity correction to unwarping (pixel shift method only)
        argument: ``--icorr``
        requires: shift_in_file
    icorr_only: (a boolean)
        apply intensity correction only
        argument: ``--icorronly``
        requires: unwarped_file
    mask_file: (a pathlike object or string representing an existing
        file)
        filename for loading valid mask
        argument: ``--mask=%s``
    nokspace: (a boolean)
        do not use k-space forward warping
        argument: ``--nokspace``

```

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```

save_shift: (a boolean)
    write pixel shift volume
    mutually_exclusive: save_unmasked_shift
shift_out_file: (a pathlike object or string representing a file)
    filename for saving pixel shift volume
    argument: ``--saveshift=%s``
save_unmasked_shift: (a boolean)
    saves the unmasked shiftmap when using --saveshift
    argument: ``--unmaskshift``
    mutually_exclusive: save_shift
save_fmap: (a boolean)
    write field map volume
    mutually_exclusive: save_unmasked_fmap
fmap_out_file: (a pathlike object or string representing a file)
    filename for saving fieldmap (rad/s)
    argument: ``--savefmap=%s``
save_unmasked_fmap: (a boolean)
    saves the unmasked fieldmap when using --savefmap
    argument: ``--unmaskfmap``
    mutually_exclusive: save_fmap
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

unwarped_file: (a pathlike object or string representing a file)
    unwarped file
warped_file: (a pathlike object or string representing a file)
    forward warped file
shift_out_file: (a pathlike object or string representing a file)
    voxel shift map file
fmap_out_file: (a pathlike object or string representing a file)
    fieldmap file

```

References:

None

63.8.9 MCFLIRT[Link to code](#)

Wraps the executable command mcflirt.

FSL MCFLIRT wrapper for within-modality motion correction

For complete details, see the [MCFLIRT Documentation](#).

Examples

```
>>> from nipy.interfaces import fsl
>>> mcflt = fsl.MCFLIRT()
>>> mcflt.inputs.in_file = 'functional.nii'
>>> mcflt.inputs.cost = 'mutualinfo'
>>> mcflt.inputs.out_file = 'moco.nii'
>>> mcflt.cmdline
'mcflirt -in functional.nii -cost mutualinfo -out moco.nii'
>>> res = mcflt.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         timeseries to motion-correct
         argument: ``-in %s``, position: 0

[Optional]
out_file: (a pathlike object or string representing a file)
         file to write
         argument: ``-out %s``
cost: ('mutualinfo' or 'woods' or 'corratio' or 'normcorr' or
       'normmi' or 'least squares')
      cost function to optimize
      argument: ``-cost %s``
bins: (an integer (int or long))
      number of histogram bins
      argument: ``-bins %d``
dof: (an integer (int or long))
     degrees of freedom for the transformation
     argument: ``-dof %d``
ref_vol: (an integer (int or long))
        volume to align frames to
        argument: ``-refvol %d``
scaling: (a float)
        scaling factor to use
        argument: ``-scaling %.2f``
smooth: (a float)
        smoothing factor for the cost function
        argument: ``-smooth %.2f``
rotation: (an integer (int or long))
         scaling factor for rotation tolerances
         argument: ``-rotation %d``
stages: (an integer (int or long))
        stages (if 4, perform final search with sinc interpolation)
        argument: ``-stages %d``
init: (a pathlike object or string representing an existing file)
      initial transformation matrix
      argument: ``-init %s``
interpolation: ('spline' or 'nn' or 'sinc')
              interpolation method for transformation
              argument: ``-%s_final``
use_gradient: (a boolean)
              run search on gradient images
              argument: ``-gdt``
use_contour: (a boolean)
             run search on contour images
```

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```

        argument: ``-edge``
mean_vol: (a boolean)
        register to mean volume
        argument: ``-meanvol``
stats_imgs: (a boolean)
        produce variance and std. dev. images
        argument: ``-stats``
save_mats: (a boolean)
        save transformation matrices
        argument: ``-mats``
save_plots: (a boolean)
        save transformation parameters
        argument: ``-plots``
save_rms: (a boolean)
        save rms displacement parameters
        argument: ``-rmsabs -rmsrel``
ref_file: (a pathlike object or string representing an existing file)
        target image for motion correction
        argument: ``-reffile %s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
        FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        motion-corrected timeseries
variance_img: (a pathlike object or string representing an existing
        file)
        variance image
std_img: (a pathlike object or string representing an existing file)
        standard deviation image
mean_img: (a pathlike object or string representing an existing file)
        mean timeseries image (if mean_vol=True)
par_file: (a pathlike object or string representing an existing file)
        text-file with motion parameters
mat_file: (a list of items which are a pathlike object or string
        representing an existing file)
        transformation matrices
rms_files: (a list of items which are a pathlike object or string
        representing an existing file)
        absolute and relative displacement parameters

```

References:

None

63.8.10 PRELUDE[Link to code](#)

Wraps the executable command `prelude`.
FSL prelude wrapper for phase unwrapping

Examples

Please insert examples for use of this command

Inputs:

```
[Mandatory]
complex_phase_file: (a pathlike object or string representing an
    existing file)
    complex phase input volume
    argument: ``--complex=%s``
    mutually_exclusive: magnitude_file, phase_file
magnitude_file: (a pathlike object or string representing an existing
    file)
    file containing magnitude image
    argument: ``--abs=%s``
    mutually_exclusive: complex_phase_file
phase_file: (a pathlike object or string representing an existing
    file)
    raw phase file
    argument: ``--phase=%s``
    mutually_exclusive: complex_phase_file

[Optional]
unwrapped_phase_file: (a pathlike object or string representing a
    file)
    file containing unwrapped phase
    argument: ``--unwrap=%s``
num_partitions: (an integer (int or long))
    number of phase partitions to use
    argument: ``--numphasesplit=%d``
labelprocess2d: (a boolean)
    does label processing in 2D (slice at a time)
    argument: ``--labelslices``
process2d: (a boolean)
    does all processing in 2D (slice at a time)
    argument: ``--slices``
    mutually_exclusive: labelprocess2d
process3d: (a boolean)
    forces all processing to be full 3D
    argument: ``--force3D``
    mutually_exclusive: labelprocess2d, process2d
threshold: (a float)
    intensity threshold for masking
    argument: ``--thresh=%.10f``
mask_file: (a pathlike object or string representing an existing
    file)
    filename of mask input volume
    argument: ``--mask=%s``
start: (an integer (int or long))
    first image number to process (default 0)
    argument: ``--start=%d``
end: (an integer (int or long))
    final image number to process (default Inf)
    argument: ``--end=%d``
savemask_file: (a pathlike object or string representing a file)
```

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```

    saving the mask volume
    argument: ``--savemask=%s``
rawphase_file: (a pathlike object or string representing a file)
    saving the raw phase output
    argument: ``--rawphase=%s``
label_file: (a pathlike object or string representing a file)
    saving the area labels output
    argument: ``--labels=%s``
removeramps: (a boolean)
    remove phase ramps during unwrapping
    argument: ``--removeramps``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

unwrapped_phase_file: (a pathlike object or string representing an
                       existing file)
                       unwrapped phase file

```

References:

None

63.8.11 SUSAN[Link to code](#)

Wraps the executable command susan.

FSL SUSAN wrapper to perform smoothing

For complete details, see the [SUSAN Documentation](#).**Examples**

```

>>> from nipy.interfaces import fsl
>>> from nipy.testing import example_data
>>> anatfile # doctest: +SKIP
anatomical.nii # doctest: +SKIP
>>> sus = fsl.SUSAN()
>>> sus.inputs.in_file = example_data('structural.nii')
>>> sus.inputs.brightness_threshold = 2000.0
>>> sus.inputs.fwhm = 8.0
>>> result = sus.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         filename of input timeseries

```

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```

        argument: ``%s``, position: 1
brightness_threshold: (a float)
    brightness threshold and should be greater than noise level and less
    than contrast of edges to be preserved.
    argument: ``%.10f``, position: 2
fwhm: (a float)
    fwhm of smoothing, in mm, gets converted using  $\sqrt{8 \cdot \log(2)}$ 
    argument: ``%.10f``, position: 3

[Optional]
dimension: (3 or 2, nipy default value: 3)
    within-plane (2) or fully 3D (3)
    argument: ``%d``, position: 4
use_median: (1 or 0, nipy default value: 1)
    whether to use a local median filter in the cases where single-point
    noise is detected
    argument: ``%d``, position: 5
usans: (a list of at most 2 items which are a tuple of the form: (a
    pathlike object or string representing an existing file, a float),
    nipy default value: [])
    determines whether the smoothing area (USAN) is to be found from
    secondary images (0, 1 or 2). A negative value for any brightness
    threshold will auto-set the threshold at 10% of the robust range
out_file: (a pathlike object or string representing a file)
    output file name
    argument: ``%s``, position: -1
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

smoothed_file: (a pathlike object or string representing an existing
    file)
    smoothed output file

```

References:

None

63.8.12 SliceTimer[Link to code](#)Wraps the executable command `slicetimer`.FSL `slicetimer` wrapper to perform slice timing correction

Examples

```
>>> from nipyre.interfaces import fsl
>>> from nipyre.testing import example_data
>>> st = fsl.SliceTimer()
>>> st.inputs.in_file = example_data('functional.nii')
>>> st.inputs.interleaved = True
>>> result = st.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        filename of input timeseries
        argument: ``--in=%s``, position: 0

[Optional]
out_file: (a pathlike object or string representing a file)
        filename of output timeseries
        argument: ``--out=%s``
index_dir: (a boolean)
        slice indexing from top to bottom
        argument: ``--down``
time_repetition: (a float)
        Specify TR of data - default is 3s
        argument: ``--repeat=%f``
slice_direction: (1 or 2 or 3)
        direction of slice acquisition (x=1, y=2, z=3) - default is z
        argument: ``--direction=%d``
interleaved: (a boolean)
        use interleaved acquisition
        argument: ``--odd``
custom_timings: (a pathlike object or string representing an existing
        file)
        slice timings, in fractions of TR, range 0:1 (default is 0.5 = no
        shift)
        argument: ``--tcustom=%s``
global_shift: (a float)
        shift in fraction of TR, range 0:1 (default is 0.5 = no shift)
        argument: ``--tglobal``
custom_order: (a pathlike object or string representing an existing
        file)
        filename of single-column custom interleave order file (first slice
        is referred to as 1 not 0)
        argument: ``--ocustom=%s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
        'NIFTI_PAIR_GZ')
        FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipyre default value: {})
        Environment variables
```

Outputs:

```
slice_time_corrected_file: (a pathlike object or string representing
    an existing file)
    slice time corrected file
```

References:

None

63.9 interfaces.fsl.utils**63.9.1 AvScale**

[Link to code](#)

Wraps the executable command avscale.

Use FSL avscale command to extract info from mat file output of FLIRT

Examples

```
>>> avscale = AvScale()
>>> avscale.inputs.mat_file = 'flirt.mat'
>>> res = avscale.run() # doctest: +SKIP
```

Inputs:

```
[Optional]
all_param: (a boolean)
    argument: ``--allparams``
mat_file: (a pathlike object or string representing an existing file)
    mat file to read
    argument: ``%s``, position: -2
ref_file: (a pathlike object or string representing an existing file)
    reference file to get center of rotation
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables
```

Outputs:

```
rotation_translation_matrix: (a list of items which are a list of
    items which are a float)
    Rotation and Translation Matrix
scales: (a list of items which are a float)
    Scales (x,y,z)
skews: (a list of items which are a float)
    Skews
average_scaling: (a float)
    Average Scaling
determinant: (a float)
    Determinant
forward_half_transform: (a list of items which are a list of items
    which are a float)
```

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```

    Forward Half Transform
backward_half_transform: (a list of items which are a list of items
    which are a float)
    Backwards Half Transform
left_right_orientation_preserved: (a boolean)
    True if LR orientation preserved
rot_angles: (a list of items which are a float)
    rotation angles
translations: (a list of items which are a float)
    translations

```

63.9.2 Complex

[Link to code](#)

Wraps the executable command `fslcomplex`.
`fslcomplex` is a tool for converting complex data

Examples

```

>>> cplx = Complex()
>>> cplx.inputs.complex_in_file = "complex.nii"
>>> cplx.real_polar = True
>>> res = cplx.run() # doctest: +SKIP

```

Inputs:

```

[Optional]
complex_in_file: (a pathlike object or string representing an
    existing file)
    argument: ``%s``, position: 2
complex_in_file2: (a pathlike object or string representing an
    existing file)
    argument: ``%s``, position: 3
real_in_file: (a pathlike object or string representing an existing
    file)
    argument: ``%s``, position: 2
imaginary_in_file: (a pathlike object or string representing an
    existing file)
    argument: ``%s``, position: 3
magnitude_in_file: (a pathlike object or string representing an
    existing file)
    argument: ``%s``, position: 2
phase_in_file: (a pathlike object or string representing an existing
    file)
    argument: ``%s``, position: 3
complex_out_file: (a pathlike object or string representing a file)
    argument: ``%s``, position: -3
mutually_exclusive: complex_out_file, magnitude_out_file,
    phase_out_file, real_out_file, imaginary_out_file, real_polar,
    real_cartesian
magnitude_out_file: (a pathlike object or string representing a file)
    argument: ``%s``, position: -4
mutually_exclusive: complex_out_file, real_out_file,
    imaginary_out_file, real_cartesian, complex_cartesian,
    complex_polar, complex_split, complex_merge

```

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```

phase_out_file: (a pathlike object or string representing a file)
    argument: ``%s``, position: -3
    mutually_exclusive: complex_out_file, real_out_file,
        imaginary_out_file, real_cartesian, complex_cartesian,
        complex_polar, complex_split, complex_merge
real_out_file: (a pathlike object or string representing a file)
    argument: ``%s``, position: -4
    mutually_exclusive: complex_out_file, magnitude_out_file,
        phase_out_file, real_polar, complex_cartesian, complex_polar,
        complex_split, complex_merge
imaginary_out_file: (a pathlike object or string representing a file)
    argument: ``%s``, position: -3
    mutually_exclusive: complex_out_file, magnitude_out_file,
        phase_out_file, real_polar, complex_cartesian, complex_polar,
        complex_split, complex_merge
start_vol: (an integer (int or long))
    argument: ``%d``, position: -2
end_vol: (an integer (int or long))
    argument: ``%d``, position: -1
real_polar: (a boolean)
    argument: ``-realpolar``, position: 1
    mutually_exclusive: real_polar, real_cartesian, complex_cartesian,
        complex_polar, complex_split, complex_merge
real_cartesian: (a boolean)
    argument: ``-realcartesian``, position: 1
    mutually_exclusive: real_polar, real_cartesian, complex_cartesian,
        complex_polar, complex_split, complex_merge
complex_cartesian: (a boolean)
    argument: ``-complex``, position: 1
    mutually_exclusive: real_polar, real_cartesian, complex_cartesian,
        complex_polar, complex_split, complex_merge
complex_polar: (a boolean)
    argument: ``-complexpolar``, position: 1
    mutually_exclusive: real_polar, real_cartesian, complex_cartesian,
        complex_polar, complex_split, complex_merge
complex_split: (a boolean)
    argument: ``-complexsplit``, position: 1
    mutually_exclusive: real_polar, real_cartesian, complex_cartesian,
        complex_polar, complex_split, complex_merge
complex_merge: (a boolean)
    argument: ``-complexmerge``, position: 1
    mutually_exclusive: real_polar, real_cartesian, complex_cartesian,
        complex_polar, complex_split, complex_merge, start_vol, end_vol
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

magnitude_out_file: (a pathlike object or string representing a file)

```

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```

phase_out_file: (a pathlike object or string representing a file)
real_out_file: (a pathlike object or string representing a file)
imaginary_out_file: (a pathlike object or string representing a file)
complex_out_file: (a pathlike object or string representing a file)

```

References:

None

63.9.3 ConvertWarp[Link to code](#)Wraps the executable command `convertwarp`.Use FSL [convertwarp](#) for combining multiple transforms into one.**Examples**

```

>>> from nipy.interfaces.fsl import ConvertWarp
>>> warputils = ConvertWarp()
>>> warputils.inputs.warpl = "warpfield.nii"
>>> warputils.inputs.reference = "T1.nii"
>>> warputils.inputs.relwarp = True
>>> warputils.inputs.output_type = "NIFTI_GZ"
>>> warputils.cmdline # doctest: +ELLIPSIS
'convertwarp --ref=T1.nii --rel --warpl=warpfield.nii --out=T1_concatwarp.nii.gz'
>>> res = warputils.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
reference: (a pathlike object or string representing an existing
           file)
           Name of a file in target space of the full transform.
           argument: ``--ref=%s``, position: 1

[Optional]
out_file: (a pathlike object or string representing a file)
           Name of output file, containing warps that are the combination of
           all those given as arguments. The format of this will be a field-
           file (rather than spline coefficients) with any affine components
           included.
           argument: ``--out=%s``, position: -1
premat: (a pathlike object or string representing an existing file)
         filename for pre-transform (affine matrix)
         argument: ``--premat=%s``
warpl: (a pathlike object or string representing an existing file)
        Name of file containing initial warp-fields/coefficients (follows
        premat). This could e.g. be a fnirt-transform from a subjects
        structural scan to an average of a group of subjects.
        argument: ``--warpl=%s``
midmat: (a pathlike object or string representing an existing file)
         Name of file containing mid-warp-affine transform
         argument: ``--midmat=%s``
warp2: (a pathlike object or string representing an existing file)
        Name of file containing secondary warp-fields/coefficients (after

```

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```

warp1/midmat but before postmat). This could e.g. be a fnirt-
transform from the average of a group of subjects to some standard
space (e.g. MNI152).
argument: ``--warp2=%s``
postmat: (a pathlike object or string representing an existing file)
Name of file containing an affine transform (applied last). It could
e.g. be an affine transform that maps the MNI152-space into a better
approximation to the Talairach-space (if indeed there is one).
argument: ``--postmat=%s``
shift_in_file: (a pathlike object or string representing an existing
file)
Name of file containing a "shiftmap", a non-linear transform with
displacements only in one direction (applied first, before premat).
This would typically be a fieldmap that has been pre-processed using
fugue that maps a subjects functional (EPI) data onto an undistorted
space (i.e. a space that corresponds to his/her true anatomy).
argument: ``--shiftmap=%s``
shift_direction: ('y-' or 'y' or 'x' or 'x-' or 'z' or 'z-')
Indicates the direction that the distortions from --shiftmap goes.
It depends on the direction and polarity of the phase-encoding in
the EPI sequence.
argument: ``--shiftdir=%s``
requires: shift_in_file
cons_jacobian: (a boolean)
Constrain the Jacobian of the warpfield to lie within specified
min/max limits.
argument: ``--constrainj``
jacobian_min: (a float)
Minimum acceptable Jacobian value for constraint (default 0.01)
argument: ``--jmin=%f``
jacobian_max: (a float)
Maximum acceptable Jacobian value for constraint (default 100.0)
argument: ``--jmax=%f``
abswarp: (a boolean)
If set it indicates that the warps in --warp1 and --warp2 should be
interpreted as absolute. I.e. the values in --warp1/2 are the
coordinates in the next space, rather than displacements. This flag
is ignored if --warp1/2 was created by fnirt, which always creates
relative displacements.
argument: ``--abs``
mutually_exclusive: relwarp
relwarp: (a boolean)
If set it indicates that the warps in --warp1/2 should be
interpreted as relative. I.e. the values in --warp1/2 are
displacements from the coordinates in the next space.
argument: ``--rel``
mutually_exclusive: abswarp
out_abswarp: (a boolean)
If set it indicates that the warps in --out should be absolute, i.e.
the values in --out are displacements from the coordinates in --ref.
argument: ``--absout``
mutually_exclusive: out_relwarp
out_relwarp: (a boolean)
If set it indicates that the warps in --out should be relative, i.e.
the values in --out are displacements from the coordinates in --ref.
argument: ``--relout``
mutually_exclusive: out_abswarp

```

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```

output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          Name of output file, containing the warp as field or coefficients.

```

References:

None

63.9.4 ConvertXFM[Link to code](#)Wraps the executable command `convert_xfm`.Use the FSL utility `convert_xfm` to modify FLIRT transformation matrices.**Examples**

```

>>> import nipy.interfaces.fsl as fsl
>>> invt = fsl.ConvertXFM()
>>> invt.inputs.in_file = "flirt.mat"
>>> invt.inputs.invert_xfm = True
>>> invt.inputs.out_file = 'flirt_inv.mat'
>>> invt.cmdline
'convert_xfm -omat flirt_inv.mat -inverse flirt.mat'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input transformation matrix
         argument: ``%s``, position: -1

[Optional]
in_file2: (a pathlike object or string representing an existing file)
          second input matrix (for use with fix_scale_skew or concat_xfm)
          argument: ``%s``, position: -2
invert_xfm: (a boolean)
            invert input transformation
            argument: ``-inverse``, position: -3
            mutually_exclusive: invert_xfm, concat_xfm, fix_scale_skew
concat_xfm: (a boolean)
            write joint transformation of two input matrices
            argument: ``-concat``, position: -3
            mutually_exclusive: invert_xfm, concat_xfm, fix_scale_skew
            requires: in_file2

```

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```

fix_scale_skew: (a boolean)
    use secondary matrix to fix scale and skew
    argument: ``-fixscaleskew``, position: -3
    mutually_exclusive: invert_xfm, concat_xfm, fix_scale_skew
    requires: in_file2
out_file: (a pathlike object or string representing a file)
    final transformation matrix
    argument: ``-omat %s``, position: 1
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output transformation matrix

```

References:

None

63.9.5 CopyGeom[Link to code](#)Wraps the executable command `fslcpgeom`.

Use `fslcpgeom` to copy the header geometry information to another image. Copy certain parts of the header information (image dimensions, voxel dimensions, voxel dimensions units string, image orientation/origin or qform/sform info) from one image to another. Note that only copies from Analyze to Analyze or Nifti to Nifti will work properly. Copying from different files will result in loss of information or potentially incorrect settings.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    source image
    argument: ``%s``, position: 0
dest_file: (a pathlike object or string representing an existing
    file)
    destination image
    argument: ``%s``, position: 1

[Optional]
ignore_dims: (a boolean)
    Do not copy image dimensions
    argument: ``-d``, position: -1
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command

```

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```

        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          image with new geometry header

```

References:

None

63.9.6 ExtractROI[Link to code](#)

Wraps the executable command fslroi.

Uses FSL Fslroi command to extract region of interest (ROI) from an image.

You can a) take a 3D ROI from a 3D data set (or if it is 4D, the same ROI is taken from each time point and a new 4D data set is created), b) extract just some time points from a 4D data set, or c) control time and space limits to the ROI. Note that the arguments are minimum index and size (not maximum index). So to extract voxels 10 to 12 inclusive you would specify 10 and 3 (not 10 and 12).

Examples

```

>>> from nipy.interfaces.fsl import ExtractROI
>>> from nipy.testing import anatfile
>>> fslroi = ExtractROI(in_file=anatfile, roi_file='bar.nii', t_min=0,
...                    t_size=1)
>>> fslroi.cmdline == 'fslroi %s bar.nii 0 1' % anatfile
True

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file
         argument: ``%s``, position: 0

[Optional]
roi_file: (a pathlike object or string representing a file)
          output file
          argument: ``%s``, position: 1
x_min: (an integer (int or long))
        argument: ``%d``, position: 2
x_size: (an integer (int or long))
        argument: ``%d``, position: 3
y_min: (an integer (int or long))
        argument: ``%d``, position: 4
y_size: (an integer (int or long))
        argument: ``%d``, position: 5
z_min: (an integer (int or long))
        argument: ``%d``, position: 6
z_size: (an integer (int or long))

```

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```

        argument: ``%d``, position: 7
t_min: (an integer (int or long))
        argument: ``%d``, position: 8
t_size: (an integer (int or long))
        argument: ``%d``, position: 9
crop_list: (a list of items which are a tuple of the form: (an
            integer (int or long), an integer (int or long)))
            list of two tuples specifying crop options
        argument: ``%s``, position: 2
        mutually_exclusive: x_min, x_size, y_min, y_size, z_min, z_size,
            t_min, t_size
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
            'NIFTI_PAIR_GZ')
            FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
            of class 'str' and with values which are a bytes or None or a
            value of class 'str', nipyre default value: {})
            Environment variables

```

Outputs:

```
roi_file: (a pathlike object or string representing an existing file)
```

References:

None

63.9.7 FilterRegressor[Link to code](#)Wraps the executable command `fsl_regfilt`.

Data de-noising by regressing out part of a design matrix

Uses simple OLS regression on 4D images

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input file name (4D image)
        argument: ``-i %s``, position: 1
design_file: (a pathlike object or string representing an existing
            file)
            name of the matrix with time courses (e.g. GLM design or MELODIC
            mixing matrix)
            argument: ``-d %s``, position: 3
filter_columns: (a list of items which are an integer (int or long))
                (1-based) column indices to filter out of the data
                argument: ``-f '%s'``, position: 4
                mutually_exclusive: filter_all
filter_all: (a boolean)
            use all columns in the design file in denoising
            argument: ``-f '%s'``, position: 4
            mutually_exclusive: filter_columns

```

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```
[Optional]
out_file: (a pathlike object or string representing a file)
    output file name for the filtered data
    argument: ``-o %s``, position: 2
mask: (a pathlike object or string representing an existing file)
    mask image file name
    argument: ``-m %s``
var_norm: (a boolean)
    perform variance-normalization on data
    argument: ``--vn``
out_vnscales: (a boolean)
    output scaling factors for variance normalization
    argument: ``--out_vnscales``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
    output file name for the filtered data
```

References:

None

63.9.8 ImageMaths[Link to code](#)Wraps the executable command `fslmaths`.Use FSL `fslmaths` command to allow mathematical manipulation of images [FSL info](#)**Examples**

```
>>> from nipy.interfaces import fsl
>>> from nipy.testing import anatfile
>>> maths = fsl.ImageMaths(in_file=anatfile, op_string= '-add 5',
...                        out_file='foo_maths.nii')
>>> maths.cmdline == 'fslmaths %s -add 5 foo_maths.nii' % anatfile
True
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    argument: ``%s``, position: 1

[Optional]
in_file2: (a pathlike object or string representing an existing file)
```

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```

    argument: ``%s``, position: 3
mask_file: (a pathlike object or string representing an existing
            file)
            use (following image>0) to mask current image
            argument: ``-mas %s``
out_file: (a pathlike object or string representing a file)
            argument: ``%s``, position: -2
op_string: (a unicode string)
            string defining the operation, i. e. -add
            argument: ``%s``, position: 2
suffix: (a unicode string)
            out_file suffix
out_data_type: ('char' or 'short' or 'int' or 'float' or 'double' or
                'input')
                output datatype, one of (char, short, int, float, double, input)
            argument: ``-odt %s``, position: -1
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

References:

None

63.9.9 ImageMeants[Link to code](#)

Wraps the executable command fslmeants.

Use fslmeants for printing the average timeseries (intensities) to the screen (or saves to a file). The average is taken over all voxels in the mask (or all voxels in the image if no mask is specified)

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file for computing the average timeseries
         argument: ``-i %s``, position: 0

[Optional]
out_file: (a pathlike object or string representing a file)
          name of output text matrix
          argument: ``-o %s``
mask: (a pathlike object or string representing an existing file)
       input 3D mask
       argument: ``-m %s``
spatial_coord: (a list of items which are an integer (int or long))

```

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```

    <x y z> requested spatial coordinate (instead of mask)
    argument: ``-c %s``
use_mm: (a boolean)
    use mm instead of voxel coordinates (for -c option)
    argument: ``--usemm``
show_all: (a boolean)
    show all voxel time series (within mask) instead of averaging
    argument: ``--showall``
eig: (a boolean)
    calculate Eigenvariate(s) instead of mean (output will have 0 mean)
    argument: ``--eig``
order: (an integer (int or long), nipy default value: 1)
    select number of Eigenvariates
    argument: ``--order=%d``
nobin: (a boolean)
    do not binarise the mask for calculation of Eigenvariates
    argument: ``--no_bin``
transpose: (a boolean)
    output results in transpose format (one row per voxel/mean)
    argument: ``--transpose``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    path/name of output text matrix

```

References:

None

63.9.10 ImageStats[Link to code](#)Wraps the executable command `fsstats`.Use FSL `fsstats` command to calculate stats from images [FSL info](#)**Examples**

```

>>> from nipy.interfaces.fsl import ImageStats
>>> from nipy.testing import funcfile
>>> stats = ImageStats(in_file=funcfile, op_string= '-M')
>>> stats.cmdline == 'fsstats %s -M'%funcfile
True

```

Inputs:


```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to generate stats of
         argument: ``%s``, position: 3
op_string: (a unicode string)
           string defining the operation, options are applied in order, e.g. -M
           -l 10 -M will report the non-zero mean, apply a threshold and then
           report the new nonzero mean
           argument: ``%s``, position: 4

[Optional]
split_4d: (a boolean)
          give a separate output line for each 3D volume of a 4D timeseries
          argument: ``-t``, position: 1
mask_file: (a pathlike object or string representing an existing
           file)
           mask file used for option -k %s
index_mask_file: (a pathlike object or string representing an
                 existing file)
                 generate separate n submasks from indexMask, for indexvalues 1..n
                 where n is the maximum index value in indexMask, and generate
                 statistics for each submask
                 argument: ``-K %s``, position: 2
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_stat: (any value)
          stats output
```

References:

None

63.9.11 InvWarp

[Link to code](#)

Wraps the executable command `invwarp`.

Use FSL `Invwarp` to invert a FNIRT warp

Examples

```
>>> from nipy.interfaces.fsl import InvWarp
>>> invwarp = InvWarp()
>>> invwarp.inputs.warp = "struct2mni.nii"
>>> invwarp.inputs.reference = "anatomical.nii"
>>> invwarp.inputs.output_type = "NIFTI_GZ"
```

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```
>>> invwarp.cmdline
'invwarp --out=struct2mni_inverse.nii.gz --ref=anatomical.nii --warp=struct2mni.
↳nii'
>>> res = invwarp.run() # doctest: +SKIP
```

Inputs:

[Mandatory]

warp: (a pathlike object or string representing an existing file)
 Name of file containing warp-coefficients/fields. This would typically be the output from the `--cout` switch of `fnirt` (but can also use fields, like the output from `--fout`).
 argument: `--warp=%s``

reference: (a pathlike object or string representing an existing file)
 Name of a file in target space. Note that the target space is now different from the target space that was used to create the `--warp` file. It would typically be the file that was specified with the `--in` argument when running `fnirt`.
 argument: `--ref=%s``

[Optional]

inverse_warp: (a pathlike object or string representing a file)
 Name of output file, containing warps that are the "reverse" of those in `--warp`. This will be a field-file (rather than a file of spline coefficients), and it will have any affine component included as part of the displacements.
 argument: `--out=%s``

absolute: (a boolean)
 If set it indicates that the warps in `--warp` should be interpreted as absolute, provided that it is not created by `fnirt` (which always uses relative warps). If set it also indicates that the output `--out` should be absolute.
 argument: `--abs``
 mutually_exclusive: relative

relative: (a boolean)
 If set it indicates that the warps in `--warp` should be interpreted as relative. I.e. the values in `--warp` are displacements from the coordinates in the `--ref` space. If set it also indicates that the output `--out` should be relative.
 argument: `--rel``
 mutually_exclusive: absolute

niter: (an integer (int or long))
 Determines how many iterations of the gradient-descent search that should be run.
 argument: `--niter=%d``

regularise: (a float)
 Regularization strength (default=1.0).
 argument: `--regularise=%f``

noconstraint: (a boolean)
 Do not apply Jacobian constraint
 argument: `--noconstraint``

jacobian_min: (a float)
 Minimum acceptable Jacobian value for constraint (default 0.01)
 argument: `--jmin=%f``

jacobian_max: (a float)
 Maximum acceptable Jacobian value for constraint (default 100.0)

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```

        argument: ``--jmax=%f``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
              FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

inverse_warp: (a pathlike object or string representing an existing
              file)
              Name of output file, containing warps that are the "reverse" of
              those in --warp.

```

References:

None

63.9.12 Merge[Link to code](#)Wraps the executable command `fslmerge`.Use `fslmerge` to concatenate images

Images can be concatenated across time, x, y, or z dimensions. Across the time (t) dimension the TR is set by default to 1 sec.

Note: to set the TR to a different value, specify 't' for dimension and specify the TR value in seconds for the tr input. The dimension will be automatically updated to 'tr'.

Examples

```

>>> from nipy.interfaces.fsl import Merge
>>> merger = Merge()
>>> merger.inputs.in_files = ['functional2.nii', 'functional3.nii']
>>> merger.inputs.dimension = 't'
>>> merger.inputs.output_type = 'NIFTI_GZ'
>>> merger.cmdline
'fslmerge -t functional2_merged.nii.gz functional2.nii functional3.nii'
>>> merger.inputs.tr = 2.25
>>> merger.cmdline
'fslmerge -tr functional2_merged.nii.gz functional2.nii functional3.nii 2.25'

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string
          representing an existing file)
          argument: ``%s``, position: 2
dimension: ('t' or 'x' or 'y' or 'z' or 'a')
          dimension along which to merge, optionally set tr input when
          dimension is t
          argument: ``-%s``, position: 0

```

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```
[Optional]
tr: (a float)
    use to specify TR in seconds (default is 1.00 sec), overrides
    dimension and sets it to tr
    argument: ``%.2f``, position: -1
merged_file: (a pathlike object or string representing a file)
    argument: ``%s``, position: 1
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
merged_file: (a pathlike object or string representing an existing
              file)
```

References:

None

63.9.13 MotionOutliers[Link to code](#)

Wraps the executable command `fsl_motion_outliers`.

Use FSL `fsl_motion_outliers` <http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FSLMotionOutliers> to find outliers in time-series (4d) data. Examples ~~~~~>>> from nipy.interfaces.fsl import MotionOutliers>>> mo = MotionOutliers()>>> mo.inputs.in_file = "epi.nii">>> mo.cmdline # doctest: +ELLIPSIS 'fsl_motion_outliers -i epi.nii -o epi_outliers.txt -p epi_metrics.png -s epi_metrics.txt'>>> res = mo.run() # doctest: +SKIP

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    unfiltered 4D image
    argument: ``-i %s``

[Optional]
out_file: (a pathlike object or string representing a file)
    output outlier file name
    argument: ``-o %s``
mask: (a pathlike object or string representing an existing file)
    mask image for calculating metric
    argument: ``-m %s``
metric: ('refrms' or 'dvars' or 'refmse' or 'fd' or 'fdrms')
    metrics: refrms - RMS intensity difference to reference volume as
    metric [default metric], refmse - Mean Square Error version of
    refrms (used in original version of fsl_motion_outliers), dvars -
    DVARS, fd - frame displacement, fdrms - FD with RMS matrix
    calculation
```

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```

        argument: ``--%s``
threshold: (a float)
    specify absolute threshold value (otherwise use box-plot cutoff =
    P75 + 1.5*IQR)
    argument: ``--thresh=%g``
no_motion_correction: (a boolean)
    do not run motion correction (assumed already done)
    argument: ``--nomoco``
dummy: (an integer (int or long))
    number of dummy scans to delete (before running anything and
    creating EVs)
    argument: ``--dummy=%d``
out_metric_values: (a pathlike object or string representing a file)
    output metric values (DVARs etc.) file name
    argument: ``-s %s``
out_metric_plot: (a pathlike object or string representing a file)
    output metric values plot (DVARs etc.) file name
    argument: ``-p %s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
out_metric_values: (a pathlike object or string representing an
    existing file)
out_metric_plot: (a pathlike object or string representing an
    existing file)

```

References:

None

63.9.14 Overlay[Link to code](#)

Wraps the executable command overlay.

Use FSL's overlay command to combine background and statistical images into one volume**Examples**

```

>>> from nipy.interfaces import fsl
>>> combine = fsl.Overlay()
>>> combine.inputs.background_image = 'mean_func.nii.gz'
>>> combine.inputs.auto_thresh_bg = True
>>> combine.inputs.stat_image = 'zstat1.nii.gz'
>>> combine.inputs.stat_thresh = (3.5, 10)

```

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```
>>> combine.inputs.show_negative_stats = True
>>> res = combine.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
background_image: (a pathlike object or string representing an
    existing file)
    image to use as background
    argument: ``%s``, position: 4
auto_thresh_bg: (a boolean)
    automatically threshold the background image
    argument: ``-a``, position: 5
    mutually_exclusive: auto_thresh_bg, full_bg_range, bg_thresh
full_bg_range: (a boolean)
    use full range of background image
    argument: ``-A``, position: 5
    mutually_exclusive: auto_thresh_bg, full_bg_range, bg_thresh
bg_thresh: (a tuple of the form: (a float, a float))
    min and max values for background intensity
    argument: ``%.3f %.3f``, position: 5
    mutually_exclusive: auto_thresh_bg, full_bg_range, bg_thresh
stat_image: (a pathlike object or string representing an existing
    file)
    statistical image to overlay in color
    argument: ``%s``, position: 6
stat_thresh: (a tuple of the form: (a float, a float))
    min and max values for the statistical overlay
    argument: ``%.2f %.2f``, position: 7

[Optional]
transparency: (a boolean, nipy default value: True)
    make overlay colors semi-transparent
    argument: ``%s``, position: 1
out_type: ('float' or 'int', nipy default value: float)
    write output with float or int
    argument: ``%s``, position: 2
use_checkerboard: (a boolean)
    use checkerboard mask for overlay
    argument: ``-c``, position: 3
show_negative_stats: (a boolean)
    display negative statistics in overlay
    argument: ``%s``, position: 8
    mutually_exclusive: stat_image2
stat_image2: (a pathlike object or string representing an existing
    file)
    second statistical image to overlay in color
    argument: ``%s``, position: 9
    mutually_exclusive: show_negative_stats
stat_thresh2: (a tuple of the form: (a float, a float))
    min and max values for second statistical overlay
    argument: ``%.2f %.2f``, position: 10
out_file: (a pathlike object or string representing a file)
    combined image volume
    argument: ``%s``, position: -1
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
```

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```

    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    combined image volume

```

References:

None

63.9.15 PlotMotionParams[Link to code](#)Wraps the executable command `fsl_tsplo`.Use `fsl_tsplo` to plot the estimated motion parameters from a realignment program.**Examples**

```

>>> import nipyte.interfaces.fsl as fsl
>>> plotter = fsl.PlotMotionParams()
>>> plotter.inputs.in_file = 'functional.par'
>>> plotter.inputs.in_source = 'fsl'
>>> plotter.inputs.plot_type = 'rotations'
>>> res = plotter.run() #doctest: +SKIP

```

Notes

The ‘`in_source`’ attribute determines the order of columns that are expected in the source file. FSL prints motion parameters in the order rotations, translations, while SPM prints them in the opposite order. This interface should be able to plot timecourses of motion parameters generated from other sources as long as they fall under one of these two patterns. For more flexibility, see the `fsl.PlotTimeSeries` interface.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file
    or a list of items which are a pathlike object or string
    representing an existing file)
    file with motion parameters
    argument: ``%s``, position: 1
in_source: ('spm' or 'fsl')
    which program generated the motion parameter file - fsl, spm
plot_type: ('rotations' or 'translations' or 'displacement')
    which motion type to plot - rotations, translations, displacement
    argument: ``%s``

[Optional]
plot_size: (a tuple of the form: (an integer (int or long), an

```

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```

        integer (int or long))
    plot image height and width
    argument: ``%s``
out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``-o %s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    image to write

```

References:

None

63.9.16 PlotTimeSeries[Link to code](#)Wraps the executable command `fsl_tsplot`.Use `fsl_tsplot` to create images of time course plots.**Examples**

```

>>> import nipy.interfaces.fsl as fsl
>>> plotter = fsl.PlotTimeSeries()
>>> plotter.inputs.in_file = 'functional.par'
>>> plotter.inputs.title = 'Functional timeseries'
>>> plotter.inputs.labels = ['run1', 'run2']
>>> plotter.run() #doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file
    or a list of items which are a pathlike object or string
    representing an existing file)
    file or list of files with columns of timecourse information
    argument: ``%s``, position: 1

[Optional]
plot_start: (an integer (int or long))
    first column from in-file to plot
    argument: ``--start=%d``
    mutually_exclusive: plot_range
plot_finish: (an integer (int or long))

```

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```

        final column from in-file to plot
        argument: ``--finish=%d``
        mutually_exclusive: plot_range
plot_range: (a tuple of the form: (an integer (int or long), an
            integer (int or long)))
            first and last columns from the in-file to plot
            argument: ``%s``
            mutually_exclusive: plot_start, plot_finish
title: (a unicode string)
        plot title
        argument: ``%s``
legend_file: (a pathlike object or string representing an existing
            file)
            legend file
            argument: ``--legend=%s``
labels: (a unicode string or a list of items which are a unicode
        string)
        label or list of labels
        argument: ``%s``
y_min: (a float)
        mininum y value
        argument: ``--ymin=%.2f``
        mutually_exclusive: y_range
y_max: (a float)
        maximum y value
        argument: ``--ymax=%.2f``
        mutually_exclusive: y_range
y_range: (a tuple of the form: (a float, a float))
        min and max y axis values
        argument: ``%s``
        mutually_exclusive: y_min, y_max
x_units: (an integer (int or long), nipy default value: 1)
        scaling units for x-axis (between 1 and length of in file)
        argument: ``-u %d``
plot_size: (a tuple of the form: (an integer (int or long), an
            integer (int or long)))
            plot image height and width
            argument: ``%s``
x_precision: (an integer (int or long))
        precision of x-axis labels
        argument: ``--precision=%d``
sci_notation: (a boolean)
        switch on scientific notation
        argument: ``--sci``
out_file: (a pathlike object or string representing a file)
        image to write
        argument: ``-o %s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
            'NIFTI_PAIR_GZ')
            FSL output type
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          image to write
```

References:

None

63.9.17 PowerSpectrum

[Link to code](#)

Wraps the executable command `fslpspec`.

Use FSL PowerSpectrum command for power spectrum estimation.

Examples

```
>>> from nipy.interfaces import fsl
>>> pspec = fsl.PowerSpectrum()
>>> pspec.inputs.in_file = 'functional.nii'
>>> res = pspec.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input 4D file to estimate the power spectrum
         argument: ``%s``, position: 0

[Optional]
out_file: (a pathlike object or string representing a file)
         name of output 4D file for power spectrum
         argument: ``%s``, position: 1
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
            FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          path/name of the output 4D power spectrum file
```

References:

None

63.9.18 Reorient2Std

[Link to code](#)

Wraps the executable command `fslreorient2std`.

fslreorient2std is a tool for reorienting the image to match the approximate orientation of the standard template images (MNI152).

Examples

```
>>> reorient = Reorient2Std()
>>> reorient.inputs.in_file = "functional.nii"
>>> res = reorient.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         argument: ``%s``

[Optional]
out_file: (a pathlike object or string representing a file)
         argument: ``%s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
            FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

References:

None

63.9.19 RobustFOV

[Link to code](#)

Wraps the executable command robustfov.

Automatically crops an image removing lower head and neck.

Interface is stable 5.0.0 to 5.0.9, but default brainsize changed from 150mm to 170mm.

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input filename
         argument: ``-i %s``, position: 0

[Optional]
out_roi: (a pathlike object or string representing a file)
         ROI volume output name
         argument: ``-r %s``
brainsize: (an integer (int or long))
           size of brain in z-dimension (default 170mm/150mm)
           argument: ``-b %d``
```

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```

out_transform: (a pathlike object or string representing a file)
    Transformation matrix in_file to out_roi output name
    argument: ``-m %s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_roi: (a pathlike object or string representing an existing file)
    ROI volume output name
out_transform: (a pathlike object or string representing an existing
    file)
    Transformation matrix in_file to out_roi output name

```

References:

None

63.9.20 SigLoss[Link to code](#)

Wraps the executable command sigloss.

Estimates signal loss from a field map (in rad/s)

Examples

```

>>> sigloss = SigLoss()
>>> sigloss.inputs.in_file = "phase.nii"
>>> sigloss.inputs.echo_time = 0.03
>>> res = sigloss.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    b0 fieldmap file
    argument: ``-i %s``

[Optional]
out_file: (a pathlike object or string representing a file)
    output signal loss estimate file
    argument: ``-s %s``
mask_file: (a pathlike object or string representing an existing
    file)
    brain mask file
    argument: ``-m %s``
echo_time: (a float)
    echo time in seconds

```

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```

        argument: ``--te=%f``
slice_direction: ('x' or 'y' or 'z')
    slicing direction
    argument: ``-d %s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    signal loss estimate file

```

References:

None

63.9.21 Slice[Link to code](#)Wraps the executable command `fslslice`.Use `fslslice` to split a 3D file into lots of 2D files (along z-axis).**Examples**

```

>>> from nipype.interfaces.fsl import Slice
>>> slice = Slice()
>>> slice.inputs.in_file = 'functional.nii'
>>> slice.inputs.out_base_name = 'sl'
>>> slice.cmdline
'fslslice functional.nii sl'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    input filename
    argument: ``%s``, position: 0

[Optional]
out_base_name: (a unicode string)
    outputs prefix
    argument: ``%s``, position: 1
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``

```

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```
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
Environment variables
```

Outputs:

```
out_files: (a list of items which are a pathlike object or string
           representing an existing file)
```

References:

None

63.9.22 Slicer[Link to code](#)Wraps the executable command `slicer`.Use FSL's `slicer` command to output a png image from a volume.**Examples**

```
>>> from nipy.interfaces import fsl
>>> from nipy.testing import example_data
>>> slice = fsl.Slicer()
>>> slice.inputs.in_file = example_data('functional.nii')
>>> slice.inputs.all_axial = True
>>> slice.inputs.image_width = 750
>>> res = slice.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input volume
         argument: ``%s``, position: 1

[Optional]
image_edges: (a pathlike object or string representing an existing
             file)
             volume to display edge overlay for (useful for checking registration)
             argument: ``%s``, position: 2
label_slices: (a boolean, nipy default value: True)
              display slice number
              argument: ``-L``, position: 3
colour_map: (a pathlike object or string representing an existing
            file)
            use different colour map from that stored in nifti header
            argument: ``-l %s``, position: 4
intensity_range: (a tuple of the form: (a float, a float))
                 min and max intensities to display
                 argument: ``-i %.3f %.3f``, position: 5
threshold_edges: (a float)
                 use threshold for edges
                 argument: ``-e %.3f``, position: 6
dither_edges: (a boolean)
```

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```

        produce semi-transparent (dithered) edges
        argument: ``-t``, position: 7
nearest_neighbour: (a boolean)
    use nearest neighbor interpolation for output
    argument: ``-n``, position: 8
show_orientation: (a boolean, nipy default value: True)
    label left-right orientation
    argument: ``%s``, position: 9
single_slice: ('x' or 'y' or 'z')
    output picture of single slice in the x, y, or z plane
    argument: ``-%s``, position: 10
    mutually_exclusive: single_slice, middle_slices, all_axial,
        sample_axial
    requires: slice_number
slice_number: (an integer (int or long))
    slice number to save in picture
    argument: ``-%d``, position: 11
middle_slices: (a boolean)
    output picture of mid-sagittal, axial, and coronal slices
    argument: ``-a``, position: 10
    mutually_exclusive: single_slice, middle_slices, all_axial,
        sample_axial
all_axial: (a boolean)
    output all axial slices into one picture
    argument: ``-A``, position: 10
    mutually_exclusive: single_slice, middle_slices, all_axial,
        sample_axial
    requires: image_width
sample_axial: (an integer (int or long))
    output every n axial slices into one picture
    argument: ``-S %d``, position: 10
    mutually_exclusive: single_slice, middle_slices, all_axial,
        sample_axial
    requires: image_width
image_width: (an integer (int or long))
    max picture width
    argument: ``%d``, position: -2
out_file: (a pathlike object or string representing a file)
    picture to write
    argument: ``%s``, position: -1
scaling: (a float)
    image scale
    argument: ``-s %f``, position: 0
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)

```

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picture to write

References:

None

63.9.23 Smooth[Link to code](#)Wraps the executable command `fslmaths`.Use `fslmaths` to smooth the image**Examples**

Setting the kernel width using sigma:

```
>>> sm = Smooth()
>>> sm.inputs.output_type = 'NIFTI_GZ'
>>> sm.inputs.in_file = 'functional2.nii'
>>> sm.inputs.sigma = 8.0
>>> sm.cmdline # doctest: +ELLIPSIS
'fslmaths functional2.nii -kernel gauss 8.000 -fmean functional2_smooth.nii.gz'
```

Setting the kernel width using fwhm:

```
>>> sm = Smooth()
>>> sm.inputs.output_type = 'NIFTI_GZ'
>>> sm.inputs.in_file = 'functional2.nii'
>>> sm.inputs.fwhm = 8.0
>>> sm.cmdline # doctest: +ELLIPSIS
'fslmaths functional2.nii -kernel gauss 3.397 -fmean functional2_smooth.nii.gz'
```

One of sigma or fwhm must be set:

```
>>> from nipy.interfaces.fsl import Smooth
>>> sm = Smooth()
>>> sm.inputs.output_type = 'NIFTI_GZ'
>>> sm.inputs.in_file = 'functional2.nii'
>>> sm.cmdline #doctest: +ELLIPSIS
Traceback (most recent call last):
  ~~~
ValueError: Smooth requires a value for one of the inputs ...
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         argument: ``%s``, position: 0
sigma: (a float)
        gaussian kernel sigma in mm (not voxels)
        argument: ``-kernel gauss %.03f -fmean``, position: 1
        mutually_exclusive: fwhm
fwhm: (a float)
       gaussian kernel fwhm, will be converted to sigma in mm (not voxels)
       argument: ``-kernel gauss %.03f -fmean``, position: 1
       mutually_exclusive: sigma
```

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```
[Optional]
smoothed_file: (a pathlike object or string representing a file)
    argument: ``%s``, position: 2
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
smoothed_file: (a pathlike object or string representing an existing
    file)
```

References:

None

63.9.24 Split[Link to code](#)Wraps the executable command `fslsplit`.Uses FSL `Fslsplit` command to separate a volume into images in time, x, y or z dimension.**Inputs:**

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    input filename
    argument: ``%s``, position: 0
dimension: ('t' or 'x' or 'y' or 'z')
    dimension along which the file will be split
    argument: ``-%s``, position: 2

[Optional]
out_base_name: (a unicode string)
    outputs prefix
    argument: ``%s``, position: 1
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_files: (a list of items which are a pathlike object or string
    representing an existing file)
```

References:

None

63.9.25 SwapDimensions

[Link to code](#)

Wraps the executable command `fslswapdim`.

Use `fslswapdim` to alter the orientation of an image.

This interface accepts a three-tuple corresponding to the new orientation. You may either provide dimension ids in the form of (-)x, (-)y, or (-)z, or nifti-style dimension codes (RL, LR, AP, PA, IS, SI).

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input image
         argument: ``%s``, position: 1
new_dims: (a tuple of the form: ('x' or '-x' or 'y' or '-y' or 'z' or
                                '-z' or 'RL' or 'LR' or 'AP' or 'PA' or 'IS' or 'SI', 'x' or '-x'
                                or 'y' or '-y' or 'z' or '-z' or 'RL' or 'LR' or 'AP' or 'PA' or
                                'IS' or 'SI', 'x' or '-x' or 'y' or '-y' or 'z' or '-z' or 'RL' or
                                'LR' or 'AP' or 'PA' or 'IS' or 'SI'))
         3-tuple of new dimension order
         argument: ``%s %s %s``

[Optional]
out_file: (a pathlike object or string representing a file)
         image to write
         argument: ``%s``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
              'NIFTI_PAIR_GZ')
            FSL output type
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          image with new dimensions
```

References:

None

63.9.26 WarpPoints

[Link to code](#)

Wraps the executable command `img2imgcoord`.

Use FSL `img2imgcoord` to transform point sets. Accepts plain text files and vtk files.

Note: transformation of TrackVis trk files is not yet implemented

Examples

```
>>> from nipy.interfaces.fsl import WarpPoints
>>> warppoints = WarpPoints()
>>> warppoints.inputs.in_coords = 'surf.txt'
>>> warppoints.inputs.src_file = 'epi.nii'
>>> warppoints.inputs.dest_file = 'T1.nii'
>>> warppoints.inputs.warp_file = 'warpfield.nii'
>>> warppoints.inputs.coord_mm = True
>>> warppoints.cmdline # doctest: +ELLIPSIS
'img2imgcoord -mm -dest T1.nii -src epi.nii -warp warpfield.nii surf.txt'
>>> res = warppoints.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
src_file: (a pathlike object or string representing an existing file)
    filename of source image
    argument: ``-src %s``
dest_file: (a pathlike object or string representing an existing
    file)
    filename of destination image
    argument: ``-dest %s``
in_coords: (a pathlike object or string representing an existing
    file)
    filename of file containing coordinates
    argument: ``%s``, position: -1

[Optional]
xfm_file: (a pathlike object or string representing an existing file)
    filename of affine transform (e.g. source2dest.mat)
    argument: ``-xfm %s``
    mutually_exclusive: warp_file
warp_file: (a pathlike object or string representing an existing
    file)
    filename of warpfield (e.g. intermediate2dest_warp.nii.gz)
    argument: ``-warp %s``
    mutually_exclusive: xfm_file
coord_vox: (a boolean)
    all coordinates in voxels - default
    argument: ``-vox``
    mutually_exclusive: coord_mm
coord_mm: (a boolean)
    all coordinates in mm
    argument: ``-mm``
    mutually_exclusive: coord_vox
out_file: (a pathlike object or string representing a file)
    output file name
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          Name of output file, containing the warp as field or coefficients.
```

63.9.27 WarpPointsFromStd

[Link to code](#)

Wraps the executable command std2imgcoord.

Use FSL `std2imgcoord` to transform point sets to standard space coordinates. Accepts plain text coordinates files.

Examples

```
>>> from nipy.interfaces.fsl import WarpPointsFromStd
>>> warppoints = WarpPointsFromStd()
>>> warppoints.inputs.in_coords = 'surf.txt'
>>> warppoints.inputs.img_file = 'T1.nii'
>>> warppoints.inputs.std_file = 'mni.nii'
>>> warppoints.inputs.warp_file = 'warpfield.nii'
>>> warppoints.inputs.coord_mm = True
>>> warppoints.cmdline # doctest: +ELLIPSIS
'std2imgcoord -mm -img T1.nii -std mni.nii -warp warpfield.nii surf.txt'
>>> res = warppoints.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
img_file: (a pathlike object or string representing an existing file)
          filename of a destination image
          argument: ``-img %s``
std_file: (a pathlike object or string representing an existing file)
          filename of the image in standard space
          argument: ``-std %s``
in_coords: (a pathlike object or string representing an existing
           file)
           filename of file containing coordinates
           argument: ``%s``, position: -2

[Optional]
xfm_file: (a pathlike object or string representing an existing file)
          filename of affine transform (e.g. source2dest.mat)
          argument: ``-xfm %s``
          mutually_exclusive: warp_file
warp_file: (a pathlike object or string representing an existing
           file)
           filename of warpfield (e.g. intermediate2dest_warp.nii.gz)
           argument: ``-warp %s``
           mutually_exclusive: xfm_file
coord_vox: (a boolean)
           all coordinates in voxels - default
           argument: ``-vox``
           mutually_exclusive: coord_mm
coord_mm: (a boolean)
           all coordinates in mm
           argument: ``-mm``
           mutually_exclusive: coord_vox
args: (a unicode string)
```

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```

Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          Name of output file, containing the warp as field or coefficients.

```

63.9.28 WarpPointsToStd[Link to code](#)Wraps the executable command `img2stdcoord`.Use FSL `img2stdcoord` to transform point sets to standard space coordinates. Accepts plain text files and vtk files.**Note:** transformation of TrackVis trk files is not yet implemented**Examples**

```

>>> from nipy.interfaces.fsl import WarpPointsToStd
>>> warppoints = WarpPointsToStd()
>>> warppoints.inputs.in_coords = 'surf.txt'
>>> warppoints.inputs.img_file = 'T1.nii'
>>> warppoints.inputs.std_file = 'mni.nii'
>>> warppoints.inputs.warp_file = 'warpfield.nii'
>>> warppoints.inputs.coord_mm = True
>>> warppoints.cmdline # doctest: +ELLIPSIS
'img2stdcoord -mm -img T1.nii -std mni.nii -warp warpfield.nii surf.txt'
>>> res = warppoints.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
img_file: (a pathlike object or string representing an existing file)
          filename of input image
          argument: ``-img %s``
std_file: (a pathlike object or string representing an existing file)
          filename of destination image
          argument: ``-std %s``
in_coords: (a pathlike object or string representing an existing
            file)
            filename of file containing coordinates
            argument: ``%s``, position: -1

[Optional]
premat_file: (a pathlike object or string representing an existing
              file)
              filename of pre-warp affine transform (e.g.
              example_func2highres.mat)
              argument: ``-premat %s``
xfm_file: (a pathlike object or string representing an existing file)

```

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```

        filename of affine transform (e.g. source2dest.mat)
        argument: ``-xfm %s``
        mutually_exclusive: warp_file
warp_file: (a pathlike object or string representing an existing
            file)
        filename of warpfield (e.g. intermediate2dest_warp.nii.gz)
        argument: ``-warp %s``
        mutually_exclusive: xfm_file
coord_vox: (a boolean)
            all coordinates in voxels - default
            argument: ``-vox``
            mutually_exclusive: coord_mm
coord_mm: (a boolean)
            all coordinates in mm
            argument: ``-mm``
            mutually_exclusive: coord_vox
out_file: (a pathlike object or string representing a file)
            output file name
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
            of class 'str' and with values which are a bytes or None or a
            value of class 'str', nipy default value: {})
            Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
            Name of output file, containing the warp as field or coefficients.

```

63.9.29 WarpUtils[Link to code](#)Wraps the executable command `fnirtfileutils`.Use FSL `fnirtfileutils` to convert field->coefficients, coefficients->field, coefficients->other_coefficients etc**Examples**

```

>>> from nipy.interfaces.fsl import WarpUtils
>>> warputils = WarpUtils()
>>> warputils.inputs.in_file = "warpfield.nii"
>>> warputils.inputs.reference = "T1.nii"
>>> warputils.inputs.out_format = 'spline'
>>> warputils.inputs.warp_resolution = (10,10,10)
>>> warputils.inputs.output_type = "NIFTI_GZ"
>>> warputils.cmdline # doctest: +ELLIPSIS
'fnirtfileutils --in=warpfield.nii --outformat=spline --ref=T1.nii --warpres=10.
↪0000,10.0000,10.0000 --out=warpfield_coeffs.nii.gz'
>>> res = invwarp.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
            Name of file containing warp-coefficients/fields. This would

```

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```

    typically be the output from the --cout switch of fnirt (but can
    also use fields, like the output from --fout).
    argument: ``--in=%s``
reference: (a pathlike object or string representing an existing
    file)
    Name of a file in target space. Note that the target space is now
    different from the target space that was used to create the --warp
    file. It would typically be the file that was specified with the
    --in argument when running fnirt.
    argument: ``--ref=%s``
write_jacobian: (a boolean, nipy default value: False)
    Switch on --jac flag with automatically generated filename

[Optional]
out_format: ('spline' or 'field')
    Specifies the output format. If set to field (default) the output
    will be a (4D) field-file. If set to spline the format will be a
    (4D) file of spline coefficients.
    argument: ``--outformat=%s``
warp_resolution: (a tuple of the form: (a float, a float, a float))
    Specifies the resolution/knot-spacing of the splines pertaining to
    the coefficients in the --out file. This parameter is only relevant
    if --outformat is set to spline. It should be noted that if the --in
    file has a higher resolution, the resulting coefficients will
    pertain to the closest (in a least-squares sense) file in the space
    of fields with the --warpres resolution. It should also be noted
    that the resolution will always be an integer multiple of the voxel
    size.
    argument: ``--warpres=%0.4f,%0.4f,%0.4f``
knot_space: (a tuple of the form: (an integer (int or long), an
    integer (int or long), an integer (int or long)))
    Alternative (to --warpres) specification of the resolution of the
    output spline-field.
    argument: ``--knotspace=%d,%d,%d``
out_file: (a pathlike object or string representing a file)
    Name of output file. The format of the output depends on what other
    parameters are set. The default format is a (4D) field-file. If the
    --outformat is set to spline the format will be a (4D) file of
    spline coefficients.
    argument: ``--out=%s``, position: -1
out_jacobian: (a pathlike object or string representing a file)
    Specifies that a (3D) file of Jacobian determinants corresponding to
    --in should be produced and written to filename.
    argument: ``--jac=%s``
with_affine: (a boolean)
    Specifies that the affine transform (i.e. that which was specified
    for the --aff parameter in fnirt) should be included as
    displacements in the --out file. That can be useful for interfacing
    with software that cannot decode FSL/fnirt coefficient-files (where
    the affine transform is stored separately from the displacements).
    argument: ``--withaff``
output_type: ('NIFTI' or 'NIFTI_PAIR' or 'NIFTI_GZ' or
    'NIFTI_PAIR_GZ')
    FSL output type
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``

```

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```
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
          Name of output file, containing the warp as field or coefficients.
out_jacobian: (a pathlike object or string representing a file)
          Name of output file, containing the map of the determinant of the
          Jacobian
```

References:

None

64.1 interfaces.minc.base

64.1.1 aggregate_filename()

[Link to code](#)

Try to work out a sensible name given a set of files that have been combined in some way (e.g. averaged). If we can't work out a sensible prefix, we use the first filename in the list.

Examples

```
>>> from nipy.interfaces.minc.base import aggregate_filename
>>> f = aggregate_filename(['/tmp/fool.mnc', '/tmp/foo2.mnc', '/tmp/foo3.mnc'],
↪ 'averaged')
>>> os.path.split(f)[1] # This has a full path, so just check the filename.
'foo_averaged.mnc'
```

```
>>> f = aggregate_filename(['/tmp/fool.mnc', '/tmp/blah1.mnc'], 'averaged')
>>> os.path.split(f)[1] # This has a full path, so just check the filename.
'fool_averaged.mnc'
```

64.2 interfaces.minc.minc

64.2.1 Average

[Link to code](#)

Wraps the executable command mincaverage.
Average a number of MINC files.

Examples

```
>>> from nipy.interfaces.minc import Average
>>> from nipy.interfaces.minc.testdata import nonempty_minc_data
```

```
>>> files = [nonempty_minc_data(i) for i in range(3)]
>>> average = Average(input_files=files, output_file='/tmp/tmp.mnc')
>>> average.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_files: (a list of items which are a pathlike object or string
              representing an existing file)
              input file(s)
              argument: ``%s``, position: -2
              mutually_exclusive: input_files, filelist
filelist: (a pathlike object or string representing an existing file)
           Specify the name of a file containing input file names.
           argument: ``-filelist %s``
           mutually_exclusive: input_files, filelist

[Optional]
output_file: (a pathlike object or string representing a file)
              output file
              argument: ``%s``, position: -1
two: (a boolean)
      Create a MINC 2 output file.
      argument: ``-2``
clobber: (a boolean, nipy default value: True)
          Overwrite existing file.
          argument: ``-clobber``
verbose: (a boolean)
          Print out log messages (default).
          argument: ``-verbose``
          mutually_exclusive: verbose, quiet
quiet: (a boolean)
        Do not print out log messages.
        argument: ``-quiet``
        mutually_exclusive: verbose, quiet
debug: (a boolean)
        Print out debugging messages.
        argument: ``-debug``
check_dimensions: (a boolean)
                  Check that dimension info matches across files (default).
                  argument: ``-check_dimensions``
                  mutually_exclusive: check_dimensions, no_check_dimensions
no_check_dimensions: (a boolean)
                     Do not check dimension info.
                     argument: ``-nocheck_dimensions``
                     mutually_exclusive: check_dimensions, no_check_dimensions
format_filetype: (a boolean)
                 Use data type of first file (default).
                 argument: ``-filetype``
                 mutually_exclusive: format_filetype, format_byte, format_short,
                 format_int, format_long, format_float, format_double,
                 format_signed, format_unsigned
format_byte: (a boolean)
              Write out byte data.
              argument: ``-byte``
              mutually_exclusive: format_filetype, format_byte, format_short,
              format_int, format_long, format_float, format_double,
              format_signed, format_unsigned
```

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```

format_short: (a boolean)
    Write out short integer data.
    argument: ``-short``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_int: (a boolean)
    Write out 32-bit integer data.
    argument: ``-int``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_long: (a boolean)
    Superseded by -int.
    argument: ``-long``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_float: (a boolean)
    Write out single-precision floating-point data.
    argument: ``-float``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_double: (a boolean)
    Write out double-precision floating-point data.
    argument: ``-double``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_signed: (a boolean)
    Write signed integer data.
    argument: ``-signed``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_unsigned: (a boolean)
    Write unsigned integer data (default).
    argument: ``-unsigned``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
max_buffer_size_in_kb: (a long integer >= 0, nipy default value:
    4096)
    Specify the maximum size of the internal buffers (in kbytes).
    argument: ``-max_buffer_size_in_kb %d``
normalize: (a boolean)
    Normalize data sets for mean intensity.
    argument: ``-normalize``
    mutually_exclusive: normalize, nonnormalize
nonnormalize: (a boolean)
    Do not normalize data sets (default).
    argument: ``-nonnormalize``
    mutually_exclusive: normalize, nonnormalize
voxel_range: (a tuple of the form: (an integer (int or long), an
    integer (int or long)))
    Valid range for output data.

```

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```

        argument: ``-range %d %d``
sdfilename: (a pathlike object or string representing a file)
    Specify an output sd file (default=None).
    argument: ``-sdfilename %s``
copy_header: (a boolean)
    Copy all of the header from the first file (default for one file).
    argument: ``-copy_header``
    mutually_exclusive: copy_header, no_copy_header
no_copy_header: (a boolean)
    Do not copy all of the header from the first file (default for many
    files)).
    argument: ``-nocopy_header``
    mutually_exclusive: copy_header, no_copy_header
avgdim: (a unicode string)
    Specify a dimension along which we wish to average.
    argument: ``-avgdim %s``
binarize: (a boolean)
    Binarize the volume by looking for values in a given range.
    argument: ``-binarize``
binrange: (a tuple of the form: (a float, a float))
    Specify a range for binarization. Default value: 1.79769e+308
    -1.79769e+308.
    argument: ``-binrange %s %s``
binvalue: (a float)
    Specify a target value (+/- 0.5) for binarization. Default value:
    -1.79769e+308
    argument: ``-binvalue %s``
weights: (a list of items which are a unicode string)
    Specify weights for averaging ("

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
    file)
    output file

```

64.2.2 BBox[Link to code](#)

Wraps the executable command mincbbox.

Determine a bounding box of image.

Examples

```
>>> from nipyre.interfaces.minc import BBox
>>> from nipyre.interfaces.minc.testdata import nonempty_minc_data
```

```
>>> file0 = nonempty_minc_data(0)
>>> bbox = BBox(input_file=file0)
>>> bbox.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_file: (a pathlike object or string representing an existing
            file)
            input file
            argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
            output file containing bounding box corners
threshold: (an integer (int or long))
            VIO_Real value threshold for bounding box. Default value: 0.
            argument: ``-threshold``
one_line: (a boolean)
            Output on one line (default): start_x y z width_x y z
            argument: ``-one_line``
            mutually_exclusive: one_line, two_lines
two_lines: (a boolean)
            Output on two lines: start_x y z
            width_x y z
            argument: ``-two_lines``
            mutually_exclusive: one_line, two_lines
format_mincre-sample: (a boolean)
            Output format for mincre-sample: (-step x y z -start x y z -nelements
            x y z
            argument: ``-mincre-sample``
format_mincre-shape: (a boolean)
            Output format for mincre-shape: (-start x,y,z -count dx,dy,dz
            argument: ``-mincre-shape``
format_minccrop: (a boolean)
            Output format for minccrop: (-xlim x1 x2 -ylim y1 y2 -zlim z1 z2
            argument: ``-minccrop``
out_file: (a pathlike object or string representing a file)
            argument: ``> %s``, position: -1
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
            of class 'str' and with values which are a bytes or None or a
            value of class 'str', nipyre default value: {})
            Environment variables
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
            file)
            output file containing bounding box corners
```

64.2.3 Beast

[Link to code](#)

Wraps the executable command mincbeast.

Extract brain image using BEaST (Brain Extraction using non-local Segmentation Technique).

Examples

```
>>> from nipy.interfaces.minc import Beast
>>> from nipy.interfaces.minc.testdata import nonempty_minc_data
```

```
>>> file0 = nonempty_minc_data(0)
>>> beast = Beast(input_file=file0)
>>> beast.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
library_dir: (a pathlike object or string representing a directory)
    library directory
    argument: ``%s``, position: -3
input_file: (a pathlike object or string representing a file)
    input file
    argument: ``%s``, position: -2

[Optional]
probability_map: (a boolean)
    Output the probability map instead of crisp mask.
    argument: ``-probability``
flip_images: (a boolean)
    Flip images around the mid-sagittal plane to increase patch count.
    argument: ``-flip``
load_moments: (a boolean)
    Do not calculate moments instead use precalculatedlibrary moments.
    (for optimization purposes)
    argument: ``-load_moments``
fill_holes: (a boolean)
    Fill holes in the binary output.
    argument: ``-fill``
median_filter: (a boolean)
    Apply a median filter on the probability map.
    argument: ``-median``
nlm_filter: (a boolean)
    Apply an NLM filter on the probability map (experimental).
    argument: ``-nlm_filter``
clobber: (a boolean, nipy default value: True)
    Overwrite existing file.
    argument: ``-clobber``
configuration_file: (a pathlike object or string representing a file)
    Specify configuration file.
    argument: ``-configuration %s``
voxel_size: (an integer (int or long), nipy default value: 4)
    Specify voxel size for calculations (4, 2, or 1).Default value: 4.
    Assumes no multiscale. Use configurationfile for multiscale.
    argument: ``-voxel_size %s``
abspath: (a boolean, nipy default value: True)
    File paths in the library are absolute (default is relative to
```

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```

        library root).
        argument: ``-abspath``
patch_size: (an integer (int or long), nipy default value: 1)
    Specify patch size for single scale approach. Default value: 1.
    argument: ``-patch_size %s``
search_area: (an integer (int or long), nipy default value: 2)
    Specify size of search area for single scale approach. Default
    value: 2.
    argument: ``-search_area %s``
confidence_level_alpha: (a float, nipy default value: 0.5)
    Specify confidence level Alpha. Default value: 0.5
    argument: ``-alpha %s``
smoothness_factor_beta: (a float, nipy default value: 0.5)
    Specify smoothness factor Beta. Default value: 0.25
    argument: ``-beta %s``
threshold_patch_selection: (a float, nipy default value: 0.95)
    Specify threshold for patch selection. Default value: 0.95
    argument: ``-threshold %s``
number_selected_images: (an integer (int or long), nipy default
    value: 20)
    Specify number of selected images. Default value: 20
    argument: ``-selection_num %s``
same_resolution: (a boolean)
    Output final mask with the same resolution as input file.
    argument: ``-same_resolution``
output_file: (a pathlike object or string representing a file)
    output file
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
    file)
    output mask file

```

64.2.4 BestLinReg[Link to code](#)

Wraps the executable command bestlinreg.

Hierachial linear fitting between two files.

The bestlinreg script is part of the EZminc package:

<https://github.com/BIC-MNI/EZminc/blob/master/scripts/bestlinreg.pl>**Examples**

```

>>> from nipy.interfaces.minc import BestLinReg
>>> from nipy.interfaces.minc.testdata import nonempty_minc_data

```

```
>>> input_file = nonempty_minc_data(0)
>>> target_file = nonempty_minc_data(1)
>>> linreg = BestLinReg(source=input_file, target=target_file)
>>> linreg.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
source: (a pathlike object or string representing an existing file)
        source Minc file
        argument: ``%s``, position: -4
target: (a pathlike object or string representing an existing file)
        target Minc file
        argument: ``%s``, position: -3

[Optional]
output_xfm: (a pathlike object or string representing a file)
            output xfm file
            argument: ``%s``, position: -2
output_mnc: (a pathlike object or string representing a file)
            output mnc file
            argument: ``%s``, position: -1
verbose: (a boolean)
          Print out log messages. Default: False.
          argument: ``-verbose``
clobber: (a boolean, nipyre default value: True)
          Overwrite existing file.
          argument: ``-clobber``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyre default value: {})
          Environment variables
```

Outputs:

```
output_xfm: (a pathlike object or string representing an existing
            file)
            output xfm file
output_mnc: (a pathlike object or string representing an existing
            file)
            output mnc file
```

64.2.5 BigAverage

[Link to code](#)

Wraps the executable command `mincbigaverage`.

Average 1000's of MINC files in linear time.

`mincbigaverage` is designed to discretise the problem of averaging either a large number of input files or averaging a smaller number of large files. (>1GB each). There is also some code included to perform “robust” averaging in which only the most common features are kept via down-weighting outliers beyond a standard deviation.

One advantage of `mincbigaverage` is that it avoids issues around the number of possible open files in HDF/netCDF. In short if you have more than 100 files open at once while averaging things will slow down significantly.

`mincbigaverage` does this via a iterative approach to averaging files and is a direct drop in replacement for

mincaverage. That said not all the arguments of mincaverage are supported in mincbigaverage but they should be.

This tool is part of the minc-widgets package:

<https://github.com/BIC-MNI/minc-widgets/blob/master/mincbigaverage/mincbigaverage>

Examples

```
>>> from nipyte.interfaces.minc import BigAverage
>>> from nipyte.interfaces.minc.testdata import nonempty_minc_data
```

```
>>> files = [nonempty_minc_data(i) for i in range(3)]
>>> average = BigAverage(input_files=files, output_float=True, robust=True)
>>> average.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_files: (a list of items which are a pathlike object or string
              representing an existing file)
              input file(s)
              argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
              output file
              argument: ``%s``, position: -1
verbose: (a boolean)
          Print out log messages. Default: False.
          argument: ``--verbose``
clobber: (a boolean, nipyte default value: True)
          Overwrite existing file.
          argument: ``--clobber``
output_float: (a boolean)
              Output files with float precision.
              argument: ``--float``
robust: (a boolean)
        Perform robust averaging, features that are outside 1
        standarddeviation from the mean are downweighted. Works well for
        noisydata with artifacts. see the --tmpdir option if you have a large
        number of input files.
        argument: ``-robust``
tmpdir: (a pathlike object or string representing a directory)
        temporary files directory
        argument: ``-tmpdir %s``
sd_file: (a pathlike object or string representing a file)
        Place standard deviation image in specified file.
        argument: ``--sdfile %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyte default value: {})
          Environment variables
```

Outputs:

```

output_file: (a pathlike object or string representing an existing
              file)
              output file
sd_file: (a pathlike object or string representing an existing file)
          standard deviation image

```

64.2.6 Blob

[Link to code](#)

Wraps the executable command mincblob.

Calculate blobs from minc deformation grids.

Examples

```

>>> from nipy.interfaces.minc import Blob
>>> from nipy.interfaces.minc.testdata import minc2Dfile

```

```

>>> blob = Blob(input_file=minc2Dfile, output_file='/tmp/tmp.mnc', trace=True)
>>> blob.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
input_file: (a pathlike object or string representing an existing
             file)
             input file to blob
             argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
              output file
              argument: ``%s``, position: -1
trace: (a boolean)
        compute the trace (approximate growth and shrinkage) -- FAST
        argument: ``-trace``
determinant: (a boolean)
              compute the determinant (exact growth and shrinkage) -- SLOW
              argument: ``-determinant``
translation: (a boolean)
              compute translation (structure displacement)
              argument: ``-translation``
magnitude: (a boolean)
            compute the magnitude of the displacement vector
            argument: ``-magnitude``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
              file)
              output file

```

64.2.7 Blur

[Link to code](#)

Wraps the executable command `mincblur`.

Convolve an input volume with a Gaussian blurring kernel of user-defined width. Optionally, the first partial derivatives and the gradient magnitude volume can be calculated.

Examples

```
>>> from nipy.interfaces.minc import Blur
>>> from nipy.interfaces.minc.testdata import minc3Dfile
```

(1) Blur an input volume with a 6mm fwhm isotropic Gaussian blurring kernel:

```
>>> blur = Blur(input_file=minc3Dfile, fwhm=6, output_file_base='/tmp/out_6')
>>> blur.run() # doctest: +SKIP
```

`mincblur` will create `/tmp/out_6_blur.mnc`.

(2) Calculate the blurred and gradient magnitude data:

```
>>> blur = Blur(input_file=minc3Dfile, fwhm=6, gradient=True, output_file_base='/
↳tmp/out_6')
>>> blur.run() # doctest: +SKIP
```

will create `/tmp/out_6_blur.mnc` and `/tmp/out_6_dxyz.mnc`.

(3) Calculate the blurred data, the partial derivative volumes and the gradient magnitude for the same data:

```
>>> blur = Blur(input_file=minc3Dfile, fwhm=6, partial=True, output_file_base='/
↳tmp/out_6')
>>> blur.run() # doctest: +SKIP
```

will create `/tmp/out_6_blur.mnc`, `/tmp/out_6_dx.mnc`, `/tmp/out_6_dy.mnc`, `/tmp/out_6_dz.mnc` and `/tmp/out_6_dxyz.mnc`.

Inputs:

```
[Mandatory]
input_file: (a pathlike object or string representing an existing
             file)
             input file
             argument: ``%s``, position: -2
fwhm: (a float)
      Full-width-half-maximum of gaussian kernel. Default value: 0.
      argument: ``-fwhm %s``
      mutually_exclusive: fwhm, fwhm3d, standard_dev
standard_dev: (a float)
              Standard deviation of gaussian kernel. Default value: 0.
              argument: ``-standarddev %s``
              mutually_exclusive: fwhm, fwhm3d, standard_dev
fwhm3d: (a tuple of the form: (a float, a float, a float))
        Full-width-half-maximum of gaussian kernel. Default value:
        -1.79769e+308 -1.79769e+308 -1.79769e+308.
        argument: ``-3dfwhm %s %s %s``
        mutually_exclusive: fwhm, fwhm3d, standard_dev

[Optional]
output_file_base: (a pathlike object or string representing a file)
                  output file base
                  argument: ``%s``, position: -1
clobber: (a boolean, nipy default value: True)
```

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```

        Overwrite existing file.
        argument: ``-clobber``
gaussian: (a boolean)
        Use a gaussian smoothing kernel (default).
        argument: ``-gaussian``
        mutually_exclusive: gaussian, rect
rect: (a boolean)
        Use a rect (box) smoothing kernel.
        argument: ``-rect``
        mutually_exclusive: gaussian, rect
gradient: (a boolean)
        Create the gradient magnitude volume as well.
        argument: ``-gradient``
partial: (a boolean)
        Create the partial derivative and gradient magnitude volumes as
        well.
        argument: ``-partial``
no_apodize: (a boolean)
        Do not apodize the data before blurring.
        argument: ``-no_apodize``
dimensions: (3 or 1 or 2)
        Number of dimensions to blur (either 1,2 or 3). Default value: 3.
        argument: ``-dimensions %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
        file)
        Blurred output file.
gradient_dxyz: (a pathlike object or string representing a file)
        Gradient dxyz.
partial_dx: (a pathlike object or string representing a file)
        Partial gradient dx.
partial_dy: (a pathlike object or string representing a file)
        Partial gradient dy.
partial_dz: (a pathlike object or string representing a file)
        Partial gradient dz.
partial_dxyz: (a pathlike object or string representing a file)
        Partial gradient dxyz.

```

64.2.8 Calc[Link to code](#)

Wraps the executable command minccalc.

Compute an expression using MINC files as input.

Examples

```
>>> from nipyre.interfaces.minc import Calc
>>> from nipyre.interfaces.minc.testdata import nonempty_minc_data
```

```
>>> file0 = nonempty_minc_data(0)
>>> file1 = nonempty_minc_data(1)
>>> calc = Calc(input_files=[file0, file1], output_file='/tmp/calc.mnc',
↳expression='A[0] + A[1]') # add files together
>>> calc.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_files: (a list of items which are a pathlike object or string
              representing an existing file)
              input file(s) for calculation
              argument: ``%s``, position: -2
filelist: (a pathlike object or string representing a file)
           Specify the name of a file containing input file names.
           argument: ``-filelist %s``
           mutually_exclusive: input_files, filelist
expression: (a unicode string)
            Expression to use in calculations.
            argument: ``-expression '%s'``
            mutually_exclusive: expression, expfile
expfile: (a pathlike object or string representing a file)
          Name of file containing expression.
          argument: ``-expfile %s``
          mutually_exclusive: expression, expfile

[Optional]
output_file: (a pathlike object or string representing a file)
             output file
             argument: ``%s``, position: -1
two: (a boolean)
      Create a MINC 2 output file.
      argument: ``-2``
clobber: (a boolean, nipyre default value: True)
          Overwrite existing file.
          argument: ``-clobber``
verbose: (a boolean)
          Print out log messages (default).
          argument: ``-verbose``
          mutually_exclusive: verbose, quiet
quiet: (a boolean)
        Do not print out log messages.
        argument: ``-quiet``
        mutually_exclusive: verbose, quiet
debug: (a boolean)
        Print out debugging messages.
        argument: ``-debug``
copy_header: (a boolean)
              Copy all of the header from the first file.
              argument: ``-copy_header``
              mutually_exclusive: copy_header, no_copy_header
no_copy_header: (a boolean)
                 Do not copy all of the header from the first file.
```

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```

        argument: ``-nocopy_header``
        mutually_exclusive: copy_header, no_copy_header
format_filetype: (a boolean)
    Use data type of first file (default).
    argument: ``-filetype``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_byte: (a boolean)
    Write out byte data.
    argument: ``-byte``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_short: (a boolean)
    Write out short integer data.
    argument: ``-short``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_int: (a boolean)
    Write out 32-bit integer data.
    argument: ``-int``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_long: (a boolean)
    Superseded by -int.
    argument: ``-long``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_float: (a boolean)
    Write out single-precision floating-point data.
    argument: ``-float``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_double: (a boolean)
    Write out double-precision floating-point data.
    argument: ``-double``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_signed: (a boolean)
    Write signed integer data.
    argument: ``-signed``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_unsigned: (a boolean)
    Write unsigned integer data (default).
    argument: ``-unsigned``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
voxel_range: (a tuple of the form: (an integer (int or long), an

```

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```

        integer (int or long))
        Valid range for output data.
        argument: ``-range %d %d``
max_buffer_size_in_kb: (a long integer >= 0)
        Specify the maximum size of the internal buffers (in kbytes).
        argument: ``-max_buffer_size_in_kb %d``
check_dimensions: (a boolean)
        Check that files have matching dimensions (default).
        argument: ``-check_dimensions``
        mutually_exclusive: check_dimensions, no_check_dimensions
no_check_dimensions: (a boolean)
        Do not check that files have matching dimensions.
        argument: ``-nocheck_dimensions``
        mutually_exclusive: check_dimensions, no_check_dimensions
ignore_nan: (a boolean)
        Ignore invalid data (NaN) for accumulations.
        argument: ``-ignore_nan``
propagate_nan: (a boolean)
        Invalid data in any file at a voxel produces a NaN (default).
        argument: ``-propagate_nan``
output_nan: (a boolean)
        Output NaN when an illegal operation is done (default).
        argument: ``-nan``
        mutually_exclusive: output_nan, output_zero, output_illegal_value
output_zero: (a boolean)
        Output zero when an illegal operation is done.
        argument: ``-zero``
        mutually_exclusive: output_nan, output_zero, output_illegal_value
output_illegal: (a boolean)
        Value to write out when an illegal operation is done. Default value:
        1.79769e+308
        argument: ``-illegal_value``
        mutually_exclusive: output_nan, output_zero, output_illegal_value
outfiles: (a list of items which are a tuple of the form: (a unicode
        string, a pathlike object or string representing a file))
eval_width: (an integer (int or long))
        Number of voxels to evaluate simultaneously.
        argument: ``-eval_width %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
        file)
        output file

```

64.2.9 Convert[Link to code](#)

Wraps the executable command mincconvert.
 convert between MINC 1 to MINC 2 format.

Examples

```
>>> from nipyre.interfaces.minc import Convert
>>> from nipyre.interfaces.minc.testdata import minc2Dfile
>>> c = Convert(input_file=minc2Dfile, output_file='/tmp/out.mnc', two=True) # 
↳ Convert to MINC2 format.
>>> c.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_file: (a pathlike object or string representing an existing
            file)
            input file for converting
            argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
            output file
            argument: ``%s``, position: -1
clobber: (a boolean, nipyre default value: True)
            Overwrite existing file.
            argument: ``-clobber``
two: (a boolean)
            Create a MINC 2 output file.
            argument: ``-2``
template: (a boolean)
            Create a template file. The dimensions, variables, and attributes of
            the input file are preserved but all data is set to zero.
            argument: ``-template``
compression: (0 or 1 or 2 or 3 or 4 or 5 or 6 or 7 or 8 or 9)
            Set the compression level, from 0 (disabled) to 9 (maximum).
            argument: ``-compress %s``
chunk: (a long integer >= 0)
            Set the target block size for chunking (0 default, >1 block size).
            argument: ``-chunk %d``
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyre default value: {})
            Environment variables
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
            file)
            output file
```

64.2.10 Copy

[Link to code](#)

Wraps the executable command `minccopy`.

Copy image values from one MINC file to another. Both the input and output files must exist, and the images in both files must have an equal number of dimensions and equal dimension lengths.

NOTE: This program is intended primarily for use with scripts such as `mincedit`. It does not follow the typical design rules of most MINC command-line tools and therefore should be used only with caution.

Inputs:

```
[Mandatory]
input_file: (a pathlike object or string representing an existing
            file)
            input file to copy
            argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
            output file
            argument: ``%s``, position: -1
pixel_values: (a boolean)
            Copy pixel values as is.
            argument: ``-pixel_values``
            mutually_exclusive: pixel_values, real_values
real_values: (a boolean)
            Copy real pixel intensities (default).
            argument: ``-real_values``
            mutually_exclusive: pixel_values, real_values
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
            file)
            output file
```

64.2.11 Dump

[Link to code](#)

Wraps the executable command mincdump.

Dump a MINC file. Typically used in conjunction with mincgen (see Gen).

Examples

```
>>> from nipy.interfaces.minc import Dump
>>> from nipy.interfaces.minc.testdata import minc2Dfile
```

```
>>> dump = Dump(input_file=minc2Dfile)
>>> dump.run() # doctest: +SKIP
```

```
>>> dump = Dump(input_file=minc2Dfile, output_file='/tmp/out.txt', precision=(3,
↪4))
>>> dump.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_file: (a pathlike object or string representing an existing
```

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```

        file)
    input file
    argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
    output file
coordinate_data: (a boolean)
    Coordinate variable data and header information.
    argument: ``-c``
    mutually_exclusive: coordinate_data, header_data
header_data: (a boolean)
    Header information only, no data.
    argument: ``-h``
    mutually_exclusive: coordinate_data, header_data
annotations_brief: ('c' or 'f')
    Brief annotations for C or Fortran indices in data.
    argument: ``-b %s``
    mutually_exclusive: annotations_brief, annotations_full
annotations_full: ('c' or 'f')
    Full annotations for C or Fortran indices in data.
    argument: ``-f %s``
    mutually_exclusive: annotations_brief, annotations_full
variables: (a list of items which are a unicode string)
    Output data for specified variables only.
    argument: ``-v %s``
line_length: (a long integer >= 0)
    Line length maximum in data section (default 80).
    argument: ``-l %d``
netcdf_name: (a unicode string)
    Name for netCDF (default derived from file name).
    argument: ``-n %s``
precision: (an integer (int or long) or a tuple of the form: (an
    integer (int or long), an integer (int or long)))
    Display floating-point values with less precision
    argument: ``%s``
out_file: (a pathlike object or string representing a file)
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
    file)
    output file

```

64.2.12 Extract[Link to code](#)

Wraps the executable command mincextract.

Dump a hyperslab of MINC file data.

Examples

```
>>> from nipyre.interfaces.minc import Extract
>>> from nipyre.interfaces.minc.testdata import minc2Dfile
```

```
>>> extract = Extract(input_file=minc2Dfile)
>>> extract.run() # doctest: +SKIP
```

```
>>> extract = Extract(input_file=minc2Dfile, start=[3, 10, 5], count=[4, 4, 4]) #_
↪extract a 4x4x4 slab at offset [3, 10, 5]
>>> extract.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_file: (a pathlike object or string representing an existing
            file)
            input file
            argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
            output file
write_ascii: (a boolean)
            Write out data as ascii strings (default).
            argument: ``-ascii``
            mutually_exclusive: write_ascii, write_ascii, write_byte,
            write_short, write_int, write_long, write_float, write_double,
            write_signed, write_unsigned
write_byte: (a boolean)
            Write out data as bytes.
            argument: ``-byte``
            mutually_exclusive: write_ascii, write_ascii, write_byte,
            write_short, write_int, write_long, write_float, write_double,
            write_signed, write_unsigned
write_short: (a boolean)
            Write out data as short integers.
            argument: ``-short``
            mutually_exclusive: write_ascii, write_ascii, write_byte,
            write_short, write_int, write_long, write_float, write_double,
            write_signed, write_unsigned
write_int: (a boolean)
            Write out data as 32-bit integers.
            argument: ``-int``
            mutually_exclusive: write_ascii, write_ascii, write_byte,
            write_short, write_int, write_long, write_float, write_double,
            write_signed, write_unsigned
write_long: (a boolean)
            Superseded by write_int.
            argument: ``-long``
            mutually_exclusive: write_ascii, write_ascii, write_byte,
            write_short, write_int, write_long, write_float, write_double,
            write_signed, write_unsigned
write_float: (a boolean)
            Write out data as single precision floating-point values.
            argument: ``-float``
            mutually_exclusive: write_ascii, write_ascii, write_byte,
```

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```

        write_short, write_int, write_long, write_float, write_double,
        write_signed, write_unsigned
write_double: (a boolean)
    Write out data as double precision floating-point values.
    argument: ``-double``
    mutually_exclusive: write_ascii, write_ascii, write_byte,
        write_short, write_int, write_long, write_float, write_double,
        write_signed, write_unsigned
write_signed: (a boolean)
    Write out signed data.
    argument: ``-signed``
    mutually_exclusive: write_signed, write_unsigned
write_unsigned: (a boolean)
    Write out unsigned data.
    argument: ``-unsigned``
    mutually_exclusive: write_signed, write_unsigned
write_range: (a tuple of the form: (a float, a float))
    Specify the range of output values
    Default value: 1.79769e+308 1.79769e+308.
    argument: ``-range %s %s``
normalize: (a boolean)
    Normalize integer pixel values to file max and min.
    argument: ``-normalize``
    mutually_exclusive: normalize, nonnormalize
nonnormalize: (a boolean)
    Turn off pixel normalization.
    argument: ``-nonnormalize``
    mutually_exclusive: normalize, nonnormalize
image_range: (a tuple of the form: (a float, a float))
    Specify the range of real image values for normalization.
    argument: ``-image_range %s %s``
image_minimum: (a float)
    Specify the minimum real image value for normalization.Default
    value: 1.79769e+308.
    argument: ``-image_minimum %s``
image_maximum: (a float)
    Specify the maximum real image value for normalization.Default
    value: 1.79769e+308.
    argument: ``-image_maximum %s``
start: (a list of items which are an integer (int or long))
    Specifies corner of hyperslab (C conventions for indices).
    argument: ``-start %s``
count: (a list of items which are an integer (int or long))
    Specifies edge lengths of hyperslab to read.
    argument: ``-count %s``
flip_positive_direction: (a boolean)
    Flip images to always have positive direction.
    argument: ``-positive_direction``
    mutually_exclusive: flip_positive_direction,
        flip_negative_direction, flip_any_direction
flip_negative_direction: (a boolean)
    Flip images to always have negative direction.
    argument: ``-negative_direction``
    mutually_exclusive: flip_positive_direction,
        flip_negative_direction, flip_any_direction
flip_any_direction: (a boolean)
    Do not flip images (Default).

```

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```

    argument: ``-any_direction``
    mutually_exclusive: flip_positive_direction,
        flip_negative_direction, flip_any_direction
flip_x_positive: (a boolean)
    Flip images to give positive xspace:step value (left-to-right).
    argument: ``+xdirection``
    mutually_exclusive: flip_x_positive, flip_x_negative, flip_x_any
flip_x_negative: (a boolean)
    Flip images to give negative xspace:step value (right-to-left).
    argument: ``-xdirection``
    mutually_exclusive: flip_x_positive, flip_x_negative, flip_x_any
flip_x_any: (a boolean)
    Don't flip images along x-axis (default).
    argument: ``-xanydirection``
    mutually_exclusive: flip_x_positive, flip_x_negative, flip_x_any
flip_y_positive: (a boolean)
    Flip images to give positive yspace:step value (post-to-ant).
    argument: ``+ydirection``
    mutually_exclusive: flip_y_positive, flip_y_negative, flip_y_any
flip_y_negative: (a boolean)
    Flip images to give negative yspace:step value (ant-to-post).
    argument: ``-ydirection``
    mutually_exclusive: flip_y_positive, flip_y_negative, flip_y_any
flip_y_any: (a boolean)
    Don't flip images along y-axis (default).
    argument: ``-yanydirection``
    mutually_exclusive: flip_y_positive, flip_y_negative, flip_y_any
flip_z_positive: (a boolean)
    Flip images to give positive zspace:step value (inf-to-sup).
    argument: ``+zdirection``
    mutually_exclusive: flip_z_positive, flip_z_negative, flip_z_any
flip_z_negative: (a boolean)
    Flip images to give negative zspace:step value (sup-to-inf).
    argument: ``-zdirection``
    mutually_exclusive: flip_z_positive, flip_z_negative, flip_z_any
flip_z_any: (a boolean)
    Don't flip images along z-axis (default).
    argument: ``-zanydirection``
    mutually_exclusive: flip_z_positive, flip_z_negative, flip_z_any
out_file: (a pathlike object or string representing a file)
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
    file)
    output file in raw/text format

```

64.2.13 Gennlxfm

[Link to code](#)

Wraps the executable command `gennlxfm`.

Generate nonlinear xfms. Currently only identity xfms are supported!

This tool is part of minc-widgets:

<https://github.com/BIC-MNI/minc-widgets/blob/master/gennlxfm/gennlxfm>

Examples

```
>>> from nipy.interfaces.minc import Gennlxfm
>>> from nipy.interfaces.minc.testdata import minc2Dfile
>>> gennlxfm = Gennlxfm(step=1, like=minc2Dfile)
>>> gennlxfm.run() # doctest: +SKIP
```

Inputs:

```
[Optional]
output_file: (a pathlike object or string representing a file)
    output file
    argument: ``%s``, position: -1
verbose: (a boolean)
    Print out log messages. Default: False.
    argument: ``-verbose``
clobber: (a boolean, nipy default value: True)
    Overwrite existing file.
    argument: ``-clobber``
ident: (a boolean)
    Generate an identity xfm. Default: False.
    argument: ``-ident``
step: (an integer (int or long))
    Output ident xfm step [default: 1].
    argument: ``-step %s``
like: (a pathlike object or string representing an existing file)
    Generate a nlxfm like this file.
    argument: ``-like %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
    file)
    output file
output_grid: (a pathlike object or string representing an existing
    file)
    output grid
```

64.2.14 Math

[Link to code](#)

Wraps the executable command `mincmath`.

Various mathematical operations supplied by mincmath.

Examples

```
>>> from nipy.interfaces.minc import Math
>>> from nipy.interfaces.minc.testdata import minc2Dfile
```

Scale: volume*3.0 + 2:

```
>>> scale = Math(input_files=[minc2Dfile], scale=(3.0, 2))
>>> scale.run() # doctest: +SKIP
```

Test if >= 1.5:

```
>>> gt = Math(input_files=[minc2Dfile], test_gt=1.5)
>>> gt.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_files: (a list of items which are a pathlike object or string
              representing an existing file)
              input file(s) for calculation
              argument: ``%s``, position: -2
              mutually_exclusive: input_files, filelist
filelist: (a pathlike object or string representing an existing file)
           Specify the name of a file containing input file names.
           argument: ``-filelist %s``
           mutually_exclusive: input_files, filelist

[Optional]
output_file: (a pathlike object or string representing a file)
              output file
              argument: ``%s``, position: -1
clobber: (a boolean, nipy default value: True)
           Overwrite existing file.
           argument: ``-clobber``
two: (a boolean)
      Create a MINC 2 output file.
      argument: ``-2``
copy_header: (a boolean)
              Copy all of the header from the first file (default for one file).
              argument: ``-copy_header``
              mutually_exclusive: copy_header, no_copy_header
no_copy_header: (a boolean)
                 Do not copy all of the header from the first file (default for many
                 files)).
                 argument: ``-nocopy_header``
                 mutually_exclusive: copy_header, no_copy_header
format_filetype: (a boolean)
                  Use data type of first file (default).
                  argument: ``-filetype``
                  mutually_exclusive: format_filetype, format_byte, format_short,
                  format_int, format_long, format_float, format_double,
                  format_signed, format_unsigned
format_byte: (a boolean)
              Write out byte data.
              argument: ``-byte``
              mutually_exclusive: format_filetype, format_byte, format_short,
              format_int, format_long, format_float, format_double,
              format_signed, format_unsigned
```

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```
format_short: (a boolean)
    Write out short integer data.
    argument: ``-short``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_int: (a boolean)
    Write out 32-bit integer data.
    argument: ``-int``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_long: (a boolean)
    Superseded by -int.
    argument: ``-long``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_float: (a boolean)
    Write out single-precision floating-point data.
    argument: ``-float``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_double: (a boolean)
    Write out double-precision floating-point data.
    argument: ``-double``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_signed: (a boolean)
    Write signed integer data.
    argument: ``-signed``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
format_unsigned: (a boolean)
    Write unsigned integer data (default).
    argument: ``-unsigned``
    mutually_exclusive: format_filetype, format_byte, format_short,
        format_int, format_long, format_float, format_double,
        format_signed, format_unsigned
voxel_range: (a tuple of the form: (an integer (int or long), an
    integer (int or long)))
    Valid range for output data.
    argument: ``-range %d %d``
max_buffer_size_in_kb: (a long integer >= 0, nipy default value:
    4096)
    Specify the maximum size of the internal buffers (in kbytes).
    argument: ``-max_buffer_size_in_kb %d``
check_dimensions: (a boolean)
    Check that dimension info matches across files (default).
    argument: ``-check_dimensions``
    mutually_exclusive: check_dimensions, no_check_dimensions
no_check_dimensions: (a boolean)
    Do not check dimension info.
    argument: ``-nocheck_dimensions``
```

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```

    mutually_exclusive: check_dimensions, no_check_dimensions
dimension: (a unicode string)
    Specify a dimension along which we wish to perform a calculation.
    argument: ``-dimension %s``
ignore_nan: (a boolean)
    Ignore invalid data (NaN) for accumulations.
    argument: ``-ignore_nan``
propagate_nan: (a boolean)
    Invalid data in any file at a voxel produces a NaN (default).
    argument: ``-propagate_nan``
output_nan: (a boolean)
    Output NaN when an illegal operation is done (default).
    argument: ``-nan``
    mutually_exclusive: output_nan, output_zero, output_illegal_value
output_zero: (a boolean)
    Output zero when an illegal operation is done.
    argument: ``-zero``
    mutually_exclusive: output_nan, output_zero, output_illegal_value
output_illegal: (a boolean)
    Value to write out when an illegal operation is done. Default value:
    1.79769e+308
    argument: ``-illegal_value``
    mutually_exclusive: output_nan, output_zero, output_illegal_value
test_gt: (a boolean or a float)
    Test for vol1 > vol2 or vol1 > constant.
    argument: ``-gt``
test_lt: (a boolean or a float)
    Test for vol1 < vol2 or vol1 < constant.
    argument: ``-lt``
test_eq: (a boolean or a float)
    Test for integer vol1 == vol2 or vol1 == constant.
    argument: ``-eq``
test_ne: (a boolean or a float)
    Test for integer vol1 != vol2 or vol1 != const.
    argument: ``-ne``
test_ge: (a boolean or a float)
    Test for vol1 >= vol2 or vol1 >= const.
    argument: ``-ge``
test_le: (a boolean or a float)
    Test for vol1 <= vol2 or vol1 <= const.
    argument: ``-le``
calc_add: (a boolean or a float)
    Add N volumes or volume + constant.
    argument: ``-add``
calc_sub: (a boolean or a float)
    Subtract 2 volumes or volume - constant.
    argument: ``-sub``
calc_mul: (a boolean or a float)
    Multiply N volumes or volume * constant.
    argument: ``-mult``
calc_div: (a boolean or a float)
    Divide 2 volumes or volume / constant.
    argument: ``-div``
invert: (a float)
    Calculate 1/c.
    argument: ``-invert -const %s``
calc_not: (a boolean)

```

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```

        Calculate !vol1.
        argument: ``-not``
sqrt: (a boolean)
    Take square root of a volume.
    argument: ``-sqrt``
square: (a boolean)
    Take square of a volume.
    argument: ``-square``
abs: (a boolean)
    Take absolute value of a volume.
    argument: ``-abs``
exp: (a tuple of the form: (a float, a float))
    Calculate  $c2 * \exp(c1 * x)$ . Both constants must be specified.
    argument: ``-exp -const2 %s %s``
log: (a tuple of the form: (a float, a float))
    Calculate  $\log(x/c2)/c1$ . The constants  $c1$  and  $c2$  default to 1.
    argument: ``-log -const2 %s %s``
scale: (a tuple of the form: (a float, a float))
    Scale a volume:  $\text{volume} * c1 + c2$ .
    argument: ``-scale -const2 %s %s``
clamp: (a tuple of the form: (a float, a float))
    Clamp a volume to lie between two values.
    argument: ``-clamp -const2 %s %s``
segment: (a tuple of the form: (a float, a float))
    Segment a volume using range of -const2: within range = 1, outside
    range = 0.
    argument: ``-segment -const2 %s %s``
nsegment: (a tuple of the form: (a float, a float))
    Opposite of -segment: within range = 0, outside range = 1.
    argument: ``-nsegment -const2 %s %s``
isnan: (a boolean)
    Test for NaN values in vol1.
    argument: ``-isnan``
nisnan: (a boolean)
    Negation of -isnan.
    argument: ``-nisnan``
percentdiff: (a float)
    Percent difference between 2 volumes, thresholded (const def=0.0).
    argument: ``-percentdiff``
count_valid: (a boolean)
    Count the number of valid values in N volumes.
    argument: ``-count_valid``
maximum: (a boolean)
    Find maximum of N volumes.
    argument: ``-maximum``
minimum: (a boolean)
    Find minimum of N volumes.
    argument: ``-minimum``
calc_and: (a boolean)
    Calculate  $\text{vol1} \&\& \text{vol2} (\&\& \dots)$ .
    argument: ``-and``
calc_or: (a boolean)
    Calculate  $\text{vol1} || \text{vol2} (|| \dots)$ .
    argument: ``-or``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``

```

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```
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipyte default value: {})
Environment variables
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
             file)
             output file
```

64.2.15 NlpFit

[Link to code](#)

Wraps the executable command nlpfit.

Hierarchial non-linear fitting with blurring.

This tool is part of the minc-widgets package:

<https://github.com/BIC-MNI/minc-widgets/blob/master/nlpfit/nlpfit>**Examples**

```
>>> from nipyte.interfaces.minc import NlpFit
>>> from nipyte.interfaces.minc.testdata import nonempty_minc_data, nlp_config
>>> from nipyte.testing import example_data
```

```
>>> source = nonempty_minc_data(0)
>>> target = nonempty_minc_data(1)
>>> source_mask = nonempty_minc_data(2)
>>> config = nlp_config
>>> initial = example_data('minc_initial.xfm')
>>> nlpfit = NlpFit(config_file=config, init_xfm=initial, source_mask=source_mask,
→ source=source, target=target)
>>> nlpfit.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
source: (a pathlike object or string representing an existing file)
        source Minc file
        argument: ``%s``, position: -3
target: (a pathlike object or string representing an existing file)
        target Minc file
        argument: ``%s``, position: -2
config_file: (a pathlike object or string representing an existing
             file)
             File containing the fitting configuration use.
             argument: ``-config_file %s``
init_xfm: (a pathlike object or string representing an existing file)
          Initial transformation (default identity).
          argument: ``-init_xfm %s``
source_mask: (a pathlike object or string representing an existing
             file)
             Source mask to use during fitting.
             argument: ``-source_mask %s``
```

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```
[Optional]
output_xfm: (a pathlike object or string representing a file)
    output xfm file
    argument: ``%s``, position: -1
input_grid_files: (a list of items which are a pathlike object or
    string representing a file)
    input grid file(s)
verbose: (a boolean)
    Print out log messages. Default: False.
    argument: ``-verbose``
clobber: (a boolean, nipy default value: True)
    Overwrite existing file.
    argument: ``-clobber``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
output_xfm: (a pathlike object or string representing an existing
    file)
    output xfm file
output_grid: (a pathlike object or string representing an existing
    file)
    output grid file
```

64.2.16 Norm[Link to code](#)

Wraps the executable command mincnorm.

Normalise a file between a max and minimum (possibly) using two histogram pct's.**Examples**

```
>>> from nipy.interfaces.minc import Norm
>>> from nipy.interfaces.minc.testdata import minc2Dfile
>>> n = Norm(input_file=minc2Dfile, output_file='/tmp/out.mnc') # Normalise the_
↪file.
>>> n.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_file: (a pathlike object or string representing an existing
    file)
    input file to normalise
    argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
    output file
    argument: ``%s``, position: -1
```

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```

output_threshold_mask: (a pathlike object or string representing a
    file)
    File in which to store the threshold mask.
    argument: ``-threshold_mask %s``
clobber: (a boolean, nipy default value: True)
    Overwrite existing file.
    argument: ``-clobber``
mask: (a pathlike object or string representing an existing file)
    Calculate the image normalisation within a mask.
    argument: ``-mask %s``
clamp: (a boolean, nipy default value: True)
    Force the output range between limits [default].
    argument: ``-clamp``
cutoff: (0.0 <= a floating point number <= 100.0)
    Cutoff value to use to calculate thresholds by a histogram PcT in %.
    [default: 0.01]
    argument: ``-cutoff %s``
lower: (a float)
    Lower real value to use.
    argument: ``-lower %s``
upper: (a float)
    Upper real value to use.
    argument: ``-upper %s``
out_floor: (a float)
    Output files maximum [default: 0]
    argument: ``-out_floor %s``
out_ceil: (a float)
    Output files minimum [default: 100]
    argument: ``-out_ceil %s``
threshold: (a boolean)
    Threshold the image (set values below threshold_perc to -out_floor).
    argument: ``-threshold``
threshold_perc: (0.0 <= a floating point number <= 100.0)
    Threshold percentage (0.1 == lower 10% of intensity range) [default:
    0.1].
    argument: ``-threshold_perc %s``
threshold_bmt: (a boolean)
    Use the resulting image BiModalT as the threshold.
    argument: ``-threshold_bmt``
threshold_blur: (a float)
    Blur FWHM for intensity edges then thresholding [default: 2].
    argument: ``-threshold_blur %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
    file)
    output file
output_threshold_mask: (a pathlike object or string representing a
    file)

```

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threshold mask file

64.2.17 Pik

[Link to code](#)

Wraps the executable command mincpik.

Generate images from minc files.

Mincpik uses Imagemagick to generate images from Minc files.

Examples

```
>>> from nipy.interfaces.minc import Pik
>>> from nipy.interfaces.minc.testdata import nonempty_minc_data
```

```
>>> file0 = nonempty_minc_data(0)
>>> pik = Pik(input_file=file0, title='foo')
>>> pik.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_file: (a pathlike object or string representing an existing
             file)
             input file
             argument: ``%s``, position: -2

[Optional]
jpg: (a boolean)
     Output a jpg file.
     mutually_exclusive: jpg, png
png: (a boolean)
     Output a png file (default).
     mutually_exclusive: jpg, png
output_file: (a pathlike object or string representing a file)
             output file
             argument: ``%s``, position: -1
clobber: (a boolean, nipy default value: True)
          Overwrite existing file.
          argument: ``-clobber``
scale: (an integer (int or long), nipy default value: 2)
        Scaling factor for resulting image. By default images are output at
        twice their original resolution.
        argument: ``--scale %s``
width: (an integer (int or long))
        Autoscale the resulting image to have a fixed image width (in
        pixels).
        argument: ``--width %s``
depth: (8 or 16)
        Bitdepth for resulting image 8 or 16 (MSB machines only!)
        argument: ``--depth %s``
title: (a boolean or a unicode string)
        argument: ``%s``
title_size: (an integer (int or long))
             Font point size for the title.
             argument: ``--title_size %s``
```

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```

    requires: title
annotated_bar: (a boolean)
    create an annotated bar to match the image (use height of the output
    image)
    argument: ``--anot_bar``
minc_range: (a tuple of the form: (a float, a float))
    Valid range of values for MINC file.
    argument: ``--range %s %s``
image_range: (a tuple of the form: (a float, a float))
    Range of image values to use for pixel intensity.
    argument: ``--image_range %s %s``
    mutually_exclusive: image_range, auto_range
auto_range: (a boolean)
    Automatically determine image range using a 5 and 95% PcT.
    (histogram)
    argument: ``--auto_range``
    mutually_exclusive: image_range, auto_range
start: (an integer (int or long))
    Slice number to get. (note this is in voxel co-ordinates).
    argument: ``--slice %s``
slice_z: (a boolean)
    Get an axial/transverse (z) slice.
    argument: ``-z``
    mutually_exclusive: slice_z, slice_y, slice_x
slice_y: (a boolean)
    Get a coronal (y) slice.
    argument: ``-y``
    mutually_exclusive: slice_z, slice_y, slice_x
slice_x: (a boolean)
    Get a sagittal (x) slice.
    argument: ``-x``
    mutually_exclusive: slice_z, slice_y, slice_x
triplanar: (a boolean)
    Create a triplanar view of the input file.
    argument: ``--triplanar``
tile_size: (an integer (int or long))
    Pixel size for each image in a triplanar.
    argument: ``--tilesize %s``
sagittal_offset: (an integer (int or long))
    Offset the sagittal slice from the centre.
    argument: ``--sagittal_offset %s``
sagittal_offset_perc: (0 <= a long integer <= 100)
    Offset the sagittal slice by a percentage from the centre.
    argument: ``--sagittal_offset_perc %d``
vertical_triplanar_view: (a boolean)
    Create a vertical triplanar view (Default).
    argument: ``--vertical``
    mutually_exclusive: vertical_triplanar_view,
        horizontal_triplanar_view
horizontal_triplanar_view: (a boolean)
    Create a horizontal triplanar view.
    argument: ``--horizontal``
    mutually_exclusive: vertical_triplanar_view,
        horizontal_triplanar_view
lookup: (a unicode string)
    Arguments to pass to minclookup
    argument: ``--lookup %s``

```

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```
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
              file)
              output image
```

64.2.18 Resample[Link to code](#)

Wraps the executable command mincresample.

Resample a minc file.'

Examples

```
>>> from nipy.interfaces.minc import Resample
>>> from nipy.interfaces.minc.testdata import minc2Dfile
>>> r = Resample(input_file=minc2Dfile, output_file='/tmp/out.mnc') # Resample_
↳the file.
>>> r.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_file: (a pathlike object or string representing an existing
             file)
             input file for resampling
             argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
             output file
             argument: ``%s``, position: -1
input_grid_files: (a list of items which are a pathlike object or
                  string representing a file)
                  input grid file(s)
two: (a boolean)
     Create a MINC 2 output file.
     argument: ``-2``
clobber: (a boolean, nipy default value: True)
         Overwrite existing file.
         argument: ``-clobber``
trilinear_interpolation: (a boolean)
                        Do trilinear interpolation.
                        argument: ``-trilinear``
                        mutually_exclusive: trilinear_interpolation, tricubic_interpolation,
                        nearest_neighbour_interpolation, sinc_interpolation
tricubic_interpolation: (a boolean)
                        Do tricubic interpolation.
```

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```

    argument: ``-tricubic``
    mutually_exclusive: trilinear_interpolation, tricubic_interpolation,
        nearest_neighbour_interpolation, sinc_interpolation
nearest_neighbour_interpolation: (a boolean)
    Do nearest neighbour interpolation.
    argument: ``-nearest_neighbour``
    mutually_exclusive: trilinear_interpolation, tricubic_interpolation,
        nearest_neighbour_interpolation, sinc_interpolation
sinc_interpolation: (a boolean)
    Do windowed sinc interpolation.
    argument: ``-sinc``
    mutually_exclusive: trilinear_interpolation, tricubic_interpolation,
        nearest_neighbour_interpolation, sinc_interpolation
half_width_sinc_window: (5 or 1 or 2 or 3 or 4 or 6 or 7 or 8 or 9 or
    10)
    Set half-width of sinc window (1-10). Default value: 5.
    argument: ``-width %s``
    requires: sinc_interpolation
sinc_window_hanning: (a boolean)
    Set sinc window type to Hanning.
    argument: ``-hanning``
    mutually_exclusive: sinc_window_hanning, sinc_window_hamming
    requires: sinc_interpolation
sinc_window_hamming: (a boolean)
    Set sinc window type to Hamming.
    argument: ``-hamming``
    mutually_exclusive: sinc_window_hanning, sinc_window_hamming
    requires: sinc_interpolation
transformation: (a pathlike object or string representing an existing
    file)
    File giving world transformation. (Default = identity).
    argument: ``-transformation %s``
invert_transformation: (a boolean)
    Invert the transformation before using it.
    argument: ``-invert_transformation``
vio_transform: (a boolean)
    VIO_Transform the input sampling with the transform (default).
    argument: ``-tfm_input_sampling``
    mutually_exclusive: vio_transform, no_input_sampling
no_input_sampling: (a boolean)
    Use the input sampling without transforming (old behaviour).
    argument: ``-use_input_sampling``
    mutually_exclusive: vio_transform, no_input_sampling
like: (a pathlike object or string representing an existing file)
    Specifies a model file for the resampling.
    argument: ``-like %s``
format_byte: (a boolean)
    Write out byte data.
    argument: ``-byte``
    mutually_exclusive: format_byte, format_short, format_int,
        format_long, format_float, format_double, format_signed,
        format_unsigned
format_short: (a boolean)
    Write out short integer data.
    argument: ``-short``
    mutually_exclusive: format_byte, format_short, format_int,
        format_long, format_float, format_double, format_signed,

```

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```

        format_unsigned
format_int: (a boolean)
    Write out 32-bit integer data.
    argument: ``-int``
    mutually_exclusive: format_byte, format_short, format_int,
        format_long, format_float, format_double, format_signed,
        format_unsigned
format_long: (a boolean)
    Superseded by -int.
    argument: ``-long``
    mutually_exclusive: format_byte, format_short, format_int,
        format_long, format_float, format_double, format_signed,
        format_unsigned
format_float: (a boolean)
    Write out single-precision floating-point data.
    argument: ``-float``
    mutually_exclusive: format_byte, format_short, format_int,
        format_long, format_float, format_double, format_signed,
        format_unsigned
format_double: (a boolean)
    Write out double-precision floating-point data.
    argument: ``-double``
    mutually_exclusive: format_byte, format_short, format_int,
        format_long, format_float, format_double, format_signed,
        format_unsigned
format_signed: (a boolean)
    Write signed integer data.
    argument: ``-signed``
    mutually_exclusive: format_byte, format_short, format_int,
        format_long, format_float, format_double, format_signed,
        format_unsigned
format_unsigned: (a boolean)
    Write unsigned integer data (default).
    argument: ``-unsigned``
    mutually_exclusive: format_byte, format_short, format_int,
        format_long, format_float, format_double, format_signed,
        format_unsigned
output_range: (a tuple of the form: (a float, a float))
    Valid range for output data. Default value: -1.79769e+308
    -1.79769e+308.
    argument: ``-range %s %s``
transverse_slices: (a boolean)
    Write out transverse slices.
    argument: ``-transverse``
    mutually_exclusive: transverse, sagittal, coronal
sagittal_slices: (a boolean)
    Write out sagittal slices
    argument: ``-sagittal``
    mutually_exclusive: transverse, sagittal, coronal
coronal_slices: (a boolean)
    Write out coronal slices
    argument: ``-coronal``
    mutually_exclusive: transverse, sagittal, coronal
no_fill: (a boolean)
    Use value zero for points outside of input volume.
    argument: ``-nofill``
    mutually_exclusive: nofill, fill

```

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```

fill: (a boolean)
    Use a fill value for points outside of input volume.
    argument: ``-fill``
    mutually_exclusive: nofill, fill
fill_value: (a float)
    Specify a fill value for points outside of input volume.Default
    value: 1.79769e+308.
    argument: ``-fillvalue %s``
    requires: fill
keep_real_range: (a boolean)
    Keep the real scale of the input volume.
    argument: ``-keep_real_range``
    mutually_exclusive: keep_real_range, nokeep_real_range
nokeep_real_range: (a boolean)
    Do not keep the real scale of the data (default).
    argument: ``-nokeep_real_range``
    mutually_exclusive: keep_real_range, nokeep_real_range
spacetype: (a unicode string)
    Set the spacetype attribute to a specified string.
    argument: ``-spacetype %s``
talairach: (a boolean)
    Output is in Talairach space.
    argument: ``-talairach``
origin: (a tuple of the form: (a float, a float, a float))
    Origin of first pixel in 3D space.Default value: 1.79769e+308
    1.79769e+308 1.79769e+308.
    argument: ``-origin %s %s %s``
standard_sampling: (a boolean)
    Set the sampling to standard values (step, start and dirs).
    argument: ``-standard_sampling``
units: (a unicode string)
    Specify the units of the output sampling.
    argument: ``-units %s``
nelements: (a tuple of the form: (an integer (int or long), an
    integer (int or long), an integer (int or long)))
    Number of elements along each dimension (X, Y, Z).
    argument: ``-nelements %s %s %s``
    mutually_exclusive: nelements, nelements_x_y_or_z
xnelements: (an integer (int or long))
    Number of elements along the X dimension.
    argument: ``-xnelements %s``
    mutually_exclusive: nelements, nelements_x_y_or_z
    requires: ynelements, znelements
ynelements: (an integer (int or long))
    Number of elements along the Y dimension.
    argument: ``-ynelements %s``
    mutually_exclusive: nelements, nelements_x_y_or_z
    requires: xnelements, znelements
znelements: (an integer (int or long))
    Number of elements along the Z dimension.
    argument: ``-znelements %s``
    mutually_exclusive: nelements, nelements_x_y_or_z
    requires: xnelements, ynelements
step: (a tuple of the form: (an integer (int or long), an integer
    (int or long), an integer (int or long)))
    Step size along each dimension (X, Y, Z). Default value: (0, 0, 0).
    argument: ``-step %s %s %s``

```

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```

        mutually_exclusive: nelements, nelements_x_y_or_z
xstep: (an integer (int or long))
    Step size along the X dimension. Default value: 0.
    argument: ``-xstep %s``
    mutually_exclusive: step, step_x_y_or_z
    requires: ystep, zstep
ystep: (an integer (int or long))
    Step size along the Y dimension. Default value: 0.
    argument: ``-ystep %s``
    mutually_exclusive: step, step_x_y_or_z
    requires: xstep, zstep
zstep: (an integer (int or long))
    Step size along the Z dimension. Default value: 0.
    argument: ``-zstep %s``
    mutually_exclusive: step, step_x_y_or_z
    requires: xstep, ystep
start: (a tuple of the form: (a float, a float, a float))
    Start point along each dimension (X, Y, Z).Default value:
    1.79769e+308 1.79769e+308 1.79769e+308.
    argument: ``-start %s %s %s``
    mutually_exclusive: nelements, nelements_x_y_or_z
xstart: (a float)
    Start point along the X dimension. Default value: 1.79769e+308.
    argument: ``-xstart %s``
    mutually_exclusive: start, start_x_y_or_z
    requires: ystart, zstart
ystart: (a float)
    Start point along the Y dimension. Default value: 1.79769e+308.
    argument: ``-ystart %s``
    mutually_exclusive: start, start_x_y_or_z
    requires: xstart, zstart
zstart: (a float)
    Start point along the Z dimension. Default value: 1.79769e+308.
    argument: ``-zstart %s``
    mutually_exclusive: start, start_x_y_or_z
    requires: xstart, ystart
dircos: (a tuple of the form: (a float, a float, a float))
    Direction cosines along each dimension (X, Y, Z). Default
    value:1.79769e+308 1.79769e+308 1.79769e+308 1.79769e+308 ...
    1.79769e+308 1.79769e+308 1.79769e+308 1.79769e+308 1.79769e+308.
    argument: ``-dircos %s %s %s``
    mutually_exclusive: nelements, nelements_x_y_or_z
xdircos: (a float)
    Direction cosines along the X dimension.Default value: 1.79769e+308
    1.79769e+308 1.79769e+308.
    argument: ``-xdircos %s``
    mutually_exclusive: dircos, dircos_x_y_or_z
    requires: ydircos, zdircos
ydircos: (a float)
    Direction cosines along the Y dimension.Default value: 1.79769e+308
    1.79769e+308 1.79769e+308.
    argument: ``-ydircos %s``
    mutually_exclusive: dircos, dircos_x_y_or_z
    requires: xdircos, zdircos
zdircos: (a float)
    Direction cosines along the Z dimension.Default value: 1.79769e+308
    1.79769e+308 1.79769e+308.

```

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```

    argument: ``-zdircos %s``
    mutually_exclusive: dircos, dircos_x_y_or_z
    requires: xdircos, ydircos
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
    file)
    output file

```

64.2.19 Reshape[Link to code](#)

Wraps the executable command mincreshape.

Cut a hyperslab out of a minc file, with dimension reordering.

This is also useful for rewriting with a different format, for example converting to short (see example below).

Examples

```

>>> from nipy.interfaces.minc import Reshape
>>> from nipy.interfaces.minc.testdata import nonempty_minc_data

```

```

>>> input_file = nonempty_minc_data(0)
>>> reshape_to_short = Reshape(input_file=input_file, write_short=True)
>>> reshape_to_short.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
input_file: (a pathlike object or string representing an existing
    file)
    input file
    argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
    output file
    argument: ``%s``, position: -1
verbose: (a boolean)
    Print out log messages. Default: False.
    argument: ``-verbose``
clobber: (a boolean, nipy default value: True)
    Overwrite existing file.
    argument: ``-clobber``
write_short: (a boolean)
    Convert to short integer data.
    argument: ``-short``
args: (a unicode string)

```

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```

    Additional parameters to the command
    argument: ``%s``
    environ: (a dictionary with keys which are a bytes or None or a value
              of class 'str' and with values which are a bytes or None or a
              value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
              file)
              output file

```

64.2.20 ToEcat[Link to code](#)

Wraps the executable command minctoecat.

Convert a 2D image, a 3D volumes or a 4D dynamic volumes written in MINC file format to a 2D, 3D or 4D Ecat7 file.

Examples

```

>>> from nipy.interfaces.minc import ToEcat
>>> from nipy.interfaces.minc.testdata import minc2Dfile

```

```

>>> c = ToEcat(input_file=minc2Dfile)
>>> c.run() # doctest: +SKIP

```

```

>>> c = ToEcat(input_file=minc2Dfile, voxels_as_integers=True)
>>> c.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
input_file: (a pathlike object or string representing an existing
             file)
             input file to convert
             argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
              output file
              argument: ``%s``, position: -1
ignore_patient_variable: (a boolean)
                          Ignore informations from the minc patient variable.
                          argument: ``-ignore_patient_variable``
ignore_study_variable: (a boolean)
                        Ignore informations from the minc study variable.
                        argument: ``-ignore_study_variable``
ignore_acquisition_variable: (a boolean)
                              Ignore informations from the minc acquisition variable.
                              argument: ``-ignore_acquisition_variable``
ignore_ecat_acquisition_variable: (a boolean)
                                   Ignore informations from the minc ecat_acquisition variable.
                                   argument: ``-ignore_ecat_acquisition_variable``

```

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```

ignore_ecat_main: (a boolean)
    Ignore informations from the minc ecat-main variable.
    argument: ``-ignore_ecat_main``
ignore_ecat_subheader_variable: (a boolean)
    Ignore informations from the minc ecat-subhdr variable.
    argument: ``-ignore_ecat_subheader_variable``
no_decay_corr_fctr: (a boolean)
    Do not compute the decay correction factors
    argument: ``-no_decay_corr_fctr``
voxels_as_integers: (a boolean)
    Voxel values are treated as integers, scale and calibration factors
    are set to unity
    argument: ``-label``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
    file)
    output file

```

64.2.21 ToRaw[Link to code](#)Wraps the executable command `minctoraw`.Dump a chunk of MINC file data. This program is largely superseded by `mincextract` (see `Extract`).**Examples**

```

>>> from nipy.interfaces.minc import ToRaw
>>> from nipy.interfaces.minc.testdata import minc2Dfile

```

```

>>> toraw = ToRaw(input_file=minc2Dfile)
>>> toraw.run() # doctest: +SKIP

```

```

>>> toraw = ToRaw(input_file=minc2Dfile, write_range=(0, 100))
>>> toraw.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
input_file: (a pathlike object or string representing an existing
    file)
    input file
    argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
    output file

```

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```
write_byte: (a boolean)
    Write out data as bytes.
    argument: ``-byte``
    mutually_exclusive: write_byte, write_short, write_int, write_long,
        write_float, write_double
write_short: (a boolean)
    Write out data as short integers.
    argument: ``-short``
    mutually_exclusive: write_byte, write_short, write_int, write_long,
        write_float, write_double
write_int: (a boolean)
    Write out data as 32-bit integers.
    argument: ``-int``
    mutually_exclusive: write_byte, write_short, write_int, write_long,
        write_float, write_double
write_long: (a boolean)
    Superseded by write_int.
    argument: ``-long``
    mutually_exclusive: write_byte, write_short, write_int, write_long,
        write_float, write_double
write_float: (a boolean)
    Write out data as single precision floating-point values.
    argument: ``-float``
    mutually_exclusive: write_byte, write_short, write_int, write_long,
        write_float, write_double
write_double: (a boolean)
    Write out data as double precision floating-point values.
    argument: ``-double``
    mutually_exclusive: write_byte, write_short, write_int, write_long,
        write_float, write_double
write_signed: (a boolean)
    Write out signed data.
    argument: ``-signed``
    mutually_exclusive: write_signed, write_unsigned
write_unsigned: (a boolean)
    Write out unsigned data.
    argument: ``-unsigned``
    mutually_exclusive: write_signed, write_unsigned
write_range: (a tuple of the form: (a float, a float))
    Specify the range of output values.Default value: 1.79769e+308
    1.79769e+308.
    argument: ``-range %s %s``
normalize: (a boolean)
    Normalize integer pixel values to file max and min.
    argument: ``-normalize``
    mutually_exclusive: normalize, nonnormalize
nonnormalize: (a boolean)
    Turn off pixel normalization.
    argument: ``-nonnormalize``
    mutually_exclusive: normalize, nonnormalize
out_file: (a pathlike object or string representing a file)
    argument: ``> %s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
```

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```
value of class 'str', nipyre default value: {}
Environment variables
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
              file)
              output file in raw format
```

64.2.22 VolSymm**Link to code**

Wraps the executable command volsymm.

Make a volume symmetric about an axis either linearly and/or nonlinearly. This is done by registering a volume to a flipped image of itself.

This tool is part of the minc-widgets package:

<https://github.com/BIC-MNI/minc-widgets/blob/master/volsymm/volsymm>

Examples

```
>>> from nipyre.interfaces.minc import VolSymm
>>> from nipyre.interfaces.minc.testdata import nonempty_minc_data
```

```
>>> input_file = nonempty_minc_data(0)
>>> volsymm = VolSymm(input_file=input_file)
>>> volsymm.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_file: (a pathlike object or string representing an existing
             file)
             input file
             argument: ``%s``, position: -3

[Optional]
trans_file: (a pathlike object or string representing a file)
             output xfm trans file
             argument: ``%s``, position: -2
output_file: (a pathlike object or string representing a file)
              output file
              argument: ``%s``, position: -1
input_grid_files: (a list of items which are a pathlike object or
                   string representing a file)
                   input grid file(s)
verbose: (a boolean)
          Print out log messages. Default: False.
          argument: ``-verbose``
clobber: (a boolean, nipyre default value: True)
          Overwrite existing file.
          argument: ``-clobber``
fit_linear: (a boolean)
             Fit using a linear xfm.
             argument: ``-linear``
fit_nonlinear: (a boolean)
```

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```

        Fit using a non-linear xfm.
        argument: ``-nonlinear``
nofit: (a boolean)
        Use the input transformation instead of generating one.
        argument: ``-nofit``
config_file: (a pathlike object or string representing an existing
              file)
              File containing the fitting configuration (nlpsfit -help for info).
              argument: ``-config_file %s``
x: (a boolean)
    Flip volume in x-plane (default).
    argument: ``-x``
y: (a boolean)
    Flip volume in y-plane.
    argument: ``-y``
z: (a boolean)
    Flip volume in z-plane.
    argument: ``-z``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
              file)
              output file
trans_file: (a pathlike object or string representing an existing
             file)
             xfm trans file
output_grid: (a pathlike object or string representing an existing
              file)
              output grid file

```

64.2.23 Volcentre[Link to code](#)

Wraps the executable command volcentre.

Centre a MINC image's sampling about a point, typically (0,0,0).

Example

```

>>> from nipy.interfaces.minc import Volcentre
>>> from nipy.interfaces.minc.testdata import minc2Dfile
>>> vc = Volcentre(input_file=minc2Dfile)
>>> vc.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
input_file: (a pathlike object or string representing an existing
             file)

```

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```

    input file to centre
    argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
    output file
    argument: ``%s``, position: -1
verbose: (a boolean)
    Print out log messages. Default: False.
    argument: ``-verbose``
clobber: (a boolean, nipyte default value: True)
    Overwrite existing file.
    argument: ``-clobber``
com: (a boolean)
    Use the CoM of the volume for the new centre (via mincstats).
    Default: False
    argument: ``-com``
centre: (a tuple of the form: (a float, a float, a float))
    Centre to use (x,y,z) [default: 0 0 0].
    argument: ``-centre %s %s %s``
zero_diracos: (a boolean)
    Set the direction cosines to identity [default].
    argument: ``-zero_diracos``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
    file)
    output file

```

64.2.24 Voliso

[Link to code](#)Wraps the executable command `voliso`.

Changes the steps and starts in order that the output volume has isotropic sampling.

Examples

```

>>> from nipyte.interfaces.minc import Voliso
>>> from nipyte.interfaces.minc.testdata import minc2Dfile
>>> viso = Voliso(input_file=minc2Dfile, minstep=0.1, avgstep=True)
>>> viso.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
input_file: (a pathlike object or string representing an existing
    file)
    input file to convert to isotropic sampling

```

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```

        argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
    output file
    argument: ``%s``, position: -1
verbose: (a boolean)
    Print out log messages. Default: False.
    argument: ``--verbose``
clobber: (a boolean, nipy default value: True)
    Overwrite existing file.
    argument: ``--clobber``
maxstep: (a float)
    The target maximum step desired in the output volume.
    argument: ``--maxstep %s``
minstep: (a float)
    The target minimum step desired in the output volume.
    argument: ``--minstep %s``
avgstep: (a boolean)
    Calculate the maximum step from the average steps of the input
    volume.
    argument: ``--avgstep``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

output_file: (a pathlike object or string representing an existing
    file)
    output file

```

64.2.25 Volpad[Link to code](#)

Wraps the executable command volpad.

Centre a MINC image's sampling about a point, typically (0,0,0).

Examples

```

>>> from nipy.interfaces.minc import Volpad
>>> from nipy.interfaces.minc.testdata import minc2Dfile
>>> vp = Volpad(input_file=minc2Dfile, smooth=True, smooth_distance=4)
>>> vp.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
input_file: (a pathlike object or string representing an existing
    file)
    input file to centre
    argument: ``%s``, position: -2

```

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```
[Optional]
output_file: (a pathlike object or string representing a file)
    output file
    argument: ``%s``, position: -1
verbose: (a boolean)
    Print out log messages. Default: False.
    argument: ``-verbose``
clobber: (a boolean, nipy default value: True)
    Overwrite existing file.
    argument: ``-clobber``
auto: (a boolean)
    Automatically determine padding distances (uses -distance as max).
    Default: False.
    argument: ``-auto``
auto_freq: (a float)
    Frequency of voxels over bimodal threshold to stop at [default:
    500].
    argument: ``-auto_freq %s``
distance: (an integer (int or long))
    Padding distance (in voxels) [default: 4].
    argument: ``-distance %s``
smooth: (a boolean)
    Smooth (blur) edges before padding. Default: False.
    argument: ``-smooth``
smooth_distance: (an integer (int or long))
    Smoothing distance (in voxels) [default: 4].
    argument: ``-smooth_distance %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
    file)
    output file
```

64.2.26 XfmAvg[Link to code](#)

Wraps the executable command xfmavg.

Average a number of xfm transforms using matrix logs and exponents. The program xfmavg calls Octave for numerical work.

This tool is part of the minc-widgets package:

<https://github.com/BIC-MNI/minc-widgets/tree/master/xfmavg>**Examples**

```
>>> from nipy.interfaces.minc import XfmAvg
>>> from nipy.interfaces.minc.testdata import nonempty_minc_data, nlp_config
>>> from nipy.testing import example_data
```

```
>>> xfm1 = example_data('minc_initial.xfm')
>>> xfm2 = example_data('minc_initial.xfm') # cheating for doctest
>>> xfmavg = XfmAvg(input_files=[xfm1, xfm2])
>>> xfmavg.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_files: (a list of items which are a pathlike object or string
              representing an existing file)
              input file(s)
              argument: ``%s``, position: -2

[Optional]
input_grid_files: (a list of items which are a pathlike object or
                   string representing a file)
                   input grid file(s)
output_file: (a pathlike object or string representing a file)
              output file
              argument: ``%s``, position: -1
verbose: (a boolean)
          Print out log messages. Default: False.
          argument: ``-verbose``
clobber: (a boolean, nipyre default value: True)
          Overwrite existing file.
          argument: ``-clobber``
avg_linear: (a boolean)
             average the linear part [default].
             argument: ``-avg_linear``
avg_nonlinear: (a boolean)
               average the non-linear part [default].
               argument: ``-avg_nonlinear``
ignore_linear: (a boolean)
               opposite of -avg_linear.
               argument: ``-ignore_linear``
ignore_nonlinear: (a boolean)
                  opposite of -avg_nonlinear.
                  argument: ``-ignore_nonlinear``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyre default value: {})
          Environment variables
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
              file)
              output file
output_grid: (a pathlike object or string representing an existing
              file)
              output grid file
```

64.2.27 XfmConcat

[Link to code](#)

Wraps the executable command xfmconcat.

Concatenate transforms together. The output transformation is equivalent to applying input1.xfm, then input2.xfm, ..., in that order.

Examples

```
>>> from nipyre.interfaces.minc import XfmConcat
>>> from nipyre.interfaces.minc.testdata import minc2Dfile
>>> conc = XfmConcat(input_files=['input1.xfm', 'input1.xfm'])
>>> conc.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_files: (a list of items which are a pathlike object or string
              representing an existing file)
              input file(s)
              argument: ``%s``, position: -2

[Optional]
input_grid_files: (a list of items which are a pathlike object or
                   string representing a file)
                   input grid file(s)
output_file: (a pathlike object or string representing a file)
              output file
              argument: ``%s``, position: -1
verbose: (a boolean)
          Print out log messages. Default: False.
          argument: ``-verbose``
clobber: (a boolean, nipyre default value: True)
          Overwrite existing file.
          argument: ``-clobber``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyre default value: {})
          Environment variables
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
              file)
              output file
output_grids: (a list of items which are a pathlike object or string
               representing an existing file)
               output grids
```

64.2.28 XfmInvert

[Link to code](#)

Wraps the executable command xfminvert.

Invert an xfm transform file.

Examples

```
>>> from nipyype.interfaces.minc import XfmAvg
>>> from nipyype.testing import example_data
```

```
>>> xfm = example_data('minc_initial.xfm')
>>> invert = XfmInvert(input_file=xfm)
>>> invert.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
input_file: (a pathlike object or string representing an existing
            file)
            input file
            argument: ``%s``, position: -2

[Optional]
output_file: (a pathlike object or string representing a file)
            output file
            argument: ``%s``, position: -1
verbose: (a boolean)
          Print out log messages. Default: False.
          argument: ``-verbose``
clobber: (a boolean, nipyype default value: True)
          Overwrite existing file.
          argument: ``-clobber``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyype default value: {})
          Environment variables
```

Outputs:

```
output_file: (a pathlike object or string representing an existing
            file)
            output file
output_grid: (a pathlike object or string representing an existing
            file)
            output grid file
```

64.3 interfaces.minc.testdata

64.3.1 nonempty_minc_data()

[Link to code](#)

65.1 interfaces.mipav.developer

65.1.1 JistBrainMgdmSegmentation

[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iacI.jist.cli.run de.mpg.cbs.jist.brain.JistBrainMgdmSegmentation`”.

title: MGDM Whole Brain Segmentation

category: Developer Tools

description: Estimate brain structures from an atlas for a MRI dataset (multiple input combinations are possible).

version: 2.0.RC

Inputs:

```
[Optional]
inMP2RAGE: (a pathlike object or string representing an existing
            file)
            MP2RAGE T1 Map Image
            argument: ``--inMP2RAGE %s``
inMP2RAGE2: (a pathlike object or string representing an existing
            file)
            MP2RAGE T1-weighted Image
            argument: ``--inMP2RAGE2 %s``
inPV: (a pathlike object or string representing an existing file)
       PV / Dura Image
       argument: ``--inPV %s``
inMPRAGE: (a pathlike object or string representing an existing file)
           MPRAGE T1-weighted Image
           argument: ``--inMPRAGE %s``
inFLAIR: (a pathlike object or string representing an existing file)
          FLAIR Image
          argument: ``--inFLAIR %s``
inAtlas: (a pathlike object or string representing an existing file)
          Atlas file
          argument: ``--inAtlas %s``
inData: (a float)
         Data weight
```

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```

        argument: ``--inData %f``
inCurvature: (a float)
    Curvature weight
    argument: ``--inCurvature %f``
inPosterior: (a float)
    Posterior scale (mm)
    argument: ``--inPosterior %f``
inMax: (an integer (int or long))
    Max iterations
    argument: ``--inMax %d``
inMin: (a float)
    Min change
    argument: ``--inMin %f``
inSteps: (an integer (int or long))
    Steps
    argument: ``--inSteps %d``
inTopology: ('26/6' or '6/26' or '18/6' or '6/18' or '6/6' or 'wcs'
    or 'wco' or 'no')
    Topology
    argument: ``--inTopology %s``
inCompute: ('true' or 'false')
    Compute posteriors
    argument: ``--inCompute %s``
inAdjust: ('true' or 'false')
    Adjust intensity priors
    argument: ``--inAdjust %s``
inOutput: ('segmentation' or 'memberships')
    Output images
    argument: ``--inOutput %s``
xPrefExt: ('nrrd')
    Output File Type
    argument: ``--xPrefExt %s``
outSegmented: (a boolean or a pathlike object or string representing
    a file)
    Segmented Brain Image
    argument: ``--outSegmented %s``
outLevelset: (a boolean or a pathlike object or string representing a
    file)
    Levelset Boundary Image
    argument: ``--outLevelset %s``
outPosterior2: (a boolean or a pathlike object or string representing
    a file)
    Posterior Maximum Memberships (4D)
    argument: ``--outPosterior2 %s``
outPosterior3: (a boolean or a pathlike object or string representing
    a file)
    Posterior Maximum Labels (4D)
    argument: ``--outPosterior3 %s``
null: (a unicode string)
    Execution Time
    argument: ``--null %s``
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``

```

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```

args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outSegmented: (a pathlike object or string representing an existing
    file)
    Segmented Brain Image
outLevelset: (a pathlike object or string representing an existing
    file)
    Levelset Boundary Image
outPosterior2: (a pathlike object or string representing an existing
    file)
    Posterior Maximum Memberships (4D)
outPosterior3: (a pathlike object or string representing an existing
    file)
    Posterior Maximum Labels (4D)

```

65.1.2 JistBrainMp2rageDuraEstimation[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iac1.jist.cli.run de.mpg.cbs.jist.brain.JistBrainMp2rageDuraEstimation`”.

title: MP2RAGE Dura Estimation

category: Developer Tools

description: Filters a MP2RAGE brain image to obtain a probability map of dura matter.

version: 3.0.RC

Inputs:

```

[Optional]
inSecond: (a pathlike object or string representing an existing file)
    Second inversion (Inv2) Image
    argument: ``--inSecond %s``
inSkull: (a pathlike object or string representing an existing file)
    Skull Stripping Mask
    argument: ``--inSkull %s``
inDistance: (a float)
    Distance to background (mm)
    argument: ``--inDistance %f``
inoutput: ('dura_region' or 'boundary' or 'dura_prior' or 'bg_prior'
    or 'intens_prior')
    Outputs an estimate of the dura / CSF boundary or an estimate of the
    entire dura region.
    argument: ``--inoutput %s``
xPrefExt: ('nrrd')
    Output File Type
    argument: ``--xPrefExt %s``
outDura: (a boolean or a pathlike object or string representing a
    file)
    Dura Image
    argument: ``--outDura %s``

```

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```

null: (a unicode string)
    Execution Time
    argument: ``--null %s``
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outDura: (a pathlike object or string representing an existing file)
    Dura Image

```

65.1.3 JistBrainMp2rageSkullStripping[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iac1.jist.cli.run de.mpg.cbs.jist.brain.JistBrainMp2rageSkullStripping`”.

title: MP2RAGE Skull Stripping

category: Developer Tools

description: Estimate a brain mask for a MP2RAGE dataset. At least a T1-weighted or a T1 map image is required.

version: 3.0.RC

Inputs:

```

[Optional]
inSecond: (a pathlike object or string representing an existing file)
    Second inversion (Inv2) Image
    argument: ``--inSecond %s``
inT1: (a pathlike object or string representing an existing file)
    T1 Map (T1_Images) Image (opt)
    argument: ``--inT1 %s``
inT1weighted: (a pathlike object or string representing an existing
    file)
    T1-weighted (UNI) Image (opt)
    argument: ``--inT1weighted %s``
inFilter: (a pathlike object or string representing an existing file)
    Filter Image (opt)
    argument: ``--inFilter %s``
inSkip: ('true' or 'false')
    Skip zero values
    argument: ``--inSkip %s``
xPrefExt: ('nrrd')
    Output File Type
    argument: ``--xPrefExt %s``
outBrain: (a boolean or a pathlike object or string representing a
    file)

```

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```

    Brain Mask Image
    argument: ``--outBrain %s``
outMasked: (a boolean or a pathlike object or string representing a
    file)
    Masked T1 Map Image
    argument: ``--outMasked %s``
outMasked2: (a boolean or a pathlike object or string representing a
    file)
    Masked T1-weighted Image
    argument: ``--outMasked2 %s``
outMasked3: (a boolean or a pathlike object or string representing a
    file)
    Masked Filter Image
    argument: ``--outMasked3 %s``
null: (a unicode string)
    Execution Time
    argument: ``--null %s``
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outBrain: (a pathlike object or string representing an existing file)
    Brain Mask Image
outMasked: (a pathlike object or string representing an existing
    file)
    Masked T1 Map Image
outMasked2: (a pathlike object or string representing an existing
    file)
    Masked T1-weighted Image
outMasked3: (a pathlike object or string representing an existing
    file)
    Masked Filter Image

```

65.1.4 JistBrainPartialVolumeFilter[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iac1.jist.cli.run de.mpg.cbs.jist.brain.JistBrainPartialVolumeFilter`”.

title: Partial Volume Filter

category: Developer Tools

description: Filters an image for regions of partial voluming assuming a ridge-like model of intensity.

version: 2.0.RC

Inputs:

```
[Optional]
inInput: (a pathlike object or string representing an existing file)
    Input Image
    argument: ``--inInput %s``
inPV: ('bright' or 'dark' or 'both')
    Outputs the raw intensity values or a probability score for the
    partial volume regions.
    argument: ``--inPV %s``
inoutput: ('probability' or 'intensity')
    output
    argument: ``--inoutput %s``
xPrefExt: ('nrrd')
    Output File Type
    argument: ``--xPrefExt %s``
outPartial: (a boolean or a pathlike object or string representing a
    file)
    Partial Volume Image
    argument: ``--outPartial %s``
null: (a unicode string)
    Execution Time
    argument: ``--null %s``
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outPartial: (a pathlike object or string representing an existing
    file)
    Partial Volume Image
```

65.1.5 JistCortexSurfaceMeshInflation[Link to code](#)

Wraps the executable command `“java edu.jhu.ece.iac.jist.cli.run de.mpg.cbs.jist.cortex.JistCortexSurfaceMeshInflation`

`“.`

title: Surface Mesh Inflation

category: Developer Tools

description: Inflates a cortical surface mesh. D. Tosun, M. E. Rettmann, X. Han, X. Tao, C. Xu, S. M. Resnick, D. Pham, and J. L. Prince, Cortical Surface Segmentation and Mapping, NeuroImage, vol. 23, pp. S108–S118, 2004.

version: 3.0.RC

contributor: Duygu Tosun

Inputs:

```
[Optional]
```

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```

inLevelset: (a pathlike object or string representing an existing
             file)
             Levelset Image
             argument: ``--inLevelset %s``
inSOR: (a float)
        SOR Parameter
        argument: ``--inSOR %f``
inMean: (a float)
        Mean Curvature Threshold
        argument: ``--inMean %f``
inStep: (an integer (int or long))
        Step Size
        argument: ``--inStep %d``
inMax: (an integer (int or long))
        Max Iterations
        argument: ``--inMax %d``
inLorentzian: ('true' or 'false')
              Lorentzian Norm
              argument: ``--inLorentzian %s``
inTopology: ('26/6' or '6/26' or '18/6' or '6/18' or '6/6' or 'wcs'
             or 'wco' or 'no')
             Topology
             argument: ``--inTopology %s``
xPrefExt: ('nrrd')
          Output File Type
          argument: ``--xPrefExt %s``
outOriginal: (a boolean or a pathlike object or string representing a
              file)
              Original Surface
              argument: ``--outOriginal %s``
outInflated: (a boolean or a pathlike object or string representing a
              file)
              Inflated Surface
              argument: ``--outInflated %s``
null: (a unicode string)
       Execution Time
       argument: ``--null %s``
xDefaultMem: (an integer (int or long))
              Set default maximum heap size
              argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipyte default value: 1)
              Set default maximum number of processes.
              argument: ``-xMaxProcess %d``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipyte default value: {})
          Environment variables

```

Outputs:

```

outOriginal: (a pathlike object or string representing an existing
              file)
              Original Surface
outInflated: (a pathlike object or string representing an existing

```

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```

file)
Inflated Surface

```

65.1.6 JistIntensityMp2rageMasking

[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iac1.jist.cli.run de.mpg.cbs.jist.intensity.JistIntensityMp2rageMasking`”.

title: MP2RAGE Background Masking

category: Developer Tools

description: Estimate a background signal mask for a MP2RAGE dataset.

version: 3.0.RC

Inputs:

```

[Optional]
inSecond: (a pathlike object or string representing an existing file)
           Second inversion (Inv2) Image
           argument: ``--inSecond %s``
inQuantitative: (a pathlike object or string representing an existing
                 file)
                 Quantitative T1 Map (T1_Images) Image
                 argument: ``--inQuantitative %s``
inT1weighted: (a pathlike object or string representing an existing
               file)
               T1-weighted (UNI) Image
               argument: ``--inT1weighted %s``
inBackground: ('exponential' or 'half-normal')
               Model distribution for background noise (default is half-normal,
               exponential is more stringent).
               argument: ``--inBackground %s``
inSkip: ('true' or 'false')
         Skip zero values
         argument: ``--inSkip %s``
inMasking: ('binary' or 'proba')
           Whether to use a binary threshold or a weighted average based on the
           probability.
           argument: ``--inMasking %s``
xPrefExt: ('nrrd')
          Output File Type
          argument: ``--xPrefExt %s``
outSignal: (a boolean or a pathlike object or string representing a
            file)
            Signal Proba Image
            argument: ``--outSignal_Proba %s``
outSignal2: (a boolean or a pathlike object or string representing a
             file)
             Signal Mask Image
             argument: ``--outSignal_Mask %s``
outMasked: (a boolean or a pathlike object or string representing a
            file)
            Masked T1 Map Image
            argument: ``--outMasked_T1_Map %s``
outMasked2: (a boolean or a pathlike object or string representing a
             file)
             Masked Iso Image

```

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```

        argument: ``--outMasked_T1weighted %s``
null: (a unicode string)
    Execution Time
    argument: ``--null %s``
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outSignal: (a pathlike object or string representing an existing
    file)
    Signal Proba Image
outSignal2: (a pathlike object or string representing an existing
    file)
    Signal Mask Image
outMasked: (a pathlike object or string representing an existing
    file)
    Masked T1 Map Image
outMasked2: (a pathlike object or string representing an existing
    file)
    Masked Iso Image

```

65.1.7 JistLaminarProfileCalculator[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iac.jist.cli.run de.mpg.cbs.jist.laminar.JistLaminarProfileCalculator`”.

title: Profile Calculator

category: Developer Tools

description: Compute various moments for intensities mapped along a cortical profile.

version: 3.0.RC

Inputs:

```

[Optional]
inIntensity: (a pathlike object or string representing an existing
    file)
    Intensity Profile Image
    argument: ``--inIntensity %s``
inMask: (a pathlike object or string representing an existing file)
    Mask Image (opt, 3D or 4D)
    argument: ``--inMask %s``
incomputed: ('mean' or 'stdev' or 'skewness' or 'kurtosis')
    computed statistic
    argument: ``--incomputed %s``
xPrefExt: ('nrrd')

```

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```

    Output File Type
    argument: ``--xPrefExt %s``
outResult: (a boolean or a pathlike object or string representing a
    file)
    Result
    argument: ``--outResult %s``
null: (a unicode string)
    Execution Time
    argument: ``--null %s``
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outResult: (a pathlike object or string representing an existing
    file)
    Result

```

65.1.8 JistLaminarProfileGeometry[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iac1.jist.cli.run de.mpg.cbs.jist.laminar.JistLaminarProfileGeometry`”.

title: Profile Geometry

category: Developer Tools

description: Compute various geometric quantities for a cortical layers.

version: 3.0.RC

Inputs:

```

[Optional]
inProfile: (a pathlike object or string representing an existing
    file)
    Profile Surface Image
    argument: ``--inProfile %s``
incomputed: ('thickness' or 'curvedness' or 'shape_index' or
    'mean_curvature' or 'gauss_curvature' or 'profile_length' or
    'profile_curvature' or 'profile_torsion')
    computed measure
    argument: ``--incomputed %s``
inregularization: ('none' or 'Gaussian')
    regularization
    argument: ``--inregularization %s``
insmoothing: (a float)
    smoothing parameter
    argument: ``--insmoothing %f``

```

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```

inoutside: (a float)
    outside extension (mm)
    argument: ``--inoutside %f``
xPrefExt: ('nrrd')
    Output File Type
    argument: ``--xPrefExt %s``
outResult: (a boolean or a pathlike object or string representing a
    file)
    Result
    argument: ``--outResult %s``
null: (a unicode string)
    Execution Time
    argument: ``--null %s``
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipyte default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables

```

Outputs:

```

outResult: (a pathlike object or string representing an existing
    file)
    Result

```

65.1.9 JistLaminarProfileSampling[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iac.jist.cli.run de.mpg.cbs.jist.laminar.JistLaminarProfileSampling`”.

title: Profile Sampling**category:** Developer Tools**description:** Sample some intensity image along a cortical profile across layer surfaces.**version:** 3.0.RC**Inputs:**

```

[Optional]
inProfile: (a pathlike object or string representing an existing
    file)
    Profile Surface Image
    argument: ``--inProfile %s``
inIntensity: (a pathlike object or string representing an existing
    file)
    Intensity Image
    argument: ``--inIntensity %s``
inCortex: (a pathlike object or string representing an existing file)
    Cortex Mask (opt)
    argument: ``--inCortex %s``

```

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```

xPrefExt: ('nrrd')
    Output File Type
    argument: ``--xPrefExt %s``
outProfilemapped: (a boolean or a pathlike object or string
    representing a file)
    Profile-mapped Intensity Image
    argument: ``--outProfilemapped %s``
outProfile2: (a boolean or a pathlike object or string representing a
    file)
    Profile 4D Mask
    argument: ``--outProfile2 %s``
null: (a unicode string)
    Execution Time
    argument: ``--null %s``
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outProfilemapped: (a pathlike object or string representing an
    existing file)
    Profile-mapped Intensity Image
outProfile2: (a pathlike object or string representing an existing
    file)
    Profile 4D Mask

```

65.1.10 JistLaminarROIAveraging[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iac.jist.cli.run de.mpg.cbs.jist.laminar.JistLaminarROIAveraging`”.

title: Profile ROI Averaging**category:** Developer Tools**description:** Compute an average profile over a given ROI.**version:** 3.0.RC**Inputs:**

```

[Optional]
inIntensity: (a pathlike object or string representing an existing
    file)
    Intensity Profile Image
    argument: ``--inIntensity %s``
inROI: (a pathlike object or string representing an existing file)
    ROI Mask
    argument: ``--inROI %s``

```

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```

inROI2: (a unicode string)
    ROI Name
    argument: ``--inROI2 %s``
inMask: (a pathlike object or string representing an existing file)
    Mask Image (opt, 3D or 4D)
    argument: ``--inMask %s``
xPrefExt: ('nrrd')
    Output File Type
    argument: ``--xPrefExt %s``
outROI3: (a boolean or a pathlike object or string representing a
    file)
    ROI Average
    argument: ``--outROI3 %s``
null: (a unicode string)
    Execution Time
    argument: ``--null %s``
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outROI3: (a pathlike object or string representing an existing file)
    ROI Average

```

65.1.11 JistLaminarVolumetricLayering[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iac1.jist.cli.run de.mpg.cbs.jist.laminar.JistLaminarVolumetricLayering`”.

title: Volumetric Layering

category: Developer Tools

description: Builds a continuous layering of the cortex following distance-preserving or volume-preserving models of cortical folding. Waehnert MD, Dinse J, Weiss M, Streicher MN, Waehnert P, Geyer S, Turner R, Bazin PL, Anatomically motivated modeling of cortical laminae, Neuroimage, 2013.

version: 3.0.RC

contributor: Miriam Waehnert (waehnert@cbs.mpg.de) <http://www.cbs.mpg.de/>

Inputs:

```

[Optional]
inInner: (a pathlike object or string representing an existing file)
    Inner Distance Image (GM/WM boundary)
    argument: ``--inInner %s``
inOuter: (a pathlike object or string representing an existing file)
    Outer Distance Image (CSF/GM boundary)
    argument: ``--inOuter %s``

```

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```

inNumber: (an integer (int or long))
    Number of layers
    argument: ``--inNumber %d``
inMax: (an integer (int or long))
    Max iterations for narrow band evolution
    argument: ``--inMax %d``
inMin: (a float)
    Min change ratio for narrow band evolution
    argument: ``--inMin %f``
inLayering: ('distance-preserving' or 'volume-preserving')
    Layering method
    argument: ``--inLayering %s``
inLayering2: ('outward' or 'inward')
    Layering direction
    argument: ``--inLayering2 %s``
incurvature: (an integer (int or long))
    curvature approximation scale (voxels)
    argument: ``--incurvature %d``
inratio: (a float)
    ratio smoothing kernel size (voxels)
    argument: ``--inratio %f``
inpresmooth: ('true' or 'false')
    pre-smooth cortical surfaces
    argument: ``--inpresmooth %s``
inTopology: ('26/6' or '6/26' or '18/6' or '6/18' or '6/6' or 'wcs'
    or 'wco' or 'no')
    Topology
    argument: ``--inTopology %s``
xPrefExt: ('nrrd')
    Output File Type
    argument: ``--xPrefExt %s``
outContinuous: (a boolean or a pathlike object or string representing
    a file)
    Continuous depth measurement
    argument: ``--outContinuous %s``
outDiscrete: (a boolean or a pathlike object or string representing a
    file)
    Discrete sampled layers
    argument: ``--outDiscrete %s``
outLayer: (a boolean or a pathlike object or string representing a
    file)
    Layer boundary surfaces
    argument: ``--outLayer %s``
null: (a unicode string)
    Execution Time
    argument: ``--null %s``
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a

```

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```
value of class 'str', nipy default value: {}  
Environment variables
```

Outputs:

```
outContinuous: (a pathlike object or string representing an existing  
file)  
Continuous depth measurement  
outDiscrete: (a pathlike object or string representing an existing  
file)  
Discrete sampled layers  
outLayer: (a pathlike object or string representing an existing file)  
Layer boundary surfaces
```

65.1.12 MedicAlgorithmImageCalculator[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iac.jist.cli.run edu.jhu.ece.iac.plugins.utilities.math.MedicAlgorithmImageCalculator`”.

title: Image Calculator

category: Developer Tools

description: Perform simple image calculator operations on two images. The operations include ‘Add’, ‘Subtract’, ‘Multiply’, and ‘Divide’

version: 1.10.RC

documentation-url: <http://www.iac.ece.jhu.edu/>

Inputs:

```
[Optional]  
inVolume: (a pathlike object or string representing an existing file)  
Volume 1  
argument: ``--inVolume %s``  
inVolume2: (a pathlike object or string representing an existing  
file)  
Volume 2  
argument: ``--inVolume2 %s``  
inOperation: ('Add' or 'Subtract' or 'Multiply' or 'Divide' or 'Min'  
or 'Max')  
Operation  
argument: ``--inOperation %s``  
xPrefExt: ('nrrd')  
Output File Type  
argument: ``--xPrefExt %s``  
outResult: (a boolean or a pathlike object or string representing a  
file)  
Result Volume  
argument: ``--outResult %s``  
null: (a unicode string)  
Execution Time  
argument: ``--null %s``  
xDefaultMem: (an integer (int or long))  
Set default maximum heap size  
argument: ``-xDefaultMem %d``  
xMaxProcess: (an integer (int or long), nipy default value: 1)  
Set default maximum number of processes.  
argument: ``-xMaxProcess %d``  
args: (a unicode string)
```

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```

Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

outResult: (a pathlike object or string representing an existing
           file)
           Result Volume

```

65.1.13 MedicAlgorithmLesionToads[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iac1.jist.cli.run edu.jhu.ece.iac1.plugins.classification.MedicAlgorithmLesionToads`”.

title: Lesion TOADS**category:** Developer Tools

description: Algorithm for simultaneous brain structures and MS lesion segmentation of MS Brains. The brain segmentation is topologically consistent and the algorithm can use multiple MR sequences as input data. N. Shiee, P.-L. Bazin, A.Z. Ozturk, P.A. Calabresi, D.S. Reich, D.L. Pham, “A Topology-Preserving Approach to the Segmentation of Brain Images with Multiple Sclerosis”, NeuroImage, vol. 49, no. 2, pp. 1524-1535, 2010.

version: 1.9.R**contributor:** Navid Shiee (navid.shiee@nih.gov) <http://iac1.ece.jhu.edu/~nshiee/>**Inputs:**

```

[Optional]
inT1_MPRAGE: (a pathlike object or string representing an existing
            file)
            T1_MPRAGE Image
            argument: ``--inT1_MPRAGE %s``
inT1_SPGR: (a pathlike object or string representing an existing
          file)
          T1_SPGR Image
          argument: ``--inT1_SPGR %s``
inFLAIR: (a pathlike object or string representing an existing file)
         FLAIR Image
         argument: ``--inFLAIR %s``
inAtlas: ('With Lesion' or 'No Lesion')
         Atlas to Use
         argument: ``--inAtlas %s``
inOutput: ('hard segmentation' or 'hard segmentation+memberships' or
          'cruise inputs' or 'dura removal inputs')
          Output images
          argument: ``--inOutput %s``
inOutput2: ('true' or 'false')
          Output the hard classification using maximum membership (not
          necessarily topologically correct)
          argument: ``--inOutput2 %s``
inCorrect: ('true' or 'false')
          Correct MR field inhomogeneity.
          argument: ``--inCorrect %s``
inOutput3: ('true' or 'false')
          Output the estimated inhomogeneity field

```

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```

        argument: ``--inOutput3 %s``
inAtlas2: (a pathlike object or string representing an existing file)
    Atlas File - With Lesions
    argument: ``--inAtlas2 %s``
inAtlas3: (a pathlike object or string representing an existing file)
    Atlas File - No Lesion - T1 and FLAIR
    argument: ``--inAtlas3 %s``
inAtlas4: (a pathlike object or string representing an existing file)
    Atlas File - No Lesion - T1 Only
    argument: ``--inAtlas4 %s``
inMaximum: (an integer (int or long))
    Maximum distance from the interventricular WM boundary to downweight
    the lesion membership to avoid false positives
    argument: ``--inMaximum %d``
inMaximum2: (an integer (int or long))
    Maximum Venticle Distance
    argument: ``--inMaximum2 %d``
inMaximum3: (an integer (int or long))
    Maximum InterVentricular Distance
    argument: ``--inMaximum3 %d``
inInclude: ('true' or 'false')
    Include lesion in WM class in hard classification
    argument: ``--inInclude %s``
inAtlas5: (a float)
    Controls the effect of the statistical atlas on the segmentation
    argument: ``--inAtlas5 %f``
inSmoothing: (a float)
    Controls the effect of neighborhood voxels on the membership
    argument: ``--inSmoothing %f``
inMaximum4: (a float)
    Maximum amount of relative change in the energy function considered
    as the convergence criteria
    argument: ``--inMaximum4 %f``
inMaximum5: (an integer (int or long))
    Maximum iterations
    argument: ``--inMaximum5 %d``
inAtlas6: ('rigid' or 'multi_fully_affine')
    Atlas alignment
    argument: ``--inAtlas6 %s``
inConnectivity: ('(26,6)' or '(6,26)' or '(6,18)' or '(18,6)')
    Connectivity (foreground,background)
    argument: ``--inConnectivity %s``
xPrefExt: ('nrrd')
    Output File Type
    argument: ``--xPrefExt %s``
outHard: (a boolean or a pathlike object or string representing a
    file)
    Hard segmentation
    argument: ``--outHard %s``
outHard2: (a boolean or a pathlike object or string representing a
    file)
    Hard segmentation from memberships
    argument: ``--outHard2 %s``
outInhomogeneity: (a boolean or a pathlike object or string
    representing a file)
    Inhomogeneity Field
    argument: ``--outInhomogeneity %s``

```

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```

outMembership: (a boolean or a pathlike object or string representing
    a file)
    Membership Functions
    argument: ``--outMembership %s``
outLesion: (a boolean or a pathlike object or string representing a
    file)
    Lesion Segmentation
    argument: ``--outLesion %s``
outSulcal: (a boolean or a pathlike object or string representing a
    file)
    Sulcal CSF Membership
    argument: ``--outSulcal %s``
outCortical: (a boolean or a pathlike object or string representing a
    file)
    Cortical GM Membership
    argument: ``--outCortical %s``
outFilled: (a boolean or a pathlike object or string representing a
    file)
    Filled WM Membership
    argument: ``--outFilled %s``
outWM: (a boolean or a pathlike object or string representing a file)
    WM Mask
    argument: ``--outWM %s``
null: (a unicode string)
    Execution Time
    argument: ``--null %s``
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outHard: (a pathlike object or string representing an existing file)
    Hard segmentation
outHard2: (a pathlike object or string representing an existing file)
    Hard segmentationfrom memberships
outInhomogeneity: (a pathlike object or string representing an
    existing file)
    Inhomogeneity Field
outMembership: (a pathlike object or string representing an existing
    file)
    Membership Functions
outLesion: (a pathlike object or string representing an existing
    file)
    Lesion Segmentation
outSulcal: (a pathlike object or string representing an existing
    file)

```

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```

    Sulcal CSF Membership
outCortical: (a pathlike object or string representing an existing
             file)
    Cortical GM Membership
outFilled: (a pathlike object or string representing an existing
           file)
    Filled WM Membership
outWM: (a pathlike object or string representing an existing file)
    WM Mask

```

65.1.14 MedicAlgorithmMipavReorient

[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iacI.jist.cli.run edu.jhu.ece.iacI.plugins.utilities.volume.MedicAlgorithmMipav`”.

title: Reorient Volume

category: Developer Tools

description: Reorient a volume to a particular anatomical orientation.

version: .alpha

Inputs:

```

[Optional]
inSource: (a list of items which are a pathlike object or string
          representing a file)
    Source
    argument: ``--inSource %s``
inTemplate: (a pathlike object or string representing an existing
            file)
    Template
    argument: ``--inTemplate %s``
inNew: ('Dicom axial' or 'Dicom coronal' or 'Dicom sagittal' or 'User
        defined')
    New image orientation
    argument: ``--inNew %s``
inUser: ('Unknown' or 'Patient Right to Left' or 'Patient Left to
        Right' or 'Patient Posterior to Anterior' or 'Patient Anterior to
        Posterior' or 'Patient Inferior to Superior' or 'Patient Superior
        to Inferior')
    User defined X-axis orientation (image left to right)
    argument: ``--inUser %s``
inUser2: ('Unknown' or 'Patient Right to Left' or 'Patient Left to
        Right' or 'Patient Posterior to Anterior' or 'Patient Anterior to
        Posterior' or 'Patient Inferior to Superior' or 'Patient Superior
        to Inferior')
    User defined Y-axis orientation (image top to bottom)
    argument: ``--inUser2 %s``
inUser3: ('Unknown' or 'Patient Right to Left' or 'Patient Left to
        Right' or 'Patient Posterior to Anterior' or 'Patient Anterior to
        Posterior' or 'Patient Inferior to Superior' or 'Patient Superior
        to Inferior')
    User defined Z-axis orientation (into the screen)
    argument: ``--inUser3 %s``
inUser4: ('Axial' or 'Coronal' or 'Sagittal' or 'Unknown')
    User defined Image Orientation
    argument: ``--inUser4 %s``

```

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```

inInterpolation: ('Nearest Neighbor' or 'Trilinear' or 'Bspline 3rd
                  order' or 'Bspline 4th order' or 'Cubic Lagrangian' or 'Quintic
                  Lagrangian' or 'Heptic Lagrangian' or 'Windowed Sinc')
Interpolation
argument: ``--inInterpolation %s``
inResolution: ('Unchanged' or 'Finest cubic' or 'Coarsest cubic' or
               'Same as template')
Resolution
argument: ``--inResolution %s``
xPrefExt: ('nrrd')
Output File Type
argument: ``--xPrefExt %s``
outReoriented: (a list of items which are a pathlike object or string
                representing a file)
Reoriented Volume
argument: ``--outReoriented %s``
null: (a unicode string)
Execution Time
argument: ``--null %s``
xDefaultMem: (an integer (int or long))
Set default maximum heap size
argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
Set default maximum number of processes.
argument: ``-xMaxProcess %d``
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

None

65.1.15 MedicAlgorithmN3

[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iac1.jist.cli.run edu.jhu.ece.iac1.plugins.classification.MedicAlgorithmN3`”.

title: N3 Correction

category: Developer Tools

description: Non-parametric Intensity Non-uniformity Correction, N3, originally by J.G. Sled.

version: 1.8.R

Inputs:

```

[Optional]
inInput: (a pathlike object or string representing an existing file)
Input Volume
argument: ``--inInput %s``
inSignal: (a float)
Default = min + 1, Values at less than threshold are treated as part
of the background
argument: ``--inSignal %f``

```

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```

inMaximum: (an integer (int or long))
    Maximum number of Iterations
    argument: ``--inMaximum %d``
inEnd: (a float)
    Usually 0.01-0.00001, The measure used to terminate the iterations
    is the coefficient of variation of change in field estimates between
    successive iterations.
    argument: ``--inEnd %f``
inField: (a float)
    Characteristic distance over which the field varies. The distance
    between adjacent knots in bspline fitting with at least 4 knots
    going in every dimension. The default in the dialog is one third the
    distance (resolution * extents) of the smallest dimension.
    argument: ``--inField %f``
inSubsample: (a float)
    Usually between 1-32, The factor by which the data is subsampled to
    a lower resolution in estimating the slowly varying non-uniformity
    field. Reduce sampling in the finest sampling direction by the
    shrink factor.
    argument: ``--inSubsample %f``
inKernel: (a float)
    Usually between 0.05-0.50, Width of deconvolution kernel used to
    sharpen the histogram. Larger values give faster convergence while
    smaller values give greater accuracy.
    argument: ``--inKernel %f``
inWeiner: (a float)
    Usually between 0.0-1.0
    argument: ``--inWeiner %f``
inAutomatic: ('true' or 'false')
    If true determines the threshold by histogram analysis. If true a
    VOI cannot be used and the input threshold is ignored.
    argument: ``--inAutomatic %s``
xPrefExt: ('nrrd')
    Output File Type
    argument: ``--xPrefExt %s``
outInhomogeneity: (a boolean or a pathlike object or string
    representing a file)
    Inhomogeneity Corrected Volume
    argument: ``--outInhomogeneity %s``
outInhomogeneity2: (a boolean or a pathlike object or string
    representing a file)
    Inhomogeneity Field
    argument: ``--outInhomogeneity2 %s``
null: (a unicode string)
    Execution Time
    argument: ``--null %s``
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a

```

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```

value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

outInhomogeneity: (a pathlike object or string representing an
existing file)
Inhomogeneity Corrected Volume
outInhomogeneity2: (a pathlike object or string representing an
existing file)
Inhomogeneity Field

```

65.1.16 MedicAlgorithmSPECTRE2010[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iac1.jist.cli.run edu.jhu.ece.iac1.plugins.segmentation.skull_strip.MedicAlgorithm`”.

    : SPECTRE 2010

category: Developer Tools

description: Simple Paradigm for Extra-Cranial Tissue Removal

Algorithm Version: 1.6 GUI Version: 1.10

A. Carass, M.B. Wheeler, J. Cuzzocreo, P.-L. Bazin, S.S. Bassett, and J.L. Prince, ‘A Joint Registration and Segmentation Approach to Skull Stripping’, Fourth IEEE International Symposium on Biomedical Imaging (ISBI 2007), Arlington, VA, April 12-15, 2007. A. Carass, J. Cuzzocreo, M.B. Wheeler, P.-L. Bazin, S.M. Resnick, and J.L. Prince, ‘Simple paradigm for extra-cerebral tissue removal: Algorithm and analysis’, NeuroImage 56(4):1982-1992, 2011.

version: 1.6.R

documentation-url: <http://www.iac1.ece.jhu.edu/>

contributor: Aaron Carass (aaron_carass@jhu.edu) <http://www.iac1.ece.jhu.edu/> Hanlin Wan (hanlinwan@gmail.com)

Inputs:

```

[Optional]
inInput: (a pathlike object or string representing an existing file)
Input volume to be skullstripped.
argument: ``--inInput %s``
inAtlas: (a pathlike object or string representing an existing file)
SPECTRE atlas description file. A text file enumerating atlas files
and landmarks.
argument: ``--inAtlas %s``
inInitial: (an integer (int or long))
Erosion of the initial mask, which is based on the probability mask
and the classification., The initial mask is output as the d0 volume
at the conclusion of SPECTRE.
argument: ``--inInitial %d``
inImage: ('T1_SPGR' or 'T1_ALT' or 'T1_MPRAGE' or 'T2' or 'FLAIR')
Set the image modality. MP-RAGE is recommended for most T1 sequence
images.
argument: ``--inImage %s``
inOutput: ('true' or 'false')
Determines if the output results are transformed back into the space
of the original input image.
argument: ``--inOutput %s``
inFind: ('true' or 'false')
Find Midsagittal Plane

```

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```

        argument: ``--inFind %s``
inRun: ('true' or 'false')
    Run Smooth Brain Mask
    argument: ``--inRun %s``
inResample: ('true' or 'false')
    Determines if the data is resampled to be isotropic during the
    processing.
    argument: ``--inResample %s``
inInitial2: (a float)
    Initial probability threshold
    argument: ``--inInitial2 %f``
inMinimum: (a float)
    Minimum probability threshold
    argument: ``--inMinimum %f``
inMMC: (an integer (int or long))
    The size of the dilation step within the Modified Morphological
    Closing.
    argument: ``--inMMC %d``
inMMC2: (an integer (int or long))
    The size of the erosion step within the Modified Morphological
    Closing.
    argument: ``--inMMC2 %d``
inInhomogeneity: ('true' or 'false')
    Set to false by default, this parameter will make FANTASM try to do
    inhomogeneity correction during it's iterative cycle.
    argument: ``--inInhomogeneity %s``
inSmoothing: (a float)
    argument: ``--inSmoothing %f``
inBackground: (a float)
    argument: ``--inBackground %f``
inOutput2: ('true' or 'false')
    Output Plane?
    argument: ``--inOutput2 %s``
inOutput3: ('true' or 'false')
    Output Split-Halves?
    argument: ``--inOutput3 %s``
inOutput4: ('true' or 'false')
    Output Segmentation on Plane?
    argument: ``--inOutput4 %s``
inDegrees: ('Rigid - 6' or 'Global rescale - 7' or 'Specific rescale
    - 9' or 'Affine - 12')
    Degrees of freedom
    argument: ``--inDegrees %s``
inCost: ('Correlation ratio' or 'Least squares' or 'Normalized cross
    correlation' or 'Normalized mutual information')
    Cost function
    argument: ``--inCost %s``
inRegistration: ('Trilinear' or 'Bspline 3rd order' or 'Bspline 4th
    order' or 'Cubic Lagrangian' or 'Quintic Lagrangian' or 'Heptic
    Lagrangian' or 'Windowed sinc')
    Registration interpolation
    argument: ``--inRegistration %s``
inOutput5: ('Trilinear' or 'Bspline 3rd order' or 'Bspline 4th order'
    or 'Cubic Lagrangian' or 'Quintic Lagrangian' or 'Heptic
    Lagrangian' or 'Windowed sinc' or 'Nearest Neighbor')
    Output interpolation
    argument: ``--inOutput5 %s``

```

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```

inApply: ('All' or 'X' or 'Y' or 'Z')
    Apply rotation
    argument: ``--inApply %s``
inMinimum2: (a float)
    Minimum angle
    argument: ``--inMinimum2 %f``
inMaximum: (a float)
    Maximum angle
    argument: ``--inMaximum %f``
inCoarse: (a float)
    Coarse angle increment
    argument: ``--inCoarse %f``
inFine: (a float)
    Fine angle increment
    argument: ``--inFine %f``
inMultiple: (an integer (int or long))
    Multiple of tolerance to bracket the minimum
    argument: ``--inMultiple %d``
inNumber: (an integer (int or long))
    Number of iterations
    argument: ``--inNumber %d``
inNumber2: (an integer (int or long))
    Number of minima from Level 8 to test at Level 4
    argument: ``--inNumber2 %d``
inUse: ('true' or 'false')
    Use the max of the min resolutions of the two datasets when
    resampling
    argument: ``--inUse %s``
inSubsample: ('true' or 'false')
    Subsample image for speed
    argument: ``--inSubsample %s``
inSkip: ('true' or 'false')
    Skip multilevel search (Assume images are close to alignment)
    argument: ``--inSkip %s``
inMultithreading: ('true' or 'false')
    Set to false by default, this parameter controls the multithreaded
    behavior of the linear registration.
    argument: ``--inMultithreading %s``
xPrefExt: ('nrrd')
    Output File Type
    argument: ``--xPrefExt %s``
outOriginal: (a boolean or a pathlike object or string representing a
    file)
    If Output in Original Space Flag is true then outputs the original
    input volume. Otherwise outputs the axially reoriented input volume.
    argument: ``--outOriginal %s``
outStripped: (a boolean or a pathlike object or string representing a
    file)
    Skullstripped result of the input volume with just the brain.
    argument: ``--outStripped %s``
outMask: (a boolean or a pathlike object or string representing a
    file)
    Binary Mask of the skullstripped result with just the brain
    argument: ``--outMask %s``
outPrior: (a boolean or a pathlike object or string representing a
    file)
    Probability prior from the atlas registrations

```

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```

        argument: ``--outPrior %s``
outFANTASM: (a boolean or a pathlike object or string representing a
            file)
            Tissue classification of of the whole input volume.
            argument: ``--outFANTASM %s``
outd0: (a boolean or a pathlike object or string representing a file)
        Initial Brainmask
        argument: ``--outd0 %s``
outMidsagittal: (a boolean or a pathlike object or string
                representing a file)
                Plane dividing the brain hemispheres
                argument: ``--outMidsagittal %s``
outSplitHalves: (a boolean or a pathlike object or string
                representing a file)
                Skullstripped mask of the brain with the hemispheres divided.
                argument: ``--outSplitHalves %s``
outSegmentation: (a boolean or a pathlike object or string
                representing a file)
                2D image showing the tissue classification on the midsagittal plane
                argument: ``--outSegmentation %s``
null: (a unicode string)
        Execution Time
        argument: ``--null %s``
xDefaultMem: (an integer (int or long))
        Set default maximum heap size
        argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
        Set default maximum number of processes.
        argument: ``-xMaxProcess %d``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

outOriginal: (a pathlike object or string representing an existing
            file)
            If Output in Original Space Flag is true then outputs the original
            input volume. Otherwise outputs the axially reoriented input volume.
outStripped: (a pathlike object or string representing an existing
            file)
            Skullstripped result of the input volume with just the brain.
outMask: (a pathlike object or string representing an existing file)
        Binary Mask of the skullstripped result with just the brain
outPrior: (a pathlike object or string representing an existing file)
        Probability prior from the atlas registrations
outFANTASM: (a pathlike object or string representing an existing
            file)
            Tissue classification of of the whole input volume.
outd0: (a pathlike object or string representing an existing file)
        Initial Brainmask
outMidsagittal: (a pathlike object or string representing an existing
                file)

```

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```

    Plane dividing the brain hemispheres
outSplitHalves: (a pathlike object or string representing an existing
    file)
    Skullstripped mask of the brain with the hemispheres divided.
outSegmentation: (a pathlike object or string representing an
    existing file)
    2D image showing the tissue classification on the midsagittal plane

```

65.1.17 MedicAlgorithmThresholdToBinaryMask

[Link to code](#)

Wraps the executable command “`java edu.jhu.ece.iacI.jist.cli.run edu.jhu.ece.iacI.plugins.utilities.volume.MedicAlgorithmThresh`”.

title: Threshold to Binary Mask

category: Developer Tools

description: Given a volume and an intensity range create a binary mask for values within that range.

version: 1.2.RC

documentation-url: <http://www.iacI.ece.jhu.edu/>

Inputs:

```

[Optional]
inLabel: (a list of items which are a pathlike object or string
    representing a file)
    Input volumes
    argument: ``--inLabel %s``
inMinimum: (a float)
    Minimum threshold value.
    argument: ``--inMinimum %f``
inMaximum: (a float)
    Maximum threshold value.
    argument: ``--inMaximum %f``
inUse: ('true' or 'false')
    Use the images max intensity as the max value of the range.
    argument: ``--inUse %s``
xPrefExt: ('nrrd')
    Output File Type
    argument: ``--xPrefExt %s``
outBinary: (a list of items which are a pathlike object or string
    representing a file)
    Binary Mask
    argument: ``--outBinary %s``
null: (a unicode string)
    Execution Time
    argument: ``--null %s``
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a

```

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```
value of class 'str', nipy default value: {}
Environment variables
```

Outputs:

None

65.1.18 RandomVol

[Link to code](#)

Wraps the executable command `“java edu.jhu.ece.iac.jist.cli.run edu.jhu.bme.smile.demo.RandomVol “`.

title: Random Volume Generator

category: Developer Tools

description: Generate a random scalar volume.

version: 1.12.RC

documentation-url: <http://www.nitrc.org/projects/jist/>

Inputs:

```
[Optional]
inSize: (an integer (int or long))
    Size of Volume in X direction
    argument: ``--inSize %d``
inSize2: (an integer (int or long))
    Size of Volume in Y direction
    argument: ``--inSize2 %d``
inSize3: (an integer (int or long))
    Size of Volume in Z direction
    argument: ``--inSize3 %d``
inSize4: (an integer (int or long))
    Size of Volume in t direction
    argument: ``--inSize4 %d``
inStandard: (an integer (int or long))
    Standard Deviation for Normal Distribution
    argument: ``--inStandard %d``
inLambda: (a float)
    Lambda Value for Exponential Distribution
    argument: ``--inLambda %f``
inMaximum: (an integer (int or long))
    Maximum Value
    argument: ``--inMaximum %d``
inMinimum: (an integer (int or long))
    Minimum Value
    argument: ``--inMinimum %d``
inField: ('Uniform' or 'Normal' or 'Exponential')
    Field
    argument: ``--inField %s``
xPrefExt: ('nrrd')
    Output File Type
    argument: ``--xPrefExt %s``
outRand1: (a boolean or a pathlike object or string representing a
    file)
    Rand1
    argument: ``--outRand1 %s``
null: (a unicode string)
    Execution Time
    argument: ``--null %s``
```

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```
xDefaultMem: (an integer (int or long))
    Set default maximum heap size
    argument: ``-xDefaultMem %d``
xMaxProcess: (an integer (int or long), nipy default value: 1)
    Set default maximum number of processes.
    argument: ``-xMaxProcess %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outRand1: (a pathlike object or string representing an existing file)
    Rand1
```

66.1 interfaces.mixins.reporting

66.1.1 ReportCapableInterface

[Link to code](#)

Mixin to enable reporting for Nipype interfaces

Inputs:

None

Outputs:

None

67.1 interfaces.mne.base

67.1.1 WatershedBEM

[Link to code](#)

Wraps the executable command `mne watershed_bem`.

Uses `mne_watershed_bem` to get information from dicom directories

Examples

```
>>> from nipy.interfaces.mne import WatershedBEM
>>> bem = WatershedBEM()
>>> bem.inputs.subject_id = 'subj1'
>>> bem.inputs.subjects_dir = '.'
>>> bem.cmdline
'mne watershed_bem --overwrite --subject subj1 --volume T1'
>>> bem.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
subject_id: (a unicode string)
    Subject ID (must have a complete Freesurfer directory)
    argument: ``--subject %s``
subjects_dir: (a pathlike object or string representing an existing
    directory, nipy default value: <undefined>)
    Path to Freesurfer subjects directory

[Optional]
volume: ('T1' or 'aparc+aseg' or 'aseg' or 'brain' or 'orig' or
    'brainmask' or 'ribbon', nipy default value: T1)
    The volume from the "mri" directory to use (defaults to T1)
    argument: ``--volume %s``
overwrite: (a boolean, nipy default value: True)
    Overwrites the existing files
    argument: ``--overwrite``
```

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```
atlas_mode: (a boolean)
    Use atlas mode for registration (default: no rigid alignment)
    argument: ``--atlas``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
mesh_files: (a list of items which are a pathlike object or string
    representing an existing file)
    Paths to the output meshes (brain, inner skull, outer skull, outer
    skin)
brain_surface: (a pathlike object or string representing an existing
    file)
    Brain surface (in Freesurfer format)
inner_skull_surface: (a pathlike object or string representing an
    existing file)
    Inner skull surface (in Freesurfer format)
outer_skull_surface: (a pathlike object or string representing an
    existing file)
    Outer skull surface (in Freesurfer format)
outer_skin_surface: (a pathlike object or string representing an
    existing file)
    Outer skin surface (in Freesurfer format)
fif_file: (a pathlike object or string representing an existing file)
    "fif" format file for EEG processing in MNE
cor_files: (a list of items which are a pathlike object or string
    representing an existing file)
    "COR" format files
```


68.1 interfaces.mrtrix.convert

68.1.1 MRTrix2TrackVis

[Link to code](#)

Converts MRtrix (.tck) tract files into TrackVis (.trk) format using functions from dipy Example ~~~~~~
 >>> import nipype.interfaces.mrtrix as mrt >>> tck2trk = mrt.MRTrix2TrackVis() >>> tck2trk.inputs.in_file =
 'dwi_CSD_tracked.tck' >>> tck2trk.inputs.image_file = 'diffusion.nii' >>> tck2trk.run() # doctest: +SKIP
 Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        The input file for the tracks in MRTrix (.tck) format

[Optional]
image_file: (a pathlike object or string representing an existing
            file)
            The image the tracks were generated from
matrix_file: (a pathlike object or string representing an existing
            file)
            A transformation matrix to apply to the tracts after they have been
            generated (from FLIRT - affine transformation from image_file to
            registration_image_file)
registration_image_file: (a pathlike object or string representing an
            existing file)
            The final image the tracks should be registered to.
out_filename: (a pathlike object or string representing a file,
            nipype default value: converted.trk)
            The output filename for the tracks in TrackVis (.trk) format
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

68.1.2 read_mrtrix_header()

[Link to code](#)

68.1.3 read_mrtrix_streamlines()

[Link to code](#)

68.1.4 read_mrtrix_tracks()

[Link to code](#)

68.1.5 transform_to_affine()

[Link to code](#)

68.2 interfaces.mrtrix.preprocess

68.2.1 DWI2Tensor

[Link to code](#)

Wraps the executable command dwi2tensor.

Converts diffusion-weighted images to tensor images.

Example

```
>>> import nipy.interfaces.mrtrix as mrt
>>> dwi2tensor = mrt.DWI2Tensor()
>>> dwi2tensor.inputs.in_file = 'dwi.mif'
>>> dwi2tensor.inputs.encoding_file = 'encoding.txt'
>>> dwi2tensor.cmdline
'dwi2tensor -grad encoding.txt dwi.mif dwi_tensor.mif'
>>> dwi2tensor.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a list of items which are a pathlike object or string
         representing an existing file)
         Diffusion-weighted images
         argument: ``%s``, position: -2

[Optional]
out_filename: (a pathlike object or string representing a file)
              Output tensor filename
              argument: ``%s``, position: -1
encoding_file: (a pathlike object or string representing a file)
               Encoding file supplied as a 4xN text file with each line is in the
               format [ X Y Z b ], where [ X Y Z ] describe the direction of the
               applied gradient, and b gives the b-value in units (1000 s/mm^2).
               See FSL2MRtrix()
               argument: ``-grad %s``, position: 2
ignore_slice_by_volume: (a list of from 2 to 2 items which are an
                        integer (int or long))
                        Requires two values (i.e. [34 1] for [Slice Volume] Ignores the
                        image slices specified when computing the tensor. Slice here means
                        the z coordinate of the slice to be ignored.
                        argument: ``-ignoreslices %s``, position: 2
ignore_volumes: (a list of at least 1 items which are an integer (int
                or long))
```

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```

Requires two values (i.e. [2 5 6] for [Volumes] Ignores the image
volumes specified when computing the tensor.
argument: ``-ignorevolumes %s``, position: 2
quiet: (a boolean)
Do not display information messages or progress status.
argument: ``-quiet``, position: 1
debug: (a boolean)
Display debugging messages.
argument: ``-debug``, position: 1
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

tensor: (a pathlike object or string representing an existing file)
path/name of output diffusion tensor image

```

68.2.2 Erode[Link to code](#)

Wraps the executable command erode.

Erode (or dilates) a mask (i.e. binary) image

Example

```

>>> import nipy.interfaces.mrtrix as mrt
>>> erode = mrt.Erode()
>>> erode.inputs.in_file = 'mask.mif'
>>> erode.run()                                     # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
Input mask image to be eroded
argument: ``%s``, position: -2

[Optional]
out_filename: (a pathlike object or string representing a file)
Output image filename
argument: ``%s``, position: -1
number_of_passes: (an integer (int or long))
the number of passes (default: 1)
argument: ``-npass %s``
dilate: (a boolean)
Perform dilation rather than erosion
argument: ``-dilate``, position: 1
quiet: (a boolean)
Do not display information messages or progress status.
argument: ``-quiet``, position: 1
debug: (a boolean)

```

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```

    Display debugging messages.
    argument: ``-debug``, position: 1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    the output image

```

68.2.3 GenerateWhiteMatterMask[Link to code](#)Wraps the executable command `gen_WM_mask`.

Generates a white matter probability mask from the DW images.

Example

```

>>> import nipype.interfaces.mrtrix as mrt
>>> genWM = mrt.GenerateWhiteMatterMask()
>>> genWM.inputs.in_file = 'dwi.mif'
>>> genWM.inputs.encoding_file = 'encoding.txt'
>>> genWM.run()                                     # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Diffusion-weighted images
    argument: ``%s``, position: -3
binary_mask: (a pathlike object or string representing an existing
    file)
    Binary brain mask
    argument: ``%s``, position: -2
encoding_file: (a pathlike object or string representing an existing
    file)
    Gradient encoding, supplied as a 4xN text file with each line is in
    the format [ X Y Z b ], where [ X Y Z ] describe the direction of
    the applied gradient, and b gives the b-value in units (1000
    s/mm^2). See FSL2MRTrix
    argument: ``-grad %s``, position: 1

[Optional]
out_WMProb_filename: (a pathlike object or string representing a
    file)
    Output WM probability image filename
    argument: ``%s``, position: -1
noise_level_margin: (a float)
    Specify the width of the margin on either side of the image to be
    used to estimate the noise level (default = 10)
    argument: ``-margin %s``

```

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```

args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

WMprobabilitymap: (a pathlike object or string representing an
                  existing file)
                  WMprobabilitymap

```

68.2.4 MRConvert

[Link to code](#)

Wraps the executable command `mrconvert`.

Perform conversion between different file types and optionally extract a subset of the input image.

If used correctly, this program can be a very useful workhorse. In addition to converting images between different formats, it can be used to extract specific studies from a data set, extract a specific region of interest, flip the images, or to scale the intensity of the images.

Example

```

>>> import nipy.interfaces.mrtrix as mrt
>>> mrconvert = mrt.MRConvert()
>>> mrconvert.inputs.in_file = 'dwi_FA.mif'
>>> mrconvert.inputs.out_filename = 'dwi_FA.nii'
>>> mrconvert.run()                                # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         voxel-order data filename
         argument: ``%s``, position: -2

[Optional]
out_filename: (a pathlike object or string representing a file)
              Output filename
              argument: ``%s``, position: -1
extract_at_axis: (1 or 2 or 3)
                 "Extract data only at the coordinates specified. This option
                 specifies the Axis. Must be used in conjunction with
                 extract_at_coordinate.
                 argument: ``-coord %s``, position: 1
extract_at_coordinate: (a list of from 1 to 3 items which are a
                       float)
                       "Extract data only at the coordinates specified. This option
                       specifies the coordinates. Must be used in conjunction with
                       extract_at_axis. Three comma-separated numbers giving the size of
                       each voxel in mm.
                       argument: ``%s``, position: 2
voxel_dims: (a list of from 3 to 3 items which are a float)
            Three comma-separated numbers giving the size of each voxel in mm.

```

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```

        argument: ``-vox %s``, position: 3
output_datatype: ('nii' or 'float' or 'char' or 'short' or 'int' or
                  'long' or 'double')
                  "i.e. Bfloat". Can be "char", "short", "int", "long", "float" or
                  "double"
        argument: ``-output %s``, position: 2
extension: ('mif' or 'nii' or 'float' or 'char' or 'short' or 'int'
            or 'long' or 'double', nipy default value: mif)
            "i.e. Bfloat". Can be "char", "short", "int", "long", "float" or
            "double"
layout: ('nii' or 'float' or 'char' or 'short' or 'int' or 'long' or
         'double')
         specify the layout of the data in memory. The actual layout produced
         will depend on whether the output image format can support it.
        argument: ``-output %s``, position: 2
resample: (a float)
          Apply scaling to the intensity values.
        argument: ``-scale %d``, position: 3
offset_bias: (a float)
             Apply offset to the intensity values.
        argument: ``-scale %d``, position: 3
replace_NaN_with_zero: (a boolean)
                       Replace all NaN values with zero.
        argument: ``-zero``, position: 3
prs: (a boolean)
     Assume that the DW gradients are specified in the PRS frame (Siemens
     DICOM only).
        argument: ``-prs``, position: 3
args: (a unicode string)
      Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

converted: (a pathlike object or string representing an existing
           file)
           path/name of 4D volume in voxel order

```

68.2.5 MRMultiply[Link to code](#)

Wraps the executable command mrmult.

Multiplies two images.

Example

```

>>> import nipy.interfaces.mrtrix as mrt
>>> MRmult = mrt.MRMultiply()
>>> MRmult.inputs.in_files = ['dwi.mif', 'dwi_WMPProb.mif']
>>> MRmult.run()
# doctest: +SKIP

```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
          representing an existing file)
          Input images to be multiplied
          argument: ``%s``, position: -2

[Optional]
out_filename: (a pathlike object or string representing a file)
              Output image filename
              argument: ``%s``, position: -1
quiet: (a boolean)
       Do not display information messages or progress status.
       argument: ``-quiet``, position: 1
debug: (a boolean)
       Display debugging messages.
       argument: ``-debug``, position: 1
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          the output image of the multiplication
```

68.2.6 MRTransform[Link to code](#)Wraps the executable command `mrtransform`.

Apply spatial transformations or reslice images

Example

```
>>> MRxform = MRTransform()
>>> MRxform.inputs.in_files = 'anat_coreg.mif'
>>> MRxform.run()                                # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
          representing an existing file)
          Input images to be transformed
          argument: ``%s``, position: -2

[Optional]
out_filename: (a pathlike object or string representing a file)
              Output image
              argument: ``%s``, position: -1
invert: (a boolean)
       Invert the specified transform before using it
       argument: ``-inverse``, position: 1
replace_transform: (a boolean)
```

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```

        replace the current transform by that specified, rather than
        applying it to the current transform
        argument: ``-replace``, position: 1
    transformation_file: (a pathlike object or string representing an
        existing file)
        The transform to apply, in the form of a 4x4 ascii file.
        argument: ``-transform %s``, position: 1
    template_image: (a pathlike object or string representing an existing
        file)
        Reslice the input image to match the specified template image.
        argument: ``-template %s``, position: 1
    reference_image: (a pathlike object or string representing an
        existing file)
        in case the transform supplied maps from the input image onto a
        reference image, use this option to specify the reference. Note that
        this implicitly sets the -replace option.
        argument: ``-reference %s``, position: 1
    flip_x: (a boolean)
        assume the transform is supplied assuming a coordinate system with
        the x-axis reversed relative to the MRtrix convention (i.e. x
        increases from right to left). This is required to handle transform
        matrices produced by FSL's FLIRT command. This is only used in
        conjunction with the -reference option.
        argument: ``-flipx``, position: 1
    quiet: (a boolean)
        Do not display information messages or progress status.
        argument: ``-quiet``, position: 1
    debug: (a boolean)
        Display debugging messages.
        argument: ``-debug``, position: 1
    args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
    environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipype default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        the output image of the transformation

```

68.2.7 MRtrixViewer[Link to code](#)Wraps the executable command `mrview`.

Loads the input images in the MRtrix Viewer.

Example

```

>>> import nipype.interfaces.mrtrix as mrt
>>> MRview = mrt.MRtrixViewer()
>>> MRview.inputs.in_files = 'dwi.mif'
>>> MRview.run()                                     # doctest: +SKIP

```

Inputs:


```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
          representing an existing file)
          Input images to be viewed
          argument: ``%s``, position: -2

[Optional]
quiet: (a boolean)
       Do not display information messages or progress status.
       argument: ``-quiet``, position: 1
debug: (a boolean)
       Display debugging messages.
       argument: ``-debug``, position: 1
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipype default value: {})
         Environment variables
```

Outputs:

None

68.2.8 MedianFilter3D

[Link to code](#)

Wraps the executable command median3D.

Smooth images using a 3x3x3 median filter.

Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> median3d = mrt.MedianFilter3D()
>>> median3d.inputs.in_file = 'mask.mif'
>>> median3d.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         Input images to be smoothed
         argument: ``%s``, position: -2

[Optional]
out_filename: (a pathlike object or string representing a file)
              Output image filename
              argument: ``%s``, position: -1
quiet: (a boolean)
       Do not display information messages or progress status.
       argument: ``-quiet``, position: 1
debug: (a boolean)
       Display debugging messages.
       argument: ``-debug``, position: 1
args: (a unicode string)
      Additional parameters to the command
```

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```

    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
           the output image

```

68.2.9 Tensor2ApparentDiffusion

[Link to code](#)

Wraps the executable command tensor2ADC.

Generates a map of the apparent diffusion coefficient (ADC) in each voxel

Example

```

>>> import nipy.interfaces.mrtrix as mrt
>>> tensor2ADC = mrt.Tensor2ApparentDiffusion()
>>> tensor2ADC.inputs.in_file = 'dwi_tensor.mif'
>>> tensor2ADC.run()                                     # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
          Diffusion tensor image
          argument: ``%s``, position: -2

[Optional]
out_filename: (a pathlike object or string representing a file)
              Output Fractional Anisotropy filename
              argument: ``%s``, position: -1
quiet: (a boolean)
       Do not display information messages or progress status.
       argument: ``-quiet``, position: 1
debug: (a boolean)
       Display debugging messages.
       argument: ``-debug``, position: 1
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

ADC: (a pathlike object or string representing an existing file)
      the output image of the major eigenvectors of the diffusion tensor
      image.

```

68.2.10 Tensor2FractionalAnisotropy

[Link to code](#)

Wraps the executable command `tensor2FA`.

Generates a map of the fractional anisotropy in each voxel.

Example

```
>>> import nipy.interfaces.mrtrix as mrt
>>> tensor2FA = mrt.Tensor2FractionalAnisotropy()
>>> tensor2FA.inputs.in_file = 'dwi_tensor.mif'
>>> tensor2FA.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         Diffusion tensor image
         argument: ``%s``, position: -2

[Optional]
out_filename: (a pathlike object or string representing a file)
              Output Fractional Anisotropy filename
              argument: ``%s``, position: -1
quiet: (a boolean)
       Do not display information messages or progress status.
       argument: ``-quiet``, position: 1
debug: (a boolean)
       Display debugging messages.
       argument: ``-debug``, position: 1
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
FA: (a pathlike object or string representing an existing file)
    the output image of the major eigenvectors of the diffusion tensor
    image.
```

68.2.11 Tensor2Vector

[Link to code](#)

Wraps the executable command `tensor2vector`.

Generates a map of the major eigenvectors of the tensors in each voxel.

Example

```
>>> import nipy.interfaces.mrtrix as mrt
>>> tensor2vector = mrt.Tensor2Vector()
>>> tensor2vector.inputs.in_file = 'dwi_tensor.mif'
>>> tensor2vector.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        Diffusion tensor image
        argument: ``%s``, position: -2

[Optional]
out_filename: (a pathlike object or string representing a file)
              Output vector filename
              argument: ``%s``, position: -1
quiet: (a boolean)
       Do not display information messages or progress status.
       argument: ``-quiet``, position: 1
debug: (a boolean)
       Display debugging messages.
       argument: ``-debug``, position: 1
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
vector: (a pathlike object or string representing an existing file)
        the output image of the major eigenvectors of the diffusion tensor
        image.
```

68.2.12 Threshold[Link to code](#)

Wraps the executable command `threshold`.

Create bitwise image by thresholding image intensity.

By default, the threshold level is determined using a histogram analysis to cut out the background. Otherwise, the threshold intensity can be specified using command line options. Note that only the first study is used for thresholding.

Example

```
>>> import nipy.interfaces.mrtrix as mrt
>>> thresh = mrt.Threshold()
>>> thresh.inputs.in_file = 'wm_mask.mif'
>>> thresh.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        The input image to be thresholded
        argument: ``%s``, position: -2

[Optional]
out_filename: (a pathlike object or string representing a file)
              The output binary image mask.
              argument: ``%s``, position: -1
```

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```

absolute_threshold_value: (a float)
    Specify threshold value as absolute intensity.
    argument: ``-abs %s``
percentage_threshold_value: (a float)
    Specify threshold value as a percentage of the peak intensity in the
    input image.
    argument: ``-percent %s``
invert: (a boolean)
    Invert output binary mask
    argument: ``-invert``, position: 1
replace_zeros_with_NaN: (a boolean)
    Replace all zero values with NaN
    argument: ``-nan``, position: 1
quiet: (a boolean)
    Do not display information messages or progress status.
    argument: ``-quiet``, position: 1
debug: (a boolean)
    Display debugging messages.
    argument: ``-debug``, position: 1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    The output binary image mask.

```

68.3 interfaces.mrtrix.tensors

68.3.1 ConstrainedSphericalDeconvolution

[Link to code](#)

Wraps the executable command `csdeconv`.

Perform non-negativity constrained spherical deconvolution.

Note that this program makes use of implied symmetries in the diffusion profile. First, the fact the signal attenuation profile is real implies that it has conjugate symmetry, i.e. $Y(l, -m) = Y(l, m)^*$ (where $*$ denotes the complex conjugate). Second, the diffusion profile should be antipodally symmetric (i.e. $S(x) = S(-x)$), implying that all odd l components should be zero. Therefore, this program only computes the even elements. Note that the spherical harmonics equations used here differ slightly from those conventionally used, in that the $(-1)^m$ factor has been omitted. This should be taken into account in all subsequent calculations. Each volume in the output image corresponds to a different spherical harmonic component, according to the following convention:

- [0] $Y(0,0)$
- [1] $\text{Im} \{Y(2,2)\}$
- [2] $\text{Im} \{Y(2,1)\}$
- [3] $Y(2,0)$
- [4] $\text{Re} \{Y(2,1)\}$
- [5] $\text{Re} \{Y(2,2)\}$
- [6] $\text{Im} \{Y(4,4)\}$
- [7] $\text{Im} \{Y(4,3)\}$

Example

```
>>> import nipy.interfaces.mrtrix as mrt
>>> csdeconv = mrt.ConstrainedSphericalDeconvolution()
>>> csdeconv.inputs.in_file = 'dwi.mif'
>>> csdeconv.inputs.encoding_file = 'encoding.txt'
>>> csdeconv.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         diffusion-weighted image
         argument: ``%s``, position: -3
response_file: (a pathlike object or string representing an existing
                file)
                the diffusion-weighted signal response function for a single fibre
                population (see EstimateResponse)
                argument: ``%s``, position: -2

[Optional]
out_filename: (a pathlike object or string representing a file)
              Output filename
              argument: ``%s``, position: -1
mask_image: (a pathlike object or string representing an existing
             file)
             only perform computation within the specified binary brain mask
             image
             argument: ``-mask %s``, position: 2
encoding_file: (a pathlike object or string representing an existing
               file)
               Gradient encoding, supplied as a 4xN text file with each line is in
               the format [ X Y Z b ], where [ X Y Z ] describe the direction of
               the applied gradient, and b gives the b-value in units (1000
               s/mm^2). See FSL2MRTrix
               argument: ``-grad %s``, position: 1
filter_file: (a pathlike object or string representing an existing
              file)
              a text file containing the filtering coefficients for each even
              harmonic order.the linear frequency filtering parameters used for
              the initial linear spherical deconvolution step (default = [ 1 1 1 0
              0 ]).
              argument: ``-filter %s``, position: -2
lambda_value: (a float)
              the regularisation parameter lambda that controls the strength of
              the constraint (default = 1.0).
              argument: ``-lambda %s``
maximum_harmonic_order: (an integer (int or long))
                        set the maximum harmonic order for the output series. By default,
                        the program will use the highest possible lmax given the number of
                        diffusion-weighted images.
                        argument: ``-lmax %s``
threshold_value: (a float)
                 the threshold below which the amplitude of the FOD is assumed to be
                 zero, expressed as a fraction of the mean value of the initial FOD
                 (default = 0.1)
                 argument: ``-threshold %s``
iterations: (an integer (int or long))
```

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```

        the maximum number of iterations to perform for each voxel (default
        = 50)
        argument: ``-niter %s``
debug: (a boolean)
        Display debugging messages.
        argument: ``-debug``
directions_file: (a pathlike object or string representing an
        existing file)
        a text file containing the [ el az ] pairs for the directions:
        Specify the directions over which to apply the non-negativity
        constraint (by default, the built-in 300 direction set is used)
        argument: ``-directions %s``, position: -2
normalise: (a boolean)
        normalise the DW signal to the b=0 image
        argument: ``-normalise``, position: 3
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipype default value: {})
        Environment variables

```

Outputs:

```

spherical_harmonics_image: (a pathlike object or string representing
        an existing file)
        Spherical harmonics image

```

68.3.2 DWI2SphericalHarmonicsImage[Link to code](#)

Wraps the executable command dwi2SH.

Convert base diffusion-weighted images to their spherical harmonic representation.

This program outputs the spherical harmonic decomposition for the set measured signal attenuations. The signal attenuations are calculated by identifying the b-zero images from the diffusion encoding supplied (i.e. those with zero as the b-value), and dividing the remaining signals by the mean b-zero signal intensity. The spherical harmonic decomposition is then calculated by least-squares linear fitting. Note that this program makes use of implied symmetries in the diffusion profile.

First, the fact the signal attenuation profile is real implies that it has conjugate symmetry, i.e. $Y(l, -m) = Y(l, m)^*$ (where * denotes the complex conjugate). Second, the diffusion profile should be antipodally symmetric (i.e. $S(x) = S(-x)$), implying that all odd l components should be zero. Therefore, this program only computes the even elements.

Note that the spherical harmonics equations used here differ slightly from those conventionally used, in that the $(-1)^m$ factor has been omitted. This should be taken into account in all subsequent calculations.

Each volume in the output image corresponds to a different spherical harmonic component, according to the following convention:

- [0] $Y(0,0)$
- [1] $\text{Im} \{Y(2,2)\}$
- [2] $\text{Im} \{Y(2,1)\}$
- [3] $Y(2,0)$
- [4] $\text{Re} \{Y(2,1)\}$
- [5] $\text{Re} \{Y(2,2)\}$
- [6] $\text{Im} \{Y(4,4)\}$
- [7] $\text{Im} \{Y(4,3)\}$

Example

```
>>> import nipy.interfaces.mrtrix as mrt
>>> dwi2SH = mrt.DWI2SphericalHarmonicsImage()
>>> dwi2SH.inputs.in_file = 'diffusion.nii'
>>> dwi2SH.inputs.encoding_file = 'encoding.txt'
>>> dwi2SH.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Diffusion-weighted images
    argument: ``%s``, position: -2
encoding_file: (a pathlike object or string representing an existing
    file)
    Gradient encoding, supplied as a 4xN text file with each line is in
    the format [ X Y Z b ], where [ X Y Z ] describe the direction of
    the applied gradient, and b gives the b-value in units (1000
    s/mm^2). See FSL2MRtrix
    argument: ``-grad %s``, position: 1

[Optional]
out_filename: (a pathlike object or string representing a file)
    Output filename
    argument: ``%s``, position: -1
maximum_harmonic_order: (a float)
    set the maximum harmonic order for the output series. By default,
    the program will use the highest possible lmax given the number of
    diffusion-weighted images.
    argument: ``-lmax %s``
normalise: (a boolean)
    normalise the DW signal to the b=0 image
    argument: ``-normalise``, position: 3
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
spherical_harmonics_image: (a pathlike object or string representing
    an existing file)
    Spherical harmonics image
```

68.3.3 Directions2Amplitude

[Link to code](#)

Wraps the executable command `dir2amp`.
convert directions image to amplitudes

Example

```
>>> import nipy.interfaces.mrtrix as mrt
>>> amplitudes = mrt.Directions2Amplitude()
>>> amplitudes.inputs.in_file = 'peak_directions.mif'
>>> amplitudes.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        the input directions image. Each volume corresponds to the x, y & z
        component of each direction vector in turn.
        argument: ``%s``, position: -2

[Optional]
peaks_image: (a pathlike object or string representing an existing
             file)
             the program will try to find the peaks that most closely match those
             in the image provided
             argument: ``-peaks %s``
num_peaks: (an integer (int or long))
           the number of peaks to extract (default is 3)
           argument: ``-num %s``
peak_directions: (a list of from 2 to 2 items which are a float)
                 phi theta. the direction of a peak to estimate. The algorithm will
                 attempt to find the same number of peaks as have been specified
                 using this option phi: the azimuthal angle of the direction (in
                 degrees). theta: the elevation angle of the direction (in degrees,
                 from the vertical z-axis)
                 argument: ``-direction %s``
display_info: (a boolean)
              Display information messages.
              argument: ``-info``
quiet_display: (a boolean)
              do not display information messages or progress status.
              argument: ``-quiet``
display_debug: (a boolean)
              Display debugging messages.
              argument: ``-debug``
out_file: (a pathlike object or string representing a file)
          the output amplitudes image
          argument: ``%s``, position: -1
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          amplitudes image
```

68.3.4 EstimateResponseForSH

[Link to code](#)

Wraps the executable command `estimate_response`.
Estimates the fibre response function for use in spherical deconvolution.

Example

```
>>> import nipyype.interfaces.mrtrix as mrt
>>> estresp = mrt.EstimateResponseForSH()
>>> estresp.inputs.in_file = 'dwi.mif'
>>> estresp.inputs.mask_image = 'dwi_WMPProb.mif'
>>> estresp.inputs.encoding_file = 'encoding.txt'
>>> estresp.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        Diffusion-weighted images
        argument: ``%s``, position: -3
mask_image: (a pathlike object or string representing an existing
            file)
            only perform computation within the specified binary brain mask
            image
            argument: ``%s``, position: -2
encoding_file: (a pathlike object or string representing an existing
            file)
            Gradient encoding, supplied as a 4xN text file with each line is in
            the format [ X Y Z b ], where [ X Y Z ] describe the direction of
            the applied gradient, and b gives the b-value in units (1000
            s/mm^2). See FSL2MRTrix
            argument: ``-grad %s``, position: 1

[Optional]
out_filename: (a pathlike object or string representing a file)
            Output filename
            argument: ``%s``, position: -1
maximum_harmonic_order: (an integer (int or long))
            set the maximum harmonic order for the output series. By default,
            the program will use the highest possible lmax given the number of
            diffusion-weighted images.
            argument: ``-lmax %s``
normalise: (a boolean)
            normalise the DW signal to the b=0 image
            argument: ``-normalise``
quiet: (a boolean)
            Do not display information messages or progress status.
            argument: ``-quiet``
debug: (a boolean)
            Display debugging messages.
            argument: ``-debug``
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
            of class 'str' and with values which are a bytes or None or a
            value of class 'str', nipyype default value: {})
            Environment variables
```

Outputs:

```
response: (a pathlike object or string representing an existing file)
          Spherical harmonics image
```

68.3.5 FindShPeaks

[Link to code](#)

Wraps the executable command `find_SH_peaks`.

identify the orientations of the N largest peaks of a SH profile

Example

```
>>> import nipy.interfaces.mrtrix as mrt
>>> shpeaks = mrt.FindShPeaks()
>>> shpeaks.inputs.in_file = 'csd.mif'
>>> shpeaks.inputs.directions_file = 'dirs.txt'
>>> shpeaks.inputs.num_peaks = 2
>>> shpeaks.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         the input image of SH coefficients.
         argument: ``%s``, position: -3
directions_file: (a pathlike object or string representing an
                  existing file)
                  the set of directions to use as seeds for the peak finding
                  argument: ``%s``, position: -2

[Optional]
peaks_image: (a pathlike object or string representing an existing
              file)
              the program will try to find the peaks that most closely match those
              in the image provided
              argument: ``-peaks %s``
num_peaks: (an integer (int or long))
            the number of peaks to extract (default is 3)
            argument: ``-num %s``
peak_directions: (a list of from 2 to 2 items which are a float)
                  phi theta. the direction of a peak to estimate. The algorithm will
                  attempt to find the same number of peaks as have been specified
                  using this option phi: the azimuthal angle of the direction (in
                  degrees). theta: the elevation angle of the direction (in degrees,
                  from the vertical z-axis)
                  argument: ``-direction %s``
peak_threshold: (a float)
                 only peak amplitudes greater than the threshold will be considered
                 argument: ``-threshold %s``
display_info: (a boolean)
               Display information messages.
               argument: ``-info``
quiet_display: (a boolean)
                do not display information messages or progress status.
                argument: ``-quiet``
display_debug: (a boolean)
                Display debugging messages.
```

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```

    argument: ``-debug``
out_file: (a pathlike object or string representing a file)
    the output image. Each volume corresponds to the x, y & z component
    of each peak direction vector in turn
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    Peak directions image

```

68.3.6 GenerateDirections

[Link to code](#)

Wraps the executable command gendir.

generate a set of directions evenly distributed over a hemisphere.

Example

```

>>> import nipy.interfaces.mrtrix as mrt
>>> gendir = mrt.GenerateDirections()
>>> gendir.inputs.num_dirs = 300
>>> gendir.run()                                     # doctest: +SKIP

```

Inputs:

```

[Mandatory]
num_dirs: (an integer (int or long))
    the number of directions to generate.
    argument: ``%s``, position: -2

[Optional]
power: (a float)
    specify exponent to use for repulsion power law.
    argument: ``-power %s``
niter: (an integer (int or long))
    specify the maximum number of iterations to perform.
    argument: ``-niter %s``
display_info: (a boolean)
    Display information messages.
    argument: ``-info``
quiet_display: (a boolean)
    do not display information messages or progress status.
    argument: ``-quiet``
display_debug: (a boolean)
    Display debugging messages.
    argument: ``-debug``
out_file: (a pathlike object or string representing a file)
    the text file to write the directions to, as [ az el ] pairs.

```

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```

        argument: ``%s``, position: -1
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
          directions file

```

68.3.7 concat_files()

[Link to code](#)

68.4 interfaces.mrtrix.tracking

68.4.1 DiffusionTensorStreamlineTrack

[Link to code](#)

Wraps the executable command streamtrack.

Specialized interface to StreamlineTrack. This interface is used for streamline tracking from diffusion tensor data, and calls the MRtrix function 'streamtrack' with the option 'DT_STREAM'

Example

```

>>> import nipype.interfaces.mrtrix as mrt
>>> dtstrack = mrt.DiffusionTensorStreamlineTrack()
>>> dtstrack.inputs.in_file = 'data.Bfloat'
>>> dtstrack.inputs.seed_file = 'seed_mask.nii'
>>> dtstrack.run()                                     # doctest: +SKIP

```

Inputs:

```

[Mandatory]
gradient_encoding_file: (a pathlike object or string representing an
                        existing file)
                        Gradient encoding, supplied as a 4xN text file with each line is in
                        the format [ X Y Z b ], where [ X Y Z ] describe the direction of
                        the applied gradient, and b gives the b-value in units (1000
                        s/mm^2). See FSL2MRTrix
                        argument: ``-grad %s``, position: -2
in_file: (a pathlike object or string representing an existing file)
          the image containing the source data.The type of data required
          depends on the type of tracking as set in the preceeding argument.
          For DT methods, the base DWI are needed. For SD methods, the SH
          harmonic coefficients of the FOD are needed.
          argument: ``%s``, position: -2

[Optional]
seed_file: (a pathlike object or string representing an existing
           file)

```

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```

    seed file
    argument: ``-seed %s``
    mutually_exclusive: seed_file, seed_spec
seed_spec: (a list of from 4 to 4 items which are a float)
    seed specification in mm and radius (x y z r)
    argument: ``-seed %s``, position: 2
    mutually_exclusive: seed_file, seed_spec
include_file: (a pathlike object or string representing an existing
    file)
    inclusion file
    argument: ``-include %s``
    mutually_exclusive: include_file, include_spec
include_spec: (a list of from 4 to 4 items which are a float)
    inclusion specification in mm and radius (x y z r)
    argument: ``-include %s``, position: 2
    mutually_exclusive: include_file, include_spec
exclude_file: (a pathlike object or string representing an existing
    file)
    exclusion file
    argument: ``-exclude %s``
    mutually_exclusive: exclude_file, exclude_spec
exclude_spec: (a list of from 4 to 4 items which are a float)
    exclusion specification in mm and radius (x y z r)
    argument: ``-exclude %s``, position: 2
    mutually_exclusive: exclude_file, exclude_spec
mask_file: (a pathlike object or string representing an existing
    file)
    mask file. Only tracks within mask.
    argument: ``-mask %s``
    mutually_exclusive: mask_file, mask_spec
mask_spec: (a list of from 4 to 4 items which are a float)
    Mask specification in mm and radius (x y z r). Tracks will be
    terminated when they leave the ROI.
    argument: ``-mask %s``, position: 2
    mutually_exclusive: mask_file, mask_spec
inputmodel: ('DT_STREAM' or 'SD_PROB' or 'SD_STREAM', nipy default
    value: DT_STREAM)
    input model type
    argument: ``%s``, position: -3
stop: (a boolean)
    stop track as soon as it enters any of the include regions.
    argument: ``-stop``
do_not_precompute: (a boolean)
    Turns off precomputation of the legendre polynomial values. Warning:
    this will slow down the algorithm by a factor of approximately 4.
    argument: ``-noprecomputed``
unidirectional: (a boolean)
    Track from the seed point in one direction only (default is to track
    in both directions).
    argument: ``-unidirectional``
no_mask_interpolation: (a boolean)
    Turns off trilinear interpolation of mask images.
    argument: ``-nomaskinterp``
step_size: (a float)
    Set the step size of the algorithm in mm (default is 0.2).
    argument: ``-step %s``
minimum_radius_of_curvature: (a float)

```

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```

        Set the minimum radius of curvature (default is 2 mm for DT_STREAM,
        0 for SD_STREAM, 1 mm for SD_PROB and DT_PROB)
        argument: ``-curvature %s``
desired_number_of_tracks: (an integer (int or long))
        Sets the desired number of tracks. The program will continue to
        generate tracks until this number of tracks have been selected and
        written to the output file (default is 100 for *_STREAM methods, 1000
        for *_PROB methods).
        argument: ``-number %d``
maximum_number_of_tracks: (an integer (int or long))
        Sets the maximum number of tracks to generate. The program will not
        generate more tracks than this number, even if the desired number of
        tracks hasn't yet been reached (default is 100 x number).
        argument: ``-maxnum %d``
minimum_tract_length: (a float)
        Sets the minimum length of any track in millimeters (default is 10
        mm).
        argument: ``-minlength %s``
maximum_tract_length: (a float)
        Sets the maximum length of any track in millimeters (default is 200
        mm).
        argument: ``-length %s``
cutoff_value: (a float)
        Set the FA or FOD amplitude cutoff for terminating tracks (default
        is 0.1).
        argument: ``-cutoff %s``
initial_cutoff_value: (a float)
        Sets the minimum FA or FOD amplitude for initiating tracks (default
        is twice the normal cutoff).
        argument: ``-initcutoff %s``
initial_direction: (a list of from 2 to 2 items which are an integer
        (int or long))
        Specify the initial tracking direction as a vector
        argument: ``-initdirection %s``
out_file: (a pathlike object or string representing a file)
        output data file
        argument: ``%s``, position: -1
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

tracked: (a pathlike object or string representing an existing file)
        output file containing reconstructed tracts

```

68.4.2 FilterTracks[Link to code](#)Wraps the executable command `filter_tracks`.

Use regions-of-interest to select a subset of tracks from a given MRtrix track file.

Example

```
>>> import nipy.interfaces.mrtrix as mrt
>>> filt = mrt.FilterTracks()
>>> filt.inputs.in_file = 'tracks.tck'
>>> filt.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input tracks to be filtered
         argument: ``%s``, position: -2

[Optional]
include_file: (a pathlike object or string representing an existing
              file)
              inclusion file
              argument: ``-include %s``
              mutually_exclusive: include_file, include_spec
include_spec: (a list of from 4 to 4 items which are a float)
              inclusion specification in mm and radius (x y z r)
              argument: ``-include %s``, position: 2
              mutually_exclusive: include_file, include_spec
exclude_file: (a pathlike object or string representing an existing
              file)
              exclusion file
              argument: ``-exclude %s``
              mutually_exclusive: exclude_file, exclude_spec
exclude_spec: (a list of from 4 to 4 items which are a float)
              exclusion specification in mm and radius (x y z r)
              argument: ``-exclude %s``, position: 2
              mutually_exclusive: exclude_file, exclude_spec
minimum_tract_length: (a float)
                      Sets the minimum length of any track in millimeters (default is 10
                      mm).
                      argument: ``-minlength %s``
out_file: (a pathlike object or string representing a file)
          Output filtered track filename
          argument: ``%s``, position: -1
no_mask_interpolation: (a boolean)
                       Turns off trilinear interpolation of mask images.
                       argument: ``-nomaskinterp``
invert: (a boolean)
        invert the matching process, so that tracks that would otherwise have
        been included are now excluded and vice-versa.
        argument: ``-invert``
quiet: (a boolean)
       Do not display information messages or progress status.
       argument: ``-quiet``, position: 1
debug: (a boolean)
       Display debugging messages.
       argument: ``-debug``, position: 1
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
```

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```
value of class 'str', nipyne default value: {}
Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
the output filtered tracks
```

68.4.3 ProbabilisticSphericallyDeconvolutedStreamlineTrack[Link to code](#)

Wraps the executable command `streamtrack`.

Performs probabilistic tracking using spherically deconvolved data

Specialized interface to `StreamlineTrack`. This interface is used for probabilistic tracking from spherically deconvolved data, and calls the MRtrix function `'streamtrack'` with the option `'SD_PROB'`

Example

```
>>> import nipyne.interfaces.mrtrix as mrt
>>> sdprobtrack = mrt.ProbabilisticSphericallyDeconvolutedStreamlineTrack()
>>> sdprobtrack.inputs.in_file = 'data.Bfloat'
>>> sdprobtrack.inputs.seed_file = 'seed_mask.nii'
>>> sdprobtrack.run()
↪ doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
the image containing the source data. The type of data required
depends on the type of tracking as set in the preceding argument.
For DT methods, the base DWI are needed. For SD methods, the SH
harmonic coefficients of the FOD are needed.
argument: ``%s``, position: -2

[Optional]
maximum_number_of_trials: (an integer (int or long))
Set the maximum number of sampling trials at each point (only used
for probabilistic tracking).
argument: ``-trials %s``
seed_file: (a pathlike object or string representing an existing
file)
seed file
argument: ``-seed %s``
mutually_exclusive: seed_file, seed_spec
seed_spec: (a list of from 4 to 4 items which are a float)
seed specification in mm and radius (x y z r)
argument: ``-seed %s``, position: 2
mutually_exclusive: seed_file, seed_spec
include_file: (a pathlike object or string representing an existing
file)
inclusion file
argument: ``-include %s``
mutually_exclusive: include_file, include_spec
include_spec: (a list of from 4 to 4 items which are a float)
inclusion specification in mm and radius (x y z r)
```

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```

        argument: ``-include %s``, position: 2
        mutually_exclusive: include_file, include_spec
exclude_file: (a pathlike object or string representing an existing
               file)
               exclusion file
               argument: ``-exclude %s``
               mutually_exclusive: exclude_file, exclude_spec
exclude_spec: (a list of from 4 to 4 items which are a float)
               exclusion specification in mm and radius (x y z r)
               argument: ``-exclude %s``, position: 2
               mutually_exclusive: exclude_file, exclude_spec
mask_file: (a pathlike object or string representing an existing
            file)
            mask file. Only tracks within mask.
            argument: ``-mask %s``
            mutually_exclusive: mask_file, mask_spec
mask_spec: (a list of from 4 to 4 items which are a float)
            Mask specification in mm and radius (x y z r). Tracks will be
            terminated when they leave the ROI.
            argument: ``-mask %s``, position: 2
            mutually_exclusive: mask_file, mask_spec
inputmodel: ('DT_STREAM' or 'SD_PROB' or 'SD_STREAM', nipy default
            value: DT_STREAM)
            input model type
            argument: ``%s``, position: -3
stop: (a boolean)
       stop track as soon as it enters any of the include regions.
       argument: ``-stop``
do_not_precompute: (a boolean)
                   Turns off precomputation of the legendre polynomial values. Warning:
                   this will slow down the algorithm by a factor of approximately 4.
                   argument: ``-noprecomputed``
unidirectional: (a boolean)
                Track from the seed point in one direction only (default is to track
                in both directions).
                argument: ``-unidirectional``
no_mask_interpolation: (a boolean)
                       Turns off trilinear interpolation of mask images.
                       argument: ``-nomaskinterp``
step_size: (a float)
            Set the step size of the algorithm in mm (default is 0.2).
            argument: ``-step %s``
minimum_radius_of_curvature: (a float)
                              Set the minimum radius of curvature (default is 2 mm for DT_STREAM,
                              0 for SD_STREAM, 1 mm for SD_PROB and DT_PROB)
                              argument: ``-curvature %s``
desired_number_of_tracks: (an integer (int or long))
                           Sets the desired number of tracks. The program will continue to
                           generate tracks until this number of tracks have been selected and
                           written to the output file (default is 100 for *_STREAM methods, 1000
                           for *_PROB methods).
                           argument: ``-number %d``
maximum_number_of_tracks: (an integer (int or long))
                           Sets the maximum number of tracks to generate. The program will not
                           generate more tracks than this number, even if the desired number of
                           tracks hasn't yet been reached (default is 100 x number).
                           argument: ``-maxnum %d``

```

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```

minimum_tract_length: (a float)
    Sets the minimum length of any track in millimeters (default is 10
    mm).
    argument: ``-minlength %s``
maximum_tract_length: (a float)
    Sets the maximum length of any track in millimeters (default is 200
    mm).
    argument: ``-length %s``
cutoff_value: (a float)
    Set the FA or FOD amplitude cutoff for terminating tracks (default
    is 0.1).
    argument: ``-cutoff %s``
initial_cutoff_value: (a float)
    Sets the minimum FA or FOD amplitude for initiating tracks (default
    is twice the normal cutoff).
    argument: ``-initcutoff %s``
initial_direction: (a list of from 2 to 2 items which are an integer
    (int or long))
    Specify the initial tracking direction as a vector
    argument: ``-initdirection %s``
out_file: (a pathlike object or string representing a file)
    output data file
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

tracked: (a pathlike object or string representing an existing file)
    output file containing reconstructed tracts

```

68.4.4 SphericallyDeconvolutedStreamlineTrack[Link to code](#)Wraps the executable command `streamtrack`.

Performs streamline tracking using spherically deconvolved data

Specialized interface to StreamlineTrack. This interface is used for streamline tracking from spherically deconvolved data, and calls the MRtrix function 'streamtrack' with the option 'SD_STREAM'

Example

```

>>> import nipy.interfaces.mrtrix as mrt
>>> sdtrack = mrt.SphericallyDeconvolutedStreamlineTrack()
>>> sdtrack.inputs.in_file = 'data.Bfloat'
>>> sdtrack.inputs.seed_file = 'seed_mask.nii'
>>> sdtrack.run()                                     # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)

```

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```

the image containing the source data. The type of data required
depends on the type of tracking as set in the preceeding argument.
For DT methods, the base DWI are needed. For SD methods, the SH
harmonic coefficients of the FOD are needed.
argument: ``%s``, position: -2

[Optional]
seed_file: (a pathlike object or string representing an existing
            file)
            seed file
            argument: ``-seed %s``
            mutually_exclusive: seed_file, seed_spec
seed_spec: (a list of from 4 to 4 items which are a float)
            seed specification in mm and radius (x y z r)
            argument: ``-seed %s``, position: 2
            mutually_exclusive: seed_file, seed_spec
include_file: (a pathlike object or string representing an existing
               file)
               inclusion file
               argument: ``-include %s``
               mutually_exclusive: include_file, include_spec
include_spec: (a list of from 4 to 4 items which are a float)
               inclusion specification in mm and radius (x y z r)
               argument: ``-include %s``, position: 2
               mutually_exclusive: include_file, include_spec
exclude_file: (a pathlike object or string representing an existing
               file)
               exclusion file
               argument: ``-exclude %s``
               mutually_exclusive: exclude_file, exclude_spec
exclude_spec: (a list of from 4 to 4 items which are a float)
               exclusion specification in mm and radius (x y z r)
               argument: ``-exclude %s``, position: 2
               mutually_exclusive: exclude_file, exclude_spec
mask_file: (a pathlike object or string representing an existing
            file)
            mask file. Only tracks within mask.
            argument: ``-mask %s``
            mutually_exclusive: mask_file, mask_spec
mask_spec: (a list of from 4 to 4 items which are a float)
            Mask specification in mm and radius (x y z r). Tracks will be
            terminated when they leave the ROI.
            argument: ``-mask %s``, position: 2
            mutually_exclusive: mask_file, mask_spec
inputmodel: ('DT_STREAM' or 'SD_PROB' or 'SD_STREAM', nipy default
             value: DT_STREAM)
             input model type
             argument: ``%s``, position: -3
stop: (a boolean)
       stop track as soon as it enters any of the include regions.
       argument: ``-stop``
do_not_precompute: (a boolean)
                    Turns off precomputation of the legendre polynomial values. Warning:
                    this will slow down the algorithm by a factor of approximately 4.
                    argument: ``-noprecomputed``
unidirectional: (a boolean)
                 Track from the seed point in one direction only (default is to track

```

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```

        in both directions).
        argument: ``-unidirectional``
no_mask_interpolation: (a boolean)
    Turns off trilinear interpolation of mask images.
    argument: ``-nomaskinterp``
step_size: (a float)
    Set the step size of the algorithm in mm (default is 0.2).
    argument: ``-step %s``
minimum_radius_of_curvature: (a float)
    Set the minimum radius of curvature (default is 2 mm for DT_STREAM,
    0 for SD_STREAM, 1 mm for SD_PROB and DT_PROB)
    argument: ``-curvature %s``
desired_number_of_tracks: (an integer (int or long))
    Sets the desired number of tracks. The program will continue to
    generate tracks until this number of tracks have been selected and
    written to the output file (default is 100 for *_STREAM methods, 1000
    for *_PROB methods).
    argument: ``-number %d``
maximum_number_of_tracks: (an integer (int or long))
    Sets the maximum number of tracks to generate. The program will not
    generate more tracks than this number, even if the desired number of
    tracks hasn't yet been reached (default is 100 x number).
    argument: ``-maxnum %d``
minimum_tract_length: (a float)
    Sets the minimum length of any track in millimeters (default is 10
    mm).
    argument: ``-minlength %s``
maximum_tract_length: (a float)
    Sets the maximum length of any track in millimeters (default is 200
    mm).
    argument: ``-length %s``
cutoff_value: (a float)
    Set the FA or FOD amplitude cutoff for terminating tracks (default
    is 0.1).
    argument: ``-cutoff %s``
initial_cutoff_value: (a float)
    Sets the minimum FA or FOD amplitude for initiating tracks (default
    is twice the normal cutoff).
    argument: ``-initcutoff %s``
initial_direction: (a list of from 2 to 2 items which are an integer
    (int or long))
    Specify the initial tracking direction as a vector
    argument: ``-initdirection %s``
out_file: (a pathlike object or string representing a file)
    output data file
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

tracked: (a pathlike object or string representing an existing file)

```

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```
output file containing reconstructed tracts
```

68.4.5 StreamlineTrack

[Link to code](#)

Wraps the executable command `streamtrack`.

Performs tractography using one of the following models: `'dt_prob'`, `'dt_stream'`, `'sd_prob'`, `'sd_stream'`. Where `'dt'` stands for diffusion tensor, `'sd'` stands for spherical deconvolution, and `'prob'` stands for probabilistic.

Example

```
>>> import nipy.interfaces.mrtrix as mrt
>>> strack = mrt.StreamlineTrack()
>>> strack.inputs.inputmodel = 'SD_PROB'
>>> strack.inputs.in_file = 'data.Bfloat'
>>> strack.inputs.seed_file = 'seed_mask.nii'
>>> strack.inputs.mask_file = 'mask.nii'
>>> strack.cmdline
'streamtrack -mask mask.nii -seed seed_mask.nii SD_PROB data.Bfloat data_tracked.
↳tck'
>>> strack.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         the image containing the source data. The type of data required
         depends on the type of tracking as set in the preceeding argument.
         For DT methods, the base DWI are needed. For SD methods, the SH
         harmonic coefficients of the FOD are needed.
         argument: ``%s``, position: -2

[Optional]
seed_file: (a pathlike object or string representing an existing
           file)
           seed file
           argument: ``-seed %s``
           mutually_exclusive: seed_file, seed_spec
seed_spec: (a list of from 4 to 4 items which are a float)
           seed specification in mm and radius (x y z r)
           argument: ``-seed %s``, position: 2
           mutually_exclusive: seed_file, seed_spec
include_file: (a pathlike object or string representing an existing
              file)
              inclusion file
              argument: ``-include %s``
              mutually_exclusive: include_file, include_spec
include_spec: (a list of from 4 to 4 items which are a float)
              inclusion specification in mm and radius (x y z r)
              argument: ``-include %s``, position: 2
              mutually_exclusive: include_file, include_spec
exclude_file: (a pathlike object or string representing an existing
              file)
              exclusion file
```

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```

    argument: ``-exclude %s``
    mutually_exclusive: exclude_file, exclude_spec
exclude_spec: (a list of from 4 to 4 items which are a float)
    exclusion specification in mm and radius (x y z r)
    argument: ``-exclude %s``, position: 2
    mutually_exclusive: exclude_file, exclude_spec
mask_file: (a pathlike object or string representing an existing
    file)
    mask file. Only tracks within mask.
    argument: ``-mask %s``
    mutually_exclusive: mask_file, mask_spec
mask_spec: (a list of from 4 to 4 items which are a float)
    Mask specification in mm and radius (x y z r). Tracks will be
    terminated when they leave the ROI.
    argument: ``-mask %s``, position: 2
    mutually_exclusive: mask_file, mask_spec
inputmodel: ('DT_STREAM' or 'SD_PROB' or 'SD_STREAM', nipy default
    value: DT_STREAM)
    input model type
    argument: ``%s``, position: -3
stop: (a boolean)
    stop track as soon as it enters any of the include regions.
    argument: ``-stop``
do_not_precompute: (a boolean)
    Turns off precomputation of the legendre polynomial values. Warning:
    this will slow down the algorithm by a factor of approximately 4.
    argument: ``-noprecomputed``
unidirectional: (a boolean)
    Track from the seed point in one direction only (default is to track
    in both directions).
    argument: ``-unidirectional``
no_mask_interpolation: (a boolean)
    Turns off trilinear interpolation of mask images.
    argument: ``-nomaskinterp``
step_size: (a float)
    Set the step size of the algorithm in mm (default is 0.2).
    argument: ``-step %s``
minimum_radius_of_curvature: (a float)
    Set the minimum radius of curvature (default is 2 mm for DT_STREAM,
    0 for SD_STREAM, 1 mm for SD_PROB and DT_PROB)
    argument: ``-curvature %s``
desired_number_of_tracks: (an integer (int or long))
    Sets the desired number of tracks. The program will continue to
    generate tracks until this number of tracks have been selected and
    written to the output file (default is 100 for *_STREAM methods, 1000
    for *_PROB methods).
    argument: ``-number %d``
maximum_number_of_tracks: (an integer (int or long))
    Sets the maximum number of tracks to generate. The program will not
    generate more tracks than this number, even if the desired number of
    tracks hasn't yet been reached (default is 100 x number).
    argument: ``-maxnum %d``
minimum_tract_length: (a float)
    Sets the minimum length of any track in millimeters (default is 10
    mm).
    argument: ``-minlength %s``
maximum_tract_length: (a float)

```

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```

        Sets the maximum length of any track in millimeters (default is 200
        mm).
        argument: ``-length %s``
cutoff_value: (a float)
        Set the FA or FOD amplitude cutoff for terminating tracks (default
        is 0.1).
        argument: ``-cutoff %s``
initial_cutoff_value: (a float)
        Sets the minimum FA or FOD amplitude for initiating tracks (default
        is twice the normal cutoff).
        argument: ``-initcutoff %s``
initial_direction: (a list of from 2 to 2 items which are an integer
        (int or long))
        Specify the initial tracking direction as a vector
        argument: ``-initdirection %s``
out_file: (a pathlike object or string representing a file)
        output data file
        argument: ``%s``, position: -1
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

tracked: (a pathlike object or string representing an existing file)
        output file containing reconstructed tracks

```

68.4.6 Tracks2Prob[Link to code](#)

Wraps the executable command `tracks2prob`.

Convert a tract file into a map of the fraction of tracks to enter each voxel - also known as a tract density image (TDI) - in MRtrix's image format (.mif). This can be viewed using MRview or converted to Nifti using MRconvert.

Example

```

>>> import nipy.interfaces.mrtrix as mrt
>>> tdi = mrt.Tracks2Prob()
>>> tdi.inputs.in_file = 'dwi_CSD_tracked.tck'
>>> tdi.inputs.colour = True
>>> tdi.run()
# doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        tract file
        argument: ``%s``, position: -2

[Optional]
template_file: (a pathlike object or string representing an existing

```

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```

    file)
    an image file to be used as a template for the output (the output
    image wil have the same transform and field of view)
    argument: ``-template %s``, position: 1
voxel_dims: (a list of from 3 to 3 items which are a float)
    Three comma-separated numbers giving the size of each voxel in mm.
    argument: ``-vox %s``, position: 2
colour: (a boolean)
    add colour to the output image according to the direction of the
    tracks.
    argument: ``-colour``, position: 3
fraction: (a boolean)
    produce an image of the fraction of fibres through each voxel (as a
    proportion of the total number in the file), rather than the count.
    argument: ``-fraction``, position: 3
output_datatype: ('Bit' or 'Int8' or 'UInt8' or 'Int16' or 'UInt16'
    or 'Int32' or 'UInt32' or 'float32' or 'float64')
    "i.e. Bfloat". Can be "char", "short", "int", "long", "float" or
    "double"
    argument: ``-datatype %s``, position: 2
resample: (a float)
    resample the tracks at regular intervals using Hermite
    interpolation. If omitted, the program will select an appropriate
    interpolation factor automatically.
    argument: ``-resample %d``, position: 3
out_filename: (a pathlike object or string representing a file)
    output data file
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

tract_image: (a pathlike object or string representing an existing
    file)
    Output tract count or track density image

```


69.1 interfaces.mrtrix3.base

69.1.1 MRTrix3Base

[Link to code](#)

Inputs:

```
[Optional]
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

```
None
```

69.2 interfaces.mrtrix3.connectivity

69.2.1 BuildConnectome

[Link to code](#)

Wraps the executable command `tck2connectome`.

Generate a connectome matrix from a streamlines file and a node parcellation image

Example

```
>>> import nipype.interfaces.mrtrix3 as mrt
>>> mat = mrt.BuildConnectome()
>>> mat.inputs.in_file = 'tracks.tck'
>>> mat.inputs.in_parcs = 'aparc+aseg.nii'
```

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```
>>> mat.cmdline                                # doctest: +ELLIPSIS
'tck2connectome tracks.tck aparc+aseg.nii connectome.csv'
>>> mat.run()                                  # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input tractography
         argument: ``%s``, position: -3
out_file: (a pathlike object or string representing a file, nipy
         default value: connectome.csv)
         output file after processing
         argument: ``%s``, position: -1

[Optional]
in_par: (a pathlike object or string representing an existing file)
        parcellation file
        argument: ``%s``, position: -2
nthreads: (an integer (int or long))
           number of threads. if zero, the number of available cpus will be
           used
           argument: ``-nthreads %d``
vox_lookup: (a boolean)
            use a simple voxel lookup value at each streamline endpoint
            argument: ``-assignment_voxel_lookup``
search_radius: (a float)
              perform a radial search from each streamline endpoint to locate the
              nearest node. Argument is the maximum radius in mm; if no node is
              found within this radius, the streamline endpoint is not assigned to
              any node.
              argument: ``-assignment_radial_search %f``
search_reverse: (a float)
              traverse from each streamline endpoint inwards along the streamline,
              in search of the last node traversed by the streamline. Argument is
              the maximum traversal length in mm (set to 0 to allow search to
              continue to the streamline midpoint).
              argument: ``-assignment_reverse_search %f``
search_forward: (a float)
              project the streamline forwards from the endpoint in search of
              aparc+aseg voxel. Argument is the maximum traversal length
              in mm.
              argument: ``-assignment_forward_search %f``
metric: ('count' or 'meanlength' or 'invlength' or 'invnodevolume' or
         'mean_scalar' or 'invlength_invnodevolume')
         specify the edge weight metric
         argument: ``-metric %s``
in_scalar: (a pathlike object or string representing an existing
         file)
         provide the associated image for the mean_scalar metric
         argument: ``-image %s``
in_weights: (a pathlike object or string representing an existing
         file)
         specify a text scalar file containing the streamline weights
         argument: ``-tck_weights_in %s``
keep_unassigned: (a boolean)
                 By default, the program discards the information regarding those
```

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```

        streamlines that are not successfully assigned to a node pair. Set
        this option to keep these values (will be the first row/column in
        the output matrix)
        argument: ``-keep_unassigned``
zero_diagonal: (a boolean)
        set all diagonal entries in the matrix to zero (these represent
        streamlines that connect to the same node at both ends)
        argument: ``-zero_diagonal``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipype default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        the output response file

```

69.2.2 LabelConfig

[Link to code](#)

Wraps the executable command labelconfig.

Re-configure parcellation to be incrementally defined.

Example

```

>>> import nipype.interfaces.mrtrix3 as mrt
>>> labels = mrt.LabelConfig()
>>> labels.inputs.in_file = 'aparc+aseg.nii'
>>> labels.inputs.in_config = 'mrtrix3_labelconfig.txt'
>>> labels.cmdline                                     # doctest: +ELLIPSIS
'labelconfig aparc+aseg.nii mrtrix3_labelconfig.txt parcellation.mif'
>>> labels.run()                                       # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input anatomical image
        argument: ``%s``, position: -3
out_file: (a pathlike object or string representing a file, nipype
        default value: parcellation.mif)
        output file after processing
        argument: ``%s``, position: -1

[Optional]
in_config: (a pathlike object or string representing an existing
        file)
        connectome configuration file
        argument: ``%s``, position: -2
lut_basic: (a pathlike object or string representing a file)
        get information from a basic lookup table consisting of index / name
        pairs

```

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```

        argument: ``-lut_basic %s``
lut_fs: (a pathlike object or string representing a file)
        get information from a FreeSurfer lookup table(typically
        "FreeSurferColorLUT.txt")
        argument: ``-lut_freesurfer %s``
lut_aal: (a pathlike object or string representing a file)
        get information from the AAL lookup table (typically
        "ROI_MNI_V4.txt")
        argument: ``-lut_aal %s``
lut_itksnap: (a pathlike object or string representing a file)
        get information from an ITK - SNAP lookup table(this includes the
        IIT atlas file "LUT_GM.txt")
        argument: ``-lut_itksnap %s``
spine: (a pathlike object or string representing a file)
        provide a manually-defined segmentation of the base of the spine
        where the streamlines terminate, so that this can become a node in
        the connection matrix.
        argument: ``-spine %s``
nthreads: (an integer (int or long))
        number of threads. if zero, the number of available cpus will be
        used
        argument: ``-nthreads %d``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        the output response file

```

69.2.3 LabelConvert

[Link to code](#)

Wraps the executable command labelconvert.

Re-configure parcellation to be incrementally defined.

Example

```

>>> import nipy.interfaces.mrtrix3 as mrt
>>> labels = mrt.LabelConvert()
>>> labels.inputs.in_file = 'aparc+aseg.nii'
>>> labels.inputs.in_config = 'mrtrix3_labelconfig.txt'
>>> labels.inputs.in_lut = 'FreeSurferColorLUT.txt'
>>> labels.cmdline
'labelconvert aparc+aseg.nii FreeSurferColorLUT.txt mrtrix3_labelconfig.txt_
↳parcellation.mif'
>>> labels.run()                                     # doctest: +SKIP

```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input anatomical image
         argument: ``%s``, position: -4
in_lut: (a pathlike object or string representing an existing file)
        get information from a basic lookup table consisting of index / name
        pairs
        argument: ``%s``, position: -3
out_file: (a pathlike object or string representing a file, nipy
          default value: parcellation.mif)
          output file after processing
          argument: ``%s``, position: -1

[Optional]
in_config: (a pathlike object or string representing an existing
           file)
           connectome configuration file
           argument: ``%s``, position: -2
spine: (a pathlike object or string representing a file)
        provide a manually-defined segmentation of the base of the spine
        where the streamlines terminate, so that this can become a node in
        the connection matrix.
        argument: ``-spine %s``
num_threads: (an integer (int or long))
              number of threads. if zero, the number of available cpus will be
              used
              argument: ``-nthreads %d``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          the output response file
```

69.3 interfaces.mrtrix3.preprocess

69.3.1 DWIBiasCorrect

[Link to code](#)

Wraps the executable command dwibiascorrect.

Perform B1 field inhomogeneity correction for a DWI volume series.

For more information, see <<https://mrtrix.readthedocs.io/en/latest/reference/scripts/dwibiascorrect.html>>

Example

```
>>> import nipy.interfaces.mrtrix3 as mrt
>>> bias_correct = mrt.DWIBiasCorrect()
>>> bias_correct.inputs.in_file = 'dwi.mif'
>>> bias_correct.inputs.use_ants = True
```

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```
>>> bias_correct.cmdline
'dwibiascorrect -ants dwi.mif dwi_biascorr.mif'
>>> bias_correct.run()                                # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input DWI image
         argument: ``%s``, position: -2
use_ants: (a boolean)
         use ANTS N4 to estimate the inhomogeneity field
         argument: ``-ants``
         mutually_exclusive: use_fsl
use_fsl: (a boolean)
         use FSL FAST to estimate the inhomogeneity field
         argument: ``-fsl``
         mutually_exclusive: use_ants

[Optional]
in_mask: (a pathlike object or string representing a file)
         input mask image for bias field estimation
         argument: ``-mask %s``
bias: (a pathlike object or string representing a file)
      bias field
      argument: ``-bias %s``
out_file: (a pathlike object or string representing a file)
          the output bias corrected DWI image
          argument: ``%s``, position: -1
nthreads: (an integer (int or long))
          number of threads. if zero, the number of available cpus will be
          used
          argument: ``-nthreads %d``
grad_file: (a pathlike object or string representing an existing
           file)
           dw gradient scheme (MRTrix format)
           argument: ``-grad %s``
           mutually_exclusive: grad_fsl
grad_fsl: (a tuple of the form: (a pathlike object or string
           representing an existing file, a pathlike object or string
           representing an existing file))
           (bvecs, bvals) dw gradient scheme (FSL format)
           argument: ``-fslgrad %s %s``
           mutually_exclusive: grad_file
bval_scale: ('yes' or 'no')
            specifies whether the b - values should be scaled by the square of
            the corresponding DW gradient norm, as often required for multishell
            or DSI DW acquisition schemes. The default action can also be set in
            the MRtrix config file, under the BValueScaling entry. Valid choices
            are yes / no, true / false, 0 / 1 (default: true).
            argument: ``-bvalue_scaling %s``
in_bvec: (a pathlike object or string representing an existing file)
         bvecs file in FSL format
         argument: ``-fslgrad %s %s``
in_bval: (a pathlike object or string representing an existing file)
         bvals file in FSL format
args: (a unicode string)
```

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```

Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

bias: (a pathlike object or string representing an existing file)
      the output bias field
out_file: (a pathlike object or string representing an existing file)
          the output bias corrected DWI image

```

69.3.2 DWIDenoise[Link to code](#)

Wraps the executable command dwidenoise.

Denoise DWI data and estimate the noise level based on the optimal threshold for PCA.

DWI data denoising and noise map estimation by exploiting data redundancy in the PCA domain using the prior knowledge that the eigenspectrum of random covariance matrices is described by the universal Marchenko Pastur distribution.

Important note: image denoising must be performed as the first step of the image processing pipeline. The routine will fail if interpolation or smoothing has been applied to the data prior to denoising.

Note that this function does not correct for non-Gaussian noise biases.

For more information, see <<https://mrtrix.readthedocs.io/en/latest/reference/commands/dwidenoise.html>>**Example**

```

>>> import nipy.interfaces.mrtrix3 as mrt
>>> denoise = mrt.DWIDenoise()
>>> denoise.inputs.in_file = 'dwi.mif'
>>> denoise.inputs.mask = 'mask.mif'
>>> denoise.inputs.noise = 'noise.mif'
>>> denoise.cmdline                                # doctest: +ELLIPSIS
'dwidenoise -mask mask.mif -noise noise.mif dwi.mif dwi_denoised.mif'
>>> denoise.run()                                  # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input DWI image
         argument: ``%s``, position: -2

[Optional]
mask: (a pathlike object or string representing an existing file)
      mask image
      argument: ``-mask %s``, position: 1
extent: (a tuple of the form: (an integer (int or long), an integer
                               (int or long), an integer (int or long)))
         set the window size of the denoising filter. (default = 5,5,5)
         argument: ``-extent %d,%d,%d``
noise: (a pathlike object or string representing a file)
       the output noise map

```

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```

    argument: ``-noise %s``
out_file: (a pathlike object or string representing a file)
    the output denoised DWI image
    argument: ``%s``, position: -1
nthreads: (an integer (int or long))
    number of threads. if zero, the number of available cpus will be
    used
    argument: ``-nthreads %d``
grad_file: (a pathlike object or string representing an existing
    file)
    dw gradient scheme (MRtrix format)
    argument: ``-grad %s``
    mutually_exclusive: grad_fsl
grad_fsl: (a tuple of the form: (a pathlike object or string
    representing an existing file, a pathlike object or string
    representing an existing file))
    (bvecs, bvals) dw gradient scheme (FSL format)
    argument: ``-fslgrad %s %s``
    mutually_exclusive: grad_file
bval_scale: ('yes' or 'no')
    specifies whether the b - values should be scaled by the square of
    the corresponding DW gradient norm, as often required for multishell
    or DSI DW acquisition schemes. The default action can also be set in
    the MRtrix config file, under the BValueScaling entry. Valid choices
    are yes / no, true / false, 0 / 1 (default: true).
    argument: ``-bvalue_scaling %s``
in_bvec: (a pathlike object or string representing an existing file)
    bvecs file in FSL format
    argument: ``-fslgrad %s %s``
in_bval: (a pathlike object or string representing an existing file)
    bvals file in FSL format
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

noise: (a pathlike object or string representing an existing file)
    the output noise map
out_file: (a pathlike object or string representing an existing file)
    the output denoised DWI image

```

69.3.3 MRDeGibbs[Link to code](#)

Wraps the executable command `mrdegibbs`.

Remove Gibbs ringing artifacts.

This application attempts to remove Gibbs ringing artefacts from MRI images using the method of local subvoxel-shifts proposed by Kellner et al.

This command is designed to run on data directly after it has been reconstructed by the scanner, before any interpolation of any kind has taken place. You should not run this command after any form of motion correction (e.g. not after `dwipreproc`). Similarly, if you intend running `dwidenoise`, you should run this command afterwards, since it has the potential to alter the noise structure, which would impact on `dwidenoise`'s performance.

Note that this method is designed to work on images acquired with full k-space coverage. Running this method on partial Fourier ('half-scan') data may lead to suboptimal and/or biased results, as noted in the original reference below. There is currently no means of dealing with this; users should exercise caution when using this method on partial Fourier data, and inspect its output for any obvious artefacts.

For more information, see <<https://mrtrix.readthedocs.io/en/latest/reference/commands/mrdegibbs.html>>

Example

```
>>> import nipy.interfaces.mrtrix3 as mrt
>>> unring = mrt.MRDeGibbs()
>>> unring.inputs.in_file = 'dwi.mif'
>>> unring.cmdline
'mrdegibbs -axes 0,1 -maxW 3 -minW 1 -nshifts 20 dwi.mif dwi_unr.mif'
>>> unring.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input DWI image
         argument: ``%s``, position: -2

[Optional]
axes: (a list of items which are a value of class 'int', nipy
      default value: [0, 1])
      indicate the plane in which the data was acquired (axial = 0,1;
      coronal = 0,2; sagittal = 1,2)
      argument: ``-axes %s``
nshifts: (an integer (int or long), nipy default value: 20)
          discretization of subpixel spacing (default = 20)
          argument: ``-nshifts %d``
minW: (an integer (int or long), nipy default value: 1)
       left border of window used for total variation (TV) computation
       (default = 1)
       argument: ``-minW %d``
maxW: (an integer (int or long), nipy default value: 3)
       right border of window used for total variation (TV) computation
       (default = 3)
       argument: ``-maxW %d``
out_file: (a pathlike object or string representing a file)
          the output unringed DWI image
          argument: ``%s``, position: -1
nthreads: (an integer (int or long))
           number of threads. if zero, the number of available cpus will be
           used
           argument: ``-nthreads %d``
grad_file: (a pathlike object or string representing an existing
            file)
            dw gradient scheme (MRTrix format)
            argument: ``-grad %s``
            mutually_exclusive: grad_fsl
grad_fsl: (a tuple of the form: (a pathlike object or string
                                representing an existing file, a pathlike object or string
                                representing an existing file))
            (bvecs, bvals) dw gradient scheme (FSL format)
            argument: ``-fslgrad %s %s``
            mutually_exclusive: grad_file
```

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```

bval_scale: ('yes' or 'no')
    specifies whether the b - values should be scaled by the square of
    the corresponding DW gradient norm, as often required for multishell
    or DSI DW acquisition schemes. The default action can also be set in
    the MRtrix config file, under the BValueScaling entry. Valid choices
    are yes / no, true / false, 0 / 1 (default: true).
    argument: ``-bvalue_scaling %s``
in_bvec: (a pathlike object or string representing an existing file)
    bvecs file in FSL format
    argument: ``-fslgrad %s %s``
in_bval: (a pathlike object or string representing an existing file)
    bvals file in FSL format
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    the output unringed DWI image

```

69.3.4 ResponseSD[Link to code](#)

Wraps the executable command dwi2response.

Estimate response function(s) for spherical deconvolution using the specified algorithm.

Example

```

>>> import nipy.interfaces.mrtrix3 as mrt
>>> resp = mrt.ResponseSD()
>>> resp.inputs.in_file = 'dwi.mif'
>>> resp.inputs.algorithm = 'tournier'
>>> resp.inputs.grad_fsl = ('bvecs', 'bvals')
>>> resp.cmdline                                # doctest: +ELLIPSIS
'dwi2response tournier -fslgrad bvecs bvals dwi.mif wm.txt'
>>> resp.run()                                  # doctest: +SKIP

```

We can also pass in multiple harmonic degrees in the case of multi-shell >>> resp.inputs.max_sh = [6,8,10]

>>> resp.cmdline 'dwi2response tournier -fslgrad bvecs bvals -lmax 6,8,10 dwi.mif wm.txt'

Inputs:

```

[Mandatory]
algorithm: ('msmt_5tt' or 'dhollander' or 'tournier' or 'tax')
    response estimation algorithm (multi-tissue)
    argument: ``%s``, position: 1
in_file: (a pathlike object or string representing an existing file)
    input DWI image
    argument: ``%s``, position: -5

[Optional]
mtt_file: (a pathlike object or string representing a file)

```

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```

    input 5tt image
    argument: ``%s``, position: -4
wm_file: (a pathlike object or string representing a file, nipy
    default value: wm.txt)
    output WM response text file
    argument: ``%s``, position: -3
gm_file: (a pathlike object or string representing a file)
    output GM response text file
    argument: ``%s``, position: -2
csf_file: (a pathlike object or string representing a file)
    output CSF response text file
    argument: ``%s``, position: -1
in_mask: (a pathlike object or string representing an existing file)
    provide initial mask image
    argument: ``-mask %s``
max_sh: (a list of items which are an integer (int or long))
    maximum harmonic degree of response function - single value for
    single-shell response, list for multi-shell response
    argument: ``-lmax %s``
nthreads: (an integer (int or long))
    number of threads. if zero, the number of available cpus will be
    used
    argument: ``-nthreads %d``
grad_file: (a pathlike object or string representing an existing
    file)
    dw gradient scheme (MRTrix format)
    argument: ``-grad %s``
    mutually_exclusive: grad_fsl
grad_fsl: (a tuple of the form: (a pathlike object or string
    representing an existing file, a pathlike object or string
    representing an existing file))
    (bvecs, bvals) dw gradient scheme (FSL format)
    argument: ``-fslgrad %s %s``
    mutually_exclusive: grad_file
bval_scale: ('yes' or 'no')
    specifies whether the b - values should be scaled by the square of
    the corresponding DW gradient norm, as often required for multishell
    or DSI DW acquisition schemes. The default action can also be set in
    the MRtrix config file, under the BValueScaling entry. Valid choices
    are yes / no, true / false, 0 / 1 (default: true).
    argument: ``-bvalue_scaling %s``
in_bvec: (a pathlike object or string representing an existing file)
    bvecs file in FSL format
    argument: ``-fslgrad %s %s``
in_bval: (a pathlike object or string representing an existing file)
    bvals file in FSL format
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

wm_file: (a pathlike object or string representing a file)

```

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```

        output WM response text file
        argument: ``%s``
gm_file: (a pathlike object or string representing a file)
        output GM response text file
        argument: ``%s``
csf_file: (a pathlike object or string representing a file)
        output CSF response text file
        argument: ``%s``

```

69.4 interfaces.mrtrix3.reconst

69.4.1 EstimateFOD

[Link to code](#)

Wraps the executable command `dwi2fod`.

Estimate fibre orientation distributions from diffusion data using spherical deconvolution

Example

```

>>> import nipy.interfaces.mrtrix3 as mrt
>>> fod = mrt.EstimateFOD()
>>> fod.inputs.algorithm = 'csd'
>>> fod.inputs.in_file = 'dwi.mif'
>>> fod.inputs.wm_txt = 'wm.txt'
>>> fod.inputs.grad_fsl = ('bvecs', 'bvals')
>>> fod.cmdline                                # doctest: +ELLIPSIS
'dwi2fod -fslgrad bvecs bvals -lmax 8 csd dwi.mif wm.txt wm.mif gm.mif csf.mif'
>>> fod.run()                                  # doctest: +SKIP

```

Inputs:

```

[Mandatory]
algorithm: ('csd' or 'msmt_csd')
    FOD algorithm
    argument: ``%s``, position: -8
in_file: (a pathlike object or string representing an existing file)
    input DWI image
    argument: ``%s``, position: -7
wm_txt: (a pathlike object or string representing a file)
    WM response text file
    argument: ``%s``, position: -6
wm_odf: (a pathlike object or string representing a file, nipy
    default value: wm.mif)
    output WM ODF
    argument: ``%s``, position: -5

[Optional]
gm_txt: (a pathlike object or string representing a file)
    GM response text file
    argument: ``%s``, position: -4
gm_odf: (a pathlike object or string representing a file, nipy
    default value: gm.mif)
    output GM ODF
    argument: ``%s``, position: -3
csf_txt: (a pathlike object or string representing a file)

```

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```

    CSF response text file
    argument: ``%s``, position: -2
csf_odf: (a pathlike object or string representing a file, nipy
    default value: csf.mif)
    output CSF ODF
    argument: ``%s``, position: -1
mask_file: (a pathlike object or string representing an existing
    file)
    mask image
    argument: ``-mask %s``
shell: (a list of items which are a float)
    specify one or more dw gradient shells
    argument: ``-shell %s``
max_sh: (a list of items which are an integer (int or long), nipy
    default value: [8])
    maximum harmonic degree of response function - single value for
    single-shell response, list for multi-shell response
    argument: ``-lmax %s``
in_dirs: (a pathlike object or string representing an existing file)
    specify the directions over which to apply the non-negativity
    constraint (by default, the built-in 300 direction set is used).
    These should be supplied as a text file containing the [ az el ]
    pairs for the directions.
    argument: ``-directions %s``
nthreads: (an integer (int or long))
    number of threads. if zero, the number of available cpus will be
    used
    argument: ``-nthreads %d``
grad_file: (a pathlike object or string representing an existing
    file)
    dw gradient scheme (MRTrix format)
    argument: ``-grad %s``
    mutually_exclusive: grad_fsl
grad_fsl: (a tuple of the form: (a pathlike object or string
    representing an existing file, a pathlike object or string
    representing an existing file))
    (bvecs, bvals) dw gradient scheme (FSL format)
    argument: ``-fslgrad %s %s``
    mutually_exclusive: grad_file
bval_scale: ('yes' or 'no')
    specifies whether the b - values should be scaled by the square of
    the corresponding DW gradient norm, as often required for multishell
    or DSI DW acquisition schemes. The default action can also be set in
    the MRtrix config file, under the BValueScaling entry. Valid choices
    are yes / no, true / false, 0 / 1 (default: true).
    argument: ``-bvalue_scaling %s``
in_bvec: (a pathlike object or string representing an existing file)
    bvecs file in FSL format
    argument: ``-fslgrad %s %s``
in_bval: (a pathlike object or string representing an existing file)
    bvals file in FSL format
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})

```

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Environment variables

Outputs:

```

wm_odf: (a pathlike object or string representing a file)
        output WM ODF
        argument: ``%s``
gm_odf: (a pathlike object or string representing a file)
        output GM ODF
        argument: ``%s``
csf_odf: (a pathlike object or string representing a file)
        output CSF ODF
        argument: ``%s``

```

69.4.2 FitTensor[Link to code](#)Wraps the executable command `dwi2tensor`.

Convert diffusion-weighted images to tensor images

Example

```

>>> import nipy.interfaces.mrtrix3 as mrt
>>> tsr = mrt.FitTensor()
>>> tsr.inputs.in_file = 'dwi.mif'
>>> tsr.inputs.in_mask = 'mask.nii.gz'
>>> tsr.inputs.grad_fsl = ('bvecs', 'bvals')
>>> tsr.cmdline                                # doctest: +ELLIPSIS
'dwi2tensor -fslgrad bvecs bvals -mask mask.nii.gz dwi.mif dti.mif'
>>> tsr.run()                                  # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input diffusion weighted images
         argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file, nipy
          default value: dti.mif)
          the output diffusion tensor image
          argument: ``%s``, position: -1

[Optional]
in_mask: (a pathlike object or string representing an existing file)
         only perform computation within the specified binary brain mask
         image
         argument: ``-mask %s``
method: ('nonlinear' or 'loglinear' or 'sech' or 'rician')
        select method used to perform the fitting
        argument: ``-method %s``
reg_term: (a float)
          specify the strength of the regularisation term on the magnitude of
          the tensor elements (default = 5000). This only applies to the non-
          linear methods
          argument: ``-regularisation %f``
nthreads: (an integer (int or long))

```

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```

        number of threads. if zero, the number of available cpus will be
        used
        argument: ``-nthreads %d``
grad_file: (a pathlike object or string representing an existing
            file)
            dw gradient scheme (MRtrix format)
            argument: ``-grad %s``
            mutually_exclusive: grad_fsl
grad_fsl: (a tuple of the form: (a pathlike object or string
            representing an existing file, a pathlike object or string
            representing an existing file))
            (bvecs, bvals) dw gradient scheme (FSL format)
            argument: ``-fslgrad %s %s``
            mutually_exclusive: grad_file
bval_scale: ('yes' or 'no')
            specifies whether the b - values should be scaled by the square of
            the corresponding DW gradient norm, as often required for multishell
            or DSI DW acquisition schemes. The default action can also be set in
            the MRtrix config file, under the BValueScaling entry. Valid choices
            are yes / no, true / false, 0 / 1 (default: true).
            argument: ``-bvalue_scaling %s``
in_bvec: (a pathlike object or string representing an existing file)
            bvecs file in FSL format
            argument: ``-fslgrad %s %s``
in_bval: (a pathlike object or string representing an existing file)
            bvals file in FSL format
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
            of class 'str' and with values which are a bytes or None or a
            value of class 'str', nipype default value: {})
            Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
            the output DTI file

```

69.5 interfaces.mrtrix3.tracking

69.5.1 Tractography

[Link to code](#)

Wraps the executable command tckgen.

Performs streamlines tractography after selecting the appropriate algorithm.

Example

```

>>> import nipype.interfaces.mrtrix3 as mrt
>>> tk = mrt.Tractography()
>>> tk.inputs.in_file = 'fods.mif'
>>> tk.inputs.roi_mask = 'mask.nii.gz'
>>> tk.inputs.seed_sphere = (80, 100, 70, 10)
>>> tk.cmdline                                     # doctest: +ELLIPSIS

```

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```
'tckgen -algorithm iFOD2 -samples 4 -output_seeds out_seeds.nii.gz -mask mask.nii.
→gz -seed_sphere 80.000000,100.000000,70.000000,10.000000 fods.mif tracked.tck'
>>> tk.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input file to be processed
         argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file, nipy
         default value: tracked.tck)
         output file containing tracks
         argument: ``%s``, position: -1

[Optional]
sph_trait: (a tuple of the form: (a float, a float, a float, a
         float))
         argument: ``%f,%f,%f,%f``
algorithm: ('iFOD2' or 'FACT' or 'iFOD1' or 'Nulldist' or 'SD_Stream'
         or 'Tensor_Det' or 'Tensor_Prob', nipy default value: iFOD2)
         tractography algorithm to be used
         argument: ``-algorithm %s``
roi_incl: (a pathlike object or string representing an existing file
         or a tuple of the form: (a float, a float, a float, a float))
         specify an inclusion region of interest, streamlines must traverse
         ALL inclusion regions to be accepted
         argument: ``-include %s``
roi_excl: (a pathlike object or string representing an existing file
         or a tuple of the form: (a float, a float, a float, a float))
         specify an exclusion region of interest, streamlines that enter ANY
         exclude region will be discarded
         argument: ``-exclude %s``
roi_mask: (a pathlike object or string representing an existing file
         or a tuple of the form: (a float, a float, a float, a float))
         specify a masking region of interest. If defined, streamlines exiting
         the mask will be truncated
         argument: ``-mask %s``
step_size: (a float)
         set the step size of the algorithm in mm (default is 0.1 x
         voxelsize; for iFOD2: 0.5 x voxelsize)
         argument: ``-step %f``
angle: (a float)
         set the maximum angle between successive steps (default is 90deg x
         stepsize / voxelsize)
         argument: ``-angle %f``
n_tracks: (an integer (int or long))
         set the desired number of tracks. The program will continue to
         generate tracks until this number of tracks have been selected and
         written to the output file
         argument: ``-number %d``
select: (an integer (int or long))
         set the desired number of tracks. The program will continue to
         generate tracks until this number of tracks have been selected and
         written to the output file
         argument: ``-select %d``
max_tracks: (an integer (int or long))
```

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```

        set the maximum number of tracks to generate. The program will not
        generate more tracks than this number, even if the desired number of
        tracks hasn't yet been reached (default is 100 x number)
        argument: ``-maxnum %d``
max_length: (a float)
        set the maximum length of any track in mm (default is 100 x
        voxelsize)
        argument: ``-maxlength %f``
min_length: (a float)
        set the minimum length of any track in mm (default is 5 x voxelsize)
        argument: ``-minlength %f``
cutoff: (a float)
        set the FA or FOD amplitude cutoff for terminating tracks (default
        is 0.1)
        argument: ``-cutoff %f``
cutoff_init: (a float)
        set the minimum FA or FOD amplitude for initiating tracks (default
        is the same as the normal cutoff)
        argument: ``-initcutoff %f``
n_trials: (an integer (int or long))
        set the maximum number of sampling trials at each point (only used
        for probabilistic tracking)
        argument: ``-trials %d``
unidirectional: (a boolean)
        track from the seed point in one direction only (default is to track
        in both directions)
        argument: ``-unidirectional``
init_dir: (a tuple of the form: (a float, a float, a float))
        specify an initial direction for the tracking (this should be
        supplied as a vector of 3 comma-separated values
        argument: ``-initdirection %f,%f,%f``
nprecomp: (a boolean)
        do NOT pre-compute legendre polynomial values. Warning: this will
        slow down the algorithm by a factor of approximately 4
        argument: ``-nprecomputed``
power: (an integer (int or long))
        raise the FOD to the power specified (default is 1/nsamples)
        argument: ``-power %d``
n_samples: (an integer (int or long), nipy default value: 4)
        set the number of FOD samples to take per step for the 2nd order
        (iFOD2) method
        argument: ``-samples %d``
use_rk4: (a boolean)
        use 4th-order Runge-Kutta integration (slower, but eliminates
        curvature overshoot in 1st-order deterministic methods)
        argument: ``-rk4``
stop: (a boolean)
        stop propagating a streamline once it has traversed all include
        regions
        argument: ``-stop``
downsample: (a float)
        downsample the generated streamlines to reduce output file size
        argument: ``-downsample %f``
act_file: (a pathlike object or string representing an existing file)
        use the Anatomically-Constrained Tractography framework during
        tracking; provided image must be in the 5TT (five - tissue - type)
        format

```

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```

        argument: ``-act %s``
backtrack: (a boolean)
    allow tracks to be truncated
    argument: ``-backtrack``
crop_at_gmwmi: (a boolean)
    crop streamline endpoints more precisely as they cross the GM-WM
    interface
    argument: ``-crop_at_gmwmi``
seed_sphere: (a tuple of the form: (a float, a float, a float, a
    float))
    spherical seed
    argument: ``-seed_sphere %f,%f,%f,%f``
seed_image: (a pathlike object or string representing an existing
    file)
    seed streamlines entirely at random within mask
    argument: ``-seed_image %s``
seed_rnd_voxel: (a tuple of the form: (a pathlike object or string
    representing an existing file, an integer (int or long)))
    seed a fixed number of streamlines per voxel in a mask image; random
    placement of seeds in each voxel
    argument: ``-seed_random_per_voxel %s %d``
    mutually_exclusive: seed_image, seed_grid_voxel
seed_grid_voxel: (a tuple of the form: (a pathlike object or string
    representing an existing file, an integer (int or long)))
    seed a fixed number of streamlines per voxel in a mask image; place
    seeds on a 3D mesh grid (grid_size argument is per axis; so a
    grid_size of 3 results in 27 seeds per voxel)
    argument: ``-seed_grid_per_voxel %s %d``
    mutually_exclusive: seed_image, seed_rnd_voxel
seed_rejection: (a pathlike object or string representing an existing
    file)
    seed from an image using rejection sampling (higher values = more
    probable to seed from
    argument: ``-seed_rejection %s``
seed_gmwmi: (a pathlike object or string representing an existing
    file)
    seed from the grey matter - white matter interface (only valid if
    using ACT framework)
    argument: ``-seed_gmwmi %s``
    requires: act_file
seed_dynamic: (a pathlike object or string representing an existing
    file)
    determine seed points dynamically using the SIFT model (must not
    provide any other seeding mechanism). Note that while this seeding
    mechanism improves the distribution of reconstructed streamlines
    density, it should NOT be used as a substitute for the SIFT method
    itself.
    argument: ``-seed_dynamic %s``
max_seed_attempts: (an integer (int or long))
    set the maximum number of times that the tracking algorithm should
    attempt to find an appropriate tracking direction from a given seed
    point
    argument: ``-max_seed_attempts %d``
out_seeds: (a pathlike object or string representing a file, nipy
    default value: out_seeds.nii.gz)
    output the seed location of all successful streamlines to a file
    argument: ``-output_seeds %s``

```

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```

nthreads: (an integer (int or long))
    number of threads. if zero, the number of available cpus will be
    used
    argument: ``-nthreads %d``
grad_file: (a pathlike object or string representing an existing
    file)
    dw gradient scheme (MRtrix format)
    argument: ``-grad %s``
    mutually_exclusive: grad_fsl
grad_fsl: (a tuple of the form: (a pathlike object or string
    representing an existing file, a pathlike object or string
    representing an existing file))
    (bvecs, bvals) dw gradient scheme (FSL format)
    argument: ``-fslgrad %s %s``
    mutually_exclusive: grad_file
bval_scale: ('yes' or 'no')
    specifies whether the b - values should be scaled by the square of
    the corresponding DW gradient norm, as often required for multishell
    or DSI DW acquisition schemes. The default action can also be set in
    the MRtrix config file, under the BValueScaling entry. Valid choices
    are yes / no, true / false, 0 / 1 (default: true).
    argument: ``-bvalue_scaling %s``
in_bvec: (a pathlike object or string representing an existing file)
    bvecs file in FSL format
    argument: ``-fslgrad %s %s``
in_bval: (a pathlike object or string representing an existing file)
    bvals file in FSL format
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    the output filtered tracks
out_seeds: (a pathlike object or string representing a file)
    output the seed location of all successful streamlines to a file

```

69.6 interfaces.mrtrix3.utils

69.6.1 BrainMask

[Link to code](#)

Wraps the executable command dwi2mask.

Convert a mesh surface to a partial volume estimation image

Example

```

>>> import nipy.interfaces.mrtrix3 as mrt
>>> bmsk = mrt.BrainMask()
>>> bmsk.inputs.in_file = 'dwi.mif'

```

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```
>>> bmsk.cmdline                                # doctest: +ELLIPSIS
'dwi2mask dwi.mif brainmask.mif'
>>> bmsk.run()                                  # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input diffusion weighted images
         argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file, nipy
         default value: brainmask.mif)
         output brain mask
         argument: ``%s``, position: -1

[Optional]
nthreads: (an integer (int or long))
          number of threads. if zero, the number of available cpus will be
          used
          argument: ``-nthreads %d``
grad_file: (a pathlike object or string representing an existing
          file)
          dw gradient scheme (MRtrix format)
          argument: ``-grad %s``
          mutually_exclusive: grad_fsl
grad_fsl: (a tuple of the form: (a pathlike object or string
          representing an existing file, a pathlike object or string
          representing an existing file))
          (bvecs, bvals) dw gradient scheme (FSL format)
          argument: ``-fslgrad %s %s``
          mutually_exclusive: grad_file
bval_scale: ('yes' or 'no')
            specifies whether the b - values should be scaled by the square of
            the corresponding DW gradient norm, as often required for multishell
            or DSI DW acquisition schemes. The default action can also be set in
            the MRtrix config file, under the BValueScaling entry. Valid choices
            are yes / no, true / false, 0 / 1 (default: true).
            argument: ``-bvalue_scaling %s``
in_bvec: (a pathlike object or string representing an existing file)
         bvecs file in FSL format
         argument: ``-fslgrad %s %s``
in_bval: (a pathlike object or string representing an existing file)
         bvals file in FSL format
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          the output response file
```

69.6.2 ComputeTDI

[Link to code](#)

Wraps the executable command `tckmap`.

Use track data as a form of contrast for producing a high-resolution image.

References

- For TDI or DEC TDI: Calamante, F.; Tournier, J.-D.; Jackson, G. D. & Connelly, A. Track-density imaging (TDI): Super-resolution white matter imaging using whole-brain track-density mapping. *NeuroImage*, 2010, 53, 1233-1243
 - If using `-contrast length` and `-stat_vox mean`: Pannek, K.; Mathias, J. L.; Bigler, E. D.; Brown, G.; Taylor, J. D. & Rose, S. E. The average pathlength map: A diffusion MRI tractography-derived index for studying brain pathology. *NeuroImage*, 2011, 55, 133-141
 - If using `-dixel` option with TDI contrast only: Smith, R.E., Tournier, J.-D., Calamante, F., Connelly, A. A novel paradigm for automated segmentation of very large whole-brain probabilistic tractography data sets. In *proc. ISMRM*, 2011, 19, 673
 - If using `-dixel` option with any other contrast: Pannek, K., Raffelt, D., Salvado, O., Rose, S. Incorporating directional information in diffusion tractography derived maps: angular track imaging (ATI). In *Proc. ISMRM*, 2012, 20, 1912
 - If using `-tod` option: Dhollander, T., Emsell, L., Van Hecke, W., Maes, F., Sunaert, S., Suetens, P. Track Orientation Density Imaging (TODI) and Track Orientation Distribution (TOD) based tractography. *NeuroImage*, 2014, 94, 312-336
 - If using other contrasts / statistics: Calamante, F.; Tournier, J.-D.; Smith, R. E. & Connelly, A. A generalised framework for super-resolution track-weighted imaging. *NeuroImage*, 2012, 59, 2494-2503
 - If using `-precise mapping` option: Smith, R. E.; Tournier, J.-D.; Calamante, F. & Connelly, A. SIFT: Spherical-deconvolution informed filtering of tractograms. *NeuroImage*, 2013, 67, 298-312 (Appendix 3)
-

Example

```
>>> import nipy.interfaces.mrtrix3 as mrt
>>> tdi = mrt.ComputeTDI()
>>> tdi.inputs.in_file = 'dti.mif'
>>> tdi.cmdline                                     # doctest: +ELLIPSIS
'tckmap dti.mif tdi.mif'
>>> tdi.run()                                       # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input tractography
         argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file, nipy
         default value: tdi.mif)
         output TDI file
         argument: ``%s``, position: -1
reference: (a pathlike object or string representing an existing
         file)
         a referenceimage to be used as template
         argument: ``-template %s``
vox_size: (a list of items which are an integer (int or long))
         voxel dimensions
         argument: ``-vox %s``
```

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```

data_type: ('float' or 'unsigned int')
    specify output image data type
    argument: ``-datatype %s``
use_dec: (a boolean)
    perform mapping in DEC space
    argument: ``-dec``
dixel: (a pathlike object or string representing a file)
    map streamlines todixels within each voxel. Directions are stored
    asazimuth elevation pairs.
    argument: ``-dixel %s``
max_tod: (an integer (int or long))
    generate a Track Orientation Distribution (TOD) in each voxel.
    argument: ``-tod %d``
contrast: ('tdi' or 'length' or 'invlength' or 'scalar_map' or
    'scalar_map_conut' or 'fod_amp' or 'curvature')
    define the desired form of contrast for the output image
    argument: ``-contrast %s``
in_map: (a pathlike object or string representing an existing file)
    provide thescalar image map for generating images with 'scalar_map'
    contrasts, or the SHs image for fod_amp
    argument: ``-image %s``
stat_vox: ('sum' or 'min' or 'mean' or 'max')
    define the statistic for choosing the finalvoxel intesities for a
    given contrast
    argument: ``-stat_vox %s``
stat_tck: ('mean' or 'sum' or 'min' or 'max' or 'median' or
    'mean_nonzero' or 'gaussian' or 'ends_min' or 'ends_mean' or
    'ends_max' or 'ends_prod')
    define the statistic for choosing the contribution to be made by
    each streamline as a function of the samples taken along their
    lengths.
    argument: ``-stat_tck %s``
fwhm_tck: (a float)
    define the statistic for choosing the contribution to be made by
    each streamline as a function of the samples taken along their
    lengths
    argument: ``-fwhm_tck %f``
map_zero: (a boolean)
    if a streamline has zero contribution based on the contrast &
    statistic, typically it is not mapped; use this option to still
    contribute to the map even if this is the case (these non-
    contributing voxels can then influence the mean value in each voxel
    of the map)
    argument: ``-map_zero``
upsample: (an integer (int or long))
    upsample the tracks by some ratio using Hermite interpolation before
    mapping
    argument: ``-upsample %d``
precise: (a boolean)
    use a more precise streamline mapping strategy, that accurately
    quantifies the length through each voxel (these lengths are then
    taken into account during TWI calculation)
    argument: ``-precise``
ends_only: (a boolean)
    only map the streamline endpoints to the image
    argument: ``-ends_only``
tck_weights: (a pathlike object or string representing an existing

```

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```

        file)
        specify a text scalar file containing the streamline weights
        argument: ``-tck_weights_in %s``
nthreads: (an integer (int or long))
        number of threads. if zero, the number of available cpus will be
        used
        argument: ``-nthreads %d``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipype default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
        output TDI file

```

69.6.3 DWIExtract[Link to code](#)

Wraps the executable command dwiextract.

Extract diffusion-weighted volumes, b=0 volumes, or certain shells from a DWI dataset

Example

```

>>> import nipype.interfaces.mrtrix3 as mrt
>>> dwiextract = mrt.DWIExtract()
>>> dwiextract.inputs.in_file = 'dwi.mif'
>>> dwiextract.inputs.bzero = True
>>> dwiextract.inputs.out_file = 'b0vols.mif'
>>> dwiextract.inputs.grad_fsl = ('bvecs', 'bvals')
>>> dwiextract.cmdline # doctest: +ELLIPSIS
'dwiextract -bzero -fslgrad bvecs bvals dwi.mif b0vols.mif'
>>> dwiextract.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input image
        argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file)
        output image
        argument: ``%s``, position: -1

[Optional]
bzero: (a boolean)
        extract b=0 volumes
        argument: ``-bzero``
nobzero: (a boolean)
        extract non b=0 volumes
        argument: ``-no_bzero``
singleshell: (a boolean)

```

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```

        extract volumes with a specific shell
        argument: ``-singleshell``
shell: (a list of items which are a float)
        specify one or more gradient shells
        argument: ``-shell %s``
nthreads: (an integer (int or long))
        number of threads. if zero, the number of available cpus will be
        used
        argument: ``-nthreads %d``
grad_file: (a pathlike object or string representing an existing
        file)
        dw gradient scheme (MRTrix format)
        argument: ``-grad %s``
        mutually_exclusive: grad_fsl
grad_fsl: (a tuple of the form: (a pathlike object or string
        representing an existing file, a pathlike object or string
        representing an existing file))
        (bvecs, bvals) dw gradient scheme (FSL format)
        argument: ``-fslgrad %s %s``
        mutually_exclusive: grad_file
bval_scale: ('yes' or 'no')
        specifies whether the b - values should be scaled by the square of
        the corresponding DW gradient norm, as often required for multishell
        or DSI DW acquisition schemes. The default action can also be set in
        the MRtrix config file, under the BValueScaling entry. Valid choices
        are yes / no, true / false, 0 / 1 (default: true).
        argument: ``-bvalue_scaling %s``
in_bvec: (a pathlike object or string representing an existing file)
        bvecs file in FSL format
        argument: ``-fslgrad %s %s``
in_bval: (a pathlike object or string representing an existing file)
        bvals file in FSL format
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        output image

```

69.6.4 Generate5tt[Link to code](#)

Wraps the executable command 5ttgen.

Generate a 5TT image suitable for ACT using the selected algorithm

Example

```

>>> import nipy.interfaces.mrtrix3 as mrt
>>> gen5tt = mrt.Generate5tt()

```

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```

>>> gen5tt.inputs.in_file = 'T1.nii.gz'
>>> gen5tt.inputs.algorithm = 'fsl'
>>> gen5tt.inputs.out_file = '5tt.mif'
>>> gen5tt.cmdline                                     # doctest: +ELLIPSIS
'5ttgen fsl T1.nii.gz 5tt.mif'
>>> gen5tt.run()                                       # doctest: +SKIP

```

Inputs:

```

[Mandatory]
algorithm: ('fsl' or 'gif' or 'freesurfer')
    tissue segmentation algorithm
    argument: ``%s``, position: -3
in_file: (a pathlike object or string representing an existing file)
    input image
    argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file)
    output image
    argument: ``%s``, position: -1

[Optional]
nthreads: (an integer (int or long))
    number of threads. if zero, the number of available cpus will be
    used
    argument: ``-nthreads %d``
grad_file: (a pathlike object or string representing an existing
    file)
    dw gradient scheme (MRtrix format)
    argument: ``-grad %s``
    mutually_exclusive: grad_fsl
grad_fsl: (a tuple of the form: (a pathlike object or string
    representing an existing file, a pathlike object or string
    representing an existing file))
    (bvecs, bvals) dw gradient scheme (FSL format)
    argument: ``-fslgrad %s %s``
    mutually_exclusive: grad_file
bval_scale: ('yes' or 'no')
    specifies whether the b - values should be scaled by the square of
    the corresponding DW gradient norm, as often required for multishell
    or DSI DW acquisition schemes. The default action can also be set in
    the MRtrix config file, under the BValueScaling entry. Valid choices
    are yes / no, true / false, 0 / 1 (default: true).
    argument: ``-bvalue_scaling %s``
in_bvec: (a pathlike object or string representing an existing file)
    bvecs file in FSL format
    argument: ``-fslgrad %s %s``
in_bval: (a pathlike object or string representing an existing file)
    bvals file in FSL format
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          output image
```

69.6.5 MRConvert

[Link to code](#)

Wraps the executable command `mrconvert`.

Perform conversion between different file types and optionally extract a subset of the input image

Example

```
>>> import nipyre.interfaces.mrtrix3 as mrt
>>> mrconvert = mrt.MRConvert()
>>> mrconvert.inputs.in_file = 'dwi.nii.gz'
>>> mrconvert.inputs.grad_fsl = ('bvecs', 'bvals')
>>> mrconvert.cmdline                               # doctest: +ELLIPSIS
'mrconvert -fslgrad bvecs bvals dwi.nii.gz dwi.mif'
>>> mrconvert.run()                                 # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input image
         argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file, nipyre
         default value: dwi.mif)
         output image
         argument: ``%s``, position: -1

[Optional]
coord: (a list of items which are a float)
       extract data at the specified coordinates
       argument: ``-coord %s``
vox: (a list of items which are a float)
     change the voxel dimensions
     argument: ``-vox %s``
axes: (a list of items which are an integer (int or long))
     specify the axes that will be used
     argument: ``-axes %s``
scaling: (a list of items which are a float)
        specify the data scaling parameter
        argument: ``-scaling %s``
nthreads: (an integer (int or long))
         number of threads. if zero, the number of available cpus will be
         used
         argument: ``-nthreads %d``
grad_file: (a pathlike object or string representing an existing
         file)
         dw gradient scheme (MRTrix format)
         argument: ``-grad %s``
         mutually_exclusive: grad_fsl
grad_fsl: (a tuple of the form: (a pathlike object or string
         representing an existing file, a pathlike object or string
         representing an existing file))
         (bvecs, bvals) dw gradient scheme (FSL format)
```

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```

        argument: ``-fslgrad %s %s``
        mutually_exclusive: grad_file
    bval_scale: ('yes' or 'no')
        specifies whether the b - values should be scaled by the square of
        the corresponding DW gradient norm, as often required for multishell
        or DSI DW acquisition schemes. The default action can also be set in
        the MRtrix config file, under the BValueScaling entry. Valid choices
        are yes / no, true / false, 0 / 1 (default: true).
        argument: ``-bvalue_scaling %s``
    in_bvec: (a pathlike object or string representing an existing file)
        bvecs file in FSL format
        argument: ``-fslgrad %s %s``
    in_bval: (a pathlike object or string representing an existing file)
        bvals file in FSL format
    args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
    environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipype default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
        output image

```

69.6.6 MRMath[Link to code](#)

Wraps the executable command mrmath.

Compute summary statistic on image intensities along a specified axis of a single image

Example

```

>>> import nipype.interfaces.mrtrix3 as mrt
>>> mrmath = mrt.MRMath()
>>> mrmath.inputs.in_file = 'dwi.mif'
>>> mrmath.inputs.operation = 'mean'
>>> mrmath.inputs.axis = 3
>>> mrmath.inputs.out_file = 'dwi_mean.mif'
>>> mrmath.inputs.grad_fsl = ('bvecs', 'bvals')
>>> mrmath.cmdline                               # doctest: +ELLIPSIS
'mrmath -axis 3 -fslgrad bvecs bvals dwi.mif mean dwi_mean.mif'
>>> mrmath.run()                                 # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        input image
        argument: ``%s``, position: -3
out_file: (a pathlike object or string representing a file)
        output image
        argument: ``%s``, position: -1
operation: ('mean' or 'median' or 'sum' or 'product' or 'rms' or

```

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```

        'norm' or 'var' or 'std' or 'min' or 'max' or 'absmax' or
        'magmax')
    operation to computer along a specified axis
    argument: ``%s``, position: -2

[Optional]
axis: (an integer (int or long))
    specied axis to perform the operation along
    argument: ``-axis %d``
nthreads: (an integer (int or long))
    number of threads. if zero, the number of available cpus will be
    used
    argument: ``-nthreads %d``
grad_file: (a pathlike object or string representing an existing
    file)
    dw gradient scheme (MRtrix format)
    argument: ``-grad %s``
    mutually_exclusive: grad_fsl
grad_fsl: (a tuple of the form: (a pathlike object or string
    representing an existing file, a pathlike object or string
    representing an existing file))
    (bvecs, bvals) dw gradient scheme (FSL format)
    argument: ``-fslgrad %s %s``
    mutually_exclusive: grad_file
bval_scale: ('yes' or 'no')
    specifies whether the b - values should be scaled by the square of
    the corresponding DW gradient norm, as often required for multishell
    or DSI DW acquisition schemes. The default action can also be set in
    the MRtrix config file, under the BValueScaling entry. Valid choices
    are yes / no, true / false, 0 / 1 (default: true).
    argument: ``-bvalue_scaling %s``
in_bvec: (a pathlike object or string representing an existing file)
    bvecs file in FSL format
    argument: ``-fslgrad %s %s``
in_bval: (a pathlike object or string representing an existing file)
    bvals file in FSL format
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output image

```

69.6.7 Mesh2PVE[Link to code](#)

Wraps the executable command mesh2pve.

Convert a mesh surface to a partial volume estimation image

Example

```
>>> import nipy.interfaces.mrtrix3 as mrt
>>> m2p = mrt.Mesh2PVE()
>>> m2p.inputs.in_file = 'surfl.vtk'
>>> m2p.inputs.reference = 'dwi.mif'
>>> m2p.inputs.in_first = 'T1.nii.gz'
>>> m2p.cmdline                                     # doctest: +ELLIPSIS
'mesh2pve -first T1.nii.gz surfl.vtk dwi.mif mesh2volume.nii.gz'
>>> m2p.run()                                       # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input mesh
         argument: ``%s``, position: -3
reference: (a pathlike object or string representing an existing
           file)
           input reference image
           argument: ``%s``, position: -2
out_file: (a pathlike object or string representing a file, nipy
          default value: mesh2volume.nii.gz)
          output file containing SH coefficients
          argument: ``%s``, position: -1

[Optional]
in_first: (a pathlike object or string representing an existing file)
          indicates that the mesh file is provided by FSL FIRST
          argument: ``-first %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          the output response file
```

69.6.8 TCK2VTK

[Link to code](#)

Wraps the executable command `tck2vtk`.

Convert a track file to a vtk format, cave: coordinates are in XYZ coordinates not reference

Example

```
>>> import nipy.interfaces.mrtrix3 as mrt
>>> vtk = mrt.TCK2VTK()
>>> vtk.inputs.in_file = 'tracks.tck'
>>> vtk.inputs.reference = 'b0.nii'
>>> vtk.cmdline                                     # doctest: +ELLIPSIS
```

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```
'tck2vtk -image b0.nii tracks.tck tracks.vtk'
>>> vtk.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input tractography
         argument: ``%s``, position: -2

[Optional]
out_file: (a pathlike object or string representing a file, nipy
         default value: tracks.vtk)
         output VTK file
         argument: ``%s``, position: -1
reference: (a pathlike object or string representing an existing
         file)
         if specified, the properties of this image will be used to convert
         track point positions from real (scanner) coordinates into image
         coordinates (in mm).
         argument: ``-image %s``
voxel: (a pathlike object or string representing an existing file)
        if specified, the properties of this image will be used to convert
        track point positions from real (scanner) coordinates into image
        coordinates.
        argument: ``-image %s``
nthreads: (an integer (int or long))
           number of threads. if zero, the number of available cpus will be
           used
           argument: ``-nthreads %d``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
         output VTK file
```

69.6.9 TensorMetrics

[Link to code](#)Wraps the executable command `tensor2metric`.

Compute metrics from tensors

Example

```
>>> import nipy.interfaces.mrtrix3 as mrt
>>> comp = mrt.TensorMetrics()
>>> comp.inputs.in_file = 'dti.mif'
>>> comp.inputs.out_fa = 'fa.mif'
>>> comp.cmdline # doctest: +ELLIPSIS
```

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```
'tensor2metric -num 1 -fa fa.mif dti.mif'
>>> comp.run()                                # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         input DTI image
         argument: ``%s``, position: -1

[Optional]
out_fa: (a pathlike object or string representing a file)
        output FA file
        argument: ``-fa %s``
out_adc: (a pathlike object or string representing a file)
         output ADC file
         argument: ``-adc %s``
out_evec: (a pathlike object or string representing a file)
          output selected eigenvector(s) file
          argument: ``-vector %s``
out_eval: (a pathlike object or string representing a file)
          output selected eigenvalue(s) file
          argument: ``-value %s``
component: (a list of items which are any value, nipy default
            value: [1])
            specify the desired eigenvalue/eigenvector(s). Note that several
            eigenvalues can be specified as a number sequence
            argument: ``-num %s``
in_mask: (a pathlike object or string representing an existing file)
         only perform computation within the specified binary brain mask
         image
         argument: ``-mask %s``
modulate: ('FA' or 'none' or 'eval')
          how to modulate the magnitude of the eigenvectors
          argument: ``-modulate %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_fa: (a pathlike object or string representing a file)
        output FA file
out_adc: (a pathlike object or string representing a file)
         output ADC file
out_evec: (a pathlike object or string representing a file)
          output selected eigenvector(s) file
out_eval: (a pathlike object or string representing a file)
          output selected eigenvalue(s) file
```


70.1 interfaces.niftyfit.asl

70.1.1 FitAsl

[Link to code](#)

Wraps the executable command `fit_asl`.

Interface for executable `fit_asl` from Niftyfit platform.

Use NiftyFit to perform ASL fitting.

ASL fitting routines (following EU Cost Action White Paper recommendations) Fits Cerebral Blood Flow maps in the first instance.

[Source code](#)

Examples

```
>>> from nipy.interfaces import niftyfit
>>> node = niftyfit.FitAsl()
>>> node.inputs.source_file = 'asl.nii.gz'
>>> node.cmdline
'fit_asl -source asl.nii.gz -cbf asl_cbf.nii.gz -error asl_error.nii.gz -syn asl_
↳syn.nii.gz'
```

Inputs:

```
[Mandatory]
source_file: (a pathlike object or string representing an existing
             file)
             Filename of the 4D ASL (control/label) source image (mandatory).
             argument: ``-source %s``, position: 1

[Optional]
pasl: (a boolean)
      Fit PASL ASL data [default]
      argument: ``-pasl``
pcasl: (a boolean)
       Fit PCASL ASL data
       argument: ``-pcasl``
```

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```

cbf_file: (a pathlike object or string representing a file)
    Filename of the Cerebral Blood Flow map (in ml/100g/min).
    argument: ``-cbf %s``
error_file: (a pathlike object or string representing a file)
    Filename of the CBF error map.
    argument: ``-error %s``
syn_file: (a pathlike object or string representing a file)
    Filename of the synthetic ASL data.
    argument: ``-syn %s``
t1map: (a pathlike object or string representing an existing file)
    Filename of the estimated input T1 map (in ms).
    argument: ``-t1map %s``
m0map: (a pathlike object or string representing an existing file)
    Filename of the estimated input M0 map.
    argument: ``-m0map %s``
m0mpe: (a pathlike object or string representing an existing file)
    Filename of the estimated input M0 map error.
    argument: ``-m0mpe %s``
ir_volume: (a pathlike object or string representing an existing
    file)
    Filename of a [1,2,5]s Inversion Recovery volume (T1/M0 fitting
    carried out internally).
    argument: ``-IRvolume %s``
ir_output: (a pathlike object or string representing an existing
    file)
    Output of [1,2,5]s Inversion Recovery fitting.
    argument: ``-IRoutput %s``
mask: (a pathlike object or string representing an existing file)
    Filename of image mask.
    argument: ``-mask %s``, position: 2
t1_art_cmp: (a float)
    T1 of arterial component [1650ms].
    argument: ``-T1a %f``
plasma_coeff: (a float)
    Single plasma/tissue partition coefficient [0.9ml/g].
    argument: ``-L %f``
eff: (a float)
    Labelling efficiency [0.99 (pasl), 0.85 (pcasl)], ensure any
    background suppression pulses are included in -eff
    argument: ``-eff %f``
out: (a float)
    Outlier rejection for multi CL volumes (enter z-score threshold
    (e.g. 2.5)) [off].
    argument: ``-out %f``
pld: (a float)
    Post Labelling Delay [2000ms].
    argument: ``-PLD %f``
ldd: (a float)
    Labelling Duration [1800ms].
    argument: ``-LDD %f``
dpld: (a float)
    Difference in labelling delay per slice [0.0 ms/slice].
    argument: ``-dPLD %f``
t_inv1: (a float)
    Saturation pulse time [800ms].
    argument: ``-Tinv1 %f``
t_inv2: (a float)

```

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```

        Inversion time [2000ms].
        argument: ``-Tinv2 %f``
dt_inv2: (a float)
        Difference in inversion time per slice [0ms/slice].
        argument: ``-dTinv2 %f``
gm_t1: (a float)
        T1 of GM [1150ms].
        argument: ``-gmT1 %f``
gm_plasma: (a float)
        Plasma/GM water partition [0.95ml/g].
        argument: ``-gmL %f``
gm_ttt: (a float)
        Time to GM [ATT+0ms].
        argument: ``-gmTTT %f``
wm_t1: (a float)
        T1 of WM [800ms].
        argument: ``-wmT1 %f``
wm_plasma: (a float)
        Plasma/WM water partition [0.82ml/g].
        argument: ``-wmL %f``
wm_ttt: (a float)
        Time to WM [ATT+0ms].
        argument: ``-wmTTT %f``
seg: (a pathlike object or string representing an existing file)
        Filename of the 4D segmentation (in ASL space) for L/T1 estimation
        and PV correction {WM,GM,CSF}.
        argument: ``-seg %s``
sig: (a boolean)
        Use sigmoid to estimate L from T1: L(T1|gmL,wmL) [Off].
        argument: ``-sig``
pv0: (an integer (int or long))
        Simple PV correction (CBF=vg*CBFg + vw*CBFw, with CBFw=f*CBFg)
        [0.25].
        argument: ``-pv0 %d``
pv2: (an integer (int or long))
        In plane PV kernel size [3x3].
        argument: ``-pv2 %d``
pv3: (a tuple of the form: (an integer (int or long), an integer (int
        or long), an integer (int or long)))
        3D kernel size [3x3x1].
        argument: ``-pv3 %d %d %d``
mul: (a float)
        Multiply CBF by this value (e.g. if CL are mislabelled use -1.0).
        argument: ``-mul %f``
mulgm: (a boolean)
        Multiply CBF by segmentation [Off].
        argument: ``-sig``
pv_threshold: (a boolean)
        Set PV threshold for switching off LSQR [0.05].
        argument: ``-pvthreshold``
segstyle: (a boolean)
        Set CBF as [gm,wm] not [wm,gm].
        argument: ``-segstyle``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value

```

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```

of class 'str' and with values which are a bytes or None or a
value of class 'str', nipype default value: {})
Environment variables

```

Outputs:

```

cbf_file: (a pathlike object or string representing an existing file)
          Filename of the Cerebral Blood Flow map (in ml/100g/min).
error_file: (a pathlike object or string representing an existing
            file)
            Filename of the CBF error map.
syn_file: (a pathlike object or string representing an existing file)
           Filename of the synthetic ASL data.

```

70.2 interfaces.niftyfit.base

70.2.1 NiftyFitCommand

[Link to code](#)

Base support interface for NiftyFit commands.

Inputs:

```

[Optional]
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables

```

Outputs:**None**

70.3 interfaces.niftyfit.dwi

70.3.1 DwiTool

[Link to code](#)

Wraps the executable command dwi_tool.

Interface for executable dwi_tool from Niftyfit platform.

Use DwiTool.

Diffusion-Weighted MR Prediction. Predicts DWI from previously fitted models and calculates model derived maps.

[Source code](#)

Examples

```

>>> from nipype.interfaces import niftyfit
>>> dwi_tool = niftyfit.DwiTool(dti_flag=True)
>>> dwi_tool.inputs.source_file = 'dwi.nii.gz'
>>> dwi_tool.inputs.bvec_file = 'bvecs'

```

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```

>>> dwi_tool.inputs.bval_file = 'bvals'
>>> dwi_tool.inputs.mask_file = 'mask.nii.gz'
>>> dwi_tool.inputs.b0_file = 'b0.nii.gz'
>>> dwi_tool.inputs.rgbmap_file = 'rgb_map.nii.gz'
>>> dwi_tool.cmdline
'dwi_tool -source dwi.nii.gz -bval bvals -bvec bvecs -b0 b0.nii.gz -mask mask.nii.
↪gz -dti -famap dwi_famap.nii.gz -logdti2 dwi_logdti2.nii.gz -mcmmap dwi_mcmmap.
↪nii.gz -mdmap dwi_mdmap.nii.gz -rgbmap rgb_map.nii.gz -syn dwi_syn.nii.gz -
↪vlmap dwi_vlmap.nii.gz'

```

Inputs:

```

[Mandatory]
source_file: (a pathlike object or string representing an existing
              file)
              The source image containing the fitted model.
              argument: ``-source %s``, position: 1
bval_file: (a pathlike object or string representing an existing
            file)
            The file containing the bvalues of the source DWI.
            argument: ``-bval %s``, position: 2

[Optional]
bvec_file: (a pathlike object or string representing an existing
            file)
            The file containing the bvecs of the source DWI.
            argument: ``-bvec %s``, position: 3
b0_file: (a pathlike object or string representing an existing file)
          The B0 image corresponding to the source DWI
          argument: ``-b0 %s``, position: 4
mask_file: (a pathlike object or string representing an existing
            file)
            The image mask
            argument: ``-mask %s``, position: 5
mcmmap_file: (a pathlike object or string representing a file)
              Filename of multi-compartment model parameter map (-ivim,-ball,-nod)
              argument: ``-mcmmap %s``
syn_file: (a pathlike object or string representing a file)
           Filename of synthetic image. Requires: bvec_file/b0_file.
           argument: ``-syn %s``
           requires: bvec_file, b0_file
mdmap_file: (a pathlike object or string representing a file)
             Filename of MD map/ADC
             argument: ``-mdmap %s``
famap_file: (a pathlike object or string representing a file)
             Filename of FA map
             argument: ``-famap %s``
vlmap_file: (a pathlike object or string representing a file)
             Filename of PDD map [x,y,z]
             argument: ``-vlmap %s``
rgbmap_file: (a pathlike object or string representing a file)
              Filename of colour FA map.
              argument: ``-rgbmap %s``
logdti_file: (a pathlike object or string representing a file)
              Filename of output logdti map.
              argument: ``-logdti2 %s``
mono_flag: (a boolean)

```

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```

    Input is a single exponential to non-directional data [default with
    no b-vectors]
    argument: ``-mono``, position: 6
    mutually_exclusive: ivim_flag, dti_flag, dti_flag2, ball_flag,
        ballv_flag, nod_flag, nodv_flag
ivim_flag: (a boolean)
    Inputs is an IVIM model to non-directional data.
    argument: ``-ivim``, position: 6
    mutually_exclusive: mono_flag, dti_flag, dti_flag2, ball_flag,
        ballv_flag, nod_flag, nodv_flag
dti_flag: (a boolean)
    Input is a tensor model diag/off-diag.
    argument: ``-dti``, position: 6
    mutually_exclusive: mono_flag, ivim_flag, dti_flag2, ball_flag,
        ballv_flag, nod_flag, nodv_flag
dti_flag2: (a boolean)
    Input is a tensor model lower triangular
    argument: ``-dti2``, position: 6
    mutually_exclusive: mono_flag, ivim_flag, dti_flag, ball_flag,
        ballv_flag, nod_flag, nodv_flag
ball_flag: (a boolean)
    Input is a ball and stick model.
    argument: ``-ball``, position: 6
    mutually_exclusive: mono_flag, ivim_flag, dti_flag, dti_flag2,
        ballv_flag, nod_flag, nodv_flag
ballv_flag: (a boolean)
    Input is a ball and stick model with optimised PDD.
    argument: ``-ballv``, position: 6
    mutually_exclusive: mono_flag, ivim_flag, dti_flag, dti_flag2,
        ball_flag, nod_flag, nodv_flag
nod_flag: (a boolean)
    Input is a NODDI model
    argument: ``-nod``, position: 6
    mutually_exclusive: mono_flag, ivim_flag, dti_flag, dti_flag2,
        ball_flag, ballv_flag, nodv_flag
nodv_flag: (a boolean)
    Input is a NODDI model with optimised PDD
    argument: ``-nodv``, position: 6
    mutually_exclusive: mono_flag, ivim_flag, dti_flag, dti_flag2,
        ball_flag, ballv_flag, nod_flag
diso_val: (a float)
    Isotropic diffusivity for -nod [3e-3]
    argument: ``-diso %f``
dpr_val: (a float)
    Parallel diffusivity for -nod [1.7e-3].
    argument: ``-dpr %f``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

mcmmap_file: (a pathlike object or string representing a file)

```

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```

        Filename of multi-compartment model parameter map (-ivim,-ball,-nod)
syn_file: (a pathlike object or string representing a file)
        Filename of synthetic image
mdmap_file: (a pathlike object or string representing a file)
        Filename of MD map/ADC
famap_file: (a pathlike object or string representing a file)
        Filename of FA map
v1map_file: (a pathlike object or string representing a file)
        Filename of PDD map [x,y,z]
rgbmap_file: (a pathlike object or string representing a file)
        Filename of colour FA map
logdti_file: (a pathlike object or string representing a file)
        Filename of output logdti map

```

70.3.2 FitDwi

[Link to code](#)

Wraps the executable command `fit_dwi`.

Interface for executable `fit_dwi` from Niftyfit platform.

Use NiftyFit to perform diffusion model fitting.

Diffusion-weighted MR Fitting. Fits DWI parameter maps to multi-shell, multi-directional data.

[Source code](#)

Examples

```

>>> from nipy.interfaces import niftyfit
>>> fit_dwi = niftyfit.FitDwi(dti_flag=True)
>>> fit_dwi.inputs.source_file = 'dwi.nii.gz'
>>> fit_dwi.inputs.bvec_file = 'bvecs'
>>> fit_dwi.inputs.bval_file = 'bvals'
>>> fit_dwi.inputs.rgbmap_file = 'rgb.nii.gz'
>>> fit_dwi.cmdline
'fit_dwi -source dwi.nii.gz -bval bvals -bvec bvecs -dti -error dwi_error.nii.gz -
↳famap dwi_famap.nii.gz -mcout dwi_mcout.txt -mdmap dwi_mdmap.nii.gz -nodiff dwi_
↳no_diff.nii.gz -res dwi_resmap.nii.gz -rgbmap rgb.nii.gz -syn dwi_syn.nii.gz -
↳tenmap2 dwi_tenmap2.nii.gz -v1map dwi_v1map.nii.gz'

```

Inputs:

```

[Mandatory]
source_file: (a pathlike object or string representing an existing
             file)
             The source image containing the dwi data.
             argument: ``-source %s``, position: 1
bval_file: (a pathlike object or string representing an existing
            file)
            The file containing the bvalues of the source DWI.
            argument: ``-bval %s``, position: 2
bvec_file: (a pathlike object or string representing an existing
            file)
            The file containing the bvectors of the source DWI.
            argument: ``-bvec %s``, position: 3

[Optional]
te_file: (a pathlike object or string representing an existing file)

```

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```

    Filename of TEs (ms).
    argument: ``-TE %s``
    mutually_exclusive: te_file
te_value: (a pathlike object or string representing an existing file)
    Value of TEs (ms).
    argument: ``-TE %s``
    mutually_exclusive: te_file
mask_file: (a pathlike object or string representing an existing
    file)
    The image mask
    argument: ``-mask %s``
prior_file: (a pathlike object or string representing an existing
    file)
    Filename of parameter priors for -ball and -nod.
    argument: ``-prior %s``
rot_sform_flag: (an integer (int or long))
    Rotate the output tensors according to the q/s form of the image
    (resulting tensors will be in mm coordinates, default: 0).
    argument: ``-rotsform %d``
error_file: (a pathlike object or string representing a file)
    Filename of parameter error maps.
    argument: ``-error %s``
res_file: (a pathlike object or string representing a file)
    Filename of model residual map.
    argument: ``-res %s``
syn_file: (a pathlike object or string representing a file)
    Filename of synthetic image.
    argument: ``-syn %s``
nodiff_file: (a pathlike object or string representing a file)
    Filename of average no diffusion image.
    argument: ``-nodiff %s``
mcmap_file: (a pathlike object or string representing a file)
    Filename of multi-compartment model parameter map (-ivim,-ball,-nod)
    argument: ``-mcmap %s``
    requires: nodv_flag
mdmap_file: (a pathlike object or string representing a file)
    Filename of MD map/ADC
    argument: ``-mdmap %s``
famap_file: (a pathlike object or string representing a file)
    Filename of FA map
    argument: ``-famap %s``
vlmap_file: (a pathlike object or string representing a file)
    Filename of PDD map [x,y,z]
    argument: ``-vlmap %s``
rgbmap_file: (a pathlike object or string representing a file)
    Filename of colour-coded FA map
    argument: ``-rgbmap %s``
    requires: dti_flag
ten_type: ('lower-tri' or 'diag-off-diag', nipy default value:
    lower-tri)
    Use lower triangular (tenmap2) or diagonal, off-diagonal tensor
    format
tenmap_file: (a pathlike object or string representing a file)
    Filename of tensor map [diag,offdiag].
    argument: ``-tenmap %s``
    requires: dti_flag
tenmap2_file: (a pathlike object or string representing a file)

```

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```

        Filename of tensor map [lower tri]
        argument: ``-tenmap2 %s``
        requires: dti_flag
mono_flag: (a boolean)
        Fit single exponential to non-directional data [default with no
        b-vectors]
        argument: ``-mono``, position: 4
        mutually_exclusive: ivim_flag, dti_flag, ball_flag, ballv_flag,
        nod_flag, nodv_flag
ivim_flag: (a boolean)
        Fit IVIM model to non-directional data.
        argument: ``-ivim``, position: 4
        mutually_exclusive: mono_flag, dti_flag, ball_flag, ballv_flag,
        nod_flag, nodv_flag
dti_flag: (a boolean)
        Fit the tensor model [default with b-vectors].
        argument: ``-dti``, position: 4
        mutually_exclusive: mono_flag, ivim_flag, ball_flag, ballv_flag,
        nod_flag, nodv_flag
ball_flag: (a boolean)
        Fit the ball and stick model.
        argument: ``-ball``, position: 4
        mutually_exclusive: mono_flag, ivim_flag, dti_flag, ballv_flag,
        nod_flag, nodv_flag
ballv_flag: (a boolean)
        Fit the ball and stick model with optimised PDD.
        argument: ``-ballv``, position: 4
        mutually_exclusive: mono_flag, ivim_flag, dti_flag, ball_flag,
        nod_flag, nodv_flag
nod_flag: (a boolean)
        Fit the NODDI model
        argument: ``-nod``, position: 4
        mutually_exclusive: mono_flag, ivim_flag, dti_flag, ball_flag,
        ballv_flag, nodv_flag
nodv_flag: (a boolean)
        Fit the NODDI model with optimised PDD
        argument: ``-nodv``, position: 4
        mutually_exclusive: mono_flag, ivim_flag, dti_flag, ball_flag,
        ballv_flag, nod_flag
maxit_val: (an integer (int or long))
        Maximum number of non-linear LSQR iterations [100x2 passes]
        argument: ``-maxit %d``
        requires: gn_flag
lm_vals: (a tuple of the form: (a float, a float))
        LM parameters (initial value, decrease rate) [100,1.2].
        argument: ``-lm %f %f``
        requires: gn_flag
gn_flag: (a boolean)
        Use Gauss-Newton algorithm [Levenberg-Marquardt].
        argument: ``-gn``
        mutually_exclusive: wls_flag
vb_flag: (a boolean)
        Use Variational Bayes fitting with known prior (currently identity
        covariance...).
        argument: ``-vb``
cov_file: (a pathlike object or string representing an existing file)
        Filename of the nc*nc covariance matrix [I]

```

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```

        argument: ``-cov %s``
wls_flag: (a boolean)
    Use Variational Bayes fitting with known prior (currently identity
    covariance...).
    argument: ``-wls``
    mutually_exclusive: gn_flag
swls_val: (a float)
    Use location-weighted least squares for DTI fitting [3x3 Gaussian]
    argument: ``-swls %f``
slice_no: (an integer (int or long))
    Fit to single slice number.
    argument: ``-slice %d``
voxel: (a tuple of the form: (an integer (int or long), an integer
    (int or long), an integer (int or long)))
    Fit to single voxel only.
    argument: ``-voxel %d %d %d``
diso_val: (a float)
    Isotropic diffusivity for -nod [3e-3]
    argument: ``-diso %f``
dpr_val: (a float)
    Parallel diffusivity for -nod [1.7e-3].
    argument: ``-dpr %f``
wm_t2_val: (a float)
    White matter T2 value [80ms].
    argument: ``-wmT2 %f``
csf_t2_val: (a float)
    CSF T2 value [400ms].
    argument: ``-csfT2 %f``
perf_thr: (a float)
    Threshold for perfusion/diffusion effects [100].
    argument: ``-perfthreshold %f``
mcout: (a pathlike object or string representing a file)
    Filename of mc samples (ascii text file)
    argument: ``-mcout %s``
mcsamples: (an integer (int or long))
    Number of samples to keep [100].
    argument: ``-mcsamples %d``
mcmaxit: (an integer (int or long))
    Number of iterations to run [10,000].
    argument: ``-mcmaxit %d``
acceptance: (a float)
    Fraction of iterations to accept [0.23].
    argument: ``-acceptance %f``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

error_file: (a pathlike object or string representing a file)
    Filename of parameter error maps
res_file: (a pathlike object or string representing a file)
    Filename of model residual map

```

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```

syn_file: (a pathlike object or string representing a file)
    Filename of synthetic image
nodiff_file: (a pathlike object or string representing a file)
    Filename of average no diffusion image.
mdmap_file: (a pathlike object or string representing a file)
    Filename of MD map/ADC
famap_file: (a pathlike object or string representing a file)
    Filename of FA map
vlmap_file: (a pathlike object or string representing a file)
    Filename of PDD map [x,y,z]
rgbmap_file: (a pathlike object or string representing a file)
    Filename of colour FA map
tenmap_file: (a pathlike object or string representing a file)
    Filename of tensor map
tenmap2_file: (a pathlike object or string representing a file)
    Filename of tensor map [lower tri]
mcmap_file: (a pathlike object or string representing a file)
    Filename of multi-compartment model parameter map
    (-ivim, -ball, -nod).
mcout: (a pathlike object or string representing a file)
    Filename of mc samples (ascii text file)

```

70.4 interfaces.niftyfit.qt1

70.4.1 FitQt1

[Link to code](#)

Wraps the executable command `fit_qt1`.

Interface for executable `fit_qt1` from Niftyfit platform.

Use NiftyFit to perform Qt1 fitting.

T1 Fitting Routine (To inversion recovery or spgr data). Fits single component T1 maps in the first instance.

[Source code](#)

Examples

```

>>> from nipy.interfaces.niftyfit import FitQt1
>>> fit_qt1 = FitQt1()
>>> fit_qt1.inputs.source_file = 'TI4D.nii.gz'
>>> fit_qt1.cmdline
'fit_qt1 -source TI4D.nii.gz -comp TI4D_comp.nii.gz -error TI4D_error.nii.gz -
↪m0map TI4D_m0map.nii.gz -mcmap TI4D_mcmap.nii.gz -res TI4D_res.nii.gz -syn TI4D_
↪syn.nii.gz -t1map TI4D_t1map.nii.gz'

```

Inputs:

```

[Mandatory]
source_file: (a pathlike object or string representing an existing
    file)
    Filename of the 4D Multi-Echo T1 source image.
    argument: ``-source %s``, position: 1

[Optional]
t1map_file: (a pathlike object or string representing a file)
    Filename of the estimated output T1 map (in ms).

```

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```

    argument: ``-t1map %s``
m0map_file: (a pathlike object or string representing a file)
    Filename of the estimated input M0 map.
    argument: ``-m0map %s``
mcmap_file: (a pathlike object or string representing a file)
    Filename of the estimated output multi-parameter map.
    argument: ``-mcmap %s``
comp_file: (a pathlike object or string representing a file)
    Filename of the estimated multi-component T1 map.
    argument: ``-comp %s``
error_file: (a pathlike object or string representing a file)
    Filename of the error map (symmetric matrix, [Diag,OffDiag]).
    argument: ``-error %s``
syn_file: (a pathlike object or string representing a file)
    Filename of the synthetic ASL data.
    argument: ``-syn %s``
res_file: (a pathlike object or string representing a file)
    Filename of the model fit residuals
    argument: ``-res %s``
mask: (a pathlike object or string representing an existing file)
    Filename of image mask.
    argument: ``-mask %s``, position: 2
prior: (a pathlike object or string representing an existing file)
    Filename of parameter prior.
    argument: ``-prior %s``, position: 3
te_value: (a float)
    TE Echo Time [0ms!].
    argument: ``-TE %f``, position: 4
tr_value: (a float)
    TR Repetition Time [10s!].
    argument: ``-TR %f``, position: 5
nb_comp: (an integer (int or long))
    Number of components to fit [1] (currently IR/SR only)
    argument: ``-nc %d``, position: 6
lm_val: (a tuple of the form: (a float, a float))
    Set LM parameters (initial value, decrease rate) [100,1.2].
    argument: ``-lm %f %f``, position: 7
gn_flag: (a boolean)
    Use Gauss-Newton algorithm [Levenberg-Marquardt].
    argument: ``-gn``, position: 8
slice_no: (an integer (int or long))
    Fit to single slice number.
    argument: ``-slice %d``, position: 9
voxel: (a tuple of the form: (an integer (int or long), an integer
    (int or long), an integer (int or long)))
    Fit to single voxel only.
    argument: ``-voxel %d %d %d``, position: 10
maxit: (an integer (int or long))
    NLSQR iterations [100].
    argument: ``-maxit %d``, position: 11
sr_flag: (a boolean)
    Saturation Recovery fitting [default].
    argument: ``-SR``, position: 12
ir_flag: (a boolean)
    Inversion Recovery fitting [default].
    argument: ``-IR``, position: 13
tis: (a list of items which are a float)

```

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```

        Inversion times for T1 data [1s,2s,5s].
        argument: ``-TIs %s``, position: 14
tis_list: (a pathlike object or string representing an existing file)
        Filename of list of pre-defined TIs.
        argument: ``-TIlis %s``
tl_list: (a pathlike object or string representing an existing file)
        Filename of list of pre-defined Tls
        argument: ``-Tllis %s``
tlmin: (a float)
        Minimum tissue T1 value [400ms].
        argument: ``-Tlmin %f``
tlmax: (a float)
        Maximum tissue T1 value [4000ms].
        argument: ``-Tlmax %f``
spgr: (a boolean)
        Spoiled Gradient Echo fitting
        argument: ``-SPGR``
flips: (a list of items which are a float)
        Flip angles
        argument: ``-flips %s``
flips_list: (a pathlike object or string representing an existing
        file)
        Filename of list of pre-defined flip angles (deg).
        argument: ``-fliplis %s``
blmap: (a pathlike object or string representing an existing file)
        Filename of B1 estimate for fitting (or include in prior).
        argument: ``-blmap %s``
mcout: (a pathlike object or string representing an existing file)
        Filename of mc samples (ascii text file)
        argument: ``-mcout %s``
mcsamples: (an integer (int or long))
        Number of samples to keep [100].
        argument: ``-mcsamples %d``
mcmaxit: (an integer (int or long))
        Number of iterations to run [10,000].
        argument: ``-mcmaxit %d``
acceptance: (a float)
        Fraction of iterations to accept [0.23].
        argument: ``-acceptance %f``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

tlmap_file: (a pathlike object or string representing a file)
        Filename of the estimated output T1 map (in ms)
m0map_file: (a pathlike object or string representing a file)
        Filename of the m0 map
mcmap_file: (a pathlike object or string representing a file)
        Filename of the estimated output multi-parameter map
comp_file: (a pathlike object or string representing a file)
        Filename of the estimated multi-component T1 map.

```

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```
error_file: (a pathlike object or string representing a file)
    Filename of the error map (symmetric matrix, [Diag,OffDiag])
syn_file: (a pathlike object or string representing a file)
    Filename of the synthetic ASL data
res_file: (a pathlike object or string representing a file)
    Filename of the model fit residuals
```


71.1 interfaces.niftyreg.base

71.1.1 NiftyRegCommand

[Link to code](#)

Base support interface for NiftyReg commands.

Inputs:

```
[Optional]
omp_core_val: (an integer (int or long), nipy default value: 1)
    Number of openmp thread to use
    argument: ``-omp %i``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
None
```

71.1.2 get_custom_path()

[Link to code](#)

71.2 interfaces.niftyreg.reg

71.2.1 RegAladin

[Link to code](#)

Wraps the executable command `reg_aladin`.

Interface for executable `reg_aladin` from NiftyReg platform.

Block Matching algorithm for symmetric global registration. Based on Modat et al., “Global image registration using asymmetric block-matching approach” J. Med. Img. 1(2) 024003, 2014, doi: 10.1117/1.JMI.1.2.024003
[Source code](#)

Examples

```
>>> from nipy.interfaces import niftyreg
>>> node = niftyreg.RegAladin()
>>> node.inputs.ref_file = 'im1.nii'
>>> node.inputs.flo_file = 'im2.nii'
>>> node.inputs.rmask_file = 'mask.nii'
>>> node.inputs.omp_core_val = 4
>>> node.cmdline
'reg_aladin -aff im2_aff.txt -flo im2.nii -omp 4 -ref im1.nii -res im2_res.nii.gz
↪-rmask mask.nii'
```

Inputs:

```
[Mandatory]
ref_file: (a pathlike object or string representing an existing file)
    The input reference/target image
    argument: ``-ref %s``
flo_file: (a pathlike object or string representing an existing file)
    The input floating/source image
    argument: ``-flo %s``

[Optional]
nosym_flag: (a boolean)
    Turn off symmetric registration
    argument: ``-noSym``
rig_only_flag: (a boolean)
    Do only a rigid registration
    argument: ``-rigOnly``
aff_direct_flag: (a boolean)
    Directly optimise the affine parameters
    argument: ``-affDirect``
in_aff_file: (a pathlike object or string representing an existing
    file)
    The input affine transformation
    argument: ``-inaff %s``
rmask_file: (a pathlike object or string representing an existing
    file)
    The input reference mask
    argument: ``-rmask %s``
fmask_file: (a pathlike object or string representing an existing
    file)
    The input floating mask
    argument: ``-fmask %s``
maxit_val: (a long integer >= 0)
    Maximum number of iterations
    argument: ``-maxit %d``
ln_val: (a long integer >= 0)
    Number of resolution levels to create
    argument: ``-ln %d``
lp_val: (a long integer >= 0)
    Number of resolution levels to perform
    argument: ``-lp %d``
```

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```

smoo_r_val: (a float)
    Amount of smoothing to apply to reference image
    argument: ``-smooR %f``
smoo_f_val: (a float)
    Amount of smoothing to apply to floating image
    argument: ``-smooF %f``
nac_flag: (a boolean)
    Use nifti header to initialise transformation
    argument: ``-nac``
cog_flag: (a boolean)
    Use the masks centre of mass to initialise the transformation
    argument: ``-cog``
v_val: (a long integer >= 0)
    Percent of blocks that are active
    argument: ``-pv %d``
i_val: (a long integer >= 0)
    Percent of inlier blocks
    argument: ``-pi %d``
ref_low_val: (a float)
    Lower threshold value on reference image
    argument: ``-refLowThr %f``
ref_up_val: (a float)
    Upper threshold value on reference image
    argument: ``-refUpThr %f``
flo_low_val: (a float)
    Lower threshold value on floating image
    argument: ``-floLowThr %f``
flo_up_val: (a float)
    Upper threshold value on floating image
    argument: ``-floUpThr %f``
platform_val: (an integer (int or long))
    Platform index
    argument: ``-platf %i``
gpuid_val: (an integer (int or long))
    Device to use id
    argument: ``-gpuid %i``
verbosity_off_flag: (a boolean)
    Turn off verbose output
    argument: ``-voff``
aff_file: (a pathlike object or string representing a file)
    The output affine matrix file
    argument: ``-aff %s``
res_file: (a pathlike object or string representing a file)
    The affine transformed floating image
    argument: ``-res %s``
omp_core_val: (an integer (int or long), nipy default value: 1)
    Number of openmp thread to use
    argument: ``-omp %i``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

aff_file: (a pathlike object or string representing a file)
           The output affine file
res_file: (a pathlike object or string representing a file)
           The output transformed image
avg_output: (a string)
             Output string in the format for reg_average

```

71.2.2 RegF3D

[Link to code](#)

Wraps the executable command `reg_f3d`.

Interface for executable `reg_f3d` from NiftyReg platform.

Fast Free-Form Deformation (F3D) algorithm for non-rigid registration. Initially based on Modat et al., “Fast Free-Form Deformation using graphics processing units”, CMPB, 2010

[Source code](#)

Examples

```

>>> from nipy.interfaces import niftyreg
>>> node = niftyreg.RegF3D()
>>> node.inputs.ref_file = 'im1.nii'
>>> node.inputs.flo_file = 'im2.nii'
>>> node.inputs.rmask_file = 'mask.nii'
>>> node.inputs.omp_core_val = 4
>>> node.cmdline
'reg_f3d -cpp im2_cpp.nii.gz -flo im2.nii -omp 4 -ref im1.nii -res im2_res.nii.gz_
↪-rmask mask.nii'

```

Inputs:

```

[Mandatory]
ref_file: (a pathlike object or string representing an existing file)
           The input reference/target image
           argument: ``-ref %s``
flo_file: (a pathlike object or string representing an existing file)
           The input floating/source image
           argument: ``-flo %s``

[Optional]
aff_file: (a pathlike object or string representing an existing file)
           The input affine transformation file
           argument: ``-aff %s``
incpp_file: (a pathlike object or string representing an existing
             file)
             The input cpp transformation file
             argument: ``-incpp %s``
rmask_file: (a pathlike object or string representing an existing
             file)
             Reference image mask
             argument: ``-rmask %s``
ref_smooth_val: (a float)
                 Smoothing kernel width for reference image
                 argument: ``-smooR %f``
flo_smooth_val: (a float)
                 Smoothing kernel width for floating image
                 argument: ``-smooF %f``

```

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```

rlwth_thr_val: (a float)
    Lower threshold for reference image
    argument: ``--rLwTh %f``
rupth_thr_val: (a float)
    Upper threshold for reference image
    argument: ``--rUpTh %f``
flwth_thr_val: (a float)
    Lower threshold for floating image
    argument: ``--fLwTh %f``
fupth_thr_val: (a float)
    Upper threshold for floating image
    argument: ``--fUpTh %f``
rlwth2_thr_val: (a tuple of the form: (a long integer >= 0, a float))
    Lower threshold for reference image at the specified time point
    argument: ``-rLwTh %d %f``
rupth2_thr_val: (a tuple of the form: (a long integer >= 0, a float))
    Upper threshold for reference image at the specified time point
    argument: ``-rUpTh %d %f``
flwth2_thr_val: (a tuple of the form: (a long integer >= 0, a float))
    Lower threshold for floating image at the specified time point
    argument: ``-fLwTh %d %f``
fupth2_thr_val: (a tuple of the form: (a long integer >= 0, a float))
    Upper threshold for floating image at the specified time point
    argument: ``-fUpTh %d %f``
sx_val: (a float)
    Final grid spacing along the x axes
    argument: ``-sx %f``
sy_val: (a float)
    Final grid spacing along the y axes
    argument: ``-sy %f``
sz_val: (a float)
    Final grid spacing along the z axes
    argument: ``-sz %f``
be_val: (a float)
    Bending energy value
    argument: ``-be %f``
le_val: (a float)
    Linear elasticity penalty term
    argument: ``-le %f``
jl_val: (a float)
    Log of jacobian of deformation penalty value
    argument: ``-jl %f``
no_app_jl_flag: (a boolean)
    Do not approximate the log of jacobian penalty at control points
    only
    argument: ``-noAppJL``
nmi_flag: (a boolean)
    use NMI even when other options are specified
    argument: ``--nmi``
rbn_val: (a long integer >= 0)
    Number of bins in the histogram for reference image
    argument: ``--rbn %d``
fbn_val: (a long integer >= 0)
    Number of bins in the histogram for reference image
    argument: ``--fbn %d``
rbn2_val: (a tuple of the form: (a long integer >= 0, a long integer
    >= 0))

```

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```

        Number of bins in the histogram for reference image for given time
        point
        argument: ``-rbn %d %d``
fbn2_val: (a tuple of the form: (a long integer >= 0, a long integer
        >= 0))
        Number of bins in the histogram for reference image for given time
        point
        argument: ``-fbn %d %d``
lncc_val: (a float)
        SD of the Gaussian for computing LNCC
        argument: ``--lncc %f``
lncc2_val: (a tuple of the form: (a long integer >= 0, a float))
        SD of the Gaussian for computing LNCC for a given time point
        argument: ``-lncc %d %f``
ssd_flag: (a boolean)
        Use SSD as the similarity measure
        argument: ``--ssd``
ssd2_flag: (a long integer >= 0)
        Use SSD as the similarity measure for a given time point
        argument: ``-ssd %d``
kld_flag: (a boolean)
        Use KL divergence as the similarity measure
        argument: ``--kld``
kld2_flag: (a long integer >= 0)
        Use KL divergence as the similarity measure for a given time point
        argument: ``-kld %d``
amc_flag: (a boolean)
        Use additive NMI
        argument: ``-amc``
nox_flag: (a boolean)
        Don't optimise in x direction
        argument: ``-nox``
noy_flag: (a boolean)
        Don't optimise in y direction
        argument: ``-noy``
noz_flag: (a boolean)
        Don't optimise in z direction
        argument: ``-noz``
maxit_val: (a long integer >= 0)
        Maximum number of iterations per level
        argument: ``-maxit %d``
ln_val: (a long integer >= 0)
        Number of resolution levels to create
        argument: ``-ln %d``
lp_val: (a long integer >= 0)
        Number of resolution levels to perform
        argument: ``-lp %d``
nopy_flag: (a boolean)
        Do not use the multiresolution approach
        argument: ``-nopy``
noconj_flag: (a boolean)
        Use simple GD optimization
        argument: ``-noConj``
pert_val: (a long integer >= 0)
        Add perturbation steps after each optimization step
        argument: ``-pert %d``
vel_flag: (a boolean)

```

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```

        Use velocity field integration
        argument: ``-vel``
fmask_file: (a pathlike object or string representing an existing
            file)
            Floating image mask
            argument: ``-fmask %s``
smooth_grad_val: (a float)
            Kernel width for smoothing the metric gradient
            argument: ``-smoothGrad %f``
pad_val: (a float)
            Padding value
            argument: ``-pad %f``
verbosity_off_flag: (a boolean)
            Turn off verbose output
            argument: ``-voff``
cpp_file: (a pathlike object or string representing a file)
            The output CPP file
            argument: ``-cpp %s``
res_file: (a pathlike object or string representing a file)
            The output resampled image
            argument: ``-res %s``
omp_core_val: (an integer (int or long), nipy default value: 1)
            Number of openmp thread to use
            argument: ``-omp %i``
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
            of class 'str' and with values which are a bytes or None or a
            value of class 'str', nipy default value: {})
            Environment variables

```

Outputs:

```

cpp_file: (a pathlike object or string representing a file)
            The output CPP file
res_file: (a pathlike object or string representing a file)
            The output resampled image
invcpp_file: (a pathlike object or string representing a file)
            The output inverse CPP file
invres_file: (a pathlike object or string representing a file)
            The output inverse res file
avg_output: (a string)
            Output string in the format for reg_average

```

71.3 interfaces.niftyreg.regutils

71.3.1 RegAverage

[Link to code](#)

Wraps the executable command `reg_average`.

Interface for executable `reg_average` from NiftyReg platform.

Compute average matrix or image from a list of matrices or image. The tool can be use to resample images given input transformation parametrisation as well as to demean transformations in Euclidean or log-Euclidean space.

This interface is different than the others in the way that the options will be written in a command file that is

given as a parameter.

[Source code](#)

Examples

```
>>> from nipy.interfaces import niftyreg
>>> node = niftyreg.RegAverage()
>>> one_file = 'im1.nii'
>>> two_file = 'im2.nii'
>>> three_file = 'im3.nii'
>>> node.inputs.avg_files = [one_file, two_file, three_file]
>>> node.cmdline # doctest: +ELLIPSIS
'reg_average --cmd_file .../reg_average_cmd'
```

Inputs:

```
[Optional]
avg_files: (a list of items which are a pathlike object or string
            representing a file)
            Averaging of images/affine transformations
            argument: ``-avg %s``, position: 1
            mutually_exclusive: avg_lts_files, avg_ref_file, demean1_ref_file,
                                demean2_ref_file, demean3_ref_file, warp_files
avg_lts_files: (a list of items which are a pathlike object or string
                representing a file)
                Robust average of affine transformations
                argument: ``-avg_lts %s``, position: 1
                mutually_exclusive: avg_files, avg_ref_file, demean1_ref_file,
                                    demean2_ref_file, demean3_ref_file, warp_files
avg_ref_file: (a pathlike object or string representing a file)
               All input images are resampled into the space of <reference image>
               and averaged. A cubic spline interpolation scheme is used for
               resampling
               argument: ``-avg_tran %s``, position: 1
               mutually_exclusive: avg_files, avg_lts_files, demean1_ref_file,
                                   demean2_ref_file, demean3_ref_file
               requires: warp_files
demean1_ref_file: (a pathlike object or string representing a file)
                  Average images and demean average image that have affine
                  transformations to a common space
                  argument: ``-demean1 %s``, position: 1
                  mutually_exclusive: avg_files, avg_lts_files, avg_ref_file,
                                      demean2_ref_file, demean3_ref_file
                  requires: warp_files
demean2_ref_file: (a pathlike object or string representing a file)
                  Average images and demean average image that have non-rigid
                  transformations to a common space
                  argument: ``-demean2 %s``, position: 1
                  mutually_exclusive: avg_files, avg_lts_files, avg_ref_file,
                                      demean1_ref_file, demean3_ref_file
                  requires: warp_files
demean3_ref_file: (a pathlike object or string representing a file)
                  Average images and demean average image that have linear and non-
                  rigid transformations to a common space
                  argument: ``-demean3 %s``, position: 1
                  mutually_exclusive: avg_files, avg_lts_files, avg_ref_file,
                                      demean1_ref_file, demean2_ref_file
                  requires: warp_files
```

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```

warp_files: (a list of items which are a pathlike object or string
             representing a file)
             transformation files and floating image pairs/triplets to the
             reference space
             argument: ``%s``, position: -1
             mutually_exclusive: avg_files, avg_lts_files
out_file: (a pathlike object or string representing a file)
           Output file name
           argument: ``%s``, position: 0
omp_core_val: (an integer (int or long), nipy default value: 1)
              Number of openmp thread to use
              argument: ``-omp %i``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
          Output file name

```

71.3.2 RegJacobian[Link to code](#)Wraps the executable command `reg_jacobian`.Interface for executable `reg_resample` from NiftyReg platform.Tool to generate Jacobian determinant maps from transformation parametrisation generated by `reg_f3d`[Source code](#)**Examples**

```

>>> from nipy.interfaces import niftyreg
>>> node = niftyreg.RegJacobian()
>>> node.inputs.ref_file = 'im1.nii'
>>> node.inputs.trans_file = 'warpfield.nii'
>>> node.inputs.omp_core_val = 4
>>> node.cmdline
'reg_jacobian -omp 4 -ref im1.nii -trans warpfield.nii -jac warpfield_jac.nii.gz'

```

Inputs:

```

[Mandatory]
trans_file: (a pathlike object or string representing an existing
            file)
            The input non-rigid transformation
            argument: ``-trans %s``

[Optional]
ref_file: (a pathlike object or string representing an existing file)
          Reference/target file (required if specifying CPP transformations.
          argument: ``-ref %s``
type: ('jac' or 'jacL' or 'jacM', nipy default value: jac)

```

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```

        Type of jacobian outcome
        argument: ``-s``, position: -2
    out_file: (a pathlike object or string representing a file)
        The output jacobian determinant file name
        argument: ``s``, position: -1
    omp_core_val: (an integer (int or long), nipy default value: 1)
        Number of openmp thread to use
        argument: ``-omp %i``
    args: (a unicode string)
        Additional parameters to the command
        argument: ``s``
    environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    The output file

```

71.3.3 RegMeasure[Link to code](#)Wraps the executable command `reg_measure`.Interface for executable `reg_measure` from NiftyReg platform.

Given two input images, compute the specified measure(s) of similarity

[Source code](#)**Examples**

```

>>> from nipy.interfaces import niftyreg
>>> node = niftyreg.RegMeasure()
>>> node.inputs.ref_file = 'im1.nii'
>>> node.inputs.flo_file = 'im2.nii'
>>> node.inputs.measure_type = 'lncc'
>>> node.inputs.omp_core_val = 4
>>> node.cmdline
'reg_measure -flo im2.nii -lncc -omp 4 -out im2_lncc.txt -ref im1.nii'

```

Inputs:

```

[Mandatory]
ref_file: (a pathlike object or string representing an existing file)
    The input reference/target image
    argument: ``-ref %s``
flo_file: (a pathlike object or string representing an existing file)
    The input floating/source image
    argument: ``-flo %s``
measure_type: ('ncc' or 'lncc' or 'nmi' or 'ssd')
    Measure of similarity to compute
    argument: ``-s``

[Optional]
out_file: (a pathlike object or string representing a file)
    The output text file containing the measure

```

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```

        argument: ``-out %s``
omp_core_val: (an integer (int or long), nipy default value: 1)
    Number of openmp thread to use
        argument: ``-omp %i``
args: (a unicode string)
    Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    The output text file containing the measure

```

71.3.4 RegResample

[Link to code](#)

Wraps the executable command `reg_resample`.

Interface for executable `reg_resample` from NiftyReg platform.

Tool to resample floating image in the space of a defined reference image given a transformation parametrisation generated by `reg_aladin`, `reg_f3d` or `reg_transform`

[Source code](#)**Examples**

```

>>> from nipy.interfaces import niftyreg
>>> node = niftyreg.RegResample()
>>> node.inputs.ref_file = 'im1.nii'
>>> node.inputs.flo_file = 'im2.nii'
>>> node.inputs.trans_file = 'warpfield.nii'
>>> node.inputs.inter_val = 'LIN'
>>> node.inputs.omp_core_val = 4
>>> node.cmdline
'reg_resample -flo im2.nii -inter 1 -omp 4 -ref im1.nii -trans warpfield.nii -res_
↪im2_res.nii.gz'

```

Inputs:

```

[Mandatory]
ref_file: (a pathlike object or string representing an existing file)
    The input reference/target image
    argument: ``-ref %s``
flo_file: (a pathlike object or string representing an existing file)
    The input floating/source image
    argument: ``-flo %s``

[Optional]
trans_file: (a pathlike object or string representing an existing
    file)
    The input transformation file
    argument: ``-trans %s``
type: ('res' or 'blank', nipy default value: res)
    Type of output

```

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```

        argument: ``-s``, position: -2
out_file: (a pathlike object or string representing a file)
        The output filename of the transformed image
        argument: ``-s``, position: -1
inter_val: ('NN' or 'LIN' or 'CUB' or 'SINC')
        Interpolation type
        argument: ``-inter %d``
pad_val: (a float)
        Padding value
        argument: ``-pad %f``
tensor_flag: (a boolean)
        Resample Tensor Map
        argument: ``-tensor ``
verbosity_off_flag: (a boolean)
        Turn off verbose output
        argument: ``-voff``
psf_flag: (a boolean)
        Perform the resampling in two steps to resample an image to a lower
        resolution
        argument: ``-psf``
psf_alg: (0 or 1)
        Minimise the matrix metric (0) or the determinant (1) when
        estimating the PSF [0]
        argument: ``-psf_alg %d``
omp_core_val: (an integer (int or long), nipy default value: 1)
        Number of openmp thread to use
        argument: ``-omp %i``
args: (a unicode string)
        Additional parameters to the command
        argument: ``-s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
        The output filename of the transformed image

```

71.3.5 RegTools[Link to code](#)Wraps the executable command `reg_tools`.Interface for executable `reg_tools` from NiftyReg platform.

Tool delivering various actions related to registration such as resampling the input image to a chosen resolution or remove the nan and inf in the input image by a specified value.

[Source code](#)**Examples**

```

>>> from nipy.interfaces import niftyreg
>>> node = niftyreg.RegTools()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.mul_val = 4

```

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```
>>> node.inputs.omp_core_val = 4
>>> node.cmdline
'reg_tools -in iml.nii -mul 4.0 -omp 4 -out iml_tools.nii.gz'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        The input image file path
        argument: ``-in %s``

[Optional]
out_file: (a pathlike object or string representing a file)
        The output file name
        argument: ``-out %s``
iso_flag: (a boolean)
        Make output image isotropic
        argument: ``-iso``
noscl_flag: (a boolean)
        Set scale, slope to 0 and 1
        argument: ``-noscl``
mask_file: (a pathlike object or string representing an existing
        file)
        Values outside the mask are set to NaN
        argument: ``-nan %s``
thr_val: (a float)
        Binarise the input image with the given threshold
        argument: ``-thr %f``
bin_flag: (a boolean)
        Binarise the input image
        argument: ``-bin``
rms_val: (a pathlike object or string representing an existing file)
        Compute the mean RMS between the images
        argument: ``-rms %s``
div_val: (a float or a pathlike object or string representing an
        existing file)
        Divide the input by image or value
        argument: ``-div %s``
mul_val: (a float or a pathlike object or string representing an
        existing file)
        Multiply the input by image or value
        argument: ``-mul %s``
add_val: (a float or a pathlike object or string representing an
        existing file)
        Add to the input image or value
        argument: ``-add %s``
sub_val: (a float or a pathlike object or string representing an
        existing file)
        Add to the input image or value
        argument: ``-sub %s``
down_flag: (a boolean)
        Downsample the image by a factor of 2
        argument: ``-down``
smo_s_val: (a tuple of the form: (a float, a float, a float))
        Smooth the input image using a cubic spline kernel
        argument: ``-smoS %f %f %f``
chg_res_val: (a tuple of the form: (a float, a float, a float))
```

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```

    Change the resolution of the input image
    argument: ``-chgres %f %f %f``
smo_g_val: (a tuple of the form: (a float, a float, a float))
    Smooth the input image using a Gaussian kernel
    argument: ``-smoG %f %f %f``
inter_val: ('NN' or 'LIN' or 'CUB' or 'SINC')
    Interpolation order to use to warp the floating image
    argument: ``-interp %d``
omp_core_val: (an integer (int or long), nipy default value: 1)
    Number of openmp thread to use
    argument: ``-omp %i``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    The output file

```

71.3.6 RegTransform[Link to code](#)Wraps the executable command `reg_transform`.Interface for executable `reg_transform` from NiftyReg platform.

Tools to convert transformation parametrisation from one type to another as well as to compose, inverse or half transformations.

[Source code](#)**Examples**

```

>>> from nipy.interfaces import niftyreg
>>> node = niftyreg.RegTransform()
>>> node.inputs.def_input = 'warpfield.nii'
>>> node.inputs.omp_core_val = 4
>>> node.cmdline # doctest: +ELLIPSIS
'reg_transform -omp 4 -def warpfield.nii .../warpfield_trans.nii.gz'

```

Inputs:

```

[Optional]
ref1_file: (a pathlike object or string representing an existing
    file)
    The input reference/target image
    argument: ``-ref %s``, position: 0
ref2_file: (a pathlike object or string representing an existing
    file)
    The input second reference/target image
    argument: ``-ref2 %s``, position: 1
    requires: ref1_file
def_input: (a pathlike object or string representing an existing
    file)

```

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```

    Compute deformation field from transformation
    argument: ``-def %s``, position: -2
    mutually_exclusive: disp_input, flow_input, comp_input,
        upd_s_form_input, inv_aff_input, inv_nrr_input, half_input,
        make_aff_input, aff_2_rig_input, flirt_2_nr_input
disp_input: (a pathlike object or string representing an existing
    file)
    Compute displacement field from transformation
    argument: ``-disp %s``, position: -2
    mutually_exclusive: def_input, flow_input, comp_input,
        upd_s_form_input, inv_aff_input, inv_nrr_input, half_input,
        make_aff_input, aff_2_rig_input, flirt_2_nr_input
flow_input: (a pathlike object or string representing an existing
    file)
    Compute flow field from spline SVF
    argument: ``-flow %s``, position: -2
    mutually_exclusive: def_input, disp_input, comp_input,
        upd_s_form_input, inv_aff_input, inv_nrr_input, half_input,
        make_aff_input, aff_2_rig_input, flirt_2_nr_input
comp_input: (a pathlike object or string representing an existing
    file)
    compose two transformations
    argument: ``-comp %s``, position: -3
    mutually_exclusive: def_input, disp_input, flow_input,
        upd_s_form_input, inv_aff_input, inv_nrr_input, half_input,
        make_aff_input, aff_2_rig_input, flirt_2_nr_input
    requires: comp_input2
comp_input2: (a pathlike object or string representing an existing
    file)
    compose two transformations
    argument: ``%s``, position: -2
upd_s_form_input: (a pathlike object or string representing an
    existing file)
    Update s-form using the affine transformation
    argument: ``-updSform %s``, position: -3
    mutually_exclusive: def_input, disp_input, flow_input, comp_input,
        inv_aff_input, inv_nrr_input, half_input, make_aff_input,
        aff_2_rig_input, flirt_2_nr_input
    requires: upd_s_form_input2
upd_s_form_input2: (a pathlike object or string representing an
    existing file)
    Update s-form using the affine transformation
    argument: ``%s``, position: -2
    requires: upd_s_form_input
inv_aff_input: (a pathlike object or string representing an existing
    file)
    Invert an affine transformation
    argument: ``-invAff %s``, position: -2
    mutually_exclusive: def_input, disp_input, flow_input, comp_input,
        upd_s_form_input, inv_nrr_input, half_input, make_aff_input,
        aff_2_rig_input, flirt_2_nr_input
inv_nrr_input: (a tuple of the form: (a pathlike object or string
    representing an existing file, a pathlike object or string
    representing an existing file))
    Invert a non-linear transformation
    argument: ``-invNrr %s %s``, position: -2
    mutually_exclusive: def_input, disp_input, flow_input, comp_input,

```

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```

    upd_s_form_input, inv_aff_input, half_input, make_aff_input,
    aff_2_rig_input, flirt_2_nr_input
half_input: (a pathlike object or string representing an existing
    file)
    Half way to the input transformation
    argument: ``-half %s``, position: -2
    mutually_exclusive: def_input, disp_input, flow_input, comp_input,
        upd_s_form_input, inv_aff_input, inv_nrr_input, make_aff_input,
        aff_2_rig_input, flirt_2_nr_input
make_aff_input: (a tuple of the form: (a float, a float, a float, a
    float, a float, a float, a float, a float, a float, a float, a
    float, a float))
    Make an affine transformation matrix
    argument: ``-makeAff %f %f %f %f %f %f %f %f %f %f %f %f``,
    position: -2
    mutually_exclusive: def_input, disp_input, flow_input, comp_input,
        upd_s_form_input, inv_aff_input, inv_nrr_input, half_input,
        aff_2_rig_input, flirt_2_nr_input
aff_2_rig_input: (a pathlike object or string representing an
    existing file)
    Extract the rigid component from affine transformation
    argument: ``-aff2rig %s``, position: -2
    mutually_exclusive: def_input, disp_input, flow_input, comp_input,
        upd_s_form_input, inv_aff_input, inv_nrr_input, half_input,
        make_aff_input, flirt_2_nr_input
flirt_2_nr_input: (a tuple of the form: (a pathlike object or string
    representing an existing file, a pathlike object or string
    representing an existing file, a pathlike object or string
    representing an existing file))
    Convert a FLIRT affine transformation to niftyreg affine
    transformation
    argument: ``-flirtAff2NR %s %s %s``, position: -2
    mutually_exclusive: def_input, disp_input, flow_input, comp_input,
        upd_s_form_input, inv_aff_input, inv_nrr_input, half_input,
        make_aff_input, aff_2_rig_input
out_file: (a pathlike object or string representing a file)
    transformation file to write
    argument: ``%s``, position: -1
omp_core_val: (an integer (int or long), nipy default value: 1)
    Number of openmp thread to use
    argument: ``-omp %i``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    Output File (transformation in any format)

```


72.1 interfaces.niftyseg.base

72.1.1 NiftySegCommand

[Link to code](#)

Base support interface for NiftySeg commands.

Inputs:

```
[Optional]
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables
```

Outputs:

```
None
```

72.2 interfaces.niftyseg.em

72.2.1 EM

[Link to code](#)

Wraps the executable command `seg_EM`.

Interface for executable `seg_EM` from NiftySeg platform.

`seg_EM` is a general purpose intensity based image segmentation tool. In it's simplest form, it takes in one 2D or 3D image and segments it in `n` classes.

[Source code](#) | [Documentation](#)

Examples

```
>>> from nipy.interfaces import niftyseg
>>> node = niftyseg.EM()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.no_prior = 4
>>> node.cmdline
'seg_EM -in im1.nii -bc_order 3 -bc_thresh 0 -max_iter 100 -min_iter 0 -nopriors_
↪4 -bc_out im1_bc_em.nii.gz -out im1_em.nii.gz -out_outlier im1_outlier_em.nii.gz
↪'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Input image to segment
    argument: ``-in %s``, position: 4
no_prior: (an integer (int or long))
    Number of classes to use without prior
    argument: ``-nopriors %s``
    mutually_exclusive: prior_4D, priors
prior_4D: (a pathlike object or string representing an existing file)
    4D file containing the priors
    argument: ``-prior4D %s``
    mutually_exclusive: no_prior, priors
priors: (a list of items which are any value)
    List of priors filepaths.
    argument: ``%s``
    mutually_exclusive: no_prior, prior_4D

[Optional]
mask_file: (a pathlike object or string representing an existing
    file)
    Filename of the ROI for label fusion
    argument: ``-mask %s``
max_iter: (an integer (int or long), nipy default value: 100)
    Maximum number of iterations
    argument: ``-max_iter %s``
min_iter: (an integer (int or long), nipy default value: 0)
    Minimum number of iterations
    argument: ``-min_iter %s``
bc_order_val: (an integer (int or long), nipy default value: 3)
    Polynomial order for the bias field
    argument: ``-bc_order %s``
mrf_beta_val: (a float)
    Weight of the Markov Random Field
    argument: ``-mrf_beta %s``
bc_thresh_val: (a float, nipy default value: 0)
    Bias field correction will run only if the ratio of improvement is
    below bc_thresh. (default=0 [OFF])
    argument: ``-bc_thresh %s``
reg_val: (a float)
    Amount of regularization over the diagonal of the covariance matrix
    [above 1]
    argument: ``-reg %s``
outlier_val: (a tuple of the form: (a float, a float))
    Outlier detection as in (Van Leemput TMI 2003). <fl1> is the
    Mahalanobis threshold [recommended between 3 and 7] <fl2> is a
```

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```

        convergence ratio below which the outlier detection is going to be
        done [recommended 0.01]
        argument: ``-outlier %s %s``
    relax_priors: (a tuple of the form: (a float, a float))
        Relax Priors [relaxation factor: 0<rf<1 (recommended=0.5), gaussian
        regularization: gstd>0 (recommended=2.0)] /only 3D/
        argument: ``-rf %s %s``
    out_file: (a pathlike object or string representing a file)
        Output segmentation
        argument: ``-out %s``
    out_bc_file: (a pathlike object or string representing a file)
        Output bias corrected image
        argument: ``-bc_out %s``
    out_outlier_file: (a pathlike object or string representing a file)
        Output outlierness image
        argument: ``-out_outlier %s``
    args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
    environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
        Output segmentation
out_bc_file: (a pathlike object or string representing a file)
        Output bias corrected image
out_outlier_file: (a pathlike object or string representing a file)
        Output outlierness image

```

72.3 interfaces.niftyseg.label_fusion

72.3.1 CalcTopNCC

[Link to code](#)

Wraps the executable command seg_CalcTopNCC.

Interface for executable seg_CalcTopNCC from NiftySeg platform.

Examples

```

>>> from nipy.interfaces import niftyseg
>>> node = niftyseg.CalcTopNCC()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.num_templates = 2
>>> node.inputs.in_templates = ['im2.nii', 'im3.nii']
>>> node.inputs.top_templates = 1
>>> node.cmdline
'seg_CalcTopNCC -target im1.nii -templates 2 im2.nii im3.nii -n 1'

```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Target file
    argument: ``-target %s``, position: 1
num_templates: (an integer (int or long))
    Number of Templates
    argument: ``-templates %s``, position: 2
in_templates: (a list of items which are a pathlike object or string
    representing an existing file)
    argument: ``%s``, position: 3
top_templates: (an integer (int or long))
    Number of Top Templates
    argument: ``-n %s``, position: 4

[Optional]
mask_file: (a pathlike object or string representing an existing
    file)
    Filename of the ROI for label fusion
    argument: ``-mask %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_files: (any value)
```

72.3.2 LabelFusion

[Link to code](#)

Wraps the executable command `seg_LabFusion`.

Interface for executable `seg_LabelFusion` from NiftySeg platform using type STEPS as classifier Fusion.

This executable implements 4 fusion strategies (-STEPS, -STAPLE, -MV or -SBA), all of them using either a global (-GNCC), ROI-based (-ROINCC), local (-LNCC) or no image similarity (-ALL). Combinations of fusion algorithms and similarity metrics give rise to different variants of known algorithms. As an example, using LNCC and MV as options will run a locally weighted voting strategy with LNCC derived weights, while using STAPLE and LNCC is equivalent to running STEPS as per its original formulation. A few other options pertaining the use of an MRF (-MRF beta), the initial sensitivity and specificity estimates and the use of only non-consensus voxels (-unc) for the STAPLE and STEPS algorithm. All processing can be masked (-mask), greatly reducing memory consumption.

As an example, the command to use STEPS should be: `seg_LabFusion -in 4D_Propragated_Labels_to_fuse.nii -out FusedSegmentation.nii -STEPS 2 15 TargetImage.nii 4D_Propagated_Intensities.nii`

[Source code](#) | [Documentation](#)

Examples

```
>>> from nipy.interfaces import niftyseg
>>> node = niftyseg.LabelFusion()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.kernel_size = 2.0
>>> node.inputs.file_to_seg = 'im2.nii'
```

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```

>>> node.inputs.template_file = 'im3.nii'
>>> node.inputs.template_num = 2
>>> node.inputs.classifier_type = 'STEPS'
>>> node.cmdline
'seg_LabFusion -in im1.nii -STEPS 2.000000 2 im2.nii im3.nii -out im1_steps.nii'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Filename of the 4D integer label image.
    argument: ``-in %s``, position: 1
file_to_seg: (a pathlike object or string representing an existing
    file)
    Original image to segment (3D Image)
classifier_type: ('STEPS' or 'STAPLE' or 'MV' or 'SBA')
    Type of Classifier Fusion.
    argument: ``-%s``, position: 2

[Optional]
template_file: (a pathlike object or string representing an existing
    file)
    Registered templates (4D Image)
mask_file: (a pathlike object or string representing an existing
    file)
    Filename of the ROI for label fusion
    argument: ``-mask %s``
out_file: (a pathlike object or string representing a file)
    Output consensus segmentation
    argument: ``-out %s``
prob_flag: (a boolean)
    Probabilistic/Fuzzy segmented image
    argument: ``-outProb``
verbose: ('0' or '1' or '2')
    Verbose level [0 = off, 1 = on, 2 = debug] (default = 0)
    argument: ``-v %s``
unc: (a boolean)
    Only consider non-consensus voxels to calculate statistics
    argument: ``-unc``
kernel_size: (a float)
    Gaussian kernel size in mm to compute the local similarity
template_num: (an integer (int or long))
    Number of labels to use
sm_ranking: ('ALL' or 'GNCC' or 'ROINCC' or 'LNCC', nipy default
    value: ALL)
    Ranking for STAPLE and MV
    argument: ``-%s``, position: 3
dilation_roi: (an integer (int or long))
    Dilation of the ROI ( <int> d>=1 )
proportion: (a float)
    Proportion of the label (only for single labels).
    argument: ``-prop %s``
prob_update_flag: (a boolean)
    Update label proportions at each iteration
    argument: ``-prop_update``
set_pq: (a tuple of the form: (a float, a float))
    Value of P and Q [ 0 < (P,Q) < 1 ] (default = 0.99 0.99)

```

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```

        argument: ``-setPQ %f %f``
mrf_value: (a float)
    MRF prior strength (between 0 and 5)
    argument: ``-MRF_beta %f``
max_iter: (an integer (int or long))
    Maximum number of iterations (default = 15).
    argument: ``-max_iter %d``
unc_thresh: (a float)
    If <float> percent of labels agree, then area is not uncertain.
    argument: ``-unc thresh %f``
conv: (a float)
    Ratio for convergence (default epsilon = 10^-5).
    argument: ``-conv %f``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    image written after calculations

```

72.4 interfaces.niftyseg.lesions

72.4.1 FillLesions

[Link to code](#)Wraps the executable command `seg_FillLesions`.Interface for executable `seg_FillLesions` from NiftySeg platform.

Fill all the masked lesions with WM intensity average.

[Source code](#) | [Documentation](#)**Examples**

```

>>> from nipy.interfaces import niftyseg
>>> node = niftyseg.FillLesions()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.lesion_mask = 'im2.nii'
>>> node.cmdline
'seg_FillLesions -i im1.nii -l im2.nii -o im1_lesions_filled.nii.gz'

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Input image to fill lesions
    argument: ``-i %s``, position: 1
lesion_mask: (a pathlike object or string representing an existing
    file)
    Lesion mask
    argument: ``-l %s``, position: 2

```

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```

[Optional]
out_file: (a pathlike object or string representing a file)
    The output filename of the fill lesions results
    argument: ``-o %s``, position: 3
in_dilation: (an integer (int or long))
    Dilate the mask <int> times (in voxels, by default 0)
    argument: ``-dil %d``
match: (a float)
    Percentage of minimum number of voxels between patches <float> (by
    default 0.5).
    argument: ``-match %f``
search: (a float)
    Minimum percentage of valid voxels in target patch <float> (by
    default 0).
    argument: ``-search %f``
smooth: (a float)
    Smoothing by <float> (in minimal 6-neighbourhood voxels (by default
    0.1)).
    argument: ``-smo %f``
size: (an integer (int or long))
    Search regions size respect biggest patch size (by default 4).
    argument: ``-size %d``
cwf: (a float)
    Patch cardinality weighting factor (by default 2).
    argument: ``-cwf %f``
bin_mask: (a pathlike object or string representing a file)
    Give a binary mask with the valid search areas.
    argument: ``-mask %s``
other: (a boolean)
    Guizard et al. (FIN 2015) method, it doesn't include the
    multiresolution/hierarchical inpainting part, this part needs to be
    done with some external software such as reg_tools and reg_resample
    from NiftyReg. By default it uses the method presented in Prados et
    al. (Neuroimage 2016).
    argument: ``-other``
use_2d: (a boolean)
    Uses 2D patches in the Z axis, by default 3D.
    argument: ``-2D``
debug: (a boolean)
    Save all intermidium files (by default OFF).
    argument: ``-debug``
out_datatype: (a string)
    Set output <datatype> (char, short, int, uchar, ushort, uint, float,
    double).
    argument: ``-odt %s``
verbose: (a boolean)
    Verbose (by default OFF).
    argument: ``-v``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```
out_file: (a pathlike object or string representing a file)
          Output segmentation
```

72.5 interfaces.niftyseg.maths

72.5.1 BinaryMaths

[Link to code](#)

Wraps the executable command `seg_maths`.

Interface for executable `seg_maths` from NiftySeg platform.

Interface to use any binary mathematical operations that can be performed with the `seg_maths` command-line program.

See below for those operations:

`mul` - `<float/file>` - Multiply image `<float>` value or by other image.

`div` - `<float/file>` - Divide image by `<float>` or by other image.

`add` - `<float/file>` - Add image by `<float>` or by other image.

`sub` - `<float/file>` - Subtract image by `<float>` or by other image.

`pow` - `<float>` - Image to the power of `<float>`.

`thr` - `<float>` - Threshold the image below `<float>`.

`uthr` - `<float>` - Threshold image above `<float>`.

`smo` - `<float>` - Gaussian smoothing by std `<float>` (in voxels and up to 4-D).

`edge` - `<float>` - Calculate the edges of the image using a threshold `<float>`.

`sobel3` - `<float>` - Calculate the edges of all timepoints using a Sobel filter with a 3x3x3 kernel and applying `<float>` gaussian smoothing.

`sobel5` - `<float>` - Calculate the edges of all timepoints using a Sobel filter with a 5x5x5 kernel and applying `<float>` gaussian smoothing.

`min` - `<file>` - Get the min per voxel between `<current>` and `<file>`.

`smol` - `<float>` - Gaussian smoothing of a 3D label image.

`geo` - `<float/file>` - Geodesic distance according to the speed function `<float/file>`

`llsnorm` `<file_norm>` - Linear LS normalisation between current and `<file_norm>`

`masknan` `<file_norm>` - Assign everything outside the mask (`mask==0`) with NaNs

`hdr_copy` `<file>` - Copy header from working image to `<file>` and save in `<output>`.

`splitinter` `<x/y/z>` - Split interleaved slices in direction `<x/y/z>` into separate time points

[Source code](#) | [Documentation](#)

Examples

```
>>> import copy
>>> from nipy.interfaces import niftyseg
>>> binary = niftyseg.BinaryMaths()
>>> binary.inputs.in_file = 'im1.nii'
>>> binary.inputs.output_datatype = 'float'
>>> # Test sub operation
>>> binary_sub = copy.deepcopy(binary)
>>> binary_sub.inputs.operation = 'sub'
>>> binary_sub.inputs.operand_file = 'im2.nii'
>>> binary_sub.cmdline
'seg_maths im1.nii -sub im2.nii -odt float im1_sub.nii'
>>> binary_sub.run() # doctest: +SKIP
>>> # Test mul operation
>>> binary_mul = copy.deepcopy(binary)
>>> binary_mul.inputs.operation = 'mul'
>>> binary_mul.inputs.operand_value = 2.0
```

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```

>>> binary_mul.cmdline
'seg_maths im1.nii -mul 2.00000000 -odt float im1_mul.nii'
>>> binary_mul.run() # doctest: +SKIP
>>> # Test llsnorm operation
>>> binary_llsnorm = copy.deepcopy(binary)
>>> binary_llsnorm.inputs.operation = 'llsnorm'
>>> binary_llsnorm.inputs.operand_file = 'im2.nii'
>>> binary_llsnorm.cmdline
'seg_maths im1.nii -llsnorm im2.nii -odt float im1_llsnorm.nii'
>>> binary_llsnorm.run() # doctest: +SKIP
>>> # Test splitinter operation
>>> binary_splitinter = copy.deepcopy(binary)
>>> binary_splitinter.inputs.operation = 'splitinter'
>>> binary_splitinter.inputs.operand_str = 'z'
>>> binary_splitinter.cmdline
'seg_maths im1.nii -splitinter z -odt float im1_splitinter.nii'
>>> binary_splitinter.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
operation: ('mul' or 'div' or 'add' or 'sub' or 'pow' or 'thr' or
            'uthr' or 'smo' or 'edge' or 'sobel3' or 'sobel5' or 'min' or
            'smol' or 'geo' or 'llsnorm' or 'masknan' or 'hdr_copy' or
            'splitinter')
            operation to perform
            argument: ``-%s``, position: 4
operand_file: (a pathlike object or string representing an existing
               file)
               second image to perform operation with
               argument: ``%s``, position: 5
               mutually_exclusive: operand_value, operand_str
operand_value: (a float)
               float value to perform operation with
               argument: ``%.8f``, position: 5
               mutually_exclusive: operand_file, operand_str
operand_str: ('x' or 'y' or 'z')
              string value to perform operation splitinter
              argument: ``%s``, position: 5
              mutually_exclusive: operand_value, operand_file
in_file: (a pathlike object or string representing an existing file)
          image to operate on
          argument: ``%s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
           image to write
           argument: ``%s``, position: -2
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                  or 'input')
                  datatype to use for output (default uses input type)
                  argument: ``-odt %s``, position: -3
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a

```

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```
value of class 'str', nipy default value: {}
Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
image written after calculations
```

72.5.2 BinaryMathsInteger

[Link to code](#)

Wraps the executable command `seg_maths`.

Interface for executable `seg_maths` from NiftySeg platform.

Interface to use any integer mathematical operations that can be performed with the `seg_maths` command-line program.

See below for those operations:: (requiring integer values)

`equal - <int>` - Get voxels equal to `<int>`

`dil - <int>` - Dilate the image `<int>` times (in voxels).

`ero - <int>` - Erode the image `<int>` times (in voxels).

`tp - <int>` - Extract time point `<int>`

`crop - <int>` - Crop `<int>` voxels around each 3D volume.

`pad - <int>` - Pad `<int>` voxels with NaN value around each 3D volume.

[Source code](#) | [Documentation](#)

Examples

```
>>> import copy
>>> from nipy.interfaces.niftyseg import BinaryMathsInteger
>>> binaryi = BinaryMathsInteger()
>>> binaryi.inputs.in_file = 'im1.nii'
>>> binaryi.inputs.output_datatype = 'float'
>>> # Test dil operation
>>> binaryi_dil = copy.deepcopy(binaryi)
>>> binaryi_dil.inputs.operation = 'dil'
>>> binaryi_dil.inputs.operand_value = 2
>>> binaryi_dil.cmdline
'seg_maths im1.nii -dil 2 -odt float im1_dil.nii'
>>> binaryi_dil.run() # doctest: +SKIP
>>> # Test dil operation
>>> binaryi_ero = copy.deepcopy(binaryi)
>>> binaryi_ero.inputs.operation = 'ero'
>>> binaryi_ero.inputs.operand_value = 1
>>> binaryi_ero.cmdline
'seg_maths im1.nii -ero 1 -odt float im1_ero.nii'
>>> binaryi_ero.run() # doctest: +SKIP
>>> # Test pad operation
>>> binaryi_pad = copy.deepcopy(binaryi)
>>> binaryi_pad.inputs.operation = 'pad'
>>> binaryi_pad.inputs.operand_value = 4
>>> binaryi_pad.cmdline
'seg_maths im1.nii -pad 4 -odt float im1_pad.nii'
>>> binaryi_pad.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
operation: ('dil' or 'ero' or 'tp' or 'equal' or 'pad' or 'crop')
    operation to perform
    argument: ``-s``, position: 4
operand_value: (an integer (int or long))
    int value to perform operation with
    argument: ``d``, position: 5
in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``s``, position: -2
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for output (default uses input type)
    argument: ``-odt s``, position: -3
args: (a unicode string)
    Additional parameters to the command
    argument: ``s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
    image written after calculations
```

72.5.3 MathsCommand

[Link to code](#)

Wraps the executable command `seg_maths`.

Base Command Interface for `seg_maths` interfaces.

The executable `seg_maths` enables the sequential execution of arithmetic operations, like multiplication (`-mul`), division (`-div`) or addition (`-add`), binarisation (`-bin`) or thresholding (`-thr`) operations and convolution by a Gaussian kernel (`-smo`). It also allows mathematical morphology based operations like dilation (`-dil`), erosion (`-ero`), connected components (`-lconncomp`) and hole filling (`-fill`), Euclidean (`-euc`) and geodesic (`-geo`) distance transforms, local image similarity metric calculation (`-lnc` and `-lssd`). Finally, it allows multiple operations over the dimensionality of the image, from merging 3D images together as a 4D image (`-merge`) or splitting (`-split` or `-tp`) 4D images into several 3D images, to estimating the maximum, minimum and average over all time-points, etc.

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``s``, position: -2
```

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```

output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                  or 'input')
    datatype to use for output (default uses input type)
    argument: ``-odt %s``, position: -3
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    image written after calculations

```

72.5.4 Merge[Link to code](#)Wraps the executable command `seg_maths`.Interface for executable `seg_maths` from NiftySeg platform.Interface to use the merge operation that can be performed with the `seg_maths` command-line program.

See below for this option:

`merge <i> <d> <files>` Merge `<i>` images and the working image in the `<d>` dimension[Source code](#) | [Documentation](#)**Examples**

```

>>> from nipy.interfaces import niftyseg
>>> node = niftyseg.Merge()
>>> node.inputs.in_file = 'im1.nii'
>>> files = ['im2.nii', 'im3.nii']
>>> node.inputs.merge_files = files
>>> node.inputs.dimension = 2
>>> node.inputs.output_datatype = 'float'
>>> node.cmdline
'seg_maths im1.nii -merge 2 2 im2.nii im3.nii -odt float im1_merged.nii'

```

Inputs:

```

[Mandatory]
dimension: (an integer (int or long))
    Dimension to merge the images.
merge_files: (a list of items which are a pathlike object or string
              representing an existing file)
    List of images to merge to the working image <input>.
    argument: ``%s``, position: 4
in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``%s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)

```

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```

        image to write
        argument: ``%s``, position: -2
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
                  or 'input')
        datatype to use for output (default uses input type)
        argument: ``-odt %s``, position: -3
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
        image written after calculations

```

72.5.5 TupleMaths

[Link to code](#)Wraps the executable command `seg_maths`.Interface for executable `seg_maths` from NiftySeg platform.Interface to use any tuple mathematical operations that can be performed with the `seg_maths` command-line program.

See below for those operations:

`lncc <file> <std>` Local CC between current img and `<file>` on a kernel with `<std>``lssd <file> <std>` Local SSD between current img and `<file>` on a kernel with `<std>``lltsnorm <file_norm> <float>` Linear LTS normalisation assuming `<float>` percent outliers[Source code](#) | [Documentation](#)

Examples

```

>>> import copy
>>> from nipy.interfaces import niftyseg
>>> tuple = niftyseg.TupleMaths()
>>> tuple.inputs.in_file = 'im1.nii'
>>> tuple.inputs.output_datatype = 'float'

```

```

>>> # Test lncc operation
>>> tuple_lncc = copy.deepcopy(tuple)
>>> tuple_lncc.inputs.operation = 'lncc'
>>> tuple_lncc.inputs.operand_file1 = 'im2.nii'
>>> tuple_lncc.inputs.operand_value2 = 2.0
>>> tuple_lncc.cmdline
'seg_maths im1.nii -lncc im2.nii 2.00000000 -odt float im1_lncc.nii'
>>> tuple_lncc.run() # doctest: +SKIP

```

```

>>> # Test lssd operation
>>> tuple_lssd = copy.deepcopy(tuple)
>>> tuple_lssd.inputs.operation = 'lssd'
>>> tuple_lssd.inputs.operand_file1 = 'im2.nii'
>>> tuple_lssd.inputs.operand_value2 = 1.0

```

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```
>>> tuple_lssd.cmdline
'seg_maths im1.nii -lssd im2.nii 1.00000000 -odt float im1_lssd.nii'
>>> tuple_lssd.run() # doctest: +SKIP
```

```
>>> # Test lltsnorm operation
>>> tuple_lltsnorm = copy.deepcopy(tuple)
>>> tuple_lltsnorm.inputs.operation = 'lltsnorm'
>>> tuple_lltsnorm.inputs.operand_file1 = 'im2.nii'
>>> tuple_lltsnorm.inputs.operand_value2 = 0.01
>>> tuple_lltsnorm.cmdline
'seg_maths im1.nii -lltsnorm im2.nii 0.01000000 -odt float im1_lltsnorm.nii'
>>> tuple_lltsnorm.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
operation: ('lncc' or 'lssd' or 'lltsnorm')
    operation to perform
    argument: ``-%s``, position: 4
operand_file1: (a pathlike object or string representing an existing
    file)
    image to perform operation 1 with
    argument: ``-%s``, position: 5
    mutually_exclusive: operand_value1
operand_value1: (a float)
    float value to perform operation 1 with
    argument: ``%.8f``, position: 5
    mutually_exclusive: operand_file1
operand_file2: (a pathlike object or string representing an existing
    file)
    image to perform operation 2 with
    argument: ``-%s``, position: 6
    mutually_exclusive: operand_value2
operand_value2: (a float)
    float value to perform operation 2 with
    argument: ``%.8f``, position: 6
    mutually_exclusive: operand_file2
in_file: (a pathlike object or string representing an existing file)
    image to operate on
    argument: ``-%s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
    image to write
    argument: ``-%s``, position: -2
output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
    or 'input')
    datatype to use for output (default uses input type)
    argument: ``-odt %s``, position: -3
args: (a unicode string)
    Additional parameters to the command
    argument: ``-%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

out_file: (a pathlike **object** **or** string representing a file)
 image written after calculations

72.5.6 UnaryMaths

[Link to code](#)

Wraps the executable command `seg_maths`.

Interface for executable `seg_maths` from NiftySeg platform.

Interface to use any unary mathematical operations that can be performed with the `seg_maths` command-line program.

See below for those operations:

`sqrt` - Square root of the image.

`exp` - Exponential root of the image.

`log` - Log of the image.

`recip` - Reciprocal (1/I) of the image.

`abs` - Absolute value of the image.

`bin` - Binarise the image.

`otsu` - Otsu thresholding of the current image.

`lconcomp` - Take the largest connected component

`concomp6` - Label the different connected components with a 6NN kernel

`concomp26` - Label the different connected components with a 26NN kernel

`fill` - Fill holes in binary object (e.g. fill ventricle in brain mask).

`euc` - Euclidean distance transform

`tpmax` - Get the time point with the highest value (binarise 4D probabilities)

`tmean` - Mean value of all time points.

`tmax` - Max value of all time points.

`tmin` - Mean value of all time points.

`splitlab` - Split the integer labels into multiple timepoints

`removenan` - Remove all NaNs and replace them with 0

`isnan` - Binary image equal to 1 if the value is NaN and 0 otherwise

`subsamp2` - Subsample the image by 2 using NN sampling (qform and sform scaled)

`scl` - Reset scale and slope info.

`4to5` - Flip the 4th and 5th dimension.

`range` - Reset the image range to the min max.

[Source code](#) | [Documentation](#)

Examples

```
>>> import copy
>>> from nipy.interfaces import niftyseg
>>> unary = niftyseg.UnaryMaths()
>>> unary.inputs.output_datatype = 'float'
>>> unary.inputs.in_file = 'im1.nii'
>>> # Test sqrt operation
>>> unary_sqrt = copy.deepcopy(unary)
>>> unary_sqrt.inputs.operation = 'sqrt'
>>> unary_sqrt.cmdline
'seg_maths im1.nii -sqrt -odt float im1_sqrt.nii'
>>> unary_sqrt.run() # doctest: +SKIP
>>> # Test sqrt operation
>>> unary_abs = copy.deepcopy(unary)
>>> unary_abs.inputs.operation = 'abs'
>>> unary_abs.cmdline
```

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```
'seg_mathcs iml.nii -abs -odt float iml_abs.nii'
>>> unary_abs.run() # doctest: +SKIP
>>> # Test bin operation
>>> unary_bin = copy.deepcopy(unary)
>>> unary_bin.inputs.operation = 'bin'
>>> unary_bin.cmdline
'seg_mathcs iml.nii -bin -odt float iml_bin.nii'
>>> unary_bin.run() # doctest: +SKIP
>>> # Test otsu operation
>>> unary_otsu = copy.deepcopy(unary)
>>> unary_otsu.inputs.operation = 'otsu'
>>> unary_otsu.cmdline
'seg_mathcs iml.nii -otsu -odt float iml_otsu.nii'
>>> unary_otsu.run() # doctest: +SKIP
>>> # Test isnan operation
>>> unary_isnan = copy.deepcopy(unary)
>>> unary_isnan.inputs.operation = 'isnan'
>>> unary_isnan.cmdline
'seg_mathcs iml.nii -isnan -odt float iml_isnan.nii'
>>> unary_isnan.run() # doctest: +SKIP
```

Inputs:

[Mandatory]

operation: ('sqrt' or 'exp' or 'log' or 'recip' or 'abs' or 'bin' or 'otsu' or 'lconcomp' or 'concomp6' or 'concomp26' or 'fill' or 'euc' or 'tpmax' or 'tmean' or 'tmax' or 'tmin' or 'splitlab' or 'removenan' or 'isnan' or 'subsamp2' or 'scl' or '4to5' or 'range')

operation to perform

argument: ``-s``, position: 4

in_file: (a pathlike object or string representing an existing file)

image to operate on

argument: ``%s``, position: 2

[Optional]

out_file: (a pathlike object or string representing a file)

image to write

argument: ``%s``, position: -2

output_datatype: ('float' or 'char' or 'int' or 'short' or 'double' or 'input')

datatype to use for output (default uses input type)

argument: ``-odt %s``, position: -3

args: (a unicode string)

Additional parameters to the command

argument: ``%s``

environ: (a dictionary with keys which are a bytes or None or a value of class 'str' and with values which are a bytes or None or a value of class 'str', nipyte default value: {})

Environment variables

Outputs:

out_file: (a pathlike **object** or string representing a file)

image written after calculations

72.6 interfaces.niftyseg.patchmatch

72.6.1 PatchMatch

[Link to code](#)

Wraps the executable command `seg_PatchMatch`.

Interface for executable `seg_PatchMatch` from NiftySeg platform.

The database file is a text file and in each line we have a template file, a mask with the search region to consider and a file with the label to propagate.

Input image, input mask, template images from database and masks from database must have the same 4D resolution (same number of XxYxZ voxels, modalities and/or time-points). Label files from database must have the same 3D resolution (XxYxZ voxels) than input image but can have different number of volumes than the input image allowing to propagate multiple labels in the same execution.

[Source code](#) | [Documentation](#)

Examples

```
>>> from nipy.interfaces import niftyseg
>>> node = niftyseg.PatchMatch()
>>> node.inputs.in_file = 'im1.nii'
>>> node.inputs.mask_file = 'im2.nii'
>>> node.inputs.database_file = 'db.xml'
>>> node.cmdline
'seg_PatchMatch -i im1.nii -m im2.nii -db db.xml -o im1_pm.nii.gz'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    Input image to segment
    argument: ``-i %s``, position: 1
mask_file: (a pathlike object or string representing an existing
    file)
    Input mask for the area where applies PatchMatch
    argument: ``-m %s``, position: 2
database_file: (a pathlike object or string representing an existing
    file)
    Database with the segmentations
    argument: ``-db %s``, position: 3

[Optional]
out_file: (a pathlike object or string representing a file)
    The output filename of the patchmatch results
    argument: ``-o %s``, position: 4
patch_size: (an integer (int or long))
    Patch size, #voxels
    argument: ``-size %i``
cs_size: (an integer (int or long))
    Constrained search area size, number of times bigger than the
    patchsize
    argument: ``-cs %i``
match_num: (an integer (int or long))
    Number of better matching
    argument: ``-match %i``
pm_num: (an integer (int or long))
    Number of patchmatch executions
    argument: ``-pm %i``
```

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```

it_num: (an integer (int or long))
        Number of iterations for the patchmatch algorithm
        argument: ``-it %i``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
          Output segmentation

```

72.7 interfaces.niftyseg.stats

72.7.1 BinaryStats

[Link to code](#)Wraps the executable command `seg_stats`.Interface for executable `seg_stats` from NiftySeg platform.Interface to use any binary statistical operations that can be performed with the `seg_stats` command-line program.

See below for those operations:

`p` - <float> - The <float>th percentile of all voxels intensity (float=[0,100])`sa` - <ax> - Average of all voxels`ss` - <ax> - Standard deviation of all voxels`svp` - <ax> - Volume of all probabilistic voxels (sum(<in>) * <volume per voxel>)`al` - <in2> - Average value in <in> for each label in <in2>`d` - <in2> - Calculate the Dice score between all classes in <in> and <in2>`ncc` - <in2> - Normalized cross correlation between <in> and <in2>`nmi` - <in2> - Normalized Mutual Information between <in> and <in2>`Vl` - <csv> - Volume of each integer label <in>. Save to <csv>file.`Nl` - <csv> - Count of each label <in>. Save to <csv> file.[Source code](#) | [Documentation](#)

Examples

```

>>> import copy
>>> from nipy.interfaces import niftyseg
>>> binary = niftyseg.BinaryStats()
>>> binary.inputs.in_file = 'im1.nii'
>>> # Test sa operation
>>> binary_sa = copy.deepcopy(binary)
>>> binary_sa.inputs.operation = 'sa'
>>> binary_sa.inputs.operand_value = 2.0
>>> binary_sa.cmdline
'seg_stats im1.nii -sa 2.00000000'
>>> binary_sa.run() # doctest: +SKIP
>>> # Test ncc operation
>>> binary_ncc = copy.deepcopy(binary)

```

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```

>>> binary_ncc.inputs.operation = 'ncc'
>>> binary_ncc.inputs.operand_file = 'im2.nii'
>>> binary_ncc.cmdline
'seg_stats im1.nii -ncc im2.nii'
>>> binary_ncc.run() # doctest: +SKIP
>>> # Test Nl operation
>>> binary_nl = copy.deepcopy(binary)
>>> binary_nl.inputs.operation = 'Nl'
>>> binary_nl.inputs.operand_file = 'output.csv'
>>> binary_nl.cmdline
'seg_stats im1.nii -Nl output.csv'
>>> binary_nl.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
operation: ('p' or 'sa' or 'ss' or 'svp' or 'al' or 'd' or 'ncc' or
            'nmi' or 'Vl' or 'Nl')
            operation to perform
            argument: ``-%s``, position: 4
operand_file: (a pathlike object or string representing an existing
               file)
               second image to perform operation with
               argument: ``%s``, position: 5
               mutually_exclusive: operand_value
operand_value: (a float)
               value to perform operation with
               argument: ``%.8f``, position: 5
               mutually_exclusive: operand_file
in_file: (a pathlike object or string representing an existing file)
          image to operate on
          argument: ``%s``, position: 2

[Optional]
mask_file: (a pathlike object or string representing an existing
            file)
            statistics within the masked area
            argument: ``-m %s``, position: -2
larger_voxel: (a float)
               Only estimate statistics if voxel is larger than <float>
               argument: ``-t %f``, position: -3
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

output: (an array)
        Output array from seg_stats

```

72.7.2 StatsCommand[Link to code](#)

Wraps the executable command seg_stats.

Base Command Interface for `seg_stats` interfaces.

The executable `seg_stats` enables the estimation of image statistics on continuous voxel intensities (average, standard deviation, min/max, robust range, percentiles, sum, probabilistic volume, entropy, etc) either over the full image or on a per slice basis (slice axis can be specified), statistics over voxel coordinates (location of max, min and centre of mass, bounding box, etc) and statistics over categorical images (e.g. per region volume, count, average, Dice scores, etc). These statistics are robust to the presence of NaNs, and can be constrained by a mask and/or thresholded at a certain level.

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        image to operate on
        argument: ``%s``, position: 2

[Optional]
mask_file: (a pathlike object or string representing an existing
           file)
           statistics within the masked area
           argument: ``-m %s``, position: -2
larger_voxel: (a float)
              Only estimate statistics if voxel is larger than <float>
              argument: ``-t %f``, position: -3
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipype default value: {})
         Environment variables
```

Outputs:

```
output: (an array)
        Output array from seg_stats
```

72.7.3 UnaryStats

[Link to code](#)

Wraps the executable command `seg_stats`.

Interface for executable `seg_stats` from NiftySeg platform.

Interface to use any unary statistical operations that can be performed with the `seg_stats` command-line program.

See below for those operations:

r - The range <min max> of all voxels.

R - The robust range (assuming 2% outliers on both sides) of all voxels

a - Average of all voxels

s - Standard deviation of all voxels

v - Volume of all voxels above 0 (<# voxels> * <volume per voxel>)

vl - Volume of each integer label (<# voxels per label> * <volume per voxel>)

vp - Volume of all probabilistic voxels (sum(<in>) * <volume per voxel>)

n - Count of all voxels above 0 (<# voxels>)

np - Sum of all fuzzy voxels (sum(<in>))

e - Entropy of all voxels

ne - Normalized entropy of all voxels

x - Location (i j k x y z) of the smallest value in the image

X - Location (i j k x y z) of the largest value in the image

c - Location (i j k x y z) of the centre of mass of the object

B - Bounding box of all nonzero voxels [xmin xsize ymin ysize zmin zsize]

xvox - Output the number of voxels in the x direction. Replace x with y/z for other directions.

xdim - Output the voxel dimension in the x direction. Replace x with y/z for other directions.

[Source code](#) | [Documentation](#)

Examples

```
>>> import copy
>>> from nipy.interfaces import niftyseg
>>> unary = niftyseg.UnaryStats()
>>> unary.inputs.in_file = 'im1.nii'
>>> # Test v operation
>>> unary_v = copy.deepcopy(unary)
>>> unary_v.inputs.operation = 'v'
>>> unary_v.cmdline
'seg_stats im1.nii -v'
>>> unary_v.run() # doctest: +SKIP
>>> # Test vl operation
>>> unary_vl = copy.deepcopy(unary)
>>> unary_vl.inputs.operation = 'vl'
>>> unary_vl.cmdline
'seg_stats im1.nii -vl'
>>> unary_vl.run() # doctest: +SKIP
>>> # Test x operation
>>> unary_x = copy.deepcopy(unary)
>>> unary_x.inputs.operation = 'x'
>>> unary_x.cmdline
'seg_stats im1.nii -x'
>>> unary_x.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
operation: ('r' or 'R' or 'a' or 's' or 'v' or 'vl' or 'vp' or 'n' or
           'np' or 'e' or 'ne' or 'x' or 'X' or 'c' or 'B' or 'xvox' or
           'xdim')
           operation to perform
           argument: ``-s``, position: 4
in_file: (a pathlike object or string representing an existing file)
          image to operate on
          argument: ``%s``, position: 2

[Optional]
mask_file: (a pathlike object or string representing an existing
            file)
            statistics within the masked area
            argument: ``-m %s``, position: -2
larger_voxel: (a float)
               Only estimate statistics if voxel is larger than <float>
               argument: ``-t %f``, position: -3
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
output: (an array)
        Output array from seg_stats
```

73.1 interfaces.nipy.base

73.1.1 NipyBaseInterface

[Link to code](#)

Inputs:

None

Outputs:

None

73.2 interfaces.nipy.model

73.2.1 EstimateContrast

[Link to code](#)

Estimate contrast of a fitted model.

Inputs:

```
[Mandatory]
contrasts: (a list of items which are a tuple of the form: (a unicode
            string, 'T', a list of items which are a unicode string, a list of
            items which are a float) or a tuple of the form: (a unicode
            string, 'T', a list of items which are a unicode string, a list of
            items which are a float, a list of items which are a float) or a
            tuple of the form: (a unicode string, 'F', a list of items which
            are a tuple of the form: (a unicode string, 'T', a list of items
            which are a unicode string, a list of items which are a float) or
            a tuple of the form: (a unicode string, 'T', a list of items which
            are a unicode string, a list of items which are a float, a list of
            items which are a float)))
List of contrasts with each contrast being a list of the form:
[('name', 'stat', [condition list], [weight list], [session
```

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```

list]]). if
    session list is None or not provided, all sessions are used. For F
    contrasts, the condition list should contain previously defined
    T-contrasts.
beta: (a pathlike object or string representing an existing file)
    beta coefficients of the fitted model
nwbeta: (any value)
s2: (a pathlike object or string representing an existing file)
    squared variance of the residuals
dof: (any value)
    degrees of freedom
constants: (any value)
axis: (any value)
reg_names: (a list of items which are any value)

[Optional]
mask: (a pathlike object or string representing an existing file)

```

Outputs:

```

stat_maps: (a list of items which are a pathlike object or string
    representing an existing file)
z_maps: (a list of items which are a pathlike object or string
    representing an existing file)
p_maps: (a list of items which are a pathlike object or string
    representing an existing file)

```

73.2.2 FitGLM[Link to code](#)

Fit GLM model based on the specified design. Supports only single or concatenated runs.

Inputs:

```

[Mandatory]
session_info: (a list of from 1 to 1 items which are any value)
    Session specific information generated by ``modelgen.SpecifyModel``,
    FitGLM does not support multiple runs unless they are concatenated
    (see SpecifyModel options)
TR: (a float)

[Optional]
hrf_model: ('Canonical' or 'Canonical With Derivative' or 'FIR',
    nipype default value: Canonical)
    that specifies the hemodynamic response function it can be
    'Canonical', 'Canonical With Derivative' or 'FIR'
drift_model: ('Cosine' or 'Polynomial' or 'Blank', nipype default
    value: Cosine)
    string that specifies the desired drift model, to be chosen among
    'Polynomial', 'Cosine', 'Blank'
model: ('ar1' or 'spherical', nipype default value: ar1)
    autoregressive mode is available only for the kalman method
method: ('kalman' or 'ols', nipype default value: kalman)
    method to fit the model, ols or kalman; kalman is more time consuming
    but it supports autoregressive model
mask: (a pathlike object or string representing an existing file)
    restrict the fitting only to the region defined by this mask

```

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```

normalize_design_matrix: (a boolean, nipy default value: False)
    normalize (zscore) the regressors before fitting
save_residuals: (a boolean, nipy default value: False)
plot_design_matrix: (a boolean, nipy default value: False)

```

Outputs:

```

beta: (a pathlike object or string representing an existing file)
nvbeta: (any value)
s2: (a pathlike object or string representing an existing file)
dof: (any value)
constants: (any value)
axis: (any value)
reg_names: (a list of items which are any value)
residuals: (a pathlike object or string representing a file)
a: (a pathlike object or string representing an existing file)

```

73.3 interfaces.nipy.preprocess

73.3.1 ComputeMask

[Link to code](#)**Inputs:**

```

[Mandatory]
mean_volume: (a pathlike object or string representing an existing
    file)
    mean EPI image, used to compute the threshold for the mask

[Optional]
reference_volume: (a pathlike object or string representing an
    existing file)
    reference volume used to compute the mask. If none is give, the mean
    volume is used.
m: (a float)
    lower fraction of the histogram to be discarded
M: (a float)
    upper fraction of the histogram to be discarded
cc: (a boolean)
    Keep only the largest connected component

```

Outputs:

```

brain_mask: (a pathlike object or string representing an existing
    file)

```

73.3.2 SpaceTimeRealigner

[Link to code](#)

Simultaneous motion and slice timing correction algorithm

If slice_times is not specified, this algorithm performs spatial motion correction

This interface wraps nipy's SpaceTimeRealign algorithm [Roche2011] or simply the SpatialRealign algorithm when timing info is not provided.

Examples

```
>>> from nipy.interfaces.nipy import SpaceTimeRealigner
>>> #Run spatial realignment only
>>> realigner = SpaceTimeRealigner()
>>> realigner.inputs.in_file = ['functional.nii']
>>> res = realigner.run() # doctest: +SKIP
```

```
>>> realigner = SpaceTimeRealigner()
>>> realigner.inputs.in_file = ['functional.nii']
>>> realigner.inputs.tr = 2
>>> realigner.inputs.slice_times = list(range(0, 3, 67))
>>> realigner.inputs.slice_info = 2
>>> res = realigner.run() # doctest: +SKIP
```

References

Inputs:

```
[Mandatory]
in_file: (a list of items which are a pathlike object or string
         representing an existing file)
         File to realign

[Optional]
tr: (a float)
    TR in seconds
    requires: slice_times
slice_times: (a list of items which are a float or 'asc_alt_2' or
             'asc_alt_2_1' or 'asc_alt_half' or 'asc_alt_siemens' or
             'ascending' or 'desc_alt_2' or 'desc_alt_half' or 'descending')
             Actual slice acquisition times.
slice_info: (an integer (int or long) or a list of items which are
            any value)
            Single integer or length 2 sequence If int, the axis in `images`
            that is the slice axis. In a 4D image, this will often be axis = 2.
            If a 2 sequence, then elements are `(slice_axis,
            slice_direction)`, where `slice_axis` is the slice axis in the
            image as above, and `slice_direction` is 1 if the slices were
            acquired slice 0 first, slice -1 last, or -1 if acquired slice -1
            first, slice 0 last. If `slice_info` is an int, assume
            `slice_direction` == 1.
            requires: slice_times
```

Outputs:

```
out_file: (a list of items which are a pathlike object or string
          representing an existing file)
          Realigned files
par_file: (a list of items which are a pathlike object or string
          representing an existing file)
          Motion parameter files. Angles are not euler angles
```

73.3.3 Trim

[Link to code](#)

Simple interface to trim a few volumes from a 4d fmri nifti file

Examples

```
>>> from nipy.interfaces.nipy.preprocess import Trim
>>> trim = Trim()
>>> trim.inputs.in_file = 'functional.nii'
>>> trim.inputs.begin_index = 3 # remove 3 first volumes
>>> res = trim.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        EPI image to trim

[Optional]
begin_index: (an integer (int or long), nipy default value: 0)
            first volume
end_index: (an integer (int or long), nipy default value: 0)
          last volume indexed as in python (and 0 for last)
out_file: (a pathlike object or string representing a file)
         output filename
suffix: (a unicode string, nipy default value: _trim)
       suffix for out_file to use if no out_file provided
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

73.4 interfaces.nipy.utils

73.4.1 Similarity

[Link to code](#)

Calculates similarity between two 3D volumes. Both volumes have to be in the same coordinate system, same space within that coordinate system and with the same voxel dimensions.

Deprecated since version 0.10.0: Use `nipy.algorithms.metrics.Similarity` instead.

Example

```
>>> from nipy.interfaces.nipy.utils import Similarity
>>> similarity = Similarity()
>>> similarity.inputs.volume1 = 'rcls1.nii'
>>> similarity.inputs.volume2 = 'rcls2.nii'
>>> similarity.inputs.mask1 = 'mask.nii'
>>> similarity.inputs.mask2 = 'mask.nii'
>>> similarity.inputs.metric = 'cr'
>>> res = similarity.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
volume1: (a pathlike object or string representing an existing file)
        3D volume
volume2: (a pathlike object or string representing an existing file)
        3D volume
```

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```
[Optional]
mask1: (a pathlike object or string representing an existing file)
      3D volume
mask2: (a pathlike object or string representing an existing file)
      3D volume
metric: ('cc' or 'cr' or 'crl1' or 'mi' or 'nmi' or 'slr' or a
        callable value, nipy default value: None)
        str or callable
        Cost-function for assessing image similarity. If a string,
        one of 'cc': correlation coefficient, 'cr': correlation
        ratio, 'crl1': L1-norm based correlation ratio, 'mi': mutual
        information, 'nmi': normalized mutual information, 'slr':
        supervised log-likelihood ratio. If a callable, it should
        take a two-dimensional array representing the image joint
        histogram as an input and return a float.
```

Outputs:

```
similarity: (a float)
            Similarity between volume 1 and 2
```

74.1 interfaces.nitime.analysis

74.1.1 CoherenceAnalyzer

[Link to code](#)

Inputs:

```
[Optional]
in_file: (a pathlike object or string representing an existing file)
         csv file with ROIs on the columns and time-points on the rows. ROI
         names at the top row
         requires: TR
TR: (a float)
    The TR used to collect the data in your csv file <in_file>
in_TS: (any value)
    a nitime TimeSeries object
NFFT: (a long integer >= 32, nipype default value: 64)
    This is the size of the window used for the spectral estimation. Use
    values between 32 and the number of samples in your time-
    series. (Defaults to 64.)
n_overlap: (a long integer >= 0, nipype default value: 0)
    The number of samples which overlap between subsequent
    windows. (Defaults to 0)
frequency_range: (a list of from 2 to 2 items which are any value,
                  nipype default value: [0.02, 0.15])
    The range of frequencies over which the analysis will
    average. [low, high] (Default [0.02, 0.15])
output_csv_file: (a pathlike object or string representing a file)
    File to write outputs (coherence, time-delay) with file-names:
    file_name_{coherence, timedelay}
output_figure_file: (a pathlike object or string representing a file)
    File to write output figures (coherence, time-delay) with file-names:
    file_name_{coherence, timedelay}. Possible formats:
    .png, .svg, .pdf, .jpg, ...
figure_type: ('matrix' or 'network', nipype default value: matrix)
    The type of plot to generate, where 'matrix' denotes a matrix image
    and 'network' denotes a graph representation. Default: 'matrix'
```

Outputs:

```
coherence_array: (an array)
    The pairwise coherence valuesbetween the ROIs
timedelay_array: (an array)
    The pairwise time delays between theROIs (in seconds)
coherence_csv: (a pathlike object or string representing a file)
    A csv file containing the pairwise coherence values
timedelay_csv: (a pathlike object or string representing a file)
    A csv file containing the pairwise time delay values
coherence_fig: (a pathlike object or string representing a file)
    Figure representing coherence values
timedelay_fig: (a pathlike object or string representing a file)
    Figure representing coherence values
```

74.2 interfaces.nitime.base

74.2.1 NitimeBaseInterface

[Link to code](#)

Inputs:

```
None
```

Outputs:

```
None
```

75.1 interfaces.semtools.brains.classify

75.1.1 BRAINSPosteriorToContinuousClass

[Link to code](#)

Wraps the executable command “ BRAINSPosteriorToContinuousClass “.

title: Tissue Classification

category: BRAINS.Classify

description: This program will generate an 8-bit continuous tissue classified image based on BRAINSABC posterior images.

version: 3.0

documentation-url: <http://www.nitrc.org/plugins/mwiki/index.php/brains:BRAINSClassify>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Vincent A. Magnotta

acknowledgements: Funding for this work was provided by NIH/NINDS award NS050568

Inputs:

```
[Optional]
inputWhiteVolume: (a pathlike object or string representing an
                    existing file)
                    White Matter Posterior Volume
                    argument: ``--inputWhiteVolume %s``
inputBasalGmVolume: (a pathlike object or string representing an
                     existing file)
                     Basal Grey Matter Posterior Volume
                     argument: ``--inputBasalGmVolume %s``
inputSurfaceGmVolume: (a pathlike object or string representing an
                       existing file)
                       Surface Grey Matter Posterior Volume
                       argument: ``--inputSurfaceGmVolume %s``
inputCsfVolume: (a pathlike object or string representing an existing
                 file)
                 CSF Posterior Volume
                 argument: ``--inputCsfVolume %s``
inputVbVolume: (a pathlike object or string representing an existing
```

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```

        file)
        Venous Blood Posterior Volume
        argument: ``--inputVbVolume %s``
inputCrblGmVolume: (a pathlike object or string representing an
                    existing file)
        Cerebellum Grey Matter Posterior Volume
        argument: ``--inputCrblGmVolume %s``
inputCrblWmVolume: (a pathlike object or string representing an
                    existing file)
        Cerebellum White Matter Posterior Volume
        argument: ``--inputCrblWmVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
        Output Continuous Tissue Classified Image
        argument: ``--outputVolume %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
              file)
              Output Continuous Tissue Classified Image

```

75.2 interfaces.semtools.brains.segmentation

75.2.1 BRAINSTalairach

[Link to code](#)

Wraps the executable command “ BRAINSTalairach “.

title: BRAINS Talairach

category: BRAINS.Segmentation

description: This program creates a VTK structured grid defining the Talairach coordinate system based on four points: AC, PC, IRP, and SLA. The resulting structured grid can be written as either a classic VTK file or the new VTK XML file format. Two representations of the resulting grid can be written. The first is a bounding box representation that also contains the location of the AC and PC points. The second representation is the full Talairach grid representation that includes the additional rows of boxes added to the inferior allowing full coverage of the cerebellum.

version: 0.1

documentation-url: <http://www.nitrc.org/plugins/mwiki/index.php/brains:BRAINSTalairach>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Steven Dunn and Vincent Magnotta

acknowledgements: Funding for this work was provided by NIH/NINDS award NS050568

Inputs:

```

[Optional]
AC: (a list of items which are a float)
    Location of AC Point
    argument: ``--AC %s``

```

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```

ACisIndex: (a boolean)
    AC Point is Index
    argument: ``--ACisIndex ``
PC: (a list of items which are a float)
    Location of PC Point
    argument: ``--PC %s``
PCisIndex: (a boolean)
    PC Point is Index
    argument: ``--PCisIndex ``
SLA: (a list of items which are a float)
    Location of SLA Point
    argument: ``--SLA %s``
SLAisIndex: (a boolean)
    SLA Point is Index
    argument: ``--SLAisIndex ``
IRP: (a list of items which are a float)
    Location of IRP Point
    argument: ``--IRP %s``
IRPisIndex: (a boolean)
    IRP Point is Index
    argument: ``--IRPisIndex ``
inputVolume: (a pathlike object or string representing an existing
    file)
    Input image used to define physical space of images
    argument: ``--inputVolume %s``
outputBox: (a boolean or a pathlike object or string representing a
    file)
    Name of the resulting Talairach Bounding Box file
    argument: ``--outputBox %s``
outputGrid: (a boolean or a pathlike object or string representing a
    file)
    Name of the resulting Talairach Grid file
    argument: ``--outputGrid %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputBox: (a pathlike object or string representing an existing
    file)
    Name of the resulting Talairach Bounding Box file
outputGrid: (a pathlike object or string representing an existing
    file)
    Name of the resulting Talairach Grid file

```

75.2.2 BRAINSTalairachMask[Link to code](#)

Wraps the executable command “ BRAINSTalairachMask “.

title: Talairach Mask

category: BRAINS.Segmentation

description: This program creates a binary image representing the specified Talairach region. The input is an

example image to define the physical space for the resulting image, the Talairach grid representation in VTK format, and the file containing the Talairach box definitions to be generated. These can be combined in BRAINS to create a label map using the procedure `Brains::WorkupUtils::CreateLabelMapFromBinaryImages`.

version: 0.1

documentation-url: <http://www.nitrc.org/plugins/mwiki/index.php/brains:BRAINSTalairachMask>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Steven Dunn and Vincent Magnotta

acknowledgements: Funding for this work was provided by NIH/NINDS award NS050568

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Input image used to define physical space of resulting mask
              argument: ``--inputVolume %s``
talairachParameters: (a pathlike object or string representing an
                      existing file)
                      Name of the Talairach parameter file.
                      argument: ``--talairachParameters %s``
talairachBox: (a pathlike object or string representing an existing
              file)
              Name of the Talairach box file.
              argument: ``--talairachBox %s``
hemisphereMode: ('left' or 'right' or 'both')
                Mode for box creation: left, right, both
                argument: ``--hemisphereMode %s``
expand: (a boolean)
        Expand exterior box to include surface CSF
        argument: ``--expand ``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              Output filename for the resulting binary image
              argument: ``--outputVolume %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
              file)
              Output filename for the resulting binary image
```

75.2.3 SimilarityIndex

[Link to code](#)

Wraps the executable command “ SimilarityIndex “.

title: BRAINSCut:SimilarityIndexComputation

category: BRAINS.Segmentation

description: Automatic analysis of BRAINSCut Output

version: 1.0

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Eunyoung Regin Kim

Inputs:

```
[Optional]
outputCSVFilename: (a pathlike object or string representing an
                    existing file)
                    output CSV Filename
                    argument: ``--outputCSVFilename %s``
ANNContinuousVolume: (a pathlike object or string representing an
                      existing file)
                      ANN Continuous volume to be compared to the manual volume
                      argument: ``--ANNContinuousVolume %s``
inputManualVolume: (a pathlike object or string representing an
                   existing file)
                   input manual(reference) volume
                   argument: ``--inputManualVolume %s``
thresholdInterval: (a float)
                   Threshold interval to compute similarity index between zero and one
                   argument: ``--thresholdInterval %f``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipype default value: {})
         Environment variables
```

Outputs:

```
None
```

75.3 interfaces.semtools.brains.utilities

75.3.1 GenerateEdgeMapImage

[Link to code](#)

Wraps the executable command “GenerateEdgeMapImage”.

title: GenerateEdgeMapImage

category: BRAINS.Utilities

description: Automatic edgemap generation for edge-guided super-resolution reconstruction

version: 1.0

contributor: Ali Ghayoor

Inputs:

```
[Optional]
inputMRVolumes: (a list of items which are a pathlike object or
                 string representing an existing file)
                 List of input structural MR volumes to create the maximum edgemap
                 argument: ``--inputMRVolumes %s...``
inputMask: (a pathlike object or string representing an existing
            file)
            Input mask file name. If set, image histogram percentiles will be
            calculated within the mask
            argument: ``--inputMask %s``
minimumOutputRange: (an integer (int or long))
                    Map lower quantile and below to minimum output range. It should be a
                    small number greater than zero. Default is 1
                    argument: ``--minimumOutputRange %d``
```

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```

maximumOutputRange: (an integer (int or long))
    Map upper quantile and above to maximum output range. Default is 255
    that is the maximum range of unsigned char
    argument: ``--maximumOutputRange %d``
lowerPercentileMatching: (a float)
    Map lower quantile and below to minOutputRange. It should be a value
    between zero and one
    argument: ``--lowerPercentileMatching %f``
upperPercentileMatching: (a float)
    Map upper quantile and above to maxOutputRange. It should be a value
    between zero and one
    argument: ``--upperPercentileMatching %f``
outputEdgeMap: (a boolean or a pathlike object or string representing
    a file)
    output edgemap file name
    argument: ``--outputEdgeMap %s``
outputMaximumGradientImage: (a boolean or a pathlike object or string
    representing a file)
    output gradient image file name
    argument: ``--outputMaximumGradientImage %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputEdgeMap: (a pathlike object or string representing an existing
    file)
    (required) output file name
outputMaximumGradientImage: (a pathlike object or string representing
    an existing file)
    output gradient image file name

```

75.3.2 GeneratePurePlugMask[Link to code](#)

Wraps the executable command “GeneratePurePlugMask”.

title: GeneratePurePlugMask

category: BRAINS.Utilities

description: This program gets several modality image files and returns a binary mask that defines the pure plugs

version: 1.0

contributor: Ali Ghayoor

Inputs:

```

[Optional]
inputImageModalities: (a list of items which are a pathlike object or
    string representing an existing file)
    List of input image file names to create pure plugs mask
    argument: ``--inputImageModalities %s...``

```

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```

threshold: (a float)
    threshold value to define class membership
    argument: ``--threshold %f``
numberOfSubSamples: (a list of items which are an integer (int or
    long))
    Number of continuous index samples taken at each direction of lattice
    space for each plug volume
    argument: ``--numberOfSubSamples %s``
outputMaskFile: (a boolean or a pathlike object or string
    representing a file)
    Output binary mask file name
    argument: ``--outputMaskFile %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputMaskFile: (a pathlike object or string representing an existing
    file)
    (required) Output binary mask file name

```

75.3.3 HistogramMatchingFilter

[Link to code](#)

Wraps the executable command “HistogramMatchingFilter”.

title: Write Out Image Intensities

category: BRAINS.Utilities

description: For Analysis

version: 0.1

contributor: University of Iowa Department of Psychiatry, <http://www.psychiatry.uiowa.edu>**Inputs:**

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    The Input image to be computed for statistics
    argument: ``--inputVolume %s``
referenceVolume: (a pathlike object or string representing an
    existing file)
    The Input image to be computed for statistics
    argument: ``--referenceVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output Image File Name
    argument: ``--outputVolume %s``
referenceBinaryVolume: (a pathlike object or string representing an
    existing file)
    referenceBinaryVolume
    argument: ``--referenceBinaryVolume %s``
inputBinaryVolume: (a pathlike object or string representing an
    existing file)

```

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```

    inputBinaryVolume
    argument: ``--inputBinaryVolume %s``
numberOfMatchPoints: (an integer (int or long))
    number of histogram matching points
    argument: ``--numberOfMatchPoints %d``
numberOfHistogramBins: (an integer (int or long))
    number of histogram bin
    argument: ``--numberOfHistogramBins %d``
writeHistogram: (a unicode string)
    decide if histogram data would be written with prefixe of the file
    name
    argument: ``--writeHistogram %s``
histogramAlgorithm: ('OtsuHistogramMatching')
    histogram algrithm selection
    argument: ``--histogramAlgorithm %s``
verbose: (a boolean)
    verbose mode running for debbuging
    argument: ``--verbose ``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Output Image File Name

```

75.4 interfaces.semtools.converters

75.4.1 DWICompare

[Link to code](#)

Wraps the executable command “ DWICompare “.

title: Nrrd DWI comparison

category: Converters

description: Compares two nrrd format DWI images and verifies that gradient magnitudes, gradient directions, measurement frame, and max B0 value are identicle. Used for testing DWIConvert.

version: 0.1.0.\$Revision: 916 \$(alpha)

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/DWIConvert>license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Mark Scully (UIowa)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149. Additional support for DTI data produced on Philips scanners was contributed by Vincent Magnotta and Hans Johnson at the University of Iowa.

Inputs:

```

[Optional]
inputVolume1: (a pathlike object or string representing an existing

```

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```

    file)
    First input volume (.nhdr or .nrrd)
    argument: ``--inputVolume1 %s``
inputVolume2: (a pathlike object or string representing an existing
    file)
    Second input volume (.nhdr or .nrrd)
    argument: ``--inputVolume2 %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

None

75.4.2 DWISimpleCompare

[Link to code](#)

Wraps the executable command “ DWISimpleCompare “.

title: Nrrd DWI comparison

category: Converters

description: Compares two nrrd format DWI images and verifies that gradient magnitudes, gradient directions, measurement frame, and max B0 value are identical. Used for testing DWIConvert.

version: 0.1.0.\$Revision: 916 \$(alpha)

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/DWIConvert>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Mark Scully (UIowa)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149. Additional support for DTI data produced on Philips scanners was contributed by Vincent Magnotta and Hans Johnson at the University of Iowa.

Inputs:

```

[Optional]
inputVolume1: (a pathlike object or string representing an existing
    file)
    First input volume (.nhdr or .nrrd)
    argument: ``--inputVolume1 %s``
inputVolume2: (a pathlike object or string representing an existing
    file)
    Second input volume (.nhdr or .nrrd)
    argument: ``--inputVolume2 %s``
checkDWIData: (a boolean)
    check for existence of DWI data, and if present, compare it
    argument: ``--checkDWIData ``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

None

75.5 interfaces.semtools.diffusion.diffusion

75.5.1 DWIConvert

[Link to code](#)

Wraps the executable command “ DWIConvert “.

title: DWIConverter

category: Diffusion.Diffusion Data Conversion

description: Converts diffusion weighted MR images in dicom series into Nrrd format for analysis in Slicer. This program has been tested on only a limited subset of DTI dicom formats available from Siemens, GE, and Phillips scanners. Work in progress to support dicom multi-frame data. The program parses dicom header to extract necessary information about measurement frame, diffusion weighting directions, b-values, etc, and write out a nrrd image. For non-diffusion weighted dicom images, it loads in an entire dicom series and writes out a single dicom volume in a .nhdr/.raw pair.

version: Version 1.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/DWIConverter>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Vince Magnotta (UIowa), Hans Johnson (UIowa), Joy Matsui (UIowa), Kent Williams (UIowa), Mark Scully (UIowa), Xiaodong Tao (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149. Additional support for DTI data produced on Philips scanners was contributed by Vincent Magnotta and Hans Johnson at the University of Iowa.

Inputs:

```
[Optional]
conversionMode: ('DicomToNrrd' or 'DicomToFSL' or 'NrrdToFSL' or
                 'FSLToNrrd')
    Determine which conversion to perform. DicomToNrrd (default):
    Convert DICOM series to NRRD DicomToFSL: Convert DICOM series to
    NIfTI File + gradient/bvalue text files NrrdToFSL: Convert DWI NRRD
    file to NIfTI File + gradient/bvalue text files FSLToNrrd: Convert
    NIfTI File + gradient/bvalue text files to NRRD file.
    argument: ``--conversionMode %s``
inputVolume: (a pathlike object or string representing an existing
              file)
    Input DWI volume -- not used for DicomToNrrd mode.
    argument: ``--inputVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
               a file)
    Output filename (.nhdr or .nrrd)
    argument: ``--outputVolume %s``
inputDicomDirectory: (a pathlike object or string representing an
                      existing directory)
    Directory holding Dicom series
    argument: ``--inputDicomDirectory %s``
fslNIFTIFile: (a pathlike object or string representing an existing
               file)
    4D NIfTI file containing gradient volumes
    argument: ``--fslNIFTIFile %s``
inputBValues: (a pathlike object or string representing an existing
```

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```

    file)
    The B Values are stored in FSL .bval text file format
    argument: ``--inputBValues %s``
inputBVectors: (a pathlike object or string representing an existing
    file)
    The Gradient Vectors are stored in FSL .bvec text file format
    argument: ``--inputBVectors %s``
outputBValues: (a boolean or a pathlike object or string representing
    a file)
    The B Values are stored in FSL .bval text file format (defaults to
    <outputVolume>.bval)
    argument: ``--outputBValues %s``
outputBVectors: (a boolean or a pathlike object or string
    representing a file)
    The Gradient Vectors are stored in FSL .bvec text file format
    (defaults to <outputVolume>.bvec)
    argument: ``--outputBVectors %s``
fMRI: (a boolean)
    Output a NRRD file, but without gradients
    argument: ``--fMRI ``
writeProtocolGradientsFile: (a boolean)
    Write the protocol gradients to a file suffixed by '.txt' as they
    were specified in the procol by multiplying each diffusion gradient
    direction by the measurement frame. This file is for debugging
    purposes only, the format is not fixed, and will likely change as
    debugging of new dicom formats is necessary.
    argument: ``--writeProtocolGradientsFile ``
useIdentityMeaseurementFrame: (a boolean)
    Adjust all the gradients so that the measurement frame is an
    identity matrix.
    argument: ``--useIdentityMeaseurementFrame ``
useBMatrixGradientDirections: (a boolean)
    Fill the nhdr header with the gradient directions and bvalues
    computed out of the BMatrix. Only changes behavior for Siemens data.
    In some cases the standard public gradients are not properly
    computed. The gradients can emperically computed from the private
    BMatrix fields. In some cases the private BMatrix is consistent with
    the public grandients, but not in all cases, when it exists BMatrix
    is usually most robust.
    argument: ``--useBMatrixGradientDirections ``
outputDirectory: (a boolean or a pathlike object or string
    representing a directory)
    Directory holding the output NRRD file
    argument: ``--outputDirectory %s``
gradientVectorFile: (a boolean or a pathlike object or string
    representing a file)
    Text file giving gradient vectors
    argument: ``--gradientVectorFile %s``
smallGradientThreshold: (a float)
    If a gradient magnitude is greater than 0 and less than
    smallGradientThreshold, then DWIConvert will display an error
    message and quit, unless the useBMatrixGradientDirections option is
    set.
    argument: ``--smallGradientThreshold %f``
allowLossyConversion: (a boolean)
    The only supported output type is 'short'. Conversion from images of
    a different type may cause data loss due to rounding or truncation.

```

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```

    Use with caution!
    argument: ``--allowLossyConversion``
transposeInputBVectors: (a boolean)
    FSL input BVectors are expected to be encoded in the input file as
    one vector per line. If it is not the case, use this option to
    transpose the file as it is read.
    argument: ``--transposeInputBVectors``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Output filename (.nhdr or .nrrd)
outputBValues: (a pathlike object or string representing an existing
    file)
    The B Values are stored in FSL .bval text file format (defaults to
    <outputVolume>.bval)
outputBVectors: (a pathlike object or string representing an existing
    file)
    The Gradient Vectors are stored in FSL .bvec text file format
    (defaults to <outputVolume>.bvec)
outputDirectory: (a pathlike object or string representing an
    existing directory)
    Directory holding the output NRRD file
gradientVectorFile: (a pathlike object or string representing an
    existing file)
    Text file giving gradient vectors

```

75.5.2 dtiaverage**Link to code**

Wraps the executable command “ dtiaverage “.

title: DTIAverage (DTIPProcess)

category: Diffusion.Diffusion Tensor Images.CommandLineOnly

description: dtiaverage is a program that allows to compute the average of an arbitrary number of tensor fields (listed after)

Several average method can be used (specified by the –method option): euclidian, log-euclidian and pga.

The default being euclidian.

version: 1.0.0

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/Nightly/Extensions/DTIPProcess>

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contributor: Casey Goodlett

Inputs:

```

[Optional]
inputs: (a list of items which are a pathlike object or string

```

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```

        representing an existing file)
        List of all the tensor fields to be averaged
        argument: ``--inputs %s...``
tensor_output: (a boolean or a pathlike object or string representing
        a file)
        Averaged tensor volume
        argument: ``--tensor_output %s``
DTI_double: (a boolean)
        Tensor components are saved as doubles (cannot be visualized in
        Slicer)
        argument: ``--DTI_double ``
verbose: (a boolean)
        produce verbose output
        argument: ``--verbose ``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

tensor_output: (a pathlike object or string representing an existing
        file)
        Averaged tensor volume

```

75.5.3 dtiestim[Link to code](#)

Wraps the executable command “ dtiestim “.

title: DTIEstim (DTIProcess)

category: Diffusion.Diffusion Weighted Images

description: dtiestim is a tool that takes in a set of DWIs (with `-dwi_image` option) in nrrd format and estimates a tensor field out of it. The output tensor file name is specified with the `-tensor_output` option There are several methods to estimate the tensors which you can specify with the option `-method` `lls`/`wls`/`nls`/`ml` . Here is a short description of the different methods:

- lls** Linear least squares. Standard estimation technique that recovers the tensor parameters by multiplying the log of the normalized signal intensities by the pseudo-inverse of the gradient matrix. Default option.
- wls** Weighted least squares. This method is similar to the linear least squares method except that the gradient matrix is weighted by the original lls estimate. (See Salvador, R., Pena, A., Menon, D. K., Carpenter, T. A., Pickard, J. D., and Bullmore, E. T. Formal characterization and extension of the linearized diffusion tensor model. Human Brain Mapping 24, 2 (Feb. 2005), 144-155. for more information on this method). This method is recommended for most applications. The weight for each iteration can be specified with the `-weight_iterations`. It is not currently the default due to occasional matrix singularities.
- nls** Non-linear least squares. This method does not take the log of the signal and requires an optimization based on levenberg-marquadt to optimize the parameters of the signal. The lls estimate is used as an initialization. For this method the step size can be specified with the `-step` option.
- ml** Maximum likelihood estimation. This method is experimental and is not currently recommended. For this ml method the sigma can be specified with the option `-sigma` and the step size can be specified with the `-step` option.

You can set a threshold (`-threshold`) to have the tensor estimated to only a subset of voxels. All the baseline voxel value higher than the threshold define the voxels where the tensors are computed. If not specified the threshold is calculated using an OTSU threshold on the baseline image. The masked generated by the `-t` option

or by the otsu value can be saved with the `-B0_mask_output` option.

dtiestim also can extract a few scalar images out of the DWI set of images:

- the average baseline image (`-B0`) which is the average of all the B0s.
- the IDWI (`-idwi`) which is the geometric mean of the diffusion images.

You can also load a mask if you want to compute the tensors only where the voxels are non-zero (`-brain_mask`) or a negative mask and the tensors will be estimated where the negative mask has zero values (`-bad_region_mask`)
version: 1.2.0

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/Nightly/Extensions/DTIPProcess>

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contributor: Casey Goodlett, Francois Budin

acknowledgements: Hans Johnson(1,3,4); Kent Williams(1); (1=University of Iowa Department of Psychiatry, 3=University of Iowa Department of Biomedical Engineering, 4=University of Iowa Department of Electrical and Computer Engineering) provided conversions to make DTIPProcess compatible with Slicer execution, and simplified the stand-alone build requirements by removing the dependancies on boost and a fortran compiler.

Inputs:

```
[Optional]
dwi_image: (a pathlike object or string representing an existing
            file)
            DWI image volume (required)
            argument: ``--dwi_image %s``
tensor_output: (a boolean or a pathlike object or string representing
                a file)
                Tensor OutputImage
                argument: ``--tensor_output %s``
B0: (a boolean or a pathlike object or string representing a file)
    Baseline image, average of all baseline images
    argument: ``--B0 %s``
idwi: (a boolean or a pathlike object or string representing a file)
    idwi output image. Image with isotropic diffusion-weighted
    information = geometric mean of diffusion images
    argument: ``--idwi %s``
B0_mask_output: (a boolean or a pathlike object or string
                 representing a file)
                 B0 mask used for the estimation. B0 thresholded either with the -t
                 option value or the automatic OTSU value
                 argument: ``--B0_mask_output %s``
brain_mask: (a pathlike object or string representing an existing
             file)
             Brain mask. Image where for every voxel == 0 the tensors are not
             estimated. Be aware that in addition a threshold based masking will
             be performed by default. If such an additional threshold masking is
             NOT desired, then use option -t 0.
             argument: ``--brain_mask %s``
bad_region_mask: (a pathlike object or string representing an
                  existing file)
                  Bad region mask. Image where for every voxel > 0 the tensors are not
                  estimated
                  argument: ``--bad_region_mask %s``
method: ('lls' or 'wls' or 'nls' or 'ml')
        Estimation method (lls:linear least squares, wls:weighted least
        squares, nls:non-linear least squares, ml:maximum likelihood)
        argument: ``--method %s``
```

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```

correction: ('none' or 'zero' or 'abs' or 'nearest')
    Correct the tensors if computed tensor is not semi-definite positive
    argument: ``--correction %s``
threshold: (an integer (int or long))
    Baseline threshold for estimation. If not specified calculated using
    an OTSU threshold on the baseline image.
    argument: ``--threshold %d``
weight_iterations: (an integer (int or long))
    Number of iterations to recalculate weightings from tensor estimate
    argument: ``--weight_iterations %d``
step: (a float)
    Gradient descent step size (for nls and ml methods)
    argument: ``--step %f``
sigma: (a float)
    argument: ``--sigma %f``
DTI_double: (a boolean)
    Tensor components are saved as doubles (cannot be visualized in
    Slicer)
    argument: ``--DTI_double ``
verbose: (a boolean)
    produce verbose output
    argument: ``--verbose ``
defaultTensor: (a list of items which are a float)
    Default tensor used if estimated tensor is below a given threshold
    argument: ``--defaultTensor %s``
shiftNeg: (a boolean)
    Shift eigenvalues so all are positive (accounts for bad tensors
    related to noise or acquisition error). This is the same option as
    the one available in DWIToDTIEstimation in Slicer (but instead of
    just adding the minimum eigenvalue to all the eigenvalues if it is
    smaller than 0, we use a coefficient to have stictly positive
    eigenvalues
    argument: ``--shiftNeg ``
shiftNegCoeff: (a float)
    Shift eigenvalues so all are positive (accounts for bad tensors
    related to noise or acquisition error). Instead of just adding the
    minimum eigenvalue to all the eigenvalues if it is smaller than 0,
    we use a coefficient to have stictly positive eigenvalues.
    Coefficient must be between 1.0 and 1.001 (included).
    argument: ``--shiftNegCoeff %f``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

tensor_output: (a pathlike object or string representing an existing
    file)
    Tensor OutputImage
B0: (a pathlike object or string representing an existing file)
    Baseline image, average of all baseline images
idwi: (a pathlike object or string representing an existing file)
    idwi output image. Image with isotropic diffusion-weighted

```

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```

information = geometric mean of diffusion images
B0_mask_output: (a pathlike object or string representing an existing
                  file)
B0 mask used for the estimation. B0 thresholded either with the -t
option value or the automatic OTSU value

```

75.5.4 dtiprocess

[Link to code](#)

Wraps the executable command “ dtiprocess “.

title: DTIPProcess (DTIPProcess)

category: Diffusion.Diffusion Tensor Images

description: dtiprocess is a tool that handles tensor fields. It takes as an input a tensor field in nrrd format. It can generate diffusion scalar properties out of the tensor field such as : FA (-fa_output), Gradient FA image (-fa_gradient_output), color FA (-color_fa_output), MD (-md_output), Frobenius norm (-frobenius_norm_output), lbd1, lbd2, lbd3 (-lambda{1,2,3}_output), binary map of voxel where if any of the eigenvalue is negative, the voxel is set to 1 (-negative_eigenvector_output)

It also creates 4D images out of the tensor field such as: Highest eigenvector map (highest eigenvector at each voxel) (-principal_eigenvector_output)

Masking capabilities: For any of the processing done with dtiprocess, it’s possible to apply it on a masked region of the tensor field. You need to use the -mask option for any of the option to be applied on that tensor field sub-region only. If you want to save the masked tensor field use the option -outmask and specify the new masked tensor field file name. dtiprocess also allows a range of transformations on the tensor fields. The transformed tensor field file name is specified with the option -deformation_output. There are 3 resampling interpolation methods specified with the tag -interpolation followed by the type to use (nearestneighbor, linear, cubic) Then you have several transformations possible to apply:

- Affine transformations using as an input
- itk affine transformation file (based on the itkAffineTransform class)
- Affine transformations using rview (details and download at <http://www.doc.ic.ac.uk/~dr/software/>). There are 2 versions of rview both creating transformation files called dof files. The old version of rview outputs text files containing the transformation parameters. It can be read in with the -dof_file option. The new version outputs binary dof files. These dof files can be transformed into human readable file with the dof2mat tool which is part of the rview package. So you need to save the output of dof2mat into a text file which can then be used with the -newdof_file option. Usage example: dof2mat mynewdoffile.dof >> mynewdoffile.txt dtiprocess -dti_image mytensorfield.nhdr -newdof_file mynewdoffile.txt -rot_output myaffinetensorfield.nhdr

Non linear transformations as an input: The default transformation file type is d-field (displacement field) in nrrd format. The option to use is -forward with the name of the file. If the transformation file is a h-field you have to add the option -hField.

version: 1.0.1

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/Nightly/Extensions/DTIPProcess>

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contributor: Casey Goodlett

Inputs:

```

[Optional]
dti_image: (a pathlike object or string representing an existing
            file)
            DTI tensor volume
            argument: ``--dti_image %s``
fa_output: (a boolean or a pathlike object or string representing a

```

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```

        file)
        Fractional Anisotropy output file
        argument: ``--fa_output %s``
md_output: (a boolean or a pathlike object or string representing a
        file)
        Mean Diffusivity output file
        argument: ``--md_output %s``
sigma: (a float)
        Scale of gradients
        argument: ``--sigma %f``
fa_gradient_output: (a boolean or a pathlike object or string
        representing a file)
        Fractional Anisotropy Gradient output file
        argument: ``--fa_gradient_output %s``
fa_gradmag_output: (a boolean or a pathlike object or string
        representing a file)
        Fractional Anisotropy Gradient Magnitude output file
        argument: ``--fa_gradmag_output %s``
color_fa_output: (a boolean or a pathlike object or string
        representing a file)
        Color Fractional Anisotropy output file
        argument: ``--color_fa_output %s``
principal_eigenvector_output: (a boolean or a pathlike object or
        string representing a file)
        Principal Eigenvectors Output
        argument: ``--principal_eigenvector_output %s``
negative_eigenvector_output: (a boolean or a pathlike object or
        string representing a file)
        Negative Eigenvectors Output: create a binary image where if any of
        the eigen value is below zero, the voxel is set to 1, otherwise 0.
        argument: ``--negative_eigenvector_output %s``
frobenius_norm_output: (a boolean or a pathlike object or string
        representing a file)
        Frobenius Norm Output
        argument: ``--frobenius_norm_output %s``
lambda1_output: (a boolean or a pathlike object or string
        representing a file)
        Axial Diffusivity - Lambda 1 (largest eigenvalue) output
        argument: ``--lambda1_output %s``
lambda2_output: (a boolean or a pathlike object or string
        representing a file)
        Lambda 2 (middle eigenvalue) output
        argument: ``--lambda2_output %s``
lambda3_output: (a boolean or a pathlike object or string
        representing a file)
        Lambda 3 (smallest eigenvalue) output
        argument: ``--lambda3_output %s``
RD_output: (a boolean or a pathlike object or string representing a
        file)
        RD (Radial Diffusivity  $1/2 * (\lambda_2 + \lambda_3)$ ) output
        argument: ``--RD_output %s``
rot_output: (a boolean or a pathlike object or string representing a
        file)
        Rotated tensor output file. Must also specify the dof file.
        argument: ``--rot_output %s``
affineitk_file: (a pathlike object or string representing an existing
        file)

```

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```

Transformation file for affine transformation. ITK format.
argument: ``--affineitk_file %s``
dof_file: (a pathlike object or string representing an existing file)
Transformation file for affine transformation. This can be ITK
format (or the outdated RView).
argument: ``--dof_file %s``
newdof_file: (a pathlike object or string representing an existing
file)
Transformation file for affine transformation. RView NEW format.
(txt file output of dof2mat)
argument: ``--newdof_file %s``
mask: (a pathlike object or string representing an existing file)
Mask tensors. Specify --outmask if you want to save the masked
tensor field, otherwise the mask is applied just for the current
processing
argument: ``--mask %s``
outmask: (a boolean or a pathlike object or string representing a
file)
Name of the masked tensor field.
argument: ``--outmask %s``
hField: (a boolean)
forward and inverse transformations are h-fields instead of
displacement fields
argument: ``--hField ``
forward: (a pathlike object or string representing an existing file)
Forward transformation. Assumed to be a deformation field in world
coordinates, unless the --h-field option is specified.
argument: ``--forward %s``
deformation_output: (a boolean or a pathlike object or string
representing a file)
Warped tensor field based on a deformation field. This option
requires the --forward, -F transformation to be specified.
argument: ``--deformation_output %s``
interpolation: ('nearestneighbor' or 'linear' or 'cubic')
Interpolation type (nearestneighbor, linear, cubic)
argument: ``--interpolation %s``
reorientation: ('fs' or 'ppd')
Reorientation type (fs, ppd)
argument: ``--reorientation %s``
correction: ('none' or 'zero' or 'abs' or 'nearest')
Correct the tensors if computed tensor is not semi-definite positive
argument: ``--correction %s``
scalar_float: (a boolean)
Write scalar [FA,MD] as unscaled float (with their actual values,
otherwise scaled by 10 000). Also causes FA to be unscaled [0..1].
argument: ``--scalar_float ``
DTI_double: (a boolean)
Tensor components are saved as doubles (cannot be visualized in
Slicer)
argument: ``--DTI_double ``
verbose: (a boolean)
produce verbose output
argument: ``--verbose ``
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value

```

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of class 'str' and with values which are a bytes or None or a value of class 'str', nipype default value: {})
Environment variables

Outputs:

```
fa_output: (a pathlike object or string representing an existing
            file)
            Fractional Anisotropy output file
md_output: (a pathlike object or string representing an existing
            file)
            Mean Diffusivity output file
fa_gradient_output: (a pathlike object or string representing an
                    existing file)
                    Fractional Anisotropy Gradient output file
fa_gradmag_output: (a pathlike object or string representing an
                   existing file)
                   Fractional Anisotropy Gradient Magnitude output file
color_fa_output: (a pathlike object or string representing an
                 existing file)
                 Color Fractional Anisotropy output file
principal_eigenvector_output: (a pathlike object or string
                              representing an existing file)
                              Principal Eigenvectors Output
negative_eigenvector_output: (a pathlike object or string
                             representing an existing file)
                             Negative Eigenvectors Output: create a binary image where if any of
                             the eigen value is below zero, the voxel is set to 1, otherwise 0.
frobenius_norm_output: (a pathlike object or string representing an
                       existing file)
                       Frobenius Norm Output
lambda1_output: (a pathlike object or string representing an existing
                file)
                Axial Diffusivity - Lambda 1 (largest eigenvalue) output
lambda2_output: (a pathlike object or string representing an existing
                file)
                Lambda 2 (middle eigenvalue) output
lambda3_output: (a pathlike object or string representing an existing
                file)
                Lambda 3 (smallest eigenvalue) output
RD_output: (a pathlike object or string representing an existing
            file)
            RD (Radial Diffusivity 1/2*(lambda2+lambda3)) output
rot_output: (a pathlike object or string representing an existing
            file)
            Rotated tensor output file. Must also specify the dof file.
outmask: (a pathlike object or string representing an existing file)
          Name of the masked tensor field.
deformation_output: (a pathlike object or string representing an
                    existing file)
                    Warped tensor field based on a deformation field. This option
                    requires the --forward,-F transformation to be specified.
```

75.6 interfaces.semtools.diffusion.gtract

75.6.1 compareTractInclusion

[Link to code](#)

Wraps the executable command “ compareTractInclusion “.

title: Compare Tracts

category: Diffusion.GTRACT

description: This program will halt with a status code indicating whether a test tract is nearly enough included in a standard tract in the sense that every fiber in the test tract has a low enough sum of squares distance to some fiber in the standard tract modulo spline resampling of every fiber to a fixed number of points.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
testFiber: (a pathlike object or string representing an existing
            file)
            Required: test fiber tract file name
            argument: ``--testFiber %s``
standardFiber: (a pathlike object or string representing an existing
                file)
                Required: standard fiber tract file name
                argument: ``--standardFiber %s``
closeness: (a float)
            Closeness of every test fiber to some fiber in the standard tract,
            computed as a sum of squares of spatial differences of standard
            points
            argument: ``--closeness %f``
numberOfPoints: (an integer (int or long))
                Number of points in comparison fiber pairs
                argument: ``--numberOfPoints %d``
testForBijection: (a boolean)
                Flag to apply the closeness criterion both ways
                argument: ``--testForBijection ``
testForFiberCardinality: (a boolean)
                Flag to require the same number of fibers in both tracts
                argument: ``--testForFiberCardinality ``
writeXMLPolyDataFile: (a boolean)
                Flag to make use of XML files when reading and writing vtkPolyData.
                argument: ``--writeXMLPolyDataFile ``
numberOfThreads: (an integer (int or long))
                Explicitly specify the maximum number of threads to use.
                argument: ``--numberOfThreads %d``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

None

75.6.2 extractNrrdVectorIndex

[Link to code](#)

Wraps the executable command “`extractNrrdVectorIndex`”.

title: Extract Nrrd Index

category: Diffusion.GTRACT

description: This program will extract a 3D image (single vector) from a vector 3D image at a given vector index.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Required: input file containing the vector that will be extracted
              argument: ``--inputVolume %s``
vectorIndex: (an integer (int or long))
              Index in the vector image to extract
              argument: ``--vectorIndex %d``
setImageOrientation: ('AsAcquired' or 'Axial' or 'Coronal' or
                     'Sagittal')
              Sets the image orientation of the extracted vector (Axial, Coronal,
              Sagittal)
              argument: ``--setImageOrientation %s``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              Required: name of output NRRD file containing the vector image at
              the given index
              argument: ``--outputVolume %s``
numberOfThreads: (an integer (int or long))
              Explicitly specify the maximum number of threads to use.
              argument: ``--numberOfThreads %d``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
              file)
              Required: name of output NRRD file containing the vector image at
              the given index
```

75.6.3 gtractAnisotropyMap

[Link to code](#)

Wraps the executable command “ gtractAnisotropyMap “.

title: Anisotropy Map

category: Diffusion.GTRACT

description: This program will generate a scalar map of anisotropy, given a tensor representation. Anisotropy images are used for fiber tracking, but the anisotropy scalars are not defined along the path. Instead, the tensor representation is included as point data allowing all of these metrics to be computed using only the fiber tract point data. The images can be saved in any ITK supported format, but it is suggested that you use an image format that supports the definition of the image origin. This includes NRRD, NifTI, and Meta formats. These images can also be used for scalar analysis including regional anisotropy measures or VBM style analysis.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
inputTensorVolume: (a pathlike object or string representing an
                    existing file)
    Required: input file containing the diffusion tensor image
    argument: ``--inputTensorVolume %s``
anisotropyType: ('ADC' or 'FA' or 'RA' or 'VR' or 'AD' or 'RD' or
                'LI')
    Anisotropy Mapping Type: ADC, FA, RA, VR, AD, RD, LI
    argument: ``--anisotropyType %s``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
    Required: name of output NRRD file containing the selected kind of
    anisotropy scalar.
    argument: ``--outputVolume %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
              file)
    Required: name of output NRRD file containing the selected kind of
    anisotropy scalar.
```

75.6.4 gtractAverageBvalues

[Link to code](#)

Wraps the executable command “ gtractAverageBvalues “.

title: Average B-Values

category: Diffusion.GTRACT

description: This program will directly average together the baseline gradients (b value equals 0) within a DWI scan. This is usually used after gtractCoregBvalues.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Required: input image file name containing multiple baseline
              gradients to average
              argument: ``--inputVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              Required: name of output NRRD file containing directly averaged
              baseline images
              argument: ``--outputVolume %s``
directionsTolerance: (a float)
                    Tolerance for matching identical gradient direction pairs
                    argument: ``--directionsTolerance %f``
averageB0only: (a boolean)
              Average only baseline gradients. All other gradient directions are
              not averaged, but retained in the outputVolume
              argument: ``--averageB0only ``
numberOfThreads: (an integer (int or long))
              Explicitly specify the maximum number of threads to use.
              argument: ``--numberOfThreads %d``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
              file)
              Required: name of output NRRD file containing directly averaged
              baseline images
```

75.6.5 gtractClipAnisotropy

[Link to code](#)

Wraps the executable command “ gtractClipAnisotropy “.

title: Clip Anisotropy

category: Diffusion.GTRACT

description: This program will zero the first and/or last slice of an anisotropy image, creating a clipped anisotropy image.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Required: input image file name
              argument: ``--inputVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              Required: name of output NRRD file containing the clipped anisotropy
              image
              argument: ``--outputVolume %s``
clipFirstSlice: (a boolean)
                Clip the first slice of the anisotropy image
                argument: ``--clipFirstSlice ``
clipLastSlice: (a boolean)
               Clip the last slice of the anisotropy image
               argument: ``--clipLastSlice ``
numberOfThreads: (an integer (int or long))
                 Explicitly specify the maximum number of threads to use.
                 argument: ``--numberOfThreads %d``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
              file)
              Required: name of output NRRD file containing the clipped anisotropy
              image
```

75.6.6 gtractCoRegAnatomy

[Link to code](#)

Wraps the executable command “ gtractCoRegAnatomy “.

title: Coregister B0 to Anatomy B-Spline

category: Diffusion.GTRACT

description: This program will register a Nrrd diffusion weighted 4D vector image to a fixed anatomical image. Two registration methods are supported for alignment with anatomical images: Rigid and B-Spline. The rigid registration performs a rigid body registration with the anatomical images and should be done as well to initialize the B-Spline transform. The B-Spline transform is the deformable transform, where the user can control the amount of deformation based on the number of control points as well as the maximum distance that these points can move. The B-Spline registration places a low dimensional grid in the image, which is deformed. This allows for some susceptibility related distortions to be removed from the diffusion weighted images. In general the amount of motion in the slice selection and read-out directions direction should be kept low. The distortion is in the phase encoding direction in the images. It is recommended that skull stripped (i.e. image containing only brain with skull removed) images should be used for image co-registration with the B-Spline transform.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Required: input vector image file name. It is recommended that the
              input volume is the skull stripped baseline image of the DWI scan.
              argument: ``--inputVolume %s``
inputAnatomicalVolume: (a pathlike object or string representing an
                        existing file)
                        Required: input anatomical image file name. It is recommended that
                        that the input anatomical image has been skull stripped and has the
                        same orientation as the DWI scan.
                        argument: ``--inputAnatomicalVolume %s``
vectorIndex: (an integer (int or long))
              Vector image index in the moving image (within the DWI) to be used
              for registration.
              argument: ``--vectorIndex %d``
inputRigidTransform: (a pathlike object or string representing an
                     existing file)
                     Required (for B-Spline type co-registration): input rigid transform
                     file name. Used as a starting point for the anatomical B-Spline
                     registration.
                     argument: ``--inputRigidTransform %s``
outputTransformName: (a boolean or a pathlike object or string
                     representing a file)
                     Required: filename for the fit transform.
                     argument: ``--outputTransformName %s``
transformType: ('Rigid' or 'Bspline')
               Transform Type: Rigid|Bspline
               argument: ``--transformType %s``
numberOfIterations: (an integer (int or long))
                    Number of iterations in the selected 3D fit
                    argument: ``--numberOfIterations %d``
gridSize: (a list of items which are an integer (int or long))
           Number of grid subdivisions in all 3 directions
           argument: ``--gridSize %s``
borderSize: (an integer (int or long))
            Size of border
            argument: ``--borderSize %d``
numberOfHistogramBins: (an integer (int or long))
                       Number of histogram bins
                       argument: ``--numberOfHistogramBins %d``
spatialScale: (an integer (int or long))
              Scales the number of voxels in the image by this value to specify
              the number of voxels used in the registration
              argument: ``--spatialScale %d``
convergence: (a float)
             Convergence Factor
             argument: ``--convergence %f``
gradientTolerance: (a float)
                   Gradient Tolerance
                   argument: ``--gradientTolerance %f``
```

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```

maxBSplineDisplacement: (a float)
    Sets the maximum allowed displacements in image physical
    coordinates for BSpline control grid along each axis. A value of 0.0
    indicates that the problem should be unbounded. NOTE: This only
    constrains the BSpline portion, and does not limit the displacement
    from the associated bulk transform. This can lead to a substantial
    reduction in computation time in the BSpline optimizer.,
    argument: ``--maxBSplineDisplacement %f``

maximumStepSize: (a float)
    Maximum permitted step size to move in the selected 3D fit
    argument: ``--maximumStepSize %f``

minimumStepSize: (a float)
    Minimum required step size to move in the selected 3D fit without
    converging -- decrease this to make the fit more exacting
    argument: ``--minimumStepSize %f``

translationScale: (a float)
    How much to scale up changes in position compared to unit rotational
    changes in radians -- decrease this to put more translation in the
    fit
    argument: ``--translationScale %f``

relaxationFactor: (a float)
    Fraction of gradient from Jacobian to attempt to move in the
    selected 3D fit
    argument: ``--relaxationFactor %f``

numberOfSamples: (an integer (int or long))
    The number of voxels sampled for mutual information computation.
    Increase this for a slower, more careful fit. NOTE that it is
    suggested to use samplingPercentage instead of this option. However,
    if set, it overwrites the samplingPercentage option.
    argument: ``--numberOfSamples %d``

samplingPercentage: (a float)
    This is a number in (0.0,1.0] interval that shows the percentage of
    the input fixed image voxels that are sampled for mutual information
    computation. Increase this for a slower, more careful fit. You can
    also limit the sampling focus with ROI masks and ROIAUTO mask
    generation. The default is to use approximately 5% of voxels (for
    backwards compatibility 5% ~= 500000/(256*256*256)). Typical values
    range from 1% for low detail images to 20% for high detail images.
    argument: ``--samplingPercentage %f``

useMomentsAlign: (a boolean)
    MomentsAlign assumes that the center of mass of the images represent
    similar structures. Perform a MomentsAlign registration as part of
    the sequential registration steps. This option MUST come first, and
    CAN NOT be used with either CenterOfHeadLAlign, GeometryAlign, or
    initialTransform file. This family of options superceeds the use of
    transformType if any of them are set.
    argument: ``--useMomentsAlign``

useGeometryAlign: (a boolean)
    GeometryAlign on assumes that the center of the voxel lattice of the
    images represent similar structures. Perform a GeometryCenterAlign
    registration as part of the sequential registration steps. This
    option MUST come first, and CAN NOT be used with either
    MomentsAlign, CenterOfHeadAlign, or initialTransform file. This
    family of options superceeds the use of transformType if any of them
    are set.
    argument: ``--useGeometryAlign``

useCenterOfHeadAlign: (a boolean)

```

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```

CenterOfHeadAlign attempts to find a hemisphere full of foreground
voxels from the superior direction as an estimate of where the
center of a head shape would be to drive a center of mass estimate.
Perform a CenterOfHeadAlign registration as part of the sequential
registration steps. This option MUST come first, and CAN NOT be used
with either MomentsAlign, GeometryAlign, or initialTransform file.
This family of options superceeds the use of transformType if any of
them are set.
argument: ``--useCenterOfHeadAlign ``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

outputTransformName: (a pathlike object or string representing an
    existing file)
    Required: filename for the fit transform.

```

75.6.7 gtractConcatDwi

Link to code

Wraps the executable command “gtractConcatDwi”.

title: Concat DWI Images

category: Diffusion.GTRACT

description: This program will concatenate two DTI runs together.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```

[Optional]
inputVolume: (a list of items which are a pathlike object or string
    representing an existing file)
    Required: input file containing the first diffusion weighted image
argument: ``--inputVolume %s...``
ignoreOrigins: (a boolean)
    If image origins are different force all images to origin of first
    image
argument: ``--ignoreOrigins ``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Required: name of output NRRD file containing the combined diffusion
    weighted images.
argument: ``--outputVolume %s``
numberOfThreads: (an integer (int or long))

```

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```

        Explicitly specify the maximum number of threads to use.
        argument: ``--numberOfThreads %d``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
              file)
              Required: name of output NRRD file containing the combined diffusion
              weighted images.

```

75.6.8 gtractCopyImageOrientation[Link to code](#)

Wraps the executable command “ gtractCopyImageOrientation “.

title: Copy Image Orientation

category: Diffusion.GTRACT

description: This program will copy the orientation from the reference image into the moving image. Currently, the registration process requires that the diffusion weighted images and the anatomical images have the same image orientation (i.e. Axial, Coronal, Sagittal). It is suggested that you copy the image orientation from the diffusion weighted images and apply this to the anatomical image. This image can be subsequently removed after the registration step is complete. We anticipate that this limitation will be removed in future versions of the registration programs.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Required: input file containing the signed short image to reorient
              without resampling.
              argument: ``--inputVolume %s``
inputReferenceVolume: (a pathlike object or string representing an
                       existing file)
                       Required: input file containing orietation that will be cloned.
                       argument: ``--inputReferenceVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              Required: name of output NRRD or Nifti file containing the
              reoriented image in reference image space.
              argument: ``--outputVolume %s``
numberOfThreads: (an integer (int or long))
                  Explicitly specify the maximum number of threads to use.
                  argument: ``--numberOfThreads %d``

```

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```
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
    file)
    Required: name of output NRRD or Nifti file containing the
    reoriented image in reference image space.
```

75.6.9 gtractCoregBvalues

[Link to code](#)

Wraps the executable command “ gtractCoregBvalues “.

title: Coregister B-Values

category: Diffusion.GTRACT

description: This step should be performed after converting DWI scans from DICOM to NRRD format. This program will register all gradients in a NRRD diffusion weighted 4D vector image (moving image) to a specified index in a fixed image. It also supports co-registration with a T2 weighted image or field map in the same plane as the DWI data. The fixed image for the registration should be a b0 image. A mutual information metric cost function is used for the registration because of the differences in signal intensity as a result of the diffusion gradients. The full affine allows the registration procedure to correct for eddy current distortions that may exist in the data. If the eddyCurrentCorrection is enabled, relaxationFactor (0.25) and maximumStepSize (0.1) should be adjusted.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
movingVolume: (a pathlike object or string representing an existing
    file)
    Required: input moving image file name. In order to register
    gradients within a scan to its first gradient, set the movingVolume
    and fixedVolume as the same image.
    argument: ``--movingVolume %s``
fixedVolume: (a pathlike object or string representing an existing
    file)
    Required: input fixed image file name. It is recommended that this
    image should either contain or be a b0 image.
    argument: ``--fixedVolume %s``
fixedVolumeIndex: (an integer (int or long))
    Index in the fixed image for registration. It is recommended that
    this image should be a b0 image.
    argument: ``--fixedVolumeIndex %d``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
```

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```

Required: name of output NRRD file containing moving images
individually resampled and fit to the specified fixed image index.
argument: ``--outputVolume %s``
outputTransform: (a boolean or a pathlike object or string
    representing a file)
    Registration 3D transforms concatenated in a single output file.
    There are no tools that can use this, but can be used for debugging
    purposes.
    argument: ``--outputTransform %s``
eddyCurrentCorrection: (a boolean)
    Flag to perform eddy current corection in addition to motion
    correction (recommended)
    argument: ``--eddyCurrentCorrection ``
numberOfIterations: (an integer (int or long))
    Number of iterations in each 3D fit
    argument: ``--numberOfIterations %d``
numberOfSpatialSamples: (an integer (int or long))
    The number of voxels sampled for mutual information computation.
    Increase this for a slower, more careful fit. NOTE that it is
    suggested to use samplingPercentage instead of this option. However,
    if set, it overwrites the samplingPercentage option.
    argument: ``--numberOfSpatialSamples %d``
samplingPercentage: (a float)
    This is a number in (0.0,1.0] interval that shows the percentage of
    the input fixed image voxels that are sampled for mutual information
    computation. Increase this for a slower, more careful fit. You can
    also limit the sampling focus with ROI masks and ROIAUTO mask
    generation. The default is to use approximately 5% of voxels (for
    backwards compatibility 5% ~= 500000/(256*256*256)). Typical values
    range from 1% for low detail images to 20% for high detail images.
    argument: ``--samplingPercentage %f``
relaxationFactor: (a float)
    Fraction of gradient from Jacobian to attempt to move in each 3D fit
    step (adjust when eddyCurrentCorrection is enabled; suggested value
    = 0.25)
    argument: ``--relaxationFactor %f``
maximumStepSize: (a float)
    Maximum permitted step size to move in each 3D fit step (adjust when
    eddyCurrentCorrection is enabled; suggested value = 0.1)
    argument: ``--maximumStepSize %f``
minimumStepSize: (a float)
    Minimum required step size to move in each 3D fit step without
    converging -- decrease this to make the fit more exacting
    argument: ``--minimumStepSize %f``
spatialScale: (a float)
    How much to scale up changes in position compared to unit rotational
    changes in radians -- decrease this to put more rotation in the fit
    argument: ``--spatialScale %f``
registerB0Only: (a boolean)
    Register the B0 images only
    argument: ``--registerB0Only ``
debugLevel: (an integer (int or long))
    Display debug messages, and produce debug intermediate results.
    0=OFF, 1=Minimal, 10=Maximum debugging.
    argument: ``--debugLevel %d``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.

```

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```

    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Required: name of output NRRD file containing moving images
    individually resampled and fit to the specified fixed image index.
outputTransform: (a pathlike object or string representing an
    existing file)
    Registration 3D transforms concatenated in a single output file.
    There are no tools that can use this, but can be used for debugging
    purposes.

```

75.6.10 gtractCostFastMarching**Link to code**

Wraps the executable command “ gtractCostFastMarching “.

title: Cost Fast Marching

category: Diffusion.GTRACT

description: This program will use a fast marching fiber tracking algorithm to identify fiber tracts from a tensor image. This program is the first portion of the algorithm. The user must first run gtractFastMarchingTracking to generate the actual fiber tracts. This algorithm is roughly based on the work by G. Parker et al. from IEEE Transactions On Medical Imaging, 21(5): 505-512, 2002. An additional feature of including anisotropy into the vcl_cost function calculation is included.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris. The original code here was developed by Daisy Espino.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```

[Optional]
inputTensorVolume: (a pathlike object or string representing an
    existing file)
    Required: input tensor image file name
    argument: ``--inputTensorVolume %s``
inputAnisotropyVolume: (a pathlike object or string representing an
    existing file)
    Required: input anisotropy image file name
    argument: ``--inputAnisotropyVolume %s``
inputStartingSeedsLabelMapVolume: (a pathlike object or string
    representing an existing file)
    Required: input starting seeds LabelMap image file name
    argument: ``--inputStartingSeedsLabelMapVolume %s``
startingSeedsLabel: (an integer (int or long))

```

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```

    Label value for Starting Seeds
    argument: ``--startingSeedsLabel %d``
outputCostVolume: (a boolean or a pathlike object or string
    representing a file)
    Output vcl_cost image
    argument: ``--outputCostVolume %s``
outputSpeedVolume: (a boolean or a pathlike object or string
    representing a file)
    Output speed image
    argument: ``--outputSpeedVolume %s``
anisotropyWeight: (a float)
    Anisotropy weight used for vcl_cost function calculations
    argument: ``--anisotropyWeight %f``
stoppingValue: (a float)
    Terminating value for vcl_cost function estimation
    argument: ``--stoppingValue %f``
seedThreshold: (a float)
    Anisotropy threshold used for seed selection
    argument: ``--seedThreshold %f``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputCostVolume: (a pathlike object or string representing an
    existing file)
    Output vcl_cost image
outputSpeedVolume: (a pathlike object or string representing an
    existing file)
    Output speed image

```

75.6.11 gtractCreateGuideFiber**Link to code**

Wraps the executable command “ gtractCreateGuideFiber “.

title: Create Guide Fiber

category: Diffusion.GTRACT

description: This program will create a guide fiber by averaging fibers from a previously generated tract.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```

[Optional]
inputFiber: (a pathlike object or string representing an existing

```

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```

        file)
        Required: input fiber tract file name
        argument: ``--inputFiber %s``
numberOfPoints: (an integer (int or long))
        Number of points in output guide fiber
        argument: ``--numberOfPoints %d``
outputFiber: (a boolean or a pathlike object or string representing a
        file)
        Required: output guide fiber file name
        argument: ``--outputFiber %s``
writeXMLPolyDataFile: (a boolean)
        Flag to make use of XML files when reading and writing vtkPolyData.
        argument: ``--writeXMLPolyDataFile ``
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        argument: ``--numberOfThreads %d``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

outputFiber: (a pathlike object or string representing an existing
        file)
        Required: output guide fiber file name

```

75.6.12 gtractFastMarchingTracking**Link to code**

Wraps the executable command “ gtractFastMarchingTracking “.

title: Fast Marching Tracking

category: Diffusion.GTRACT

description: This program will use a fast marching fiber tracking algorithm to identify fiber tracts from a tensor image. This program is the second portion of the algorithm. The user must first run gtractCostFastMarching to generate the vcl_cost image. The second step of the algorithm implemented here is a gradient descent soplution from the defined ending region back to the seed points specified in gtractCostFastMarching. This algorithm is roughly based on the work by G. Parker et al. from IEEE Transactions On Medical Imaging, 21(5): 505-512, 2002. An additional feature of including anisotropy into the vcl_cost function calculation is included.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris. The original code here was developed by Daisy Espino.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```

[Optional]
inputTensorVolume: (a pathlike object or string representing an
        existing file)
        Required: input tensor image file name

```

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```

        argument: ``--inputTensorVolume %s``
inputAnisotropyVolume: (a pathlike object or string representing an
    existing file)
    Required: input anisotropy image file name
    argument: ``--inputAnisotropyVolume %s``
inputCostVolume: (a pathlike object or string representing an
    existing file)
    Required: input vcl_cost image file name
    argument: ``--inputCostVolume %s``
inputStartingSeedsLabelMapVolume: (a pathlike object or string
    representing an existing file)
    Required: input starting seeds LabelMap image file name
    argument: ``--inputStartingSeedsLabelMapVolume %s``
startingSeedsLabel: (an integer (int or long))
    Label value for Starting Seeds
    argument: ``--startingSeedsLabel %d``
outputTract: (a boolean or a pathlike object or string representing a
    file)
    Required: name of output vtkPolydata file containing tract lines and
    the point data collected along them.
    argument: ``--outputTract %s``
writeXMLPolyDataFile: (a boolean)
    Flag to make use of the XML format for vtkPolyData fiber tracts.
    argument: ``--writeXMLPolyDataFile ``
numberOfIterations: (an integer (int or long))
    Number of iterations used for the optimization
    argument: ``--numberOfIterations %d``
seedThreshold: (a float)
    Anisotropy threshold used for seed selection
    argument: ``--seedThreshold %f``
trackingThreshold: (a float)
    Anisotropy threshold used for fiber tracking
    argument: ``--trackingThreshold %f``
costStepSize: (a float)
    Cost image sub-voxel sampling
    argument: ``--costStepSize %f``
maximumStepSize: (a float)
    Maximum step size to move when tracking
    argument: ``--maximumStepSize %f``
minimumStepSize: (a float)
    Minimum step size to move when tracking
    argument: ``--minimumStepSize %f``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputTract: (a pathlike object or string representing an existing
    file)

```

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Required: name of output vtkPolydata file containing tract lines **and** the point data collected along them.

75.6.13 gtractFiberTracking

[Link to code](#)

Wraps the executable command “ gtractFiberTracking “.

title: Fiber Tracking

category: Diffusion.GTRACT

description: This program implements four fiber tracking methods (Free, Streamline, GraphSearch, Guided). The output of the fiber tracking is vtkPolyData (i.e. Polylines) that can be loaded into Slicer3 for visualization. The poly data can be saved in either old VTK format files (.vtk) or in the new VTK XML format (.xml). The polylines contain point data that defines the Tensor at each point along the fiber tract. This can then be used to rendered as glyphs in Slicer3 and can be used to define several scalar measures without referencing back to the anisotropy images. (1) Free tracking is a basic streamlines algorithm. This is a direct implementation of the method originally proposed by Basser et al. The tracking follows the primary eigenvector. The tracking begins with seed points in the starting region. Only those voxels above the specified anisotropy threshold in the starting region are used as seed points. Tracking terminates either as a result of maximum fiber length, low anisotropy, or large curvature. This is a great way to explore your data. (2) The streamlines algorithm is a direct implementation of the method originally proposed by Basser et al. The tracking follows the primary eigenvector. The tracking begins with seed points in the starting region. Only those voxels above the specified anisotropy threshold in the starting region are used as seed points. Tracking terminates either by reaching the ending region or reaching some stopping criteria. Stopping criteria are specified using the following parameters: tracking threshold, curvature threshold, and max length. Only paths terminating in the ending region are kept in this method. The TEND algorithm proposed by Lazar et al. (Human Brain Mapping 18:306-321, 2003) has been instrumented. This can be enabled using the `-useTend` option while performing Streamlines tracking. This utilizes the entire diffusion tensor to deflect the incoming vector instead of simply following the primary eigenvector. The TEND parameters are set using the `-tendF` and `-tendG` options. (3) Graph Search tracking is the first step in the full GTRACT algorithm developed by Cheng et al. (NeuroImage 31(3): 1075-1085, 2006) for finding the tracks in a tensor image. This method was developed to generate fibers in a Tensor representation where crossing fibers occur. The graph search algorithm follows the primary eigenvector in non-ambiguous regions and utilizes branching and a graph search algorithm in ambiguous regions. Ambiguous tracking regions are defined based on two criteria: Branching AI Threshold (anisotropy values below this value and above the tracking threshold) and Curvature Major Eigen (angles of the primary eigenvector direction and the current tracking direction). In regions that meet this criteria, two or three tracking paths are considered. The first is the standard primary eigenvector direction. The second is the secondary eigenvector direction. This is based on the assumption that these regions may be prolate regions. If the Random Walk option is selected then a third direction is also considered. This direction is defined by a cone pointing from the current position to the centroid of the ending region. The interior angle of the cone is specified by the user with the Branch/Guide Angle parameter. A vector contained inside of the cone is selected at random and used as the third direction. This method can also utilize the TEND option where the primary tracking direction is that specified by the TEND method instead of the primary eigenvector. The parameter `-maximumBranchPoints` allows the tracking to have this number of branches being considered at a time. If this number of branch points is exceeded at any time, then the algorithm will revert back to a streamline algorithm until the number of branches is reduced. This allows the user to constrain the computational complexity of the algorithm. (4) The second phase of the GTRACT algorithm is Guided Tracking. This method incorporates anatomical information about the track orientation using an initial guess of the fiber track. In the originally proposed GTRACT method, this would be created from the fibers resulting from the Graph Search tracking. However, in practice this can be created using any method and could be defined manually. To create the guide fiber the program `gtractCreateGuideFiber` can be used. This program will load a fiber tract that has been generated and create a centerline representation of the fiber tract (i.e. a single fiber). In this method, the fiber tracking follows the primary eigenvector direction unless it deviates from the guide fiber track by an angle greater than that specified by the `-guidedCurvatureThreshold` parameter.

The user must specify the guide fiber when running this program.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta, Greg Harris and Yongqiang Zhao.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
inputTensorVolume: (a pathlike object or string representing an
    existing file)
    Required (for Free, Streamline, GraphSearch, and Guided fiber
    tracking methods): input tensor image file name
    argument: ``--inputTensorVolume %s``
inputAnisotropyVolume: (a pathlike object or string representing an
    existing file)
    Required (for Free, Streamline, GraphSearch, and Guided fiber
    tracking methods): input anisotropy image file name
    argument: ``--inputAnisotropyVolume %s``
inputStartingSeedsLabelMapVolume: (a pathlike object or string
    representing an existing file)
    Required (for Free, Streamline, GraphSearch, and Guided fiber
    tracking methods): input starting seeds LabelMap image file name
    argument: ``--inputStartingSeedsLabelMapVolume %s``
startingSeedsLabel: (an integer (int or long))
    Label value for Starting Seeds (required if Label number used to
    create seed point in Slicer was not 1)
    argument: ``--startingSeedsLabel %d``
inputEndingSeedsLabelMapVolume: (a pathlike object or string
    representing an existing file)
    Required (for Streamline, GraphSearch, and Guided fiber tracking
    methods): input ending seeds LabelMap image file name
    argument: ``--inputEndingSeedsLabelMapVolume %s``
endingSeedsLabel: (an integer (int or long))
    Label value for Ending Seeds (required if Label number used to
    create seed point in Slicer was not 1)
    argument: ``--endingSeedsLabel %d``
inputTract: (a pathlike object or string representing an existing
    file)
    Required (for Guided fiber tracking method): guide fiber in
    vtkPolydata file containing one tract line.
    argument: ``--inputTract %s``
outputTract: (a boolean or a pathlike object or string representing a
    file)
    Required (for Free, Streamline, GraphSearch, and Guided fiber
    tracking methods): name of output vtkPolydata file containing tract
    lines and the point data collected along them.
    argument: ``--outputTract %s``
writeXMLPolyDataFile: (a boolean)
    Flag to make use of the XML format for vtkPolyData fiber tracts.
    argument: ``--writeXMLPolyDataFile ``
trackingMethod: ('Guided' or 'Free' or 'Streamline' or 'GraphSearch')
    Fiber tracking Filter Type: Guided|Free|Streamline|GraphSearch
    argument: ``--trackingMethod %s``
guidedCurvatureThreshold: (a float)
    Guided Curvature Threshold (Degrees)
```

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```

        argument: ``--guidedCurvatureThreshold %f``
maximumGuideDistance: (a float)
    Maximum distance for using the guide fiber direction
    argument: ``--maximumGuideDistance %f``
seedThreshold: (a float)
    Anisotropy threshold for seed selection (recommended for Free fiber
    tracking)
    argument: ``--seedThreshold %f``
trackingThreshold: (a float)
    Anisotropy threshold for fiber tracking (anisotropy values of the
    next point along the path)
    argument: ``--trackingThreshold %f``
curvatureThreshold: (a float)
    Curvature threshold in degrees (recommended for Free fiber tracking)
    argument: ``--curvatureThreshold %f``
branchingThreshold: (a float)
    Anisotropy Branching threshold (recommended for GraphSearch fiber
    tracking method)
    argument: ``--branchingThreshold %f``
maximumBranchPoints: (an integer (int or long))
    Maximum branch points (recommended for GraphSearch fiber tracking
    method)
    argument: ``--maximumBranchPoints %d``
useRandomWalk: (a boolean)
    Flag to use random walk.
    argument: ``--useRandomWalk ``
randomSeed: (an integer (int or long))
    Random number generator seed
    argument: ``--randomSeed %d``
branchingAngle: (a float)
    Branching angle in degrees (recommended for GraphSearch fiber
    tracking method)
    argument: ``--branchingAngle %f``
minimumLength: (a float)
    Minimum fiber length. Helpful for filtering invalid tracts.
    argument: ``--minimumLength %f``
maximumLength: (a float)
    Maximum fiber length (voxels)
    argument: ``--maximumLength %f``
stepSize: (a float)
    Fiber tracking step size
    argument: ``--stepSize %f``
useLoopDetection: (a boolean)
    Flag to make use of loop detection.
    argument: ``--useLoopDetection ``
useTend: (a boolean)
    Flag to make use of Tend F and Tend G parameters.
    argument: ``--useTend ``
tendF: (a float)
    Tend F parameter
    argument: ``--tendF %f``
tendG: (a float)
    Tend G parameter
    argument: ``--tendG %f``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``

```

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```
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outputTract: (a pathlike object or string representing an existing
    file)
    Required (for Free, Streamline, GraphSearch, and Guided fiber
    tracking methods): name of output vtkPolydata file containing tract
    lines and the point data collected along them.
```

75.6.14 gtractImageConformity[Link to code](#)

Wraps the executable command “ gtractImageConformity “.

title: Image Conformity

category: Diffusion.GTRACT

description: This program will straighten out the Direction and Origin to match the Reference Image.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    Required: input file containing the signed short image to reorient
    without resampling.
    argument: ``--inputVolume %s``
inputReferenceVolume: (a pathlike object or string representing an
    existing file)
    Required: input file containing the standard image to clone the
    characteristics of.
    argument: ``--inputReferenceVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Required: name of output Nrrd or Nifti file containing the
    reoriented image in reference image space.
    argument: ``--outputVolume %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
```

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Environment variables

Outputs:

outputVolume: (a pathlike **object** **or** string representing an existing file)
 Required: name of output Nrrd **or** Nifti file containing the reoriented image **in** reference image space.

75.6.15 gtractInvertBSplineTransform[Link to code](#)

Wraps the executable command “ gtractInvertBSplineTransform “.

title: B-Spline Transform Inversion

category: Diffusion.GTRACT

description: This program will invert a B-Spline transform using a thin-plate spline approximation.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
inputReferenceVolume: (a pathlike object or string representing an
    existing file)
    Required: input image file name to exemplify the anatomical space to
    interpolate over.
    argument: ``--inputReferenceVolume %s``
inputTransform: (a pathlike object or string representing an existing
    file)
    Required: input B-Spline transform file name
    argument: ``--inputTransform %s``
outputTransform: (a boolean or a pathlike object or string
    representing a file)
    Required: output transform file name
    argument: ``--outputTransform %s``
landmarkDensity: (a list of items which are an integer (int or long))
    Number of landmark subdivisions in all 3 directions
    argument: ``--landmarkDensity %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

outputTransform: (a pathlike **object** **or** string representing an existing file)

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Required: output transform file name

75.6.16 gtractInvertDisplacementField

[Link to code](#)

Wraps the executable command “ gtractInvertDisplacementField “.

title: Invert Displacement Field

category: Diffusion.GTRACT

description: This program will invert a deformation field. The size of the deformation field is defined by an example image provided by the user

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
baseImage: (a pathlike object or string representing an existing
            file)
            Required: base image used to define the size of the inverse field
            argument: ``--baseImage %s``
deformationImage: (a pathlike object or string representing an
                   existing file)
                   Required: Displacement field image
                   argument: ``--deformationImage %s``
outputVolume: (a boolean or a pathlike object or string representing
               a file)
               Required: Output deformation field
               argument: ``--outputVolume %s``
subsamplingFactor: (an integer (int or long))
                   Subsampling factor for the deformation field
                   argument: ``--subsamplingFactor %d``
numberOfThreads: (an integer (int or long))
                  Explicitly specify the maximum number of threads to use.
                  argument: ``--numberOfThreads %d``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               Required: Output deformation field
```

75.6.17 gtractInvertRigidTransform

[Link to code](#)

Wraps the executable command “ gtractInvertRigidTransform “.

title: Rigid Transform Inversion
 category: Diffusion.GTRACT
 description: This program will invert a Rigid transform.
 version: 4.0.0
 documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>
 license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>
 contributor: This tool was developed by Vincent Magnotta and Greg Harris.
 acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1
 Inputs:

```

[Optional]
inputTransform: (a pathlike object or string representing an existing
                 file)
                 Required: input rigid transform file name
                 argument: ``--inputTransform %s``
outputTransform: (a boolean or a pathlike object or string
                  representing a file)
                  Required: output transform file name
                  argument: ``--outputTransform %s``
numberOfThreads: (an integer (int or long))
                  Explicitly specify the maximum number of threads to use.
                  argument: ``--numberOfThreads %d``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
  
```

Outputs:

```

outputTransform: (a pathlike object or string representing an
                  existing file)
                  Required: output transform file name
  
```

75.6.18 gtractResampleAnisotropy

[Link to code](#)

Wraps the executable command “ gtractResampleAnisotropy “.

title: Resample Anisotropy
 category: Diffusion.GTRACT
 description: This program will resample a floating point image using either the Rigid or B-Spline transform. You may want to save the aligned B0 image after each of the anisotropy map co-registration steps with the anatomical image to check the registration quality with another tool.
 version: 4.0.0
 documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>
 license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>
 contributor: This tool was developed by Vincent Magnotta and Greg Harris.
 acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1
 Inputs:

```

[Optional]
inputAnisotropyVolume: (a pathlike object or string representing an
  
```

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```

    existing file)
    Required: input file containing the anisotropy image
    argument: ``--inputAnisotropyVolume %s``
inputAnatomicalVolume: (a pathlike object or string representing an
    existing file)
    Required: input file containing the anatomical image whose
    characteristics will be cloned.
    argument: ``--inputAnatomicalVolume %s``
inputTransform: (a pathlike object or string representing an existing
    file)
    Required: input Rigid OR Bspline transform file name
    argument: ``--inputTransform %s``
transformType: ('Rigid' or 'B-Spline')
    Transform type: Rigid, B-Spline
    argument: ``--transformType %s``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Required: name of output NRRD file containing the resampled
    transformed anisotropy image.
    argument: ``--outputVolume %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Required: name of output NRRD file containing the resampled
    transformed anisotropy image.

```

75.6.19 gtractResampleB0[Link to code](#)

Wraps the executable command “ gtractResampleB0 “.

title: Resample B0

category: Diffusion.GTRACT

description: This program will resample a signed short image using either a Rigid or B-Spline transform. The user must specify a template image that will be used to define the origin, orientation, spacing, and size of the resampled image.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:


```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Required: input file containing the 4D image
              argument: ``--inputVolume %s``
inputAnatomicalVolume: (a pathlike object or string representing an
                        existing file)
                        Required: input file containing the anatomical image defining the
                        origin, spacing and size of the resampled image (template)
                        argument: ``--inputAnatomicalVolume %s``
inputTransform: (a pathlike object or string representing an existing
                 file)
                 Required: input Rigid OR Bspline transform file name
                 argument: ``--inputTransform %s``
vectorIndex: (an integer (int or long))
              Index in the diffusion weighted image set for the B0 image
              argument: ``--vectorIndex %d``
transformType: ('Rigid' or 'B-Spline')
               Transform type: Rigid, B-Spline
               argument: ``--transformType %s``
outputVolume: (a boolean or a pathlike object or string representing
               a file)
               Required: name of output NRRD file containing the resampled input
               image.
               argument: ``--outputVolume %s``
numberOfThreads: (an integer (int or long))
                  Explicitly specify the maximum number of threads to use.
                  argument: ``--numberOfThreads %d``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               Required: name of output NRRD file containing the resampled input
               image.
```

75.6.20 gtractResampleCodeImage[Link to code](#)

Wraps the executable command “ gtractResampleCodeImage “.

title: Resample Code Image

category: Diffusion.GTRACT

description: This program will resample a short integer code image using either the Rigid or Inverse-B-Spline transform. The reference image is the DTI tensor anisotropy image space, and the input code image is in anatomical space.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS

R01NS050568-01A2S1

Inputs:

```
[Optional]
inputCodeVolume: (a pathlike object or string representing an
    existing file)
    Required: input file containing the code image
    argument: ``--inputCodeVolume %s``
inputReferenceVolume: (a pathlike object or string representing an
    existing file)
    Required: input file containing the standard image to clone the
    characteristics of.
    argument: ``--inputReferenceVolume %s``
inputTransform: (a pathlike object or string representing an existing
    file)
    Required: input Rigid or Inverse-B-Spline transform file name
    argument: ``--inputTransform %s``
transformType: ('Rigid' or 'Affine' or 'B-Spline' or 'Inverse-B-
    Spline' or 'None')
    Transform type: Rigid or Inverse-B-Spline
    argument: ``--transformType %s``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Required: name of output NRRD file containing the resampled code
    image in acquisition space.
    argument: ``--outputVolume %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
    file)
    Required: name of output NRRD file containing the resampled code
    image in acquisition space.
```

75.6.21 gtractResampleDWIInPlace

[Link to code](#)

Wraps the executable command “ gtractResampleDWIInPlace “.

title: Resample DWI In Place

category: Diffusion.GTRACT

description: Resamples DWI image to structural image.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta, Greg Harris, Hans Johnson, and Joy Matsui.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Required: input image is a 4D NRRD image.
              argument: ``--inputVolume %s``
referenceVolume: (a pathlike object or string representing an
                  existing file)
                  If provided, resample to the final space of the referenceVolume 3D
                  data set.
                  argument: ``--referenceVolume %s``
outputResampledB0: (a boolean or a pathlike object or string
                    representing a file)
                    Convenience function for extracting the first index location
                    (assumed to be the B0)
                    argument: ``--outputResampledB0 %s``
inputTransform: (a pathlike object or string representing an existing
                 file)
                 Required: transform file derived from rigid registration of b0 image
                 to reference structural image.
                 argument: ``--inputTransform %s``
warpDWITransform: (a pathlike object or string representing an
                   existing file)
                   Optional: transform file to warp gradient volumes.
                   argument: ``--warpDWITransform %s``
debugLevel: (an integer (int or long))
             Display debug messages, and produce debug intermediate results.
             0=OFF, 1=Minimal, 10=Maximum debugging.
             argument: ``--debugLevel %d``
imageOutputSize: (a list of items which are an integer (int or long))
                  The voxel lattice for the output image, padding is added if
                  necessary. NOTE: if 0,0,0, then the inputVolume size is used.
                  argument: ``--imageOutputSize %s``
outputVolume: (a boolean or a pathlike object or string representing
               a file)
               Required: output image (NRRD file) that has been rigidly transformed
               into the space of the structural image and padded if image padding
               was changed from 0,0,0 default.
               argument: ``--outputVolume %s``
numberOfThreads: (an integer (int or long))
                  Explicitly specify the maximum number of threads to use.
                  argument: ``--numberOfThreads %d``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputResampledB0: (a pathlike object or string representing an
                    existing file)
                    Convenience function for extracting the first index location
                    (assumed to be the B0)
outputVolume: (a pathlike object or string representing an existing
               file)
               Required: output image (NRRD file) that has been rigidly transformed
```

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into the space of the structural image **and** padded **if** image padding was changed **from** 0,0,0 default.

75.6.22 gtractResampleFibers

[Link to code](#)

Wraps the executable command “ gtractResampleFibers “.

title: Resample Fibers

category: Diffusion.GTRACT

description: This program will resample a fiber tract with respect to a pair of deformation fields that represent the forward and reverse deformation fields.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
inputForwardDeformationFieldVolume: (a pathlike object or string
    representing an existing file)
    Required: input forward deformation field image file name
    argument: ``--inputForwardDeformationFieldVolume %s``
inputReverseDeformationFieldVolume: (a pathlike object or string
    representing an existing file)
    Required: input reverse deformation field image file name
    argument: ``--inputReverseDeformationFieldVolume %s``
inputTract: (a pathlike object or string representing an existing
    file)
    Required: name of input vtkPolydata file containing tract lines.
    argument: ``--inputTract %s``
outputTract: (a boolean or a pathlike object or string representing a
    file)
    Required: name of output vtkPolydata file containing tract lines and
    the point data collected along them.
    argument: ``--outputTract %s``
writeXMLPolyDataFile: (a boolean)
    Flag to make use of the XML format for vtkPolyData fiber tracts.
    argument: ``--writeXMLPolyDataFile ``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outputTract: (a pathlike object or string representing an existing
    file)
```

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Required: name of output vtkPolydata file containing tract lines **and** the point data collected along them.

75.6.23 gtractTensor

[Link to code](#)

Wraps the executable command “ gtractTensor “.

title: Tensor Estimation

category: Diffusion.GTRACT

description: This step will convert a b-value averaged diffusion tensor image to a 3x3 tensor voxel image. This step takes the diffusion tensor image data and generates a tensor representation of the data based on the signal intensity decay, b values applied, and the diffusion difrections. The apparent diffusion coefficient for a given orientation is computed on a pixel-by-pixel basis by fitting the image data (voxel intensities) to the Stejskal-Tanner equation. If at least 6 diffusion directions are used, then the diffusion tensor can be computed. This program uses itk::DiffusionTensor3DReconstructionImageFilter. The user can adjust background threshold, median filter, and isotropic resampling.

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta and Greg Harris.

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
    Required: input image 4D NRRD image. Must contain data based on at
    least 6 distinct diffusion directions. The inputVolume is allowed to
    have multiple b0 and gradient direction images. Averaging of the b0
    image is done internally in this step. Prior averaging of the DWIs
    is not required.
    argument: ``--inputVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
    Required: name of output NRRD file containing the Tensor vector
    image
    argument: ``--outputVolume %s``
medianFilterSize: (a list of items which are an integer (int or
                  long))
    Median filter radius in all 3 directions
    argument: ``--medianFilterSize %s``
maskProcessingMode: ('NOMASK' or 'ROIAUTO' or 'ROI')
    ROIAUTO: mask is implicitly defined using a otsu foreground and hole
    filling algorithm. ROI: Uses the masks to define what parts of the
    image should be used for computing the transform. NOMASK: no mask
    used
    argument: ``--maskProcessingMode %s``
maskVolume: (a pathlike object or string representing an existing
            file)
    Mask Image, if maskProcessingMode is ROI
    argument: ``--maskVolume %s``
backgroundSuppressingThreshold: (an integer (int or long))
    Image threshold to suppress background. This sets a threshold used
```

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```

    on the b0 image to remove background voxels from processing.
    Typically, values of 100 and 500 work well for Siemens and GE DTI
    data, respectively. Check your data particularly in the globus
    pallidus to make sure the brain tissue is not being eliminated with
    this threshold.
    argument: ``--backgroundSuppressingThreshold %d``
resampleIsotropic: (a boolean)
    Flag to resample to isotropic voxels. Enabling this feature is
    recommended if fiber tracking will be performed.
    argument: ``--resampleIsotropic``
size: (a float)
    Isotropic voxel size to resample to
    argument: ``--size %f``
b0Index: (an integer (int or long))
    Index in input vector index to extract
    argument: ``--b0Index %d``
applyMeasurementFrame: (a boolean)
    Flag to apply the measurement frame to the gradient directions
    argument: ``--applyMeasurementFrame``
ignoreIndex: (a list of items which are an integer (int or long))
    Ignore diffusion gradient index. Used to remove specific gradient
    directions with artifacts.
    argument: ``--ignoreIndex %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Required: name of output NRRD file containing the Tensor vector
    image

```

75.6.24 gtractTransformToDisplacementField**Link to code**

Wraps the executable command “ gtractTransformToDisplacementField “.

title: Create Displacement Field

category: Diffusion.GTRACT

description: This program will compute forward deformation from the given Transform. The size of the DF is equal to MNI space

version: 4.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:GTRACT>

license: <http://mri.radiology.uiowa.edu/copyright/GTRACT-Copyright.txt>

contributor: This tool was developed by Vincent Magnotta, Madhura Ingahalikar, and Greg Harris

acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1

Inputs:

```
[Optional]
inputTransform: (a pathlike object or string representing an existing
    file)
    Input Transform File Name
    argument: ``--inputTransform %s``
inputReferenceVolume: (a pathlike object or string representing an
    existing file)
    Required: input image file name to exemplify the anatomical space
    over which to vcl_express the transform as a displacement field.
    argument: ``--inputReferenceVolume %s``
outputDeformationFieldVolume: (a boolean or a pathlike object or
    string representing a file)
    Output deformation field
    argument: ``--outputDeformationFieldVolume %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables
```

Outputs:

```
outputDeformationFieldVolume: (a pathlike object or string
    representing an existing file)
    Output deformation field
```

75.7 interfaces.semtools.diffusion.maxcurvature

75.7.1 maxcurvature

Link to code

Wraps the executable command “ maxcurvature “.

title: MaxCurvature-Hessian (DTIPProcess)

category: Diffusion

description: This program computes the Hessian of the FA image (–image). We use this scalar image as a registration input when doing DTI atlas building. For most adult FA we use a sigma of 2 whereas for neonate or primate images and sigma of 1 or 1.5 is more appropriate. For really noisy images, 2.5 - 4 can be considered. The final image (–output) shows the main feature of the input image.

version: 1.1.0

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/Nightly/Extensions/DTIPProcess>

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contributor: Casey Goodlett

acknowledgements: Hans Johnson(1,3,4); Kent Williams(1); (1=University of Iowa Department of Psychiatry, 3=University of Iowa Department of Biomedical Engineering, 4=University of Iowa Department of Electrical and Computer Engineering) provided conversions to make DTIPProcess compatible with Slicer execution, and simplified the stand-alone build requirements by removing the dependancies on boost and a fortran compiler.

Inputs:

```
[Optional]
image: (a pathlike object or string representing an existing file)
      FA Image
      argument: ``--image %s``
output: (a boolean or a pathlike object or string representing a
        file)
        Output File
        argument: ``--output %s``
sigma: (a float)
        Scale of Gradients
        argument: ``--sigma %f``
verbose: (a boolean)
         produce verbose output
         argument: ``--verbose``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
output: (a pathlike object or string representing an existing file)
        Output File
```

75.8 interfaces.semtools.diffusion.tractography.commandlineonly**75.8.1 fiberstats**[Link to code](#)

Wraps the executable command “ fiberstats “.

title: FiberStats (DTIPProcess)

category: Diffusion.Tractography.CommandLineOnly

description: Obsolete tool - Not used anymore

version: 1.1.0

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/Nightly/Extensions/DTIPProcess>

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contributor: Casey Goodlett

acknowledgements: Hans Johnson(1,3,4); Kent Williams(1); (1=University of Iowa Department of Psychiatry, 3=University of Iowa Department of Biomedical Engineering, 4=University of Iowa Department of Electrical and Computer Engineering) provided conversions to make DTIPProcess compatible with Slicer execution, and simplified the stand-alone build requirements by removing the dependancies on boost and a fortran compiler.

Inputs:

```
[Optional]
fiber_file: (a pathlike object or string representing an existing
            file)
            DTI Fiber File
            argument: ``--fiber_file %s``
verbose: (a boolean)
```

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```

        produce verbose output
        argument: ``--verbose ``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

None

75.9 interfaces.semtools.diffusion.tractography.fiberprocess

75.9.1 fiberprocess

[Link to code](#)

Wraps the executable command “ fiberprocess “.

title: FiberProcess (DTIPProcess)

category: Diffusion.Tractography

description: fiberprocess is a tool that manage fiber files extracted from the fibertrack tool or any fiber tracking algorithm. It takes as an input .fib and .vtk files (–fiber_file) and saves the changed fibers (–fiber_output) into the 2 same formats. The main purpose of this tool is to deform the fiber file with a transformation field as an input (–displacement_field or –h_field depending if you deal with dfield or hfield). To use that option you need to specify the tensor field from which the fiber file was extracted with the option –tensor_volume. The transformation applied on the fiber file is the inverse of the one input. If the transformation is from one case to an atlas, fiberprocess assumes that the fiber file is in the atlas space and you want it in the original case space, so it’s the inverse of the transformation which has been computed. You have 2 options for fiber modification. You can either deform the fibers (their geometry) into the space OR you can keep the same geometry but map the diffusion properties (fa, md, lbd’s...) of the original tensor field along the fibers at the corresponding locations. This is triggered by the –no_warp option. To use the previous example: when you have a tensor field in the original space and the deformed tensor field in the atlas space, you want to track the fibers in the atlas space, keeping this geometry but with the original case diffusion properties. Then you can specify the transformations field (from original case -> atlas) and the original tensor field with the –tensor_volume option. With fiberprocess you can also binarize a fiber file. Using the –voxelize option will create an image where each voxel through which a fiber is passing is set to 1. The output is going to be a binary image with the values 0 or 1 by default but the 1 value voxel can be set to any number with the –voxel_label option. Finally you can create an image where the value at the voxel is the number of fiber passing through. (–voxelize_count_fibers)

version: 1.0.0

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/Nightly/Extensions/DTIPProcess>

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contributor: Casey Goodlett

Inputs:

```

[Optional]
fiber_file: (a pathlike object or string representing an existing
            file)
            DTI fiber file

```

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```

    argument: ``--fiber_file %s``
fiber_output: (a boolean or a pathlike object or string representing
    a file)
    Output fiber file. May be warped or updated with new data depending
    on other options used.
    argument: ``--fiber_output %s``
tensor_volume: (a pathlike object or string representing an existing
    file)
    Interpolate tensor values from the given field
    argument: ``--tensor_volume %s``
h_field: (a pathlike object or string representing an existing file)
    HField for warp and statistics lookup. If this option is used
    tensor-volume must also be specified.
    argument: ``--h_field %s``
displacement_field: (a pathlike object or string representing an
    existing file)
    Displacement Field for warp and statistics lookup. If this option is
    used tensor-volume must also be specified.
    argument: ``--displacement_field %s``
saveProperties: (a boolean)
    save the tensor property as scalar data into the vtk (only works for
    vtk fiber files).
    argument: ``--saveProperties ``
no_warp: (a boolean)
    Do not warp the geometry of the tensors only obtain the new
    statistics.
    argument: ``--no_warp ``
fiber_radius: (a float)
    set radius of all fibers to this value
    argument: ``--fiber_radius %f``
index_space: (a boolean)
    Use index-space for fiber output coordinates, otherwise us world
    space for fiber output coordinates (from tensor file).
    argument: ``--index_space ``
voxelize: (a boolean or a pathlike object or string representing a
    file)
    Voxelize fiber into a label map (the labelmap filename is the
    argument of -V). The tensor file must be specified using -T for
    information about the size, origin, spacing of the image. The
    deformation is applied before the voxelization
    argument: ``--voxelize %s``
voxelize_count_fibers: (a boolean)
    Count number of fibers per-voxel instead of just setting to 1
    argument: ``--voxelize_count_fibers ``
voxel_label: (an integer (int or long))
    Label for voxelized fiber
    argument: ``--voxel_label %d``
verbose: (a boolean)
    produce verbose output
    argument: ``--verbose ``
noDataChange: (a boolean)
    Do not change data ???
    argument: ``--noDataChange ``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value

```

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```

of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

fiber_output: (a pathlike object or string representing an existing
               file)
               Output fiber file. May be warped or updated with new data depending
               on other options used.
voxelize: (a pathlike object or string representing an existing file)
           Voxelize fiber into a label map (the labelmap filename is the
           argument of -V). The tensor file must be specified using -T for
           information about the size, origin, spacing of the image. The
           deformation is applied before the voxelization

```

75.10 interfaces.semtools.diffusion.tractography.fibertrack

75.10.1 fibertrack

Link to code

Wraps the executable command “ fibertrack “.

title: FiberTrack (DTIPProcess)

category: Diffusion.Tractography

description: This program implements a simple streamline tractography method based on the principal eigenvector of the tensor field. A fourth order Runge-Kutta integration rule used to advance the streamlines. As a first parameter you have to input the tensor field (with the `-input_tensor_file` option). Then the region of interest image file is set with the `-input_roi_file`. Next you want to set the output fiber file name after the `-output_fiber_file` option. You can specify the label value in the input_roi_file with the `-target_label`, `-source_label` and `-forbidden_label` options. By default target label is 1, source label is 2 and forbidden label is 0. The source label is where the streamlines are seeded, the target label defines the voxels through which the fibers must pass by to be kept in the final fiber file and the forbidden label defines the voxels where the streamlines are stopped if they pass through it. There is also a `-whole_brain` option which, if enabled, consider both target and source labels of the roi image as target labels and all the voxels of the image are considered as sources. During the tractography, the `-fa_min` parameter is used as the minimum value needed at different voxel for the tracking to keep going along a streamline. The `-step_size` parameter is used for each iteration of the tracking algorithm and defines the length of each step. The `-max_angle` option defines the maximum angle allowed between two successive segments along the tracked fiber.

version: 1.1.0

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/Nightly/Extensions/DTIPProcess>

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See <http://www.ia.unc.edu/dev/Copyright.htm> for details. This software is distributed WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. See the above copyright notices for more information.

contributor: Casey Goodlett

acknowledgements: Hans Johnson(1,3,4); Kent Williams(1); (1=University of Iowa Department of Psychiatry, 3=University of Iowa Department of Biomedical Engineering, 4=University of Iowa Department of Electrical and Computer Engineering) provided conversions to make DTIPProcess compatible with Slicer execution, and simplified the stand-alone build requirements by removing the dependancies on boost and a fortran compiler.

Inputs:

```

[Optional]
input_tensor_file: (a pathlike object or string representing an

```

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```

    existing file)
    Tensor Image
    argument: ``--input_tensor_file %s``
input_roi_file: (a pathlike object or string representing an existing
    file)
    The filename of the image which contains the labels used for seeding
    and constraining the algorithm.
    argument: ``--input_roi_file %s``
output_fiber_file: (a boolean or a pathlike object or string
    representing a file)
    The filename for the fiber file produced by the algorithm. This file
    must end in a .fib or .vtk extension for ITK spatial object and
    vtkPolyData formats respectively.
    argument: ``--output_fiber_file %s``
source_label: (an integer (int or long))
    The label of voxels in the labelfile to use for seeding
    tractography. One tract is seeded from the center of each voxel with
    this label
    argument: ``--source_label %d``
target_label: (an integer (int or long))
    The label of voxels in the labelfile used to constrain tractography.
    Tracts that do not pass through a voxel with this label are
    rejected. Set this keep all tracts.
    argument: ``--target_label %d``
forbidden_label: (an integer (int or long))
    Forbidden label
    argument: ``--forbidden_label %d``
whole_brain: (a boolean)
    If this option is enabled all voxels in the image are used to seed
    tractography. When this option is enabled both source and target
    labels function as target labels
    argument: ``--whole_brain ``
max_angle: (a float)
    Maximum angle of change in radians
    argument: ``--max_angle %f``
step_size: (a float)
    Step size in mm for the tracking algorithm
    argument: ``--step_size %f``
min_fa: (a float)
    The minimum FA threshold to continue tractography
    argument: ``--min_fa %f``
force: (a boolean)
    Ignore sanity checks.
    argument: ``--force ``
verbose: (a boolean)
    produce verbose output
    argument: ``--verbose ``
really_verbose: (a boolean)
    Follow detail of fiber tracking algorithm
    argument: ``--really_verbose ``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

output_fiber_file: (a pathlike object or string representing an
                    existing file)
                    The filename for the fiber file produced by the algorithm. This file
                    must end in a .fib or .vtk extension for ITK spatial object and
                    vtkPolyData formats respectively.

```

75.11 interfaces.semttools.diffusion.tractography.ukftractography

75.11.1 UKFTractography

Link to code

Wraps the executable command “ UKFTractography “.

title: UKF Tractography

category: Diffusion.Tractography

description: This module traces fibers in a DWI Volume using the multiple tensor unscented Kalman Filter methodology. For more informations check the documentation.

version: 1.0

documentation-url: <http://www.nitrc.org/plugins/mwiki/index.php/ukftractography:MainPage>

contributor: Yogesh Rath, Stefan Lienhard, Yinpeng Li, Martin Styner, Ipek Oguz, Yundi Shi, Christian Baumgartner, Kent Williams, Hans Johnson, Peter Savadjiev, Carl-Fredrik Westin.

acknowledgements: The development of this module was supported by NIH grants R01 MH097979 (PI Rath), R01 MH092862 (PIs Westin and Verma), U01 NS083223 (PI Westin), R01 MH074794 (PI Westin) and P41 EB015902 (PI Kikinis).

Inputs:

```

[Optional]
dwiFile: (a pathlike object or string representing an existing file)
         Input DWI volume
         argument: ``--dwiFile %s``
seedsFile: (a pathlike object or string representing an existing
            file)
            Seeds for diffusion. If not specified, full brain tractography will
            be performed, and the algorithm will start from every voxel in the
            brain mask where the Generalized Anisotropy is bigger than 0.18
            argument: ``--seedsFile %s``
labels: (a list of items which are an integer (int or long))
         A vector of the ROI labels to be used
         argument: ``--labels %s``
maskFile: (a pathlike object or string representing an existing file)
          Mask for diffusion tractography
          argument: ``--maskFile %s``
tracts: (a boolean or a pathlike object or string representing a
         file)
         Tracts generated, with first tensor output
         argument: ``--tracts %s``
writeAsciiTracts: (a boolean)
                  Write tract file as a VTK binary data file
                  argument: ``--writeAsciiTracts ``
writeUncompressedTracts: (a boolean)
                          Write tract file as a VTK uncompressed data file
                          argument: ``--writeUncompressedTracts ``
seedsPerVoxel: (an integer (int or long))
               Each seed generates a fiber, thus using more seeds generates more

```

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```

        fibers. In general use 1 or 2 seeds, and for a more thorough result
        use 5 or 10 (depending on your machine this may take up to 2 days to
        run).,
        argument: ``--seedsPerVoxel %d``
numTensor: ('1' or '2')
    Number of tensors used
    argument: ``--numTensor %s``
freeWater: (a boolean)
    Adds a term for free water difusion to the model. (Note for experts:
    if checked, the 1T simple model is forced)
    argument: ``--freeWater``
recordFA: (a boolean)
    Whether to store FA. Attaches field 'FA', and 'FA2' for 2-tensor
    case to fiber.
    argument: ``--recordFA``
recordFreeWater: (a boolean)
    Whether to store the fraction of free water. Attaches field
    'FreeWater' to fiber.
    argument: ``--recordFreeWater``
recordTrace: (a boolean)
    Whether to store Trace. Attaches field 'Trace', and 'Trace2' for
    2-tensor case to fiber.
    argument: ``--recordTrace``
recordTensors: (a boolean)
    Recording the tensors enables Slicer to color the fiber bundles by
    FA, orientation, and so on. The fields will be called 'TensorN',
    where N is the tensor number.
    argument: ``--recordTensors``
recordNMSE: (a boolean)
    Whether to store NMSE. Attaches field 'NMSE' to fiber.
    argument: ``--recordNMSE``
recordState: (a boolean)
    Whether to attach the states to the fiber. Will generate field
    'state'.
    argument: ``--recordState``
recordCovariance: (a boolean)
    Whether to store the covariance. Will generate field 'covariance' in
    fiber.
    argument: ``--recordCovariance``
recordLength: (a float)
    Record length of tractography, in millimeters
    argument: ``--recordLength %f``
minFA: (a float)
    Abort the tractography when the Fractional Anisotropy is less than
    this value
    argument: ``--minFA %f``
minGA: (a float)
    Abort the tractography when the Generalized Anisotropy is less than
    this value
    argument: ``--minGA %f``
fullTensorModel: (a boolean)
    Whether to use the full tensor model. If unchecked, use the default
    simple tensor model
    argument: ``--fullTensorModel``
numThreads: (an integer (int or long))
    Number of threads used during computation. Set to the number of
    cores on your workstation for optimal speed. If left undefined the

```

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        number of cores detected will be used.
        argument: ``--numThreads %d``
stepLength: (a float)
    Step length of tractography, in millimeters
    argument: ``--stepLength %f``
maxHalfFiberLength: (a float)
    The max length limit of the half fibers generated during
    tractography. Here the fiber is 'half' because the tractography goes
    in only one direction from one seed point at a time
    argument: ``--maxHalfFiberLength %f``
seedFALimit: (a float)
    Seed points whose FA are below this value are excluded
    argument: ``--seedFALimit %f``
Qm: (a float)
    Process noise for angles/direction
    argument: ``--Qm %f``
Ql: (a float)
    Process noise for eigenvalues
    argument: ``--Ql %f``
Qw: (a float)
    Process noise for free water weights, ignored if no free water
    estimation
    argument: ``--Qw %f``
Rs: (a float)
    Measurement noise
    argument: ``--Rs %f``
maxBranchingAngle: (a float)
    Maximum branching angle, in degrees. When using multiple tensors, a
    new branch will be created when the tensors' major directions form
    an angle between (minBranchingAngle, maxBranchingAngle). Branching
    is suppressed when this maxBranchingAngle is set to 0.0
    argument: ``--maxBranchingAngle %f``
minBranchingAngle: (a float)
    Minimum branching angle, in degrees. When using multiple tensors, a
    new branch will be created when the tensors' major directions form
    an angle between (minBranchingAngle, maxBranchingAngle)
    argument: ``--minBranchingAngle %f``
tractsWithSecondTensor: (a boolean or a pathlike object or string
    representing a file)
    Tracts generated, with second tensor output (if there is one)
    argument: ``--tractsWithSecondTensor %s``
storeGlyphs: (a boolean)
    Store tensors' main directions as two-point lines in a separate file
    named glyphs_{tracts}. When using multiple tensors, only the major
    tensors' main directions are stored
    argument: ``--storeGlyphs``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables

```

Outputs:

```

tracts: (a pathlike object or string representing an existing file)

```

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```

Tracts generated, with first tensor output
tractsWithSecondTensor: (a pathlike object or string representing an
    existing file)
Tracts generated, with second tensor output (if there is one)

```

75.12 interfaces.semtools.featurecreator

75.12.1 GenerateCsfClippedFromClassifiedImage

[Link to code](#)

Wraps the executable command “GenerateCsfClippedFromClassifiedImage”.

title: GenerateCsfClippedFromClassifiedImage

category: FeatureCreator

description: Get the distance from a voxel to the nearest voxel of a given tissue type.

version: 0.1.0.\$Revision: 1 \$(alpha)

documentation-url: <http://www.na-mic.org/>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was written by Hans J. Johnson.

Inputs:

```

[Optional]
inputCassifiedVolume: (a pathlike object or string representing an
    existing file)
    Required: input tissue label image
    argument: ``--inputCassifiedVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Required: output image
    argument: ``--outputVolume %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Required: output image

```

75.13 interfaces.semtools.filtering.denoising

75.13.1 UnbiasedNonLocalMeans

[Link to code](#)

Wraps the executable command “UnbiasedNonLocalMeans”.

title: Unbiased NLM for MRI

category: Filtering.Denoising

description: This module implements a fast version of the popular Non-Local Means filter for image denoising. This algorithm

In the original formulation a patch with a certain radius is centered in each of the voxels, and the Mean Squared Error between each pair of corresponding voxels is computed. In this implementation, only the

mean value and gradient components are compared. This, together with an efficient memory management, can attain a speed-up of nearly 20x. Besides, the filtering is more accurate than the original with poor SNR. This code is intended for its use with MRI (or any other Rician-distributed modality): the second order moment is estimated, then we subtract twice the squared power of noise, and finally we take the square root of the result to remove the Rician bias. The original implementation of the NLM filter may be found in: A. Buades, B. Coll, J. Morel, "A review of image denoising algorithms, with a new one", Multiscale Modelling and Simulation 4(2): 490-530. 2005. The correction of the Rician bias is described in the following reference (among others): S. Aja-Fernandez, K. Krissian, "An unbiased Non-Local Means scheme for DWI filtering", in: Proceedings of the MICCAI Workshop on Computational Diffusion MRI, 2008, pp. 277-284. The whole description of this version may be found in the following paper (please, cite it if you are willing to use this software): A. Tristan-Vega, V. Garcia Perez, S. Aja-Fernandez, and C.-F. Westin, "Efficient and Robust Nonlocal Means Denoising of MR Data Based on Salient Features Matching", Computer Methods and Programs in Biomedicine. (Accepted for publication) 2011.

version: 0.0.1.\$Revision: 1 \$(beta)

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Modules:UnbiasedNonLocalMeans-Documentation-3.6>

contributor: Antonio Tristan Vega, Veronica Garcia-Perez, Santiago Aja-Fernandez, Carl-Fredrik Westin

acknowledgements: Supported by grant number FMECD-2010/71131616E from the Spanish Ministry of Education/Fulbright Committee

Inputs:

```
[Optional]
sigma: (a float)
    The root power of noise (sigma) in the complex Gaussian process the
    Rician comes from. If it is underestimated, the algorithm fails to
    remove the noise. If it is overestimated, over-blurring is likely to
    occur.
    argument: ``--sigma %f``
rs: (a list of items which are an integer (int or long))
    The algorithm search for similar voxels in a neighborhood of this
    radius (radii larger than 5,5,5 are very slow, and the results can
    be only marginally better. Small radii may fail to effectively
    remove the noise).
    argument: ``--rs %s``
rc: (a list of items which are an integer (int or long))
    Similarity between blocks is computed as the difference between mean
    values and gradients. These parameters are computed fitting a
    hyperplane with LS inside a neighborhood of this size
    argument: ``--rc %s``
hp: (a float)
    This parameter is related to noise; the larger the parameter, the
    more aggressive the filtering. Should be near 1, and only values
    between 0.8 and 1.2 are allowed
    argument: ``--hp %f``
ps: (a float)
    To accelerate computations, preselection is used: if the normalized
    difference is above this threshold, the voxel will be discarded (non
    used for average)
    argument: ``--ps %f``
inputVolume: (a pathlike object or string representing an existing
    file)
    Input MRI volume.
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output (filtered) MRI volume.
```

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```

        argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Output (filtered) MRI volume.

```

75.14 interfaces.semtools.filtering.featuredetection**75.14.1 CannyEdge**[Link to code](#)

Wraps the executable command “CannyEdge”.

title: Canny Edge Detection

category: Filtering.FeatureDetection

description: Get the distance from a voxel to the nearest voxel of a given tissue type.

version: 0.1.0.(alpha)

documentation-url: <http://www.na-mic.org/>license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was written by Hans J. Johnson.

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    Required: input tissue label image
    argument: ``--inputVolume %s``
variance: (a float)
    Variance and Maximum error are used in the Gaussian smoothing of the
    input image. See itkDiscreteGaussianImageFilter for information on
    these parameters.
    argument: ``--variance %f``
upperThreshold: (a float)
    Threshold is the lowest allowed value in the output image. Its data
    type is the same as the data type of the output image. Any values
    below the Threshold level will be replaced with the OutsideValue
    parameter value, whose default is zero.
    argument: ``--upperThreshold %f``
lowerThreshold: (a float)
    Threshold is the lowest allowed value in the output image. Its data
    type is the same as the data type of the output image. Any values
    below the Threshold level will be replaced with the OutsideValue
    parameter value, whose default is zero.
    argument: ``--lowerThreshold %f``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Required: output image

```

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```

        argument: ``--outputVolume %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Required: output image

```

75.14.2 CannySegmentationLevelSetImageFilter**Link to code**

Wraps the executable command “CannySegmentationLevelSetImageFilter”.

title: Canny Level Set Image Filter

category: Filtering.FeatureDetection

description: The CannySegmentationLevelSet is commonly used to refine a manually generated manual mask.

version: 0.3.0

license: CC

contributor: Regina Kim

acknowledgements: This command module was derived from Insight/Examples/Segmentation/CannySegmentationLevelSetImageFilter (copyright) Insight Software Consortium. See http://wiki.na-mic.org/Wiki/index.php/Slicer3:Execution_Model_Documentation for more detailed descriptions.

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    argument: ``--inputVolume %s``
initialModel: (a pathlike object or string representing an existing
    file)
    argument: ``--initialModel %s``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    argument: ``--outputVolume %s``
outputSpeedVolume: (a boolean or a pathlike object or string
    representing a file)
    argument: ``--outputSpeedVolume %s``
cannyThreshold: (a float)
    Canny Threshold Value
    argument: ``--cannyThreshold %f``
cannyVariance: (a float)
    Canny variance
    argument: ``--cannyVariance %f``
advectionWeight: (a float)
    Controls the smoothness of the resulting mask, small number are more
    smooth, large numbers allow more sharp corners.
    argument: ``--advectionWeight %f``
initialModelIsovalue: (a float)
    The identification of the input model iso-surface. (for a binary
    image with 0s and 1s use 0.5) (for a binary image with 0s and 255's

```

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```

        use 127.5).
        argument: ``--initialModelIsovalue %f``
maxIterations: (an integer (int or long))
    The
        argument: ``--maxIterations %d``
args: (a unicode string)
    Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
outputSpeedVolume: (a pathlike object or string representing an
    existing file)

```

75.14.3 DilateImage[Link to code](#)

Wraps the executable command “DilateImage”.

title: Dilate Image

category: Filtering.FeatureDetection

description: Uses mathematical morphology to dilate the input images.

version: 0.1.0.\$Revision: 1 \$(alpha)

documentation-url: <http://www.na-mic.org/>license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Mark Scully and Jeremy Bockholt.

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    Required: input image
        argument: ``--inputVolume %s``
inputMaskVolume: (a pathlike object or string representing an
    existing file)
    Required: input brain mask image
        argument: ``--inputMaskVolume %s``
inputRadius: (an integer (int or long))
    Required: input neighborhood radius
        argument: ``--inputRadius %d``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Required: output image
        argument: ``--outputVolume %s``
args: (a unicode string)
    Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               Required: output image
```

75.14.4 DilateMask[Link to code](#)

Wraps the executable command “DilateMask”.

title: Dilate Image

category: Filtering.FeatureDetection

description: Uses mathematical morphology to dilate the input images.

version: 0.1.0.\$Revision: 1 \$(alpha)

documentation-url: <http://www.na-mic.org/>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Mark Scully and Jeremy Bockholt.

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Required: input image
              argument: ``--inputVolume %s``
inputBinaryVolume: (a pathlike object or string representing an
                    existing file)
                    Required: input brain mask image
                    argument: ``--inputBinaryVolume %s``
sizeStructuralElement: (an integer (int or long))
                        size of structural element. sizeStructuralElement=1 means that 3x3x3
                        structuring element for 3D
                        argument: ``--sizeStructuralElement %d``
lowerThreshold: (a float)
                Required: lowerThreshold value
                argument: ``--lowerThreshold %f``
outputVolume: (a boolean or a pathlike object or string representing
               a file)
               Required: output image
               argument: ``--outputVolume %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               Required: output image
```

75.14.5 DistanceMaps[Link to code](#)

Wraps the executable command “DistanceMaps”.

title: Mauerer Distance
category: Filtering.FeatureDetection
description: Get the distance from a voxel to the nearest voxel of a given tissue type.
version: 0.1.0.\$Revision: 1 \$(alpha)
documentation-url: <http://www.na-mic.org/>
license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>
contributor: This tool was developed by Mark Scully and Jeremy Bockholt.
Inputs:

```
[Optional]
inputLabelVolume: (a pathlike object or string representing an
    existing file)
    Required: input tissue label image
    argument: ``--inputLabelVolume %s``
inputMaskVolume: (a pathlike object or string representing an
    existing file)
    Required: input brain mask image
    argument: ``--inputMaskVolume %s``
inputTissueLabel: (an integer (int or long))
    Required: input integer value of tissue type used to calculate
    distance
    argument: ``--inputTissueLabel %d``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Required: output image
    argument: ``--outputVolume %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
    file)
    Required: output image
```

75.14.6 DumpBinaryTrainingVectors

[Link to code](#)

Wraps the executable command “ DumpBinaryTrainingVectors “.

title: Erode Image
category: Filtering.FeatureDetection
description: Uses mathematical morphology to erode the input images.
version: 0.1.0.\$Revision: 1 \$(alpha)
documentation-url: <http://www.na-mic.org/>
license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>
contributor: This tool was developed by Mark Scully and Jeremy Bockholt.
Inputs:

```
[Optional]
inputHeaderFilename: (a pathlike object or string representing an
    existing file)
    Required: input header file name
```

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```

    argument: ``--inputHeaderFilename %s``
inputVectorFilename: (a pathlike object or string representing an
    existing file)
    Required: input vector filename
    argument: ``--inputVectorFilename %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

None

75.14.7 ErodeImage

[Link to code](#)

Wraps the executable command “ ErodeImage “.

title: Erode Image

category: Filtering.FeatureDetection

description: Uses mathematical morphology to erode the input images.

version: 0.1.0.\$Revision: 1 \$(alpha)

documentation-url: <http://www.na-mic.org/>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Mark Scully and Jeremy Bockholt.

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    Required: input image
    argument: ``--inputVolume %s``
inputMaskVolume: (a pathlike object or string representing an
    existing file)
    Required: input brain mask image
    argument: ``--inputMaskVolume %s``
inputRadius: (an integer (int or long))
    Required: input neighborhood radius
    argument: ``--inputRadius %d``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Required: output image
    argument: ``--outputVolume %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               Required: output image
```

75.14.8 FlippedDifference

[Link to code](#)

Wraps the executable command “ FlippedDifference “.

title: Flip Image

category: Filtering.FeatureDetection

description: Difference between an image and the axially flipped version of that image.

version: 0.1.0.\$Revision: 1 \$(alpha)

documentation-url: <http://www.na-mic.org/>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Mark Scully and Jeremy Bockholt.

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Required: input image
              argument: ``--inputVolume %s``
inputMaskVolume: (a pathlike object or string representing an
                  existing file)
                  Required: input brain mask image
                  argument: ``--inputMaskVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
               a file)
               Required: output image
               argument: ``--outputVolume %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               Required: output image
```

75.14.9 GenerateBrainClippedImage

[Link to code](#)

Wraps the executable command “ GenerateBrainClippedImage “.

title: GenerateBrainClippedImage

category: Filtering.FeatureDetection

description: Automatic FeatureImages using neural networks

version: 1.0

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Eun Young Kim

Inputs:


```
[Optional]
inputImg: (a pathlike object or string representing an existing file)
    input volume 1, usually t1 image
    argument: ``--inputImg %s``
inputMsk: (a pathlike object or string representing an existing file)
    input volume 2, usually t2 image
    argument: ``--inputMsk %s``
outputFileName: (a boolean or a pathlike object or string
    representing a file)
    (required) output file name
    argument: ``--outputFileName %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outputFileName: (a pathlike object or string representing an existing
    file)
    (required) output file name
```

75.14.10 GenerateSummedGradientImage**Link to code**

Wraps the executable command “GenerateSummedGradientImage”.

title: GenerateSummedGradient

category: Filtering.FeatureDetection

description: Automatic FeatureImages using neural networks

version: 1.0

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Greg Harris, Eun Young Kim

Inputs:

```
[Optional]
inputVolume1: (a pathlike object or string representing an existing
    file)
    input volume 1, usually t1 image
    argument: ``--inputVolume1 %s``
inputVolume2: (a pathlike object or string representing an existing
    file)
    input volume 2, usually t2 image
    argument: ``--inputVolume2 %s``
outputFileName: (a boolean or a pathlike object or string
    representing a file)
    (required) output file name
    argument: ``--outputFileName %s``
MaximumGradient: (a boolean)
    If set this flag, it will compute maximum gradient between two input
    volumes instead of sum of it.
    argument: ``--MaximumGradient ``
```

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```

numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputFileName: (a pathlike object or string representing an existing
    file)
    (required) output file name

```

75.14.11 GenerateTestImage**Link to code**

Wraps the executable command “GenerateTestImage”.

title: DownSampleImage

category: Filtering.FeatureDetection

description: Down sample image for testing

version: 1.0

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Eun Young Kim

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    input volume 1, usually t1 image
    argument: ``--inputVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    (required) output file name
    argument: ``--outputVolume %s``
lowerBoundOfOutputVolume: (a float)
    argument: ``--lowerBoundOfOutputVolume %f``
upperBoundOfOutputVolume: (a float)
    argument: ``--upperBoundOfOutputVolume %f``
outputVolumeSize: (a float)
    output Volume Size
    argument: ``--outputVolumeSize %f``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing

```

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```
file)
(required) output file name
```

75.14.12 GradientAnisotropicDiffusionImageFilter

[Link to code](#)

Wraps the executable command “ GradientAnisotropicDiffusionImageFilter “.

title: GradientAnisotropicDiffusionFilter

category: Filtering.FeatureDetection

description: Image Smoothing using Gradient Anisotropic Diffuesion Filer

contributor: This tool was developed by Eun Young Kim by modifying ITK Example

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Required: input image
              argument: ``--inputVolume %s``
numberOfIterations: (an integer (int or long))
                    Optional value for number of Iterations
                    argument: ``--numberOfIterations %d``
timeStep: (a float)
          Time step for diffusion process
          argument: ``--timeStep %f``
conductance: (a float)
            Conductance for diffusion process
            argument: ``--conductance %f``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              Required: output image
              argument: ``--outputVolume %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipype default value: {})
         Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
              file)
              Required: output image
```

75.14.13 HammerAttributeCreator

[Link to code](#)

Wraps the executable command “ HammerAttributeCreator “.

title: HAMMER Feature Vectors

category: Filtering.FeatureDetection

description: Create the feature vectors used by HAMMER.

version: 0.1.0.\$Revision: 1 \$(alpha)

documentation-url: <http://www.na-mic.org/>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This was extracted from the Hammer Registration source code, and wrapped up by Hans J. Johnson.
Inputs:

```
[Optional]
Scale: (an integer (int or long))
    Determine Scale of Ball
    argument: ``--Scale %d``
Strength: (a float)
    Determine Strength of Edges
    argument: ``--Strength %f``
inputGMVolume: (a pathlike object or string representing an existing
    file)
    Required: input grey matter posterior image
    argument: ``--inputGMVolume %s``
inputWMVolume: (a pathlike object or string representing an existing
    file)
    Required: input white matter posterior image
    argument: ``--inputWMVolume %s``
inputCSFVolume: (a pathlike object or string representing an existing
    file)
    Required: input CSF posterior image
    argument: ``--inputCSFVolume %s``
outputVolumeBase: (a unicode string)
    Required: output image base name to be appended for each feature
    vector.
    argument: ``--outputVolumeBase %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

None

75.14.14 NeighborhoodMean

[Link to code](#)

Wraps the executable command “NeighborhoodMean”.

title: Neighborhood Mean

category: Filtering.FeatureDetection

description: Calculates the mean, for the given neighborhood size, at each voxel of the T1, T2, and FLAIR.

version: 0.1.0.\$Revision: 1 \$(alpha)

documentation-url: <http://www.na-mic.org/>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Mark Scully and Jeremy Bockholt.

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    Required: input image
    argument: ``--inputVolume %s``
inputMaskVolume: (a pathlike object or string representing an
```

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```

    existing file)
    Required: input brain mask image
    argument: ``--inputMaskVolume %s``
inputRadius: (an integer (int or long))
    Required: input neighborhood radius
    argument: ``--inputRadius %d``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Required: output image
    argument: ``--outputVolume %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Required: output image

```

75.14.15 NeighborhoodMedian[Link to code](#)

Wraps the executable command “NeighborhoodMedian”.

title: Neighborhood Median

category: Filtering.FeatureDetection

description: Calculates the median, for the given neighborhood size, at each voxel of the input image.

version: 0.1.0.\$Revision: 1 \$(alpha)

documentation-url: <http://www.na-mic.org/>license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Mark Scully and Jeremy Bockholt.

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    Required: input image
    argument: ``--inputVolume %s``
inputMaskVolume: (a pathlike object or string representing an
    existing file)
    Required: input brain mask image
    argument: ``--inputMaskVolume %s``
inputRadius: (an integer (int or long))
    Required: input neighborhood radius
    argument: ``--inputRadius %d``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Required: output image
    argument: ``--outputVolume %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``

```

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```
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               Required: output image
```

75.14.16 STAPLEAnalysis

[Link to code](#)

Wraps the executable command “ STAPLEAnalysis “.

title: Dilate Image

category: Filtering.FeatureDetection

description: Uses mathematical morphology to dilate the input images.

version: 0.1.0.\$Revision: 1 \$(alpha)

documentation-url: <http://www.na-mic.org/>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Mark Scully and Jeremy Bockholt.

Inputs:

```
[Optional]
inputDimension: (an integer (int or long))
                 Required: input image Dimension 2 or 3
                 argument: ``--inputDimension %d``
inputLabelVolume: (a list of items which are a pathlike object or
                  string representing an existing file)
                  Required: input label volume
                  argument: ``--inputLabelVolume %s...``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              Required: output image
              argument: ``--outputVolume %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               Required: output image
```

75.14.17 TextureFromNoiseImageFilter

[Link to code](#)

Wraps the executable command “ TextureFromNoiseImageFilter “.

title: TextureFromNoiseImageFilter

category: Filtering.FeatureDetection

description: Calculate the local noise in an image.

version: 0.1.0.\$Revision: 1 \$(alpha)

documentation-url: <http://www.na-mic.org/>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Eunyoung Regina Kim

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Required: input image
              argument: ``--inputVolume %s``
inputRadius: (an integer (int or long))
              Required: input neighborhood radius
              argument: ``--inputRadius %d``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              Required: output image
              argument: ``--outputVolume %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
              file)
              Required: output image
```

75.14.18 TextureMeasureFilter

[Link to code](#)

Wraps the executable command “TextureMeasureFilter”.

title: Canny Level Set Image Filter

category: Filtering.FeatureDetection

description: The CannySegmentationLevelSet is commonly used to refine a manually generated manual mask.

version: 0.3.0

license: CC

contributor: Regina Kim

acknowledgements: This command module was derived from Insight/Examples/Segmentation/CannySegmentationLevelSetImage (copyright) Insight Software Consortium. See http://wiki.na-mic.org/Wiki/index.php/Slicer3:Execution_Model_Documentation for more detailed descriptions.

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              argument: ``--inputVolume %s``
inputMaskVolume: (a pathlike object or string representing an
                  existing file)
                  argument: ``--inputMaskVolume %s``
distance: (an integer (int or long))
          argument: ``--distance %d``
```

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```

insideROIValue: (a float)
    argument: ``--insideROIValue %f``
outputFilename: (a boolean or a pathlike object or string
    representing a file)
    argument: ``--outputFilename %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputFilename: (a pathlike object or string representing an existing
    file)

```

75.15 interfaces.semtools.legacy.registration

75.15.1 scalartransform

[Link to code](#)

Wraps the executable command “ scalartransform “.

title: ScalarTransform (DTIPProcess)

category: Legacy.Registration

version: 1.0.0

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/Nightly/Extensions/DTIPProcess>

license: Copyright (c) Casey Goodlett. All rights reserved.

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contributor: Casey Goodlett

Inputs:

```

[Optional]
input_image: (a pathlike object or string representing an existing
    file)
    Image to transform
    argument: ``--input_image %s``
output_image: (a boolean or a pathlike object or string representing
    a file)
    The transformed image
    argument: ``--output_image %s``
transformation: (a boolean or a pathlike object or string
    representing a file)
    Output file for transformation parameters
    argument: ``--transformation %s``
invert: (a boolean)
    Invert transform before applying.
    argument: ``--invert ``
deformation: (a pathlike object or string representing an existing
    file)
    Deformation field.
    argument: ``--deformation %s``

```

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```

h_field: (a boolean)
    The deformation is an h-field.
    argument: ``--h_field``
interpolation: ('nearestneighbor' or 'linear' or 'cubic')
    Interpolation type (nearestneighbor, linear, cubic)
    argument: ``--interpolation %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

output_image: (a pathlike object or string representing an existing
    file)
    The transformed image
transformation: (a pathlike object or string representing an existing
    file)
    Output file for transformation parameters

```

75.16 interfaces.semtools.registration.brainsfit

75.16.1 BRAINSFit

Link to code

Wraps the executable command “BRAINSFit”.

title: General Registration (BRAINS)

category: Registration

description: Register a three-dimensional volume to a reference volume (Mattes Mutual Information by default). Full documentation available here: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/BRAINSFit>. Method described in BRAINSFit: Mutual Information Registrations of Whole-Brain 3D Images, Using the Insight Toolkit, Johnson H.J., Harris G., Williams K., The Insight Journal, 2007. <http://hdl.handle.net/1926/1291>

version: 3.0.0

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/BRAINSFit>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Hans J. Johnson, hans-johnson -at- uiowa.edu, <http://www.psychiatry.uiowa.edu>

acknowledgements: Hans Johnson(1,3,4); Kent Williams(1); Gregory Harris(1), Vincent Magnotta(1,2,3); Andriy Fedorov(5) 1=University of Iowa Department of Psychiatry, 2=University of Iowa Department of Radiology, 3=University of Iowa Department of Biomedical Engineering, 4=University of Iowa Department of Electrical and Computer Engineering, 5=Surgical Planning Lab, Harvard

Inputs:

```

[Optional]
fixedVolume: (a pathlike object or string representing an existing
    file)
    Input fixed image (the moving image will be transformed into this
    image space).
    argument: ``--fixedVolume %s``
movingVolume: (a pathlike object or string representing an existing
    file)

```

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Input moving image (this image will be transformed into the fixed
image space).
argument: ``--movingVolume %s``
samplingPercentage: (a float)
Fraction of voxels of the fixed image that will be used for
registration. The number has to be larger than zero and less or
equal to one. Higher values increase the computation time but may
give more accurate results. You can also limit the sampling focus
with ROI masks and ROIAUTO mask generation. The default is 0.002
(use approximately 0.2% of voxels, resulting in 100000 samples in a
512x512x192 volume) to provide a very fast registration in most
cases. Typical values range from 0.01 (1%) for low detail images to
0.2 (20%) for high detail images.
argument: ``--samplingPercentage %f``
splineGridSize: (a list of items which are an integer (int or long))
Number of BSpline grid subdivisions along each axis of the fixed
image, centered on the image space. Values must be 3 or higher for
the BSpline to be correctly computed.
argument: ``--splineGridSize %s``
linearTransform: (a boolean or a pathlike object or string
representing a file)
(optional) Output estimated transform - in case the computed
transform is not BSpline. NOTE: You must set at least one output
object (transform and/or output volume).
argument: ``--linearTransform %s``
bsplineTransform: (a boolean or a pathlike object or string
representing a file)
(optional) Output estimated transform - in case the computed
transform is BSpline. NOTE: You must set at least one output object
(transform and/or output volume).
argument: ``--bsplineTransform %s``
outputVolume: (a boolean or a pathlike object or string representing
a file)
(optional) Output image: the moving image warped to the fixed image
space. NOTE: You must set at least one output object (transform
and/or output volume).
argument: ``--outputVolume %s``
initialTransform: (a pathlike object or string representing an
existing file)
Transform to be applied to the moving image to initialize the
registration. This can only be used if Initialize Transform Mode is
Off.
argument: ``--initialTransform %s``
initializeTransformMode: ('Off' or 'useMomentsAlign' or
'useCenterOfHeadAlign' or 'useGeometryAlign' or
'useCenterOfROIAlign')
Determine how to initialize the transform center. useMomentsAlign
assumes that the center of mass of the images represent similar
structures. useCenterOfHeadAlign attempts to use the top of head and
shape of neck to drive a center of mass estimate. useGeometryAlign
on assumes that the center of the voxel lattice of the images
represent similar structures. Off assumes that the physical space of
the images are close. This flag is mutually exclusive with the
Initialization transform.
argument: ``--initializeTransformMode %s``
useRigid: (a boolean)
Perform a rigid registration as part of the sequential registration

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    steps. This family of options overrides the use of transformType if
    any of them are set.
    argument: ``--useRigid ``
useScaleVersor3D: (a boolean)
    Perform a ScaleVersor3D registration as part of the sequential
    registration steps. This family of options overrides the use of
    transformType if any of them are set.
    argument: ``--useScaleVersor3D ``
useScaleSkewVersor3D: (a boolean)
    Perform a ScaleSkewVersor3D registration as part of the sequential
    registration steps. This family of options overrides the use of
    transformType if any of them are set.
    argument: ``--useScaleSkewVersor3D ``
useAffine: (a boolean)
    Perform an Affine registration as part of the sequential
    registration steps. This family of options overrides the use of
    transformType if any of them are set.
    argument: ``--useAffine ``
useBSpline: (a boolean)
    Perform a BSpline registration as part of the sequential
    registration steps. This family of options overrides the use of
    transformType if any of them are set.
    argument: ``--useBSpline ``
useSyN: (a boolean)
    Perform a SyN registration as part of the sequential registration
    steps. This family of options overrides the use of transformType if
    any of them are set.
    argument: ``--useSyN ``
useComposite: (a boolean)
    Perform a Composite registration as part of the sequential
    registration steps. This family of options overrides the use of
    transformType if any of them are set.
    argument: ``--useComposite ``
maskProcessingMode: ('NOMASK' or 'ROIAUTO' or 'ROI')
    Specifies a mask to only consider a certain image region for the
    registration. If ROIAUTO is chosen, then the mask is computed using
    Otsu thresholding and hole filling. If ROI is chosen then the mask
    has to be specified as in input.
    argument: ``--maskProcessingMode %s``
fixedBinaryVolume: (a pathlike object or string representing an
    existing file)
    Fixed Image binary mask volume, required if Masking Option is ROI.
    Image areas where the mask volume has zero value are ignored during
    the registration.
    argument: ``--fixedBinaryVolume %s``
movingBinaryVolume: (a pathlike object or string representing an
    existing file)
    Moving Image binary mask volume, required if Masking Option is ROI.
    Image areas where the mask volume has zero value are ignored during
    the registration.
    argument: ``--movingBinaryVolume %s``
outputFixedVolumeROI: (a boolean or a pathlike object or string
    representing a file)
    ROI that is automatically computed from the fixed image. Only
    available if Masking Option is ROIAUTO. Image areas where the mask
    volume has zero value are ignored during the registration.
    argument: ``--outputFixedVolumeROI %s``

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outputMovingVolumeROI: (a boolean or a pathlike object or string
    representing a file)
    ROI that is automatically computed from the moving image. Only
    available if Masking Option is ROIAUTO. Image areas where the mask
    volume has zero value are ignored during the registration.
    argument: ``--outputMovingVolumeROI %s``

useROIBSpline: (a boolean)
    If enabled then the bounding box of the input ROIs defines the
    BSpline grid support region. Otherwise the BSpline grid support
    region is the whole fixed image.
    argument: ``--useROIBSpline ``

histogramMatch: (a boolean)
    Apply histogram matching operation for the input images to make them
    more similar. This is suitable for images of the same modality that
    may have different brightness or contrast, but the same overall
    intensity profile. Do NOT use if registering images from different
    modalities.
    argument: ``--histogramMatch ``

medianFilterSize: (a list of items which are an integer (int or
    long))
    Apply median filtering to reduce noise in the input volumes. The 3
    values specify the radius for the optional MedianImageFilter
    preprocessing in all 3 directions (in voxels).
    argument: ``--medianFilterSize %s``

removeIntensityOutliers: (a float)
    Remove very high and very low intensity voxels from the input
    volumes. The parameter specifies the half percentage to decide
    outliers of image intensities. The default value is zero, which
    means no outlier removal. If the value of 0.005 is given, the 0.005%
    of both tails will be thrown away, so 0.01% of intensities in total
    would be ignored in the statistic calculation.
    argument: ``--removeIntensityOutliers %f``

fixedVolume2: (a pathlike object or string representing an existing
    file)
    Input fixed image that will be used for multimodal registration.
    (the moving image will be transformed into this image space).
    argument: ``--fixedVolume2 %s``

movingVolume2: (a pathlike object or string representing an existing
    file)
    Input moving image that will be used for multimodal
    registration(this image will be transformed into the fixed image
    space).
    argument: ``--movingVolume2 %s``

outputVolumePixelType: ('float' or 'short' or 'ushort' or 'int' or
    'uint' or 'uchar')
    Data type for representing a voxel of the Output Volume.
    argument: ``--outputVolumePixelType %s``

backgroundFillValue: (a float)
    This value will be used for filling those areas of the output image
    that have no corresponding voxels in the input moving image.
    argument: ``--backgroundFillValue %f``

scaleOutputValues: (a boolean)
    If true, and the voxel values do not fit within the minimum and
    maximum values of the desired outputVolumePixelType, then linearly
    scale the min/max output image voxel values to fit within the
    min/max range of the outputVolumePixelType.
    argument: ``--scaleOutputValues ``

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interpolationMode: ('NearestNeighbor' or 'Linear' or
    'ResampleInPlace' or 'BSpline' or 'WindowedSinc' or 'Hamming' or
    'Cosine' or 'Welch' or 'Lanczos' or 'Blackman')
    Type of interpolation to be used when applying transform to moving
    volume. Options are Linear, NearestNeighbor, BSpline, WindowedSinc,
    Hamming, Cosine, Welch, Lanczos, or ResampleInPlace. The
    ResampleInPlace option will create an image with the same discrete
    voxel values and will adjust the origin and direction of the
    physical space interpretation.
    argument: ``--interpolationMode %s``
numberOfIterations: (a list of items which are an integer (int or
    long))
    The maximum number of iterations to try before stopping the
    optimization. When using a lower value (500-1000) then the
    registration is forced to terminate earlier but there is a higher
    risk of stopping before an optimal solution is reached.
    argument: ``--numberOfIterations %s``
maximumStepLength: (a float)
    Starting step length of the optimizer. In general, higher values
    allow for recovering larger initial misalignments but there is an
    increased chance that the registration will not converge.
    argument: ``--maximumStepLength %f``
minimumStepLength: (a list of items which are a float)
    Each step in the optimization takes steps at least this big. When
    none are possible, registration is complete. Smaller values allows
    the optimizer to make smaller adjustments, but the registration time
    may increase.
    argument: ``--minimumStepLength %s``
relaxationFactor: (a float)
    Specifies how quickly the optimization step length is decreased
    during registration. The value must be larger than 0 and smaller
    than 1. Larger values result in slower step size decrease, which
    allow for recovering larger initial misalignments but it increases
    the registration time and the chance that the registration will not
    converge.
    argument: ``--relaxationFactor %f``
translationScale: (a float)
    How much to scale up changes in position (in mm) compared to unit
    rotational changes (in radians) -- decrease this to allow for more
    rotation in the search pattern.
    argument: ``--translationScale %f``
reproportionScale: (a float)
    ScaleVersor3D 'Scale' compensation factor. Increase this to allow
    for more rescaling in a ScaleVersor3D or ScaleSkewVersor3D search
    pattern. 1.0 works well with a translationScale of 1000.0
    argument: ``--reproportionScale %f``
skewScale: (a float)
    ScaleSkewVersor3D Skew compensation factor. Increase this to allow
    for more skew in a ScaleSkewVersor3D search pattern. 1.0 works well
    with a translationScale of 1000.0
    argument: ``--skewScale %f``
maxBSplineDisplacement: (a float)
    Maximum allowed displacements in image physical coordinates (mm) for
    BSpline control grid along each axis. A value of 0.0 indicates that
    the problem should be unbounded. NOTE: This only constrains the
    BSpline portion, and does not limit the displacement from the
    associated bulk transform. This can lead to a substantial reduction

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    in computation time in the BSpline optimizer.,
    argument: ``--maxBSplineDisplacement %f``
fixedVolumeTimeIndex: (an integer (int or long))
    The index in the time series for the 3D fixed image to fit. Only
    allowed if the fixed input volume is 4-dimensional.
    argument: ``--fixedVolumeTimeIndex %d``
movingVolumeTimeIndex: (an integer (int or long))
    The index in the time series for the 3D moving image to fit. Only
    allowed if the moving input volume is 4-dimensional
    argument: ``--movingVolumeTimeIndex %d``
numberOfHistogramBins: (an integer (int or long))
    The number of histogram levels used for mutual information metric
    estimation.
    argument: ``--numberOfHistogramBins %d``
numberOfMatchPoints: (an integer (int or long))
    Number of histogram match points used for mutual information metric
    estimation.
    argument: ``--numberOfMatchPoints %d``
costMetric: ('MMI' or 'MSE' or 'NC' or 'MIH')
    The cost metric to be used during fitting. Defaults to MMI. Options
    are MMI (Mattes Mutual Information), MSE (Mean Square Error), NC
    (Normalized Correlation), MC (Match Cardinality for binary images)
    argument: ``--costMetric %s``
maskInferiorCutOffFromCenter: (a float)
    If Initialize Transform Mode is set to useCenterOfHeadAlign or
    Masking Option is ROIAUTO then this value defines the how much is
    cut of from the inferior part of the image. The cut-off distance is
    specified in millimeters, relative to the image center. If the value
    is 1000 or larger then no cut-off performed.
    argument: ``--maskInferiorCutOffFromCenter %f``
ROIAutoDilateSize: (a float)
    This flag is only relevant when using ROIAUTO mode for initializing
    masks. It defines the final dilation size to capture a bit of
    background outside the tissue region. A setting of 10mm has been
    shown to help regularize a BSpline registration type so that there
    is some background constraints to match the edges of the head
    better.
    argument: ``--ROIAutoDilateSize %f``
ROIAutoClosingSize: (a float)
    This flag is only relevant when using ROIAUTO mode for initializing
    masks. It defines the hole closing size in mm. It is rounded up to
    the nearest whole pixel size in each direction. The default is to
    use a closing size of 9mm. For mouse data this value may need to be
    reset to 0.9 or smaller.
    argument: ``--ROIAutoClosingSize %f``
numberOfSamples: (an integer (int or long))
    The number of voxels sampled for mutual information computation.
    Increase this for higher accuracy, at the cost of longer computation
    time., NOTE that it is suggested to use samplingPercentage instead
    of this option. However, if set to non-zero, numberOfSamples
    overwrites the samplingPercentage option.
    argument: ``--numberOfSamples %d``
strippedOutputTransform: (a boolean or a pathlike object or string
    representing a file)
    Rigid component of the estimated affine transform. Can be used to
    rigidly register the moving image to the fixed image. NOTE: This
    value is overridden if either bsplineTransform or linearTransform is

```

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    set.
    argument: ``--strippedOutputTransform %s``
transformType: (a list of items which are a unicode string)
    Specifies a list of registration types to be used. The valid types
    are, Rigid, ScaleVersor3D, ScaleSkewVersor3D, Affine, BSpline and
    SyN. Specifying more than one in a comma separated list will
    initialize the next stage with the previous results. If
    registrationClass flag is used, it overrides this parameter setting.
    argument: ``--transformType %s``
outputTransform: (a boolean or a pathlike object or string
    representing a file)
    (optional) Filename to which save the (optional) estimated
    transform. NOTE: You must select either the outputTransform or the
    outputVolume option.
    argument: ``--outputTransform %s``
initializeRegistrationByCurrentGenericTransform: (a boolean)
    If this flag is ON, the current generic composite transform,
    resulted from the linear registration stages, is set to initialize
    the follow nonlinear registration process. However, by the default
    behaviour, the moving image is first warped based on the existant
    transform before it is passed to the BSpline registration filter. It
    is done to speed up the BSpline registration by reducing the
    computations of composite transform Jacobian.
    argument: ``--initializeRegistrationByCurrentGenericTransform ``
failureExitCode: (an integer (int or long))
    If the fit fails, exit with this status code. (It can be used to
    force a successfult exit status of (0) if the registration fails due
    to reaching the maximum number of iterations.
    argument: ``--failureExitCode %d``
writeTransformOnFailure: (a boolean)
    Flag to save the final transform even if the numberOfIterations are
    reached without convergence. (Intended for use when
    --failureExitCode 0 )
    argument: ``--writeTransformOnFailure ``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use. (default is
    auto-detected)
    argument: ``--numberOfThreads %d``
debugLevel: (an integer (int or long))
    Display debug messages, and produce debug intermediate results.
    0=OFF, 1=Minimal, 10=Maximum debugging.
    argument: ``--debugLevel %d``
costFunctionConvergenceFactor: (a float)
    From itkLBFGSBOptimizer.h: Set/Get the
    CostFunctionConvergenceFactor. Algorithm terminates when the
    reduction in cost function is less than (factor * epsmcj) where
    epsmch is the machine precision. Typical values for factor: 1e+12
    for low accuracy; 1e+7 for moderate accuracy and 1e+1 for extremely
    high accuracy. 1e+9 seems to work well.,
    argument: ``--costFunctionConvergenceFactor %f``
projectedGradientTolerance: (a float)
    From itkLBFGSBOptimizer.h: Set/Get the ProjectedGradientTolerance.
    Algorithm terminates when the project gradient is below the
    tolerance. Default lbfgsb value is 1e-5, but 1e-4 seems to work
    well.,
    argument: ``--projectedGradientTolerance %f``
maximumNumberOfEvaluations: (an integer (int or long))

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Maximum number of evaluations for line search in lbfgsb optimizer.
argument: ``--maximumNumberOfEvaluations %d``
maximumNumberOfCorrections: (an integer (int or long))
Maximum number of corrections in lbfgsb optimizer.
argument: ``--maximumNumberOfCorrections %d``
gui: (a boolean)
Display intermediate image volumes for debugging. NOTE: This is not
part of the standard build sytem, and probably does nothing on your
installation.
argument: ``--gui ``
promptUser: (a boolean)
Prompt the user to hit enter each time an image is sent to the
DebugImageViewer
argument: ``--promptUser ``
metricSamplingStrategy: ('Random')
It defines the method that registration filter uses to sample the
input fixed image. Only Random is supported for now.
argument: ``--metricSamplingStrategy %s``
logFileReport: (a boolean or a pathlike object or string representing
a file)
A file to write out final information report in CSV file: MetricName
,MetricValue,FixedImageName,FixedMaskName,MovingImageName,MovingMask
Name
argument: ``--logFileReport %s``
writeOutputTransformInFloat: (a boolean)
By default, the output registration transforms (either the output
composite transform or each transform component) are written to the
disk in double precision. If this flag is ON, the output transforms
will be written in single (float) precision. It is especially
important if the output transform is a displacement field transform,
or it is a composite transform that includes several displacement
fields.
argument: ``--writeOutputTransformInFloat ``
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

linearTransform: (a pathlike object or string representing an
existing file)
(optional) Output estimated transform - in case the computed
transform is not BSpline. NOTE: You must set at least one output
object (transform and/or output volume).
bsplineTransform: (a pathlike object or string representing an
existing file)
(optional) Output estimated transform - in case the computed
transform is BSpline. NOTE: You must set at least one output object
(transform and/or output volume).
outputVolume: (a pathlike object or string representing an existing
file)
(optional) Output image: the moving image warped to the fixed image
space. NOTE: You must set at least one output object (transform

```

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    and/or output volume).
outputFixedVolumeROI: (a pathlike object or string representing an
    existing file)
    ROI that is automatically computed from the fixed image. Only
    available if Masking Option is ROIAUTO. Image areas where the mask
    volume has zero value are ignored during the registration.
outputMovingVolumeROI: (a pathlike object or string representing an
    existing file)
    ROI that is automatically computed from the moving image. Only
    available if Masking Option is ROIAUTO. Image areas where the mask
    volume has zero value are ignored during the registration.
strippedOutputTransform: (a pathlike object or string representing an
    existing file)
    Rigid component of the estimated affine transform. Can be used to
    rigidly register the moving image to the fixed image. NOTE: This
    value is overridden if either bsplineTransform or linearTransform is
    set.
outputTransform: (a pathlike object or string representing an
    existing file)
    (optional) Filename to which save the (optional) estimated
    transform. NOTE: You must select either the outputTransform or the
    outputVolume option.
logFileReport: (a pathlike object or string representing an existing
    file)
    A file to write out final information report in CSV file: MetricName
    ,MetricValue,FixedImageName,FixedMaskName,MovingImageName,MovingMask
    Name

```

75.17 interfaces.semtools.registration.brainsresample

75.17.1 BRAINSResample

[Link to code](#)

Wraps the executable command “BRAINSResample”.

title: Resample Image (BRAINS)

category: Registration

description: This program collects together three common image processing tasks that all involve resampling an image volume: Resampling to a new resolution and spacing, applying a transformation (using an ITK transform IO mechanisms) and Warping (using a vector image deformation field). Full documentation available here: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/BRAINSResample>.

version: 3.0.0

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/BRAINSResample>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Vincent Magnotta, Greg Harris, and Hans Johnson.

acknowledgements: The development of this tool was supported by funding from grants NS050568 and NS40068 from the National Institute of Neurological Disorders and Stroke and grants MH31593, MH40856, from the National Institute of Mental Health.

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    Image To Warp

```

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    argument: ``--inputVolume %s``
referenceVolume: (a pathlike object or string representing an
    existing file)
    Reference image used only to define the output space. If not
    specified, the warping is done in the same space as the image to
    warp.
    argument: ``--referenceVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Resulting deformed image
    argument: ``--outputVolume %s``
pixelType: ('float' or 'short' or 'ushort' or 'int' or 'uint' or
    'uchar' or 'binary')
    Specifies the pixel type for the input/output images. The 'binary'
    pixel type uses a modified algorithm whereby the image is read in as
    unsigned char, a signed distance map is created, signed distance map
    is resampled, and then a thresholded image of type unsigned char is
    written to disk.
    argument: ``--pixelType %s``
deformationVolume: (a pathlike object or string representing an
    existing file)
    Displacement Field to be used to warp the image (ITKv3 or earlier)
    argument: ``--deformationVolume %s``
warpTransform: (a pathlike object or string representing an existing
    file)
    Filename for the BRAINSFit transform (ITKv3 or earlier) or composite
    transform file (ITKv4)
    argument: ``--warpTransform %s``
interpolationMode: ('NearestNeighbor' or 'Linear' or
    'ResampleInPlace' or 'BSpline' or 'WindowedSinc' or 'Hamming' or
    'Cosine' or 'Welch' or 'Lanczos' or 'Blackman')
    Type of interpolation to be used when applying transform to moving
    volume. Options are Linear, ResampleInPlace, NearestNeighbor,
    BSpline, or WindowedSinc
    argument: ``--interpolationMode %s``
inverseTransform: (a boolean)
    True/False is to compute inverse of given transformation. Default is
    false
    argument: ``--inverseTransform ``
defaultValue: (a float)
    Default voxel value
    argument: ``--defaultValue %f``
gridSpacing: (a list of items which are an integer (int or long))
    Add warped grid to output image to help show the deformation that
    occurred with specified spacing. A spacing of 0 in a dimension
    indicates that grid lines should be rendered to fall exactly (i.e.
    do not allow displacements off that plane). This is useful for
    making a 2D image of grid lines from the 3D space
    argument: ``--gridSpacing %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a

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```
value of class 'str', nipy default value: {}
Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
file)
Resulting deformed image
```

75.18 interfaces.semttools.registration.brainsresize

75.18.1 BRAINSResize

[Link to code](#)

Wraps the executable command “ BRAINSResize “.

title: Resize Image (BRAINS)

category: Registration

description: This program is useful for downsampling an image by a constant scale factor.

version: 3.0.0

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Hans Johnson.

acknowledgements: The development of this tool was supported by funding from grants NS050568 and NS40068 from the National Institute of Neurological Disorders and Stroke and grants MH31593, MH40856, from the National Institute of Mental Health.

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
file)
Image To Scale
argument: ``--inputVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
a file)
Resulting scaled image
argument: ``--outputVolume %s``
pixelType: ('float' or 'short' or 'ushort' or 'int' or 'uint' or
'uchar' or 'binary')
Specifies the pixel type for the input/output images. The 'binary'
pixel type uses a modified algorithm whereby the image is read in as
unsigned char, a signed distance map is created, signed distance map
is resampled, and then a thresholded image of type unsigned char is
written to disk.
argument: ``--pixelType %s``
scaleFactor: (a float)
The scale factor for the image spacing.
argument: ``--scaleFactor %f``
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               Resulting scaled image
```

75.19 interfaces.semtools.registration.specialized

75.19.1 BRAINSDemonWarp

[Link to code](#)

Wraps the executable command “ BRAINSDemonWarp “.

title: Demon Registration (BRAINS)

category: Registration.Specialized

description: This program finds a deformation field to warp a moving image onto a fixed image. The images must be of the same signal kind, and contain an image of the same kind of object. This program uses the Thirion Demons warp software in ITK, the Insight Toolkit. Additional information is available at: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/BRAINSDemonWarp>.

version: 3.0.0

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/BRAINSDemonWarp>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Hans J. Johnson and Greg Harris.

acknowledgements: The development of this tool was supported by funding from grants NS050568 and NS40068 from the National Institute of Neurological Disorders and Stroke and grants MH31593, MH40856, from the National Institute of Mental Health.

Inputs:

```
[Optional]
movingVolume: (a pathlike object or string representing an existing
               file)
               Required: input moving image
               argument: ``--movingVolume %s``
fixedVolume: (a pathlike object or string representing an existing
               file)
               Required: input fixed (target) image
               argument: ``--fixedVolume %s``
inputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
                Input volumes will be typecast to this format:
                float|short|ushort|int|uchar
                argument: ``--inputPixelType %s``
outputVolume: (a boolean or a pathlike object or string representing
               a file)
               Required: output resampled moving image (will have the same physical
               space as the fixedVolume).
               argument: ``--outputVolume %s``
outputDisplacementFieldVolume: (a boolean or a pathlike object or
                                string representing a file)
                                Output deformation field vector image (will have the same physical
                                space as the fixedVolume).
                                argument: ``--outputDisplacementFieldVolume %s``
outputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
                 outputVolume will be typecast to this format:
                 float|short|ushort|int|uchar
                 argument: ``--outputPixelType %s``
interpolationMode: ('NearestNeighbor' or 'Linear' or
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    'ResampleInPlace' or 'BSpline' or 'WindowedSinc' or 'Hamming' or
    'Cosine' or 'Welch' or 'Lanczos' or 'Blackman')
    Type of interpolation to be used when applying transform to moving
    volume. Options are Linear, ResampleInPlace, NearestNeighbor,
    BSpline, or WindowedSinc
    argument: ``--interpolationMode %s``
registrationFilterType: ('Demons' or 'FastSymmetricForces' or
    'Diffeomorphic')
    Registration Filter Type: Demons|FastSymmetricForces|Diffeomorphic
    argument: ``--registrationFilterType %s``
smoothDisplacementFieldSigma: (a float)
    A gaussian smoothing value to be applied to the deformation feild at
    each iteration.
    argument: ``--smoothDisplacementFieldSigma %f``
numberOfPyramidLevels: (an integer (int or long))
    Number of image pyramid levels to use in the multi-resolution
    registration.
    argument: ``--numberOfPyramidLevels %d``
minimumFixedPyramid: (a list of items which are an integer (int or
    long))
    The shrink factor for the first level of the fixed image pyramid.
    (i.e. start at 1/16 scale, then 1/8, then 1/4, then 1/2, and finally
    full scale)
    argument: ``--minimumFixedPyramid %s``
minimumMovingPyramid: (a list of items which are an integer (int or
    long))
    The shrink factor for the first level of the moving image pyramid.
    (i.e. start at 1/16 scale, then 1/8, then 1/4, then 1/2, and finally
    full scale)
    argument: ``--minimumMovingPyramid %s``
arrayOfPyramidLevelIterations: (a list of items which are an integer
    (int or long))
    The number of iterations for each pyramid level
    argument: ``--arrayOfPyramidLevelIterations %s``
histogramMatch: (a boolean)
    Histogram Match the input images. This is suitable for images of the
    same modality that may have different absolute scales, but the same
    overall intensity profile.
    argument: ``--histogramMatch ``
numberOfHistogramBins: (an integer (int or long))
    The number of histogram levels
    argument: ``--numberOfHistogramBins %d``
numberOfMatchPoints: (an integer (int or long))
    The number of match points for histogramMatch
    argument: ``--numberOfMatchPoints %d``
medianFilterSize: (a list of items which are an integer (int or
    long))
    Median filter radius in all 3 directions. When images have a lot of
    salt and pepper noise, this step can improve the registration.
    argument: ``--medianFilterSize %s``
initializeWithDisplacementField: (a pathlike object or string
    representing an existing file)
    Initial deformation field vector image file name
    argument: ``--initializeWithDisplacementField %s``
initializeWithTransform: (a pathlike object or string representing an
    existing file)
    Initial Transform filename

```

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    argument: ``--initializeWithTransform %s``
maskProcessingMode: ('NOMASK' or 'ROIAUTO' or 'ROI' or 'BOBF')
    What mode to use for using the masks: NOMASK|ROIAUTO|ROI|BOBF. If
    ROIAUTO is choosen, then the mask is implicitly defined using a otsu
    foreground and hole filling algorithm. Where the Region Of Interest
    mode uses the masks to define what parts of the image should be used
    for computing the deformation field. Brain Only Background Fill uses
    the masks to pre-process the input images by clipping and filling in
    the background with a predefined value.
    argument: ``--maskProcessingMode %s``
fixedBinaryVolume: (a pathlike object or string representing an
    existing file)
    Mask filename for desired region of interest in the Fixed image.
    argument: ``--fixedBinaryVolume %s``
movingBinaryVolume: (a pathlike object or string representing an
    existing file)
    Mask filename for desired region of interest in the Moving image.
    argument: ``--movingBinaryVolume %s``
lowerThresholdForBOBF: (an integer (int or long))
    Lower threshold for performing BOBF
    argument: ``--lowerThresholdForBOBF %d``
upperThresholdForBOBF: (an integer (int or long))
    Upper threshold for performing BOBF
    argument: ``--upperThresholdForBOBF %d``
backgroundFillValue: (an integer (int or long))
    Replacement value to overwrite background when performing BOBF
    argument: ``--backgroundFillValue %d``
seedForBOBF: (a list of items which are an integer (int or long))
    coordinates in all 3 directions for Seed when performing BOBF
    argument: ``--seedForBOBF %s``
neighborhoodForBOBF: (a list of items which are an integer (int or
    long))
    neighborhood in all 3 directions to be included when performing BOBF
    argument: ``--neighborhoodForBOBF %s``
outputDisplacementFieldPrefix: (a unicode string)
    Displacement field filename prefix for writing separate x, y, and z
    component images
    argument: ``--outputDisplacementFieldPrefix %s``
outputCheckerboardVolume: (a boolean or a pathlike object or string
    representing a file)
    Genete a checkerboard image volume between the fixedVolume and the
    deformed movingVolume.
    argument: ``--outputCheckerboardVolume %s``
checkerboardPatternSubdivisions: (a list of items which are an
    integer (int or long))
    Number of Checkerboard subdivisions in all 3 directions
    argument: ``--checkerboardPatternSubdivisions %s``
outputNormalized: (a boolean)
    Flag to warp and write the normalized images to output. In
    normalized images the image values are fit-scaled to be between 0
    and the maximum storage type value.
    argument: ``--outputNormalized ``
outputDebug: (a boolean)
    Flag to write debugging images after each step.
    argument: ``--outputDebug ``
gradient_type: ('0' or '1' or '2')
    Type of gradient used for computing the demons force (0 is

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    symmetrized, 1 is fixed image, 2 is moving image)
    argument: ``--gradient_type %s``
upFieldSmoothing: (a float)
    Smoothing sigma for the update field at each iteration
    argument: ``--upFieldSmoothing %f``
max_step_length: (a float)
    Maximum length of an update vector (0: no restriction)
    argument: ``--max_step_length %f``
use_vanilla_dem: (a boolean)
    Run vanilla demons algorithm
    argument: ``--use_vanilla_dem ``
gui: (a boolean)
    Display intermediate image volumes for debugging
    argument: ``--gui ``
promptUser: (a boolean)
    Prompt the user to hit enter each time an image is sent to the
    DebugImageViewer
    argument: ``--promptUser ``
numberOfBCHApproximationTerms: (an integer (int or long))
    Number of terms in the BCH expansion
    argument: ``--numberOfBCHApproximationTerms %d``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Required: output resampled moving image (will have the same physical
    space as the fixedVolume).
outputDisplacementFieldVolume: (a pathlike object or string
    representing an existing file)
    Output deformation field vector image (will have the same physical
    space as the fixedVolume).
outputCheckerboardVolume: (a pathlike object or string representing
    an existing file)
    Genete a checkerboard image volume between the fixedVolume and the
    deformed movingVolume.

```

75.19.2 BRAINSTransformFromFiducials**Link to code**

Wraps the executable command “ BRAINSTransformFromFiducials “.

title: Fiducial Registration (BRAINS)

category: Registration.Specialized

description: Computes a rigid, similarity or affine transform from a matched list of fiducials

version: 0.1.0.\$Revision\$

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Modules:TransformFromFiducials-Documentation-3.6>

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contributor: Casey B Goodlett

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
fixedLandmarks: (a list of items which are a list of from 3 to 3
    items which are a float)
    Ordered list of landmarks in the fixed image
    argument: ``--fixedLandmarks %s...``
movingLandmarks: (a list of items which are a list of from 3 to 3
    items which are a float)
    Ordered list of landmarks in the moving image
    argument: ``--movingLandmarks %s...``
saveTransform: (a boolean or a pathlike object or string representing
    a file)
    Save the transform that results from registration
    argument: ``--saveTransform %s``
transformType: ('Translation' or 'Rigid' or 'Similarity')
    Type of transform to produce
    argument: ``--transformType %s``
fixedLandmarksFile: (a pathlike object or string representing an
    existing file)
    An fcsv formatted file with a list of landmark points.
    argument: ``--fixedLandmarksFile %s``
movingLandmarksFile: (a pathlike object or string representing an
    existing file)
    An fcsv formatted file with a list of landmark points.
    argument: ``--movingLandmarksFile %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
saveTransform: (a pathlike object or string representing an existing
    file)
    Save the transform that results from registration
```

75.19.3 VBRAINSDemonWarp

[Link to code](#)

Wraps the executable command “ VBRAINSDemonWarp “.

title: Vector Demon Registration (BRAINS)

category: Registration.Specialized

description: This program finds a deformation field to warp a moving image onto a fixed image. The images must be of the same signal kind, and contain an image of the same kind of object. This program uses the Thirion Demons warp software in ITK, the Insight Toolkit. Additional information is available at: <http://www.nitrc.org/projects/brainsdemonwarp>.

version: 3.0.0

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/>

BRAINSDemonWarp

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Hans J. Johnson and Greg Harris.

acknowledgements: The development of this tool was supported by funding from grants NS050568 and NS40068 from the National Institute of Neurological Disorders and Stroke and grants MH31593, MH40856, from the National Institute of Mental Health.

Inputs:

```
[Optional]
movingVolume: (a list of items which are a pathlike object or string
               representing an existing file)
               Required: input moving image
               argument: ``--movingVolume %s...``
fixedVolume: (a list of items which are a pathlike object or string
              representing an existing file)
              Required: input fixed (target) image
              argument: ``--fixedVolume %s...``
inputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
                Input volumes will be typecast to this format:
                float|short|ushort|int|uchar
                argument: ``--inputPixelType %s``
outputVolume: (a boolean or a pathlike object or string representing
               a file)
               Required: output resampled moving image (will have the same physical
               space as the fixedVolume).
               argument: ``--outputVolume %s``
outputDisplacementFieldVolume: (a boolean or a pathlike object or
                                string representing a file)
                                Output deformation field vector image (will have the same physical
                                space as the fixedVolume).
                                argument: ``--outputDisplacementFieldVolume %s``
outputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
                 outputVolume will be typecast to this format:
                 float|short|ushort|int|uchar
                 argument: ``--outputPixelType %s``
interpolationMode: ('NearestNeighbor' or 'Linear' or
                    'ResampleInPlace' or 'BSpline' or 'WindowedSinc' or 'Hamming' or
                    'Cosine' or 'Welch' or 'Lanczos' or 'Blackman')
                    Type of interpolation to be used when applying transform to moving
                    volume. Options are Linear, ResampleInPlace, NearestNeighbor,
                    BSpline, or WindowedSinc
                    argument: ``--interpolationMode %s``
registrationFilterType: ('Demons' or 'FastSymmetricForces' or
                        'Diffeomorphic' or 'LogDemons' or 'SymmetricLogDemons')
                        Registration Filter Type: Demons|FastSymmetricForces|Diffeomorphic|L
                        ogDemons|SymmetricLogDemons
                        argument: ``--registrationFilterType %s``
smoothDisplacementFieldSigma: (a float)
                              A gaussian smoothing value to be applied to the deformation feild at
                              each iteration.
                              argument: ``--smoothDisplacementFieldSigma %f``
numberOfPyramidLevels: (an integer (int or long))
                       Number of image pyramid levels to use in the multi-resolution
                       registration.
                       argument: ``--numberOfPyramidLevels %d``
minimumFixedPyramid: (a list of items which are an integer (int or
                      long))
```

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    The shrink factor for the first level of the fixed image pyramid.
    (i.e. start at 1/16 scale, then 1/8, then 1/4, then 1/2, and finally
    full scale)
    argument: ``--minimumFixedPyramid %s``
minimumMovingPyramid: (a list of items which are an integer (int or
    long))
    The shrink factor for the first level of the moving image pyramid.
    (i.e. start at 1/16 scale, then 1/8, then 1/4, then 1/2, and finally
    full scale)
    argument: ``--minimumMovingPyramid %s``
arrayOfPyramidLevelIterations: (a list of items which are an integer
    (int or long))
    The number of iterations for each pyramid level
    argument: ``--arrayOfPyramidLevelIterations %s``
histogramMatch: (a boolean)
    Histogram Match the input images. This is suitable for images of the
    same modality that may have different absolute scales, but the same
    overall intensity profile.
    argument: ``--histogramMatch ``
numberOfHistogramBins: (an integer (int or long))
    The number of histogram levels
    argument: ``--numberOfHistogramBins %d``
numberOfMatchPoints: (an integer (int or long))
    The number of match points for histogramMatch
    argument: ``--numberOfMatchPoints %d``
medianFilterSize: (a list of items which are an integer (int or
    long))
    Median filter radius in all 3 directions. When images have a lot of
    salt and pepper noise, this step can improve the registration.
    argument: ``--medianFilterSize %s``
initializeWithDisplacementField: (a pathlike object or string
    representing an existing file)
    Initial deformation field vector image file name
    argument: ``--initializeWithDisplacementField %s``
initializeWithTransform: (a pathlike object or string representing an
    existing file)
    Initial Transform filename
    argument: ``--initializeWithTransform %s``
makeBOBF: (a boolean)
    Flag to make Brain-Only Background-Filled versions of the input and
    target volumes.
    argument: ``--makeBOBF ``
fixedBinaryVolume: (a pathlike object or string representing an
    existing file)
    Mask filename for desired region of interest in the Fixed image.
    argument: ``--fixedBinaryVolume %s``
movingBinaryVolume: (a pathlike object or string representing an
    existing file)
    Mask filename for desired region of interest in the Moving image.
    argument: ``--movingBinaryVolume %s``
lowerThresholdForBOBF: (an integer (int or long))
    Lower threshold for performing BOBF
    argument: ``--lowerThresholdForBOBF %d``
upperThresholdForBOBF: (an integer (int or long))
    Upper threshold for performing BOBF
    argument: ``--upperThresholdForBOBF %d``
backgroundFillValue: (an integer (int or long))

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Replacement value to overwrite background when performing BOBF
argument: ``--backgroundFillValue %d``
seedForBOBF: (a list of items which are an integer (int or long))
coordinates in all 3 directions for Seed when performing BOBF
argument: ``--seedForBOBF %s``
neighborhoodForBOBF: (a list of items which are an integer (int or
long))
neighborhood in all 3 directions to be included when performing BOBF
argument: ``--neighborhoodForBOBF %s``
outputDisplacementFieldPrefix: (a unicode string)
Displacement field filename prefix for writing separate x, y, and z
component images
argument: ``--outputDisplacementFieldPrefix %s``
outputCheckerboardVolume: (a boolean or a pathlike object or string
representing a file)
Generate a checkerboard image volume between the fixedVolume and the
deformed movingVolume.
argument: ``--outputCheckerboardVolume %s``
checkerboardPatternSubdivisions: (a list of items which are an
integer (int or long))
Number of Checkerboard subdivisions in all 3 directions
argument: ``--checkerboardPatternSubdivisions %s``
outputNormalized: (a boolean)
Flag to warp and write the normalized images to output. In
normalized images the image values are fit-scaled to be between 0
and the maximum storage type value.
argument: ``--outputNormalized ``
outputDebug: (a boolean)
Flag to write debugging images after each step.
argument: ``--outputDebug ``
weightFactors: (a list of items which are a float)
Weight factors for each input images
argument: ``--weightFactors %s``
gradient_type: ('0' or '1' or '2')
Type of gradient used for computing the demons force (0 is
symmetrized, 1 is fixed image, 2 is moving image)
argument: ``--gradient_type %s``
upFieldSmoothing: (a float)
Smoothing sigma for the update field at each iteration
argument: ``--upFieldSmoothing %f``
max_step_length: (a float)
Maximum length of an update vector (0: no restriction)
argument: ``--max_step_length %f``
use_vanilla_dem: (a boolean)
Run vanilla demons algorithm
argument: ``--use_vanilla_dem ``
gui: (a boolean)
Display intermediate image volumes for debugging
argument: ``--gui ``
promptUser: (a boolean)
Prompt the user to hit enter each time an image is sent to the
DebugImageViewer
argument: ``--promptUser ``
numberOfBCHApproximationTerms: (an integer (int or long))
Number of terms in the BCH expansion
argument: ``--numberOfBCHApproximationTerms %d``
numberOfThreads: (an integer (int or long))

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        Explicitly specify the maximum number of threads to use.
        argument: ``--numberOfThreads %d``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
        file)
        Required: output resampled moving image (will have the same physical
        space as the fixedVolume).
outputDisplacementFieldVolume: (a pathlike object or string
        representing an existing file)
        Output deformation field vector image (will have the same physical
        space as the fixedVolume).
outputCheckerboardVolume: (a pathlike object or string representing
        an existing file)
        Genete a checkerboard image volume between the fixedVolume and the
        deformed movingVolume.

```

75.20 interfaces.semtools.segmentation.specialized

75.20.1 BRAINSABC

[Link to code](#)

Wraps the executable command “ BRAINSABC “.

title: Intra-subject registration, bias Correction, and tissue classification (BRAINS)

category: Segmentation.Specialized

description: Atlas-based tissue segmentation method. This is an algorithmic extension of work done by XXXX at UNC and Utah XXXX need more description here.

Inputs:

```

[Optional]
inputVolumes: (a list of items which are a pathlike object or string
        representing an existing file)
        The list of input image files to be segmented.
        argument: ``--inputVolumes %s...``
atlasDefinition: (a pathlike object or string representing an
        existing file)
        Contains all parameters for Atlas
        argument: ``--atlasDefinition %s``
restoreState: (a pathlike object or string representing an existing
        file)
        The initial state for the registration process
        argument: ``--restoreState %s``
saveState: (a boolean or a pathlike object or string representing a
        file)
        (optional) Filename to which save the final state of the
        registration
        argument: ``--saveState %s``

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inputVolumeTypes: (a list of items which are a unicode string)
    The list of input image types corresponding to the inputVolumes.
    argument: ``--inputVolumeTypes %s``
outputDir: (a boolean or a pathlike object or string representing a
    directory)
    Output directory
    argument: ``--outputDir %s``
atlasToSubjectTransformType: ('Identity' or 'Rigid' or 'Affine' or
    'BSpline' or 'SyN')
    What type of linear transform type do you want to use to register
    the atlas to the reference subject image.
    argument: ``--atlasToSubjectTransformType %s``
atlasToSubjectTransform: (a boolean or a pathlike object or string
    representing a file)
    The transform from atlas to the subject
    argument: ``--atlasToSubjectTransform %s``
atlasToSubjectInitialTransform: (a boolean or a pathlike object or
    string representing a file)
    The initial transform from atlas to the subject
    argument: ``--atlasToSubjectInitialTransform %s``
subjectIntermodeTransformType: ('Identity' or 'Rigid' or 'Affine' or
    'BSpline')
    What type of linear transform type do you want to use to register
    the atlas to the reference subject image.
    argument: ``--subjectIntermodeTransformType %s``
outputVolumes: (a boolean or a list of items which are a pathlike
    object or string representing a file)
    Corrected Output Images: should specify the same number of images as
    inputVolume, if only one element is given, then it is used as a file
    pattern where %s is replaced by the imageVolumeType, and %d by the
    index list location.
    argument: ``--outputVolumes %s...``
outputLabels: (a boolean or a pathlike object or string representing
    a file)
    Output Label Image
    argument: ``--outputLabels %s``
outputDirtyLabels: (a boolean or a pathlike object or string
    representing a file)
    Output Dirty Label Image
    argument: ``--outputDirtyLabels %s``
posteriorTemplate: (a unicode string)
    filename template for Posterior output files
    argument: ``--posteriorTemplate %s``
outputFormat: ('NIFTI' or 'Meta' or 'Nrrd')
    Output format
    argument: ``--outputFormat %s``
interpolationMode: ('BSpline' or 'NearestNeighbor' or 'WindowedSinc'
    or 'Linear' or 'ResampleInPlace' or 'Hamming' or 'Cosine' or
    'Welch' or 'Lanczos' or 'Blackman')
    Type of interpolation to be used when applying transform to moving
    volume. Options are Linear, NearestNeighbor, BSpline, WindowedSinc,
    or ResampleInPlace. The ResampleInPlace option will create an image
    with the same discrete voxel values and will adjust the origin and
    direction of the physical space interpretation.
    argument: ``--interpolationMode %s``
maxIterations: (an integer (int or long))
    Filter iterations

```

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        argument: ``--maxIterations %d``
medianFilterSize: (a list of items which are an integer (int or
                    long))
    The radius for the optional MedianImageFilter preprocessing in all 3
    directions.
        argument: ``--medianFilterSize %s``
filterIteration: (an integer (int or long))
    Filter iterations
        argument: ``--filterIteration %d``
filterTimeStep: (a float)
    Filter time step should be less than (PixelSpacing/(1^(DIM+1))),
    value is set to negative, then allow automatic setting of this
    value.
        argument: ``--filterTimeStep %f``
filterMethod: ('None' or 'CurvatureFlow' or
               'GradientAnisotropicDiffusion' or 'Median')
    Filter method for preprocessing of registration
        argument: ``--filterMethod %s``
maxBiasDegree: (an integer (int or long))
    Maximum bias degree
        argument: ``--maxBiasDegree %d``
useKNN: (a boolean)
    Use the KNN stage of estimating posteriors.
        argument: ``--useKNN ``
purePlugsThreshold: (a float)
    If this threshold value is greater than zero, only pure samples are
    used to compute the distributions in EM classification, and only
    pure samples are used for KNN training. The default value is set to
    0, that means not using pure plugs. However, a value of 0.2 is
    suggested if you want to activate using pure plugs option.
        argument: ``--purePlugsThreshold %f``
numberOfSubSamplesInEachPlugArea: (a list of items which are an
                                    integer (int or long))
    Number of continous index samples taken at each direction of lattice
    space for each plug volume.
        argument: ``--numberOfSubSamplesInEachPlugArea %s``
atlasWarpingOff: (a boolean)
    Deformable registration of atlas to subject
        argument: ``--atlasWarpingOff ``
gridSize: (a list of items which are an integer (int or long))
    Grid size for atlas warping with BSplines
        argument: ``--gridSize %s``
defaultSuffix: (a unicode string)
        argument: ``--defaultSuffix %s``
implicitOutputs: (a boolean or a list of items which are a pathlike
                  object or string representing a file)
    Outputs to be made available to NiPype. Needed because not all
    BRAINSABC outputs have command line arguments.
        argument: ``--implicitOutputs %s...``
debuglevel: (an integer (int or long))
    Display debug messages, and produce debug intermediate results.
    0=OFF, 1=Minimal, 10=Maximum debugging.
        argument: ``--debuglevel %d``
writeLess: (a boolean)
    Does not write posteriors and filtered, bias corrected images
        argument: ``--writeLess ``
numberOfThreads: (an integer (int or long))

```

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```

        Explicitly specify the maximum number of threads to use.
        argument: ``--numberOfThreads %d``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

saveState: (a pathlike object or string representing an existing
        file)
        (optional) Filename to which save the final state of the
        registration
outputDir: (a pathlike object or string representing an existing
        directory)
        Output directory
atlasToSubjectTransform: (a pathlike object or string representing an
        existing file)
        The transform from atlas to the subject
atlasToSubjectInitialTransform: (a pathlike object or string
        representing an existing file)
        The initial transform from atlas to the subject
outputVolumes: (a list of items which are a pathlike object or string
        representing an existing file)
        Corrected Output Images: should specify the same number of images as
        inputVolume, if only one element is given, then it is used as a file
        pattern where %s is replaced by the imageVolumeType, and %d by the
        index list location.
outputLabels: (a pathlike object or string representing an existing
        file)
        Output Label Image
outputDirtyLabels: (a pathlike object or string representing an
        existing file)
        Output Dirty Label Image
implicitOutputs: (a list of items which are a pathlike object or
        string representing an existing file)
        Outputs to be made available to NiPype. Needed because not all
        BRAINSABC outputs have command line arguments.

```

75.20.2 BRAINSConstellationDetector[Link to code](#)

Wraps the executable command “ BRAINSConstellationDetector “.

title: Brain Landmark Constellation Detector (BRAINS)

category: Segmentation.Specialized

description: This program will find the mid-sagittal plane, a constellation of landmarks in a volume, and create an AC/PC aligned data set with the AC point at the center of the voxel lattice (labeled at the origin of the image physical space.) Part of this work is an extension of the algorithms originally described by Dr. Babak A. Ardekani, Alvin H. Bachman, Model-based automatic detection of the anterior and posterior commissures on MRI scans, NeuroImage, Volume 46, Issue 3, 1 July 2009, Pages 677-682, ISSN 1053-8119, DOI: 10.1016/j.neuroimage.2009.02.030. (<http://www.sciencedirect.com/science/article/B6WNP-4VRP25C-4/2/8207b962a38aa83c822c6379bc43fe4c>)

version: 1.0

documentation-url: <http://www.nitrc.org/projects/brainscdetector/>

Inputs:

```
[Optional]
houghEyeDetectorMode: (an integer (int or long))
    , This flag controls the mode of Hough eye detector. By default,
    value of 1 is for T1W images, while the value of 0 is for T2W and PD
    images.,
    argument: ``--houghEyeDetectorMode %d``
inputTemplateModel: (a pathlike object or string representing an
    existing file)
    User-specified template model.,
    argument: ``--inputTemplateModel %s``
LLSModel: (a pathlike object or string representing an existing file)
    Linear least squares model filename in HD5 format
    argument: ``--LLSModel %s``
inputVolume: (a pathlike object or string representing an existing
    file)
    Input image in which to find ACPC points
    argument: ``--inputVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    ACPC-aligned output image with the same voxels, but updated origin,
    and direction cosign so that the AC point would fall at the physical
    location (0.0,0.0,0.0), and the mid-sagittal plane is the plane where
    physical L/R coordinate is 0.0.
    argument: ``--outputVolume %s``
outputResampledVolume: (a boolean or a pathlike object or string
    representing a file)
    ACPC-aligned output image in a resampled unifor space. Currently
    this is a 1mm, 256^3, Identity direction image.
    argument: ``--outputResampledVolume %s``
outputTransform: (a boolean or a pathlike object or string
    representing a file)
    The filename for the original space to ACPC alignment to be written
    (in .h5 format).,
    argument: ``--outputTransform %s``
outputLandmarksInInputSpace: (a boolean or a pathlike object or
    string representing a file)
    , The filename for the new subject-specific landmark definition file
    in the same format produced by Slicer3 (.fcsv) with the landmarks in
    the original image space (the detected RP, AC, PC, and VN4) in it to
    be written.,
    argument: ``--outputLandmarksInInputSpace %s``
outputLandmarksInACPCAlignedSpace: (a boolean or a pathlike object or
    string representing a file)
    , The filename for the new subject-specific landmark definition file
    in the same format produced by Slicer3 (.fcsv) with the landmarks in
    the output image space (the detected RP, AC, PC, and VN4) in it to
    be written.,
    argument: ``--outputLandmarksInACPCAlignedSpace %s``
outputMRML: (a boolean or a pathlike object or string representing a
    file)
    , The filename for the new subject-specific scene definition file in
    the same format produced by Slicer3 (in .mrml format). Only the
    components that were specified by the user on command line would be
    generated. Compatible components include inputVolume, outputVolume,
    outputLandmarksInInputSpace, outputLandmarksInACPCAlignedSpace, and
```

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```

        outputTransform.,
        argument: ``--outputMRML %s``
outputVerificationScript: (a boolean or a pathlike object or string
    representing a file)
    , The filename for the Slicer3 script that verifies the aligned
    landmarks against the aligned image file. This will happen only in
    conjunction with saveOutputLandmarks and an outputVolume.,
    argument: ``--outputVerificationScript %s``
mspQualityLevel: (an integer (int or long))
    , Flag cotrols how aggressive the MSP is estimated. 0=quick estimate
    (9 seconds), 1=normal estimate (11 seconds), 2=great estimate (22
    seconds), 3=best estimate (58 seconds), NOTE: -1= Prealigned so no
    estimate!.,
    argument: ``--mspQualityLevel %d``
otsuPercentileThreshold: (a float)
    , This is a parameter to FindLargestForegroundFilledMask, which is
    employed when acLowerBound is set and an
    outputUntransformedClippedVolume is requested.,
    argument: ``--otsuPercentileThreshold %f``
acLowerBound: (a float)
    , When generating a resampled output image, replace the image with
    the BackgroundFillValue everywhere below the plane This Far in
    physical units (millimeters) below (inferior to) the AC point (as
    found by the model.) The oversize default was chosen to have no
    effect. Based on visualizing a thousand masks in the IPIG study, we
    recommend a limit no smaller than 80.0 mm.,
    argument: ``--acLowerBound %f``
cutOutHeadInOutputVolume: (a boolean)
    , Flag to cut out just the head tissue when producing an
    (un)transformed clipped volume.,
    argument: ``--cutOutHeadInOutputVolume ``
outputUntransformedClippedVolume: (a boolean or a pathlike object or
    string representing a file)
    Output image in which to store neck-clipped input image, with the
    use of --acLowerBound and maybe --cutOutHeadInUntransformedVolume.
    argument: ``--outputUntransformedClippedVolume %s``
rescaleIntensities: (a boolean)
    , Flag to turn on rescaling image intensities on input.,
    argument: ``--rescaleIntensities ``
trimRescaledIntensities: (a float)
    , Turn on clipping the rescaled image one-tailed on input. Units of
    standard deviations above the mean. Very large values are very
    permissive. Non-positive value turns clipping off. Defaults to
    removing 0.00001 of a normal tail above the mean.,
    argument: ``--trimRescaledIntensities %f``
rescaleIntensitiesOutputRange: (a list of items which are an integer
    (int or long))
    , This pair of integers gives the lower and upper bounds on the
    signal portion of the output image. Out-of-field voxels are taken
    from BackgroundFillValue.,
    argument: ``--rescaleIntensitiesOutputRange %s``
BackgroundFillValue: (a unicode string)
    Fill the background of image with specified short int value. Enter
    number or use BIGNEG for a large negative number.
    argument: ``--BackgroundFillValue %s``
interpolationMode: ('NearestNeighbor' or 'Linear' or
    'ResampleInPlace' or 'BSpline' or 'WindowedSinc' or 'Hamming' or

```

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    'Cosine' or 'Welch' or 'Lanczos' or 'Blackman')
    Type of interpolation to be used when applying transform to moving
    volume. Options are Linear, ResampleInPlace, NearestNeighbor,
    BSpline, or WindowedSinc
    argument: ``--interpolationMode %s``
forceACPoint: (a list of items which are a float)
    , Use this flag to manually specify the AC point from the original
    image on the command line.,
    argument: ``--forceACPoint %s``
forcePCPoint: (a list of items which are a float)
    , Use this flag to manually specify the PC point from the original
    image on the command line.,
    argument: ``--forcePCPoint %s``
forceVN4Point: (a list of items which are a float)
    , Use this flag to manually specify the VN4 point from the original
    image on the command line.,
    argument: ``--forceVN4Point %s``
forceRPPoint: (a list of items which are a float)
    , Use this flag to manually specify the RP point from the original
    image on the command line.,
    argument: ``--forceRPPoint %s``
inputLandmarksEMSP: (a pathlike object or string representing an
    existing file)
    , The filename for the new subject-specific landmark definition file
    in the same format produced by Slicer3 (in .fcsv) with the landmarks
    in the estimated MSP aligned space to be loaded. The detector will
    only process landmarks not enlisted on the file.,
    argument: ``--inputLandmarksEMSP %s``
forceHoughEyeDetectorReportFailure: (a boolean)
    , Flag indicates whether the Hough eye detector should report
    failure,
    argument: ``--forceHoughEyeDetectorReportFailure ``
rmpj: (a float)
    , Search radius for MPJ in unit of mm,
    argument: ``--rmpj %f``
rac: (a float)
    , Search radius for AC in unit of mm,
    argument: ``--rac %f``
rpc: (a float)
    , Search radius for PC in unit of mm,
    argument: ``--rpc %f``
rVN4: (a float)
    , Search radius for VN4 in unit of mm,
    argument: ``--rVN4 %f``
debug: (a boolean)
    , Show internal debugging information.,
    argument: ``--debug ``
verbose: (a boolean)
    , Show more verbose output,
    argument: ``--verbose ``
writeBranded2DImage: (a boolean or a pathlike object or string
    representing a file)
    , The filename for the 2D .png branded midline debugging image. This
    will happen only in conjunction with requesting an outputVolume.,
    argument: ``--writeBranded2DImage %s``
resultsDir: (a boolean or a pathlike object or string representing a
    directory)

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    , The directory for the debugging images to be written.,
    argument: ``--resultsDir %s``
writedebuggingImagesLevel: (an integer (int or long))
    , This flag controls if debugging images are produced. By default
    value of 0 is no images. Anything greater than zero will be
    increasing level of debugging images.,
    argument: ``--writedebuggingImagesLevel %d``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
atlasVolume: (a pathlike object or string representing an existing
    file)
    Atlas volume image to be used for BRAINSFit registration
    argument: ``--atlasVolume %s``
atlasLandmarks: (a pathlike object or string representing an existing
    file)
    Atlas landmarks to be used for BRAINSFit registration
    initialization,
    argument: ``--atlasLandmarks %s``
atlasLandmarkWeights: (a pathlike object or string representing an
    existing file)
    Weights associated with atlas landmarks to be used for BRAINSFit
    registration initialization,
    argument: ``--atlasLandmarkWeights %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    ACPC-aligned output image with the same voxels, but updated origin,
    and direction cosign so that the AC point would fall at the physical
    location (0.0,0.0,0.0), and the mid-sagittal plane is the plane where
    physical L/R coordinate is 0.0.
outputResampledVolume: (a pathlike object or string representing an
    existing file)
    ACPC-aligned output image in a resampled unifor space. Currently
    this is a 1mm, 256^3, Identity direction image.
outputTransform: (a pathlike object or string representing an
    existing file)
    The filename for the original space to ACPC alignment to be written
    (in .h5 format)..
outputLandmarksInInputSpace: (a pathlike object or string
    representing an existing file)
    , The filename for the new subject-specific landmark definition file
    in the same format produced by Slicer3 (.fcsv) with the landmarks in
    the original image space (the detected RP, AC, PC, and VN4) in it to
    be written.,
outputLandmarksInACPCAlignedSpace: (a pathlike object or string
    representing an existing file)
    , The filename for the new subject-specific landmark definition file

```

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```

    in the same format produced by Slicer3 (.fcsv) with the landmarks in
    the output image space (the detected RP, AC, PC, and VN4) in it to
    be written.,
outputMRML: (a pathlike object or string representing an existing
    file)
    , The filename for the new subject-specific scene definition file in
    the same format produced by Slicer3 (in .mrml format). Only the
    components that were specified by the user on command line would be
    generated. Compatible components include inputVolume, outputVolume,
    outputLandmarksInInputSpace, outputLandmarksInACPCAlignedSpace, and
    outputTransform.,
outputVerificationScript: (a pathlike object or string representing
    an existing file)
    , The filename for the Slicer3 script that verifies the aligned
    landmarks against the aligned image file. This will happen only in
    conjunction with saveOutputLandmarks and an outputVolume.,
outputUntransformedClippedVolume: (a pathlike object or string
    representing an existing file)
    Output image in which to store neck-clipped input image, with the
    use of --acLowerBound and maybe --cutOutHeadInUntransformedVolume.
writeBranded2DImage: (a pathlike object or string representing an
    existing file)
    , The filename for the 2D .png branded midline debugging image. This
    will happen only in conjunction with requesting an outputVolume.,
resultsDir: (a pathlike object or string representing an existing
    directory)
    , The directory for the debugging images to be written.,

```

75.20.3 BRAINSCreateLabelMapFromProbabilityMaps

[Link to code](#)

Wraps the executable command “ BRAINSCreateLabelMapFromProbabilityMaps “.

title: Create Label Map From Probability Maps (BRAINS)

category: Segmentation.Specialized

description: Given A list of Probability Maps, generate a LabelMap.

Inputs:

```

[Optional]
inputProbabilityVolume: (a list of items which are a pathlike object
    or string representing an existing file)
    The list of proobabilityimages.
    argument: ``--inputProbabilityVolume %s...``
priorLabelCodes: (a list of items which are an integer (int or long))
    A list of PriorLabelCode values used for coding the output label
    images
    argument: ``--priorLabelCodes %s``
foregroundPriors: (a list of items which are an integer (int or
    long))
    A list: For each Prior Label, 1 if foreground, 0 if background
    argument: ``--foregroundPriors %s``
nonAirRegionMask: (a pathlike object or string representing an
    existing file)
    a mask representing the 'NonAirRegion' -- Just force pixels in this
    region to zero
    argument: ``--nonAirRegionMask %s``
inclusionThreshold: (a float)

```

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    tolerance for inclusion
    argument: ``--inclusionThreshold %f``
dirtyLabelVolume: (a boolean or a pathlike object or string
    representing a file)
    the labels prior to cleaning
    argument: ``--dirtyLabelVolume %s``
cleanLabelVolume: (a boolean or a pathlike object or string
    representing a file)
    the foreground labels volume
    argument: ``--cleanLabelVolume %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

dirtyLabelVolume: (a pathlike object or string representing an
    existing file)
    the labels prior to cleaning
cleanLabelVolume: (a pathlike object or string representing an
    existing file)
    the foreground labels volume

```

75.20.4 BRAINSCut[Link to code](#)

Wraps the executable command “ BRAINSCut “.

title: BRAINSCut (BRAINS)

category: Segmentation.Specialized

description: Automatic Segmentation using neural networks

version: 1.0

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Vince Magnotta, Hans Johnson, Greg Harris, Kent Williams, Eunyoung Regina Kim

Inputs:

```

[Optional]
netConfiguration: (a pathlike object or string representing an
    existing file)
    XML File defining BRAINSCut parameters. OLD NAME. PLEASE USE
    modelConfigurationFilename instead.
    argument: ``--netConfiguration %s``
modelConfigurationFilename: (a pathlike object or string representing
    an existing file)
    XML File defining BRAINSCut parameters
    argument: ``--modelConfigurationFilename %s``
trainModelStartIndex: (an integer (int or long))
    Starting iteration for training
    argument: ``--trainModelStartIndex %d``
verbose: (an integer (int or long))
    print out some debugging information
    argument: ``--verbose %d``
multiStructureThreshold: (a boolean)

```

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```

        multiStructureThreshold module to deal with overlaping area
        argument: ``--multiStructureThreshold ``
    histogramEqualization: (a boolean)
        A Histogram Equalization process could be added to the
        creating/applying process from Subject To Atlas. Default is false,
        which genreate input vectors without Histogram Equalization.
        argument: ``--histogramEqualization ``
    computeSSEOn: (a boolean)
        compute Sum of Square Error (SSE) along the trained model until the
        number of iteration given in the modelConfigurationFilename file
        argument: ``--computeSSEOn ``
    generateProbability: (a boolean)
        Generate probability map
        argument: ``--generateProbability ``
    createVectors: (a boolean)
        create vectors for training neural net
        argument: ``--createVectors ``
    trainModel: (a boolean)
        train the neural net
        argument: ``--trainModel ``
    NoTrainingVectorShuffling: (a boolean)
        If this flag is on, there will be no shuffling.
        argument: ``--NoTrainingVectorShuffling ``
    applyModel: (a boolean)
        apply the neural net
        argument: ``--applyModel ``
    validate: (a boolean)
        validate data set. Just need for the first time run ( This is for
        validation of xml file and not working yet )
        argument: ``--validate ``
    method: ('RandomForest' or 'ANN')
        argument: ``--method %s``
    numberOfTrees: (an integer (int or long))
        Random tree: number of trees. This is to be used when only one
        model with specified depth wish to be created.
        argument: ``--numberOfTrees %d``
    randomTreeDepth: (an integer (int or long))
        Random tree depth. This is to be used when only one model with
        specified depth wish to be created.
        argument: ``--randomTreeDepth %d``
    modelFilename: (a unicode string)
        model file name given from user (not by xml configuration file)
        argument: ``--modelFilename %s``
    args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
    environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipyte default value: {})
        Environment variables

```

Outputs:

None

75.20.5 BRAINSMultiSTAPLE

[Link to code](#)

Wraps the executable command “ BRAINSMultiSTAPLE “.

title: Create best representative label map)

category: Segmentation.Specialized

description: given a list of label map images, create a representative/average label map.

Inputs:

```
[Optional]
inputCompositeT1Volume: (a pathlike object or string representing an
    existing file)
    Composite T1, all label maps transofrmed into the space for this
    image.
    argument: ``--inputCompositeT1Volume %s``
inputLabelVolume: (a list of items which are a pathlike object or
    string representing an existing file)
    The list of proobabilityimages.
    argument: ``--inputLabelVolume %s...``
inputTransform: (a list of items which are a pathlike object or
    string representing an existing file)
    transforms to apply to label volumes
    argument: ``--inputTransform %s...``
labelForUndecidedPixels: (an integer (int or long))
    Label for undecided pixels
    argument: ``--labelForUndecidedPixels %d``
resampledVolumePrefix: (a unicode string)
    if given, write out resampled volumes with this prefix
    argument: ``--resampledVolumePrefix %s``
skipResampling: (a boolean)
    Omit resampling images into reference space
    argument: ``--skipResampling ``
outputMultiSTAPLE: (a boolean or a pathlike object or string
    representing a file)
    the MultiSTAPLE average of input label volumes
    argument: ``--outputMultiSTAPLE %s``
outputConfusionMatrix: (a boolean or a pathlike object or string
    representing a file)
    Confusion Matrix
    argument: ``--outputConfusionMatrix %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {}))
    Environment variables
```

Outputs:

```
outputMultiSTAPLE: (a pathlike object or string representing an
    existing file)
    the MultiSTAPLE average of input label volumes
outputConfusionMatrix: (a pathlike object or string representing an
    existing file)
    Confusion Matrix
```

75.20.6 BRAINSROIAuto

[Link to code](#)

Wraps the executable command “ BRAINSROIAuto “.

title: Foreground masking (BRAINS)

category: Segmentation.Specialized

description: This program is used to create a mask over the most prominent foreground region in an image. This is accomplished via a combination of otsu thresholding and a closing operation. More documentation is available here: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/ForegroundMasking>.

version: 2.4.1

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Hans J. Johnson, hans-johnson -at- uiowa.edu, <http://www.psychiatry.uiowa.edu>

acknowledgements: Hans Johnson(1,3,4); Kent Williams(1); Gregory Harris(1), Vincent Magnotta(1,2,3); Andriy Fedorov(5), fedorov -at- bwh.harvard.edu (Slicer integration); (1=University of Iowa Department of Psychiatry, 2=University of Iowa Department of Radiology, 3=University of Iowa Department of Biomedical Engineering, 4=University of Iowa Department of Electrical and Computer Engineering, 5=Surgical Planning Lab, Harvard)

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              The input image for finding the largest region filled mask.
              argument: ``--inputVolume %s``
outputROIMaskVolume: (a boolean or a pathlike object or string
                      representing a file)
                      The ROI automatically found from the input image.
                      argument: ``--outputROIMaskVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              The inputVolume with optional [maskOutput|cropOutput] to the region
              of the brain mask.
              argument: ``--outputVolume %s``
maskOutput: (a boolean)
             The inputVolume multiplied by the ROI mask.
             argument: ``--maskOutput ``
cropOutput: (a boolean)
             The inputVolume cropped to the region of the ROI mask.
             argument: ``--cropOutput ``
otsuPercentileThreshold: (a float)
                         Parameter to the Otsu threshold algorithm.
                         argument: ``--otsuPercentileThreshold %f``
thresholdCorrectionFactor: (a float)
                           A factor to scale the Otsu algorithm's result threshold, in case
                           clipping mangles the image.
                           argument: ``--thresholdCorrectionFactor %f``
closingSize: (a float)
             The Closing Size (in millimeters) for largest connected filled mask.
             This value is divided by image spacing and rounded to the next
             largest voxel number.
             argument: ``--closingSize %f``
ROIAutoDilateSize: (a float)
                  This flag is only relevant when using ROIAUTO mode for initializing
                  masks. It defines the final dilation size to capture a bit of
                  background outside the tissue region. At setting of 10mm has been
                  shown to help regularize a BSpline registration type so that there
                  is some background constraints to match the edges of the head
```

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```

    better.
    argument: ``--ROIAutoDilateSize %f``
outputVolumePixelType: ('float' or 'short' or 'ushort' or 'int' or
    'uint' or 'uchar')
    The output image Pixel Type is the scalar datatype for
    representation of the Output Volume.
    argument: ``--outputVolumePixelType %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputROIMaskVolume: (a pathlike object or string representing an
    existing file)
    The ROI automatically found from the input image.
outputVolume: (a pathlike object or string representing an existing
    file)
    The inputVolume with optional [maskOutput|cropOutput] to the region
    of the brain mask.

```

75.20.7 BinaryMaskEditorBasedOnLandmarks**Link to code**

Wraps the executable command “ BinaryMaskEditorBasedOnLandmarks “.

title: BRAINS Binary Mask Editor Based On Landmarks(BRAINS)

category: Segmentation.Specialized

version: 1.0

documentation-url: <http://www.nitrc.org/projects/brainscdetector/>

Inputs:

```

[Optional]
inputBinaryVolume: (a pathlike object or string representing an
    existing file)
    Input binary image in which to be edited
    argument: ``--inputBinaryVolume %s``
outputBinaryVolume: (a boolean or a pathlike object or string
    representing a file)
    Output binary image in which to be edited
    argument: ``--outputBinaryVolume %s``
inputLandmarksFilename: (a pathlike object or string representing an
    existing file)
    The filename for the landmark definition file in the same format
    produced by Slicer3 (.fcsv).
    argument: ``--inputLandmarksFilename %s``
inputLandmarkNames: (a list of items which are a unicode string)
    A target input landmark name to be edited. This should be listed in
    the inputLandmakrFilename Given.
    argument: ``--inputLandmarkNames %s``

```

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```

setCutDirectionForLandmark: (a list of items which are a unicode
    string)
    Setting the cutting out direction of the input binary image to the
    one of anterior, posterior, left, right, superior or posterior.
    (ENUMERATION: ANTERIOR, POSTERIOR, LEFT, RIGHT, SUPERIOR, POSTERIOR)
    argument: ``--setCutDirectionForLandmark %s``
setCutDirectionForObliquePlane: (a list of items which are a unicode
    string)
    If this is true, the mask will be thresholded out to the direction
    of inferior, posterior, and/or left. Default behavior is that
    cutting out to the direction of superior, anterior and/or right.
    argument: ``--setCutDirectionForObliquePlane %s``
inputLandmarkNamesForObliquePlane: (a list of items which are a
    unicode string)
    Three subset landmark names of inputLandmarksFilename for a oblique
    plane computation. The plane computed for binary volume editing.
    argument: ``--inputLandmarkNamesForObliquePlane %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputBinaryVolume: (a pathlike object or string representing an
    existing file)
    Output binary image in which to be edited

```

75.20.8 ESLR[Link to code](#)Wraps the executable command “**ESLR**”.

title: Clean Contiguous Label Map (BRAINS)

category: Segmentation.Specialized

description: From a range of label map values, extract the largest contiguous region of those labels

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    Input Label Volume
    argument: ``--inputVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output Label Volume
    argument: ``--outputVolume %s``
low: (an integer (int or long))
    The lower bound of the labels to be used.
    argument: ``--low %d``
high: (an integer (int or long))
    The higher bound of the labels to be used.
    argument: ``--high %d``
closingSize: (an integer (int or long))

```

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```

        The closing size for hole filling.
        argument: ``--closingSize %d``
openingSize: (an integer (int or long))
        The opening size for hole filling.
        argument: ``--openingSize %d``
safetySize: (an integer (int or long))
        The safetySize size for the clipping region.
        argument: ``--safetySize %d``
preserveOutside: (a boolean)
        For values outside the specified range, preserve those values.
        argument: ``--preserveOutside ``
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        argument: ``--numberOfThreads %d``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
        file)
        Output Label Volume

```

75.21 interfaces.semtools.utilities.brains

75.21.1 BRAINSAlignMSP

[Link to code](#)

Wraps the executable command “ BRAINSAlignMSP “.

title: Align Mid Saggital Brain (BRAINS)

category: Utilities.BRAINS

description: Resample an image into ACPC alignment ACPCDetect

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
        file)
        , The Image to be resampled,
        argument: ``--inputVolume %s``
OutputresampleMSP: (a boolean or a pathlike object or string
        representing a file)
        , The image to be output.,
        argument: ``--OutputresampleMSP %s``
verbose: (a boolean)
        , Show more verbose output,
        argument: ``--verbose ``
resultsDir: (a boolean or a pathlike object or string representing a
        directory)
        , The directory for the results to be written.,
        argument: ``--resultsDir %s``

```

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```
writedebuggingImagesLevel: (an integer (int or long))
    , This flag controls if debugging images are produced. By default
    value of 0 is no images. Anything greater than zero will be
    increasing level of debugging images.,
    argument: ``--writedebuggingImagesLevel %d``
mspQualityLevel: (an integer (int or long))
    , Flag cotrols how agressive the MSP is estimated. 0=quick estimate
    (9 seconds), 1=normal estimate (11 seconds), 2=great estimate (22
    seconds), 3=best estimate (58 seconds).,
    argument: ``--mspQualityLevel %d``
rescaleIntensities: (a boolean)
    , Flag to turn on rescaling image intensities on input.,
    argument: ``--rescaleIntensities ``
trimRescaledIntensities: (a float)
    , Turn on clipping the rescaled image one-tailed on input. Units of
    standard deviations above the mean. Very large values are very
    permissive. Non-positive value turns clipping off. Defaults to
    removing 0.00001 of a normal tail above the mean.,
    argument: ``--trimRescaledIntensities %f``
rescaleIntensitiesOutputRange: (a list of items which are an integer
    (int or long))
    , This pair of integers gives the lower and upper bounds on the
    signal portion of the output image. Out-of-field voxels are taken
    from BackgroundFillValue.,
    argument: ``--rescaleIntensitiesOutputRange %s``
BackgroundFillValue: (a unicode string)
    Fill the background of image with specified short int value. Enter
    number or use BIGNEG for a large negative number.
    argument: ``--BackgroundFillValue %s``
interpolationMode: ('NearestNeighbor' or 'Linear' or
    'ResampleInPlace' or 'BSpline' or 'WindowedSinc' or 'Hamming' or
    'Cosine' or 'Welch' or 'Lanczos' or 'Blackman')
    Type of interpolation to be used when applying transform to moving
    volume. Options are Linear, ResampleInPlace, NearestNeighbor,
    BSpline, or WindowedSinc
    argument: ``--interpolationMode %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
OutputresampleMSP: (a pathlike object or string representing an
    existing file)
    , The image to be output.,
resultsDir: (a pathlike object or string representing an existing
    directory)
    , The directory for the results to be written.,
```

75.21.2 BRAINSClipInferior

[Link to code](#)

Wraps the executable command “ BRAINSClipInferior “.

title: Clip Inferior of Center of Brain (BRAINS)

category: Utilities.BRAINS

description: This program will read the inputVolume as a short int image, write the BackgroundFillValue everywhere inferior to the lower bound, and write the resulting clipped short int image in the outputVolume.

version: 1.0

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Input image to make a clipped short int copy from.
              argument: ``--inputVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              Output image, a short int copy of the upper portion of the input
              image, filled with BackgroundFillValue.
              argument: ``--outputVolume %s``
acLowerBound: (a float)
              , When the input image to the output image, replace the image with
              the BackgroundFillValue everywhere below the plane This Far in
              physical units (millimeters) below (inferior to) the AC point
              (assumed to be the voxel field middle.) The oversize default was
              chosen to have no effect. Based on visualizing a thousand masks in
              the IPIG study, we recommend a limit no smaller than 80.0 mm.,
              argument: ``--acLowerBound %f``
BackgroundFillValue: (a unicode string)
              Fill the background of image with specified short int value. Enter
              number or use BIGNEG for a large negative number.
              argument: ``--BackgroundFillValue %s``
numberOfThreads: (an integer (int or long))
              Explicitly specify the maximum number of threads to use.
              argument: ``--numberOfThreads %d``
args: (a unicode string)
              Additional parameters to the command
              argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
              file)
              Output image, a short int copy of the upper portion of the input
              image, filled with BackgroundFillValue.
```

75.21.3 BRAINSConstellationModeler

[Link to code](#)

Wraps the executable command “ BRAINSConstellationModeler “.

title: Generate Landmarks Model (BRAINS)

category: Utilities.BRAINS

description: Train up a model for BRAINSConstellationDetector

Inputs:

```
[Optional]
verbose: (a boolean)
    , Show more verbose output,
    argument: ``--verbose ``
inputTrainingList: (a pathlike object or string representing an
    existing file)
    , Setup file, giving all parameters for training up a template model
    for each landmark.,
    argument: ``--inputTrainingList %s``
outputModel: (a boolean or a pathlike object or string representing a
    file)
    , The full filename of the output model file.,
    argument: ``--outputModel %s``
saveOptimizedLandmarks: (a boolean)
    , Flag to make a new subject-specific landmark definition file in
    the same format produced by Slicer3 with the optimized landmark (the
    detected RP, AC, and PC) in it. Useful to tighten the variances in
    the ConstellationModeler.,
    argument: ``--saveOptimizedLandmarks ``
optimizedLandmarksFilenameExtender: (a unicode string)
    , If the trainingList is (indexFullPathName) and contains landmark
    data filenames [path]/[filename].fcsv , make the optimized landmarks
    filenames out of [path]/[filename](thisExtender) and the optimized
    version of the input trainingList out of
    (indexFullPathName)(thisExtender) , when you rewrite all the
    landmarks according to the saveOptimizedLandmarks flag.,
    argument: ``--optimizedLandmarksFilenameExtender %s``
resultsDir: (a boolean or a pathlike object or string representing a
    directory)
    , The directory for the results to be written.,
    argument: ``--resultsDir %s``
mspQualityLevel: (an integer (int or long))
    , Flag cotrols how aggressive the MSP is estimated. 0=quick estimate
    (9 seconds), 1=normal estimate (11 seconds), 2=great estimate (22
    seconds), 3=best estimate (58 seconds)。，
    argument: ``--mspQualityLevel %d``
rescaleIntensities: (a boolean)
    , Flag to turn on rescaling image intensities on input.,
    argument: ``--rescaleIntensities ``
trimRescaledIntensities: (a float)
    , Turn on clipping the rescaled image one-tailed on input. Units of
    standard deviations above the mean. Very large values are very
    permissive. Non-positive value turns clipping off. Defaults to
    removing 0.00001 of a normal tail above the mean.,
    argument: ``--trimRescaledIntensities %f``
rescaleIntensitiesOutputRange: (a list of items which are an integer
    (int or long))
    , This pair of integers gives the lower and upper bounds on the
    signal portion of the output image. Out-of-field voxels are taken
    from BackgroundFillValue.,
    argument: ``--rescaleIntensitiesOutputRange %s``
BackgroundFillValue: (a unicode string)
    Fill the background of image with specified short int value. Enter
    number or use BIGNEG for a large negative number.
    argument: ``--BackgroundFillValue %s``
writedebuggingImagesLevel: (an integer (int or long))
```

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```

, This flag controls if debugging images are produced. By default
value of 0 is no images. Anything greater than zero will be
increasing level of debugging images.,
argument: ``--writedebuggingImagesLevel %d``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputModel: (a pathlike object or string representing an existing
    file)
    , The full filename of the output model file.,
resultsDir: (a pathlike object or string representing an existing
    directory)
    , The directory for the results to be written.,

```

75.21.4 BRAINSEyeDetector[Link to code](#)

Wraps the executable command “ BRAINSEyeDetector “.

title: Eye Detector (BRAINS)

category: Utilities.BRAINS

version: 1.0

documentation-url: <http://www.nitrc.org/projects/brainscdetector/>**Inputs:**

```

[Optional]
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
inputVolume: (a pathlike object or string representing an existing
    file)
    The input volume
    argument: ``--inputVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    The output volume
    argument: ``--outputVolume %s``
debugDir: (a unicode string)
    A place for debug information
    argument: ``--debugDir %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               The output volume
```

75.21.5 BRAINSInitializedControlPoints[Link to code](#)

Wraps the executable command “BRAINSInitializedControlPoints”.

title: Initialized Control Points (BRAINS)

category: Utilities.BRAINS

description: Outputs bspline control points as landmarks

version: 0.1.0.\$Revision: 916 \$(alpha)

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Mark Scully

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149. Additional support for Mark Scully and Hans Johnson at the University of Iowa.

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Input Volume
              argument: ``--inputVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
               a file)
               Output Volume
               argument: ``--outputVolume %s``
splineGridSize: (a list of items which are an integer (int or long))
                 The number of subdivisions of the BSpline Grid to be centered on the
                 image space. Each dimension must have at least 3 subdivisions for
                 the BSpline to be correctly computed.
                 argument: ``--splineGridSize %s``
permuteOrder: (a list of items which are an integer (int or long))
               The permutation order for the images. The default is 0,1,2 (i.e. no
               permutation)
               argument: ``--permuteOrder %s``
outputLandmarksFile: (a unicode string)
                     Output filename
                     argument: ``--outputLandmarksFile %s``
numberOfThreads: (an integer (int or long))
                  Explicitly specify the maximum number of threads to use.
                  argument: ``--numberOfThreads %d``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
```

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Output Volume

75.21.6 BRAINSLandmarkInitializer

[Link to code](#)

Wraps the executable command “ BRAINSLandmarkInitializer “.

title: BRAINSLandmarkInitializer

category: Utilities.BRAINS

description: Create transformation file (*mat) from a pair of landmarks (*fcsv) files.

version: 1.0

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Eunyoung Regina Kim

Inputs:

```
[Optional]
inputFixedLandmarkFilename: (a pathlike object or string representing
                             an existing file)
                             input fixed landmark. *.fcsv
                             argument: ``--inputFixedLandmarkFilename %s``
inputMovingLandmarkFilename: (a pathlike object or string
                              representing an existing file)
                              input moving landmark. *.fcsv
                              argument: ``--inputMovingLandmarkFilename %s``
inputWeightFilename: (a pathlike object or string representing an
                      existing file)
                      Input weight file name for landmarks. Higher weighted landmark will
                      be considered more heavily. Weights are propotional, that is the
                      magnitude of weights will be normalized by its minimum and maximum
                      value.
                      argument: ``--inputWeightFilename %s``
outputTransformFilename: (a boolean or a pathlike object or string
                          representing a file)
                          output transform file name (ex: ./outputTransform.mat)
                          argument: ``--outputTransformFilename %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

```
outputTransformFilename: (a pathlike object or string representing an
                          existing file)
                          output transform file name (ex: ./outputTransform.mat)
```

75.21.7 BRAINSLinearModelerEPCA

[Link to code](#)

Wraps the executable command “ BRAINSLinearModelerEPCA “.

title: Landmark Linear Modeler (BRAINS)

category: Utilities.BRAINS

description: Training linear model using EPCA. Implementation based on my MS thesis, “A METHOD

FOR AUTOMATED LANDMARK CONSTELLATION DETECTION USING EVOLUTIONARY PRINCIPAL COMPONENTS AND STATISTICAL SHAPE MODELS”

version: 1.0

documentation-url: <http://www.nitrc.org/projects/brainscdetector/>

Inputs:

```
[Optional]
inputTrainingList: (a pathlike object or string representing an
                    existing file)
                    Input Training Landmark List Filename,
                    argument: ``--inputTrainingList %s``
numberOfThreads: (an integer (int or long))
                  Explicitly specify the maximum number of threads to use.
                  argument: ``--numberOfThreads %d``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

None

75.21.8 BRAINSLmkTransform[Link to code](#)

Wraps the executable command “ BRAINSLmkTransform “.

title: Landmark Transform (BRAINS)

category: Utilities.BRAINS

description: This utility program estimates the affine transform to align the fixed landmarks to the moving landmarks, and then generate the resampled moving image to the same physical space as that of the reference image.

version: 1.0

documentation-url: <http://www.nitrc.org/projects/brainscdetector/>

Inputs:

```
[Optional]
inputMovingLandmarks: (a pathlike object or string representing an
                      existing file)
                      Input Moving Landmark list file in fcsv,
                      argument: ``--inputMovingLandmarks %s``
inputFixedLandmarks: (a pathlike object or string representing an
                     existing file)
                     Input Fixed Landmark list file in fcsv,
                     argument: ``--inputFixedLandmarks %s``
outputAffineTransform: (a boolean or a pathlike object or string
                       representing a file)
                       The filename for the estimated affine transform,
                       argument: ``--outputAffineTransform %s``
inputMovingVolume: (a pathlike object or string representing an
                   existing file)
                   The filename of input moving volume
                   argument: ``--inputMovingVolume %s``
inputReferenceVolume: (a pathlike object or string representing an
```

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```

    existing file)
    The filename of the reference volume
    argument: ``--inputReferenceVolume %s``
outputResampledVolume: (a boolean or a pathlike object or string
    representing a file)
    The filename of the output resampled volume
    argument: ``--outputResampledVolume %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputAffineTransform: (a pathlike object or string representing an
    existing file)
    The filename for the estimated affine transform,
outputResampledVolume: (a pathlike object or string representing an
    existing file)
    The filename of the output resampled volume

```

75.21.9 BRAINSMush[Link to code](#)

Wraps the executable command “ BRAINSMush “.

title: Brain Extraction from T1/T2 image (BRAINS)

category: Utilities.BRAINS

description: This program: 1) generates a weighted mixture image optimizing the mean and variance and 2) produces a mask of the brain volume

version: 0.1.0.\$Revision: 1.4 \$(alpha)

documentation-url: <http://mri.radiology.uiowa.edu>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool is a modification by Steven Dunn of a program developed by Greg Harris and Ron Pierson.

acknowledgements: This work was developed by the University of Iowa Departments of Radiology and Psychiatry. This software was supported in part of NIH/NINDS award NS050568.

Inputs:

```

[Optional]
inputFirstVolume: (a pathlike object or string representing an
    existing file)
    Input image (1) for mixture optimization
    argument: ``--inputFirstVolume %s``
inputSecondVolume: (a pathlike object or string representing an
    existing file)
    Input image (2) for mixture optimization
    argument: ``--inputSecondVolume %s``
inputMaskVolume: (a pathlike object or string representing an
    existing file)
    Input label image for mixture optimization

```

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```

        argument: ``--inputMaskVolume %s``
outputWeightsFile: (a boolean or a pathlike object or string
    representing a file)
    Output Weights File
    argument: ``--outputWeightsFile %s``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    The MUSH image produced from the T1 and T2 weighted images
    argument: ``--outputVolume %s``
outputMask: (a boolean or a pathlike object or string representing a
    file)
    The brain volume mask generated from the MUSH image
    argument: ``--outputMask %s``
seed: (a list of items which are an integer (int or long))
    Seed Point for Brain Region Filling
    argument: ``--seed %s``
desiredMean: (a float)
    Desired mean within the mask for weighted sum of both images.
    argument: ``--desiredMean %f``
desiredVariance: (a float)
    Desired variance within the mask for weighted sum of both images.
    argument: ``--desiredVariance %f``
lowerThresholdFactorPre: (a float)
    Lower threshold factor for finding an initial brain mask
    argument: ``--lowerThresholdFactorPre %f``
upperThresholdFactorPre: (a float)
    Upper threshold factor for finding an initial brain mask
    argument: ``--upperThresholdFactorPre %f``
lowerThresholdFactor: (a float)
    Lower threshold factor for defining the brain mask
    argument: ``--lowerThresholdFactor %f``
upperThresholdFactor: (a float)
    Upper threshold factor for defining the brain mask
    argument: ``--upperThresholdFactor %f``
boundingBoxSize: (a list of items which are an integer (int or long))
    Size of the cubic bounding box mask used when no brain mask is
    present
    argument: ``--boundingBoxSize %s``
boundingBoxStart: (a list of items which are an integer (int or
    long))
    XYZ point-coordinate for the start of the cubic bounding box mask
    used when no brain mask is present
    argument: ``--boundingBoxStart %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```
outputWeightsFile: (a pathlike object or string representing an
```

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```

    existing file)
    Output Weights File
outputVolume: (a pathlike object or string representing an existing
    file)
    The MUSH image produced from the T1 and T2 weighted images
outputMask: (a pathlike object or string representing an existing
    file)
    The brain volume mask generated from the MUSH image

```

75.21.10 BRAINSSnapShotWriter

[Link to code](#)

Wraps the executable command “ BRAINSSnapShotWriter “.

title: BRAINSSnapShotWriter

category: Utilities.BRAINS

description: Create 2D snapshot of input images. Mask images are color-coded

version: 1.0

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Eunyoung Regina Kim

Inputs:

```

[Optional]
inputVolumes: (a list of items which are a pathlike object or string
    representing an existing file)
    Input image volume list to be extracted as 2D image. Multiple input
    is possible. At least one input is required.
    argument: ``--inputVolumes %s...``
inputBinaryVolumes: (a list of items which are a pathlike object or
    string representing an existing file)
    Input mask (binary) volume list to be extracted as 2D image.
    Multiple input is possible.
    argument: ``--inputBinaryVolumes %s...``
inputSliceToExtractInPhysicalPoint: (a list of items which are a
    float)
    2D slice number of input images. For autoWorkUp output, which AC-PC
    aligned, 0,0,0 will be the center.
    argument: ``--inputSliceToExtractInPhysicalPoint %s``
inputSliceToExtractInIndex: (a list of items which are an integer
    (int or long))
    2D slice number of input images. For size of 256*256*256 image, 128
    is usually used.
    argument: ``--inputSliceToExtractInIndex %s``
inputSliceToExtractInPercent: (a list of items which are an integer
    (int or long))
    2D slice number of input images. Percentage input from 0%-100%. (ex.
    --inputSliceToExtractInPercent 50,50,50
    argument: ``--inputSliceToExtractInPercent %s``
inputPlaneDirection: (a list of items which are an integer (int or
    long))
    Plane to display. In general, 0=sagittal, 1=coronal, and 2=axial
    plane.
    argument: ``--inputPlaneDirection %s``
outputFilename: (a boolean or a pathlike object or string
    representing a file)
    2D file name of input images. Required.

```

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```

    argument: ``--outputFilename %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputFilename: (a pathlike object or string representing an existing
    file)
    2D file name of input images. Required.

```

75.21.11 BRAINSTransformConvert**Link to code**

Wraps the executable command “ BRAINSTransformConvert “.

title: BRAINS Transform Convert

category: Utilities.BRAINS

description: Convert ITK transforms to higher order transforms

version: 1.0

documentation-url: A utility to convert between transform file formats.

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Hans J. Johnson,Kent Williams, Ali Ghayoor

Inputs:

```

[Optional]
inputTransform: (a pathlike object or string representing an existing
    file)
    argument: ``--inputTransform %s``
referenceVolume: (a pathlike object or string representing an
    existing file)
    argument: ``--referenceVolume %s``
outputTransformType: ('Affine' or 'VersorRigid' or 'ScaleVersor' or
    'ScaleSkewVersor' or 'DisplacementField' or 'Same')
    The target transformation type. Must be conversion-compatible with
    the input transform type
    argument: ``--outputTransformType %s``
outputPrecisionType: ('double' or 'float')
    Precision type of the output transform. It can be either single
    precision or double precision
    argument: ``--outputPrecisionType %s``
displacementVolume: (a boolean or a pathlike object or string
    representing a file)
    argument: ``--displacementVolume %s``
outputTransform: (a boolean or a pathlike object or string
    representing a file)
    argument: ``--outputTransform %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})

```

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Environment variables

Outputs:

displacementVolume: (a pathlike object or string representing an existing file)
 outputTransform: (a pathlike object or string representing an existing file)

75.21.12 BRAINSTrimForegroundInDirection[Link to code](#)

Wraps the executable command “ BRAINSTrimForegroundInDirection “.

title: Trim Foreground In Direction (BRAINS)

category: Utilities.BRAINS

description: This program will trim off the neck and also air-filling noise from the inputImage.

version: 0.1

documentation-url: <http://www.nitrc.org/projects/art/>**Inputs:**

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Input image to trim off the neck (and also air-filling noise.)
              argument: ``--inputVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              Output image with neck and air-filling noise trimmed isotropic image
              with AC at center of image.
              argument: ``--outputVolume %s``
directionCode: (an integer (int or long))
              , This flag chooses which dimension to compare. The sign lets you
              flip direction.,
              argument: ``--directionCode %d``
otsuPercentileThreshold: (a float)
              , This is a parameter to FindLargestForegroundFilledMask, which is
              employed to trim off air-filling noise.,
              argument: ``--otsuPercentileThreshold %f``
closingSize: (an integer (int or long))
              , This is a parameter to FindLargestForegroundFilledMask,
              argument: ``--closingSize %d``
headSizeLimit: (a float)
              , Use this to vary from the command line our search for how much
              upper tissue is head for the center-of-mass calculation. Units are
              CCs, not cubic millimeters.,
              argument: ``--headSizeLimit %f``
BackgroundFillValue: (a unicode string)
              Fill the background of image with specified short int value. Enter
              number or use BIGNEG for a large negative number.
              argument: ``--BackgroundFillValue %s``
numberOfThreads: (an integer (int or long))
              Explicitly specify the maximum number of threads to use.
              argument: ``--numberOfThreads %d``
args: (a unicode string)
              Additional parameters to the command
              argument: ``%s``
```

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```
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
              file)
              Output image with neck and air-filling noise trimmed isotropic image
              with AC at center of image.
```

75.21.13 CleanUpOverlapLabels

[Link to code](#)

Wraps the executable command “ CleanUpOverlapLabels “.

title: Clean Up Overla Labels

category: Utilities.BRAINS

description: Take a series of input binary images and clean up for those overlapped area. Binary volumes given first always wins out

version: 0.1.0

contributor: Eun Young Kim

Inputs:

```
[Optional]
inputBinaryVolumes: (a list of items which are a pathlike object or
                    string representing an existing file)
                    The list of binary images to be checked and cleaned up. Order is
                    important. Binary volume given first always wins out.
                    argument: ``--inputBinaryVolumes %s...``
outputBinaryVolumes: (a boolean or a list of items which are a
                    pathlike object or string representing a file)
                    The output label map images, with integer values in it. Each label
                    value specified in the inputLabels is combined into this output
                    label map volume
                    argument: ``--outputBinaryVolumes %s...``
args: (a unicode string)
     Additional parameters to the command
     argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
outputBinaryVolumes: (a list of items which are a pathlike object or
                    string representing an existing file)
                    The output label map images, with integer values in it. Each label
                    value specified in the inputLabels is combined into this output
                    label map volume
```

75.21.14 FindCenterOfBrain

[Link to code](#)

Wraps the executable command “ FindCenterOfBrain “.

title: Center Of Brain (BRAINS)

category: Utilities.BRAINS

description: Finds the center point of a brain

version: 3.0.0

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Hans J. Johnson, hans-johnson -at- uiowa.edu, <http://www.psychiatry.uiowa.edu>

acknowledgements: Hans Johnson(1,3,4); Kent Williams(1); (1=University of Iowa Department of Psychiatry, 3=University of Iowa Department of Biomedical Engineering, 4=University of Iowa Department of Electrical and Computer Engineering

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              The image in which to find the center.
              argument: ``--inputVolume %s``
imageMask: (a pathlike object or string representing an existing
            file)
            argument: ``--imageMask %s``
clippedImageMask: (a boolean or a pathlike object or string
                  representing a file)
                  argument: ``--clippedImageMask %s``
maximize: (a boolean)
           argument: ``--maximize ``
axis: (an integer (int or long))
       argument: ``--axis %d``
otsuPercentileThreshold: (a float)
                          argument: ``--otsuPercentileThreshold %f``
closingSize: (an integer (int or long))
             argument: ``--closingSize %d``
headSizeLimit: (a float)
               argument: ``--headSizeLimit %f``
headSizeEstimate: (a float)
                  argument: ``--headSizeEstimate %f``
backgroundValue: (an integer (int or long))
                 argument: ``--backgroundValue %d``
generateDebugImages: (a boolean)
                     argument: ``--generateDebugImages ``
debugDistanceImage: (a boolean or a pathlike object or string
                    representing a file)
                    argument: ``--debugDistanceImage %s``
debugGridImage: (a boolean or a pathlike object or string
                 representing a file)
                 argument: ``--debugGridImage %s``
debugAfterGridComputationsForegroundImage: (a boolean or a pathlike
                                             object or string representing a file)
                                             argument: ``--debugAfterGridComputationsForegroundImage %s``
debugClippedImageMask: (a boolean or a pathlike object or string
                        representing a file)
                        argument: ``--debugClippedImageMask %s``
debugTrimmedImage: (a boolean or a pathlike object or string
                   representing a file)
                   argument: ``--debugTrimmedImage %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
```

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```

of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

clippedImageMask: (a pathlike object or string representing an
existing file)
debugDistanceImage: (a pathlike object or string representing an
existing file)
debugGridImage: (a pathlike object or string representing an existing
file)
debugAfterGridComputationsForegroundImage: (a pathlike object or
string representing an existing file)
debugClippedImageMask: (a pathlike object or string representing an
existing file)
debugTrimmedImage: (a pathlike object or string representing an
existing file)

```

75.21.15 GenerateLabelMapFromProbabilityMap[Link to code](#)

Wraps the executable command “GenerateLabelMapFromProbabilityMap”.

title: Label Map from Probability Images

category: Utilities.BRAINS

description: Given a list of probability maps for labels, create a discrete label map where only the highest probability region is used for the labeling.

version: 0.1

contributor: University of Iowa Department of Psychiatry, <http://www.psychiatry.uiowa.edu>**Inputs:**

```

[Optional]
inputVolumes: (a list of items which are a pathlike object or string
representing an existing file)
The Input probaiblity images to be computed for lable maps
argument: ``--inputVolumes %s...``
outputLabelVolume: (a boolean or a pathlike object or string
representing a file)
The Input binary image for region of interest
argument: ``--outputLabelVolume %s``
numberOfThreads: (an integer (int or long))
Explicitly specify the maximum number of threads to use.
argument: ``--numberOfThreads %d``
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

outputLabelVolume: (a pathlike object or string representing an
existing file)
The Input binary image for region of interest

```

75.21.16 ImageRegionPlotter

[Link to code](#)

Wraps the executable command “ ImageRegionPlotter “.

title: Write Out Image Intensities

category: Utilities.BRAINS

description: For Analysis

version: 0.1

contributor: University of Iowa Department of Psychiatry, <http://www.psychiatry.uiowa.edu>

Inputs:

```
[Optional]
inputVolume1: (a pathlike object or string representing an existing
               file)
               The Input image to be computed for statistics
               argument: ``--inputVolume1 %s``
inputVolume2: (a pathlike object or string representing an existing
               file)
               The Input image to be computed for statistics
               argument: ``--inputVolume2 %s``
inputBinaryROIVolume: (a pathlike object or string representing an
                       existing file)
                       The Input binary image for region of interest
                       argument: ``--inputBinaryROIVolume %s``
inputLabelVolume: (a pathlike object or string representing an
                   existing file)
                   The Label Image
                   argument: ``--inputLabelVolume %s``
numberOfHistogramBins: (an integer (int or long))
                       the number of histogram levels
                       argument: ``--numberOfHistogramBins %d``
outputJointHistogramData: (a unicode string)
                          output data file name
                          argument: ``--outputJointHistogramData %s``
useROIAUTO: (a boolean)
            Use ROIAUTO to compute region of interest. This cannot be used with
            inputLabelVolume
            argument: ``--useROIAUTO ``
useIntensityForHistogram: (a boolean)
                          Create Intensity Joint Histogram instead of Quantile Joint
                          Histogram
                          argument: ``--useIntensityForHistogram ``
verbose: (a boolean)
          print debugging information,
          argument: ``--verbose ``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

None

75.21.17 JointHistogram

[Link to code](#)

Wraps the executable command “ JointHistogram “.

title: Write Out Image Intensities

category: Utilities.BRAINS

description: For Analysis

version: 0.1

contributor: University of Iowa Department of Psychiatry, <http://www.psychiatry.uiowa.edu>

Inputs:

```

[Optional]
inputVolumeInXAxis: (a pathlike object or string representing an
    existing file)
    The Input image to be computed for statistics
    argument: ``--inputVolumeInXAxis %s``
inputVolumeInYAxis: (a pathlike object or string representing an
    existing file)
    The Input image to be computed for statistics
    argument: ``--inputVolumeInYAxis %s``
inputMaskVolumeInXAxis: (a pathlike object or string representing an
    existing file)
    Input mask volume for inputVolumeInXAxis. Histogram will be computed
    just for the masked region
    argument: ``--inputMaskVolumeInXAxis %s``
inputMaskVolumeInYAxis: (a pathlike object or string representing an
    existing file)
    Input mask volume for inputVolumeInYAxis. Histogram will be computed
    just for the masked region
    argument: ``--inputMaskVolumeInYAxis %s``
outputJointHistogramImage: (a unicode string)
    output joint histogram image file name. Histogram is usually 2D
    image.
    argument: ``--outputJointHistogramImage %s``
verbose: (a boolean)
    print debugging information,
    argument: ``--verbose ``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

None

75.21.18 ShuffleVectorsModule

[Link to code](#)

Wraps the executable command “ ShuffleVectorsModule “.

title: ShuffleVectors

category: Utilities.BRAINS

description: Automatic Segmentation using neural networks

version: 1.0

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Hans Johnson

Inputs:

```
[Optional]
inputVectorFileBaseName: (a pathlike object or string representing an
    existing file)
    input vector file name prefix. Usually end with .txt and header file
    has prost fix of .txt.hdr
    argument: ``--inputVectorFileBaseName %s``
outputVectorFileBaseName: (a boolean or a pathlike object or string
    representing a file)
    output vector file name prefix. Usually end with .txt and header
    file has prost fix of .txt.hdr
    argument: ``--outputVectorFileBaseName %s``
resampleProportion: (a float)
    downsample size of 1 will be the same size as the input images,
    downsample size of 3 will throw 2/3 the vectors away.
    argument: ``--resampleProportion %f``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables
```

Outputs:

```
outputVectorFileBaseName: (a pathlike object or string representing
    an existing file)
    output vector file name prefix. Usually end with .txt and header
    file has prost fix of .txt.hdr
```

75.21.19 fcsv_to_hdf5

[Link to code](#)

Wraps the executable command “ fcsv_to_hdf5 “.

title: fcsv_to_hdf5 (BRAINS)

category: Utilities.BRAINS

description: Convert a collection of fcsv files to a HDF5 format file

Inputs:

```
[Optional]
versionID: (a unicode string)
    , Current version ID. It should be match with the version of BCD
    that will be using the output model file,
    argument: ``--versionID %s``
landmarksInformationFile: (a boolean or a pathlike object or string
    representing a file)
    , name of HDF5 file to write matrices into,
    argument: ``--landmarksInformationFile %s``
landmarkTypesList: (a pathlike object or string representing an
    existing file)
    , file containing list of landmark types,
    argument: ``--landmarkTypesList %s``
modelFile: (a boolean or a pathlike object or string representing a
    file)
```

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```

, name of HDF5 file containing BRAINSConstellationDetector Model
file (LLSMatrices, LLSMeans and LLSSearchRadii),
argument: ``--modelFile %s``
landmarkGlobPattern: (a unicode string)
Glob pattern to select fcsv files
argument: ``--landmarkGlobPattern %s``
numberOfThreads: (an integer (int or long))
Explicitly specify the maximum number of threads to use.
argument: ``--numberOfThreads %d``
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipype default value: {})
Environment variables

```

Outputs:

```

landmarksInformationFile: (a pathlike object or string representing
an existing file)
, name of HDF5 file to write matrices into,
modelFile: (a pathlike object or string representing an existing
file)
, name of HDF5 file containing BRAINSConstellationDetector Model
file (LLSMatrices, LLSMeans and LLSSearchRadii),

```

75.21.20 insertMidACPCpoint[Link to code](#)

Wraps the executable command “insertMidACPCpoint”.

title: MidACPC Landmark Insertion

category: Utilities.BRAINS

description: This program gets a landmark fcsv file and adds a new landmark as the midpoint between AC and PC points to the output landmark fcsv file

contributor: Ali Ghayoor

Inputs:

```

[Optional]
inputLandmarkFile: (a pathlike object or string representing an
existing file)
Input landmark file (.fcsv)
argument: ``--inputLandmarkFile %s``
outputLandmarkFile: (a boolean or a pathlike object or string
representing a file)
Output landmark file (.fcsv)
argument: ``--outputLandmarkFile %s``
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipype default value: {})
Environment variables

```

Outputs:

```
outputLandmarkFile: (a pathlike object or string representing an
    existing file)
    Output landmark file (.fcsv)
```

75.21.21 landmarksConstellationAligner

[Link to code](#)

Wraps the executable command “ landmarksConstellationAligner “.

title: MidACPC Landmark Insertion

category: Utilities.BRAINS

description: This program converts the original landmark files to the acpc-aligned landmark files

contributor: Ali Ghayoor

Inputs:

```
[Optional]
inputLandmarksPaired: (a pathlike object or string representing an
    existing file)
    Input landmark file (.fcsv)
    argument: ``--inputLandmarksPaired %s``
outputLandmarksPaired: (a boolean or a pathlike object or string
    representing a file)
    Output landmark file (.fcsv)
    argument: ``--outputLandmarksPaired %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables
```

Outputs:

```
outputLandmarksPaired: (a pathlike object or string representing an
    existing file)
    Output landmark file (.fcsv)
```

75.21.22 landmarksConstellationWeights

[Link to code](#)

Wraps the executable command “ landmarksConstellationWeights “.

title: Generate Landmarks Weights (BRAINS)

category: Utilities.BRAINS

description: Train up a list of Weights for the Landmarks in BRAINSConstellationDetector

Inputs:

```
[Optional]
inputTrainingList: (a pathlike object or string representing an
    existing file)
    , Setup file, giving all parameters for training up a Weight list
    for landmark.,
    argument: ``--inputTrainingList %s``
inputTemplateModel: (a pathlike object or string representing an
    existing file)
    User-specified template model.,
    argument: ``--inputTemplateModel %s``
```

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```
LLSModel: (a pathlike object or string representing an existing file)
    Linear least squares model filename in HD5 format
    argument: ``--LLSModel %s``
outputWeightsList: (a boolean or a pathlike object or string
    representing a file)
    , The filename of a csv file which is a list of landmarks and their
    corresponding weights.,
    argument: ``--outputWeightsList %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outputWeightsList: (a pathlike object or string representing an
    existing file)
    , The filename of a csv file which is a list of landmarks and their
    corresponding weights.,
```


76.1 interfaces.slicer.base

76.1.1 SlicerCommandLine

[Link to code](#)

Inputs:

```
[Optional]
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
None
```

76.2 interfaces.slicer.converters

76.2.1 DicomToNrrdConverter

[Link to code](#)

Wraps the executable command “DicomToNrrdConverter”.

title: DICOM to NRRD Converter

category: Converters

description: Converts diffusion weighted MR images in dicom series into Nrrd format for analysis in Slicer. This program has been tested on only a limited subset of DTI dicom formats available from Siemens, GE, and Phillips scanners. Work in progress to support dicom multi-frame data. The program parses dicom header to extract necessary information about measurement frame, diffusion weighting directions, b-values, etc, and write out a nrrd image. For non-diffusion weighted dicom images, it loads in an entire dicom series and writes out a single dicom volume in a .nhdr/.raw pair.

version: 0.2.0.\$Revision: 916 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/DicomToNrrdConverter>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: Xiaodong Tao (GE), Vince Magnotta (UIowa), Hans Johnson (UIowa)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149. Additional support for DTI data produced on Philips scanners was contributed by Vincent Magnotta and Hans Johnson at the University of Iowa.

Inputs:

```
[Optional]
inputDicomDirectory: (a pathlike object or string representing an
    existing directory)
    Directory holding Dicom series
    argument: ``--inputDicomDirectory %s``
outputDirectory: (a boolean or a pathlike object or string
    representing a directory)
    Directory holding the output NRRD format
    argument: ``--outputDirectory %s``
outputVolume: (a unicode string)
    Output filename (.nhdr or .nrrd)
    argument: ``--outputVolume %s``
smallGradientThreshold: (a float)
    If a gradient magnitude is greater than 0 and less than
    smallGradientThreshold, then DicomToNrrdConverter will display an
    error message and quit, unless the useBMatrixGradientDirections
    option is set.
    argument: ``--smallGradientThreshold %f``
writeProtocolGradientsFile: (a boolean)
    Write the protocol gradients to a file suffixed by '.txt' as they
    were specified in the procol by multiplying each diffusion gradient
    direction by the measurement frame. This file is for debugging
    purposes only, the format is not fixed, and will likely change as
    debugging of new dicom formats is necessary.
    argument: ``--writeProtocolGradientsFile ``
useIdentityMeaseurementFrame: (a boolean)
    Adjust all the gradients so that the measurement frame is an
    identity matrix.
    argument: ``--useIdentityMeaseurementFrame ``
useBMatrixGradientDirections: (a boolean)
    Fill the nhdr header with the gradient directions and bvalues
    computed out of the BMatrix. Only changes behavior for Siemens data.
    argument: ``--useBMatrixGradientDirections ``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outputDirectory: (a pathlike object or string representing an
    existing directory)
    Directory holding the output NRRD format
```

76.2.2 OrientScalarVolume

[Link to code](#)

Wraps the executable command “OrientScalarVolume”.

title: Orient Scalar Volume

category: Converters

description: Orients an output volume. Rearranges the slices in a volume according to the selected orientation. The slices are not interpolated. They are just reordered and/or permuted. The resulting volume will cover the original volume. NOTE: since Slicer takes into account the orientation of a volume, the re-oriented volume will not show any difference from the original volume, To see the difference, save the volume and display it with a system that either ignores the orientation of the image (e.g. Paraview) or displays individual images.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/OrientImage>

contributor: Bill Lorensen (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
inputVolume1: (a pathlike object or string representing an existing
               file)
               Input volume 1
               argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
               a file)
               The oriented volume
               argument: ``%s``, position: -1
orientation: ('Axial' or 'Coronal' or 'Sagittal' or 'RIP' or 'LIP' or
              'RSP' or 'LSP' or 'RIA' or 'LIA' or 'RSA' or 'LSA' or 'IRP' or
              'ILP' or 'SRP' or 'SLP' or 'IRA' or 'ILA' or 'SRA' or 'SLA' or
              'RPI' or 'LPI' or 'RAI' or 'LAI' or 'RPS' or 'LPS' or 'RAS' or
              'LAS' or 'PRI' or 'PLI' or 'ARI' or 'ALI' or 'PRS' or 'PLS' or
              'ARS' or 'ALS' or 'IPR' or 'SPR' or 'IAR' or 'SAR' or 'IPL' or
              'SPL' or 'IAL' or 'SAL' or 'PIR' or 'PSR' or 'AIR' or 'ASR' or
              'PIL' or 'PSL' or 'AIL' or 'ASL')
Orientation choices
argument: ``--orientation %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               The oriented volume
```

76.3 interfaces.slicer.diffusion.diffusion

76.3.1 DTIexport

[Link to code](#)

Wraps the executable command “DTIexport”.

title: DTIexport

category: Diffusion.Diffusion Data Conversion

description: Export DTI data to various file formats

version: 1.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/DTIExport>

contributor: Sonia Pujol (SPL, BWH)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NA-MIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
inputTensor: (a pathlike object or string representing an existing
              file)
              Input DTI volume
              argument: ``%s``, position: -2
outputFile: (a boolean or a pathlike object or string representing a
             file)
             Output DTI file
             argument: ``%s``, position: -1
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputFile: (a pathlike object or string representing an existing
             file)
             Output DTI file
```

76.3.2 DTIimport

[Link to code](#)

Wraps the executable command “DTIimport”.

title: DTIimport

category: Diffusion.Diffusion Data Conversion

description: Import tensor datasets from various formats, including the NifTi file format

version: 1.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/DTIImport>

contributor: Sonia Pujol (SPL, BWH)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NA-MIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
inputFile: (a pathlike object or string representing an existing
            file)
            Input DTI file
            argument: ``%s``, position: -2
outputTensor: (a boolean or a pathlike object or string representing
               a file)
               Output DTI volume
               argument: ``%s``, position: -1
```

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```

testingmode: (a boolean)
    Enable testing mode. Sample helix file (helix-DTI.nhdr) will be
    loaded into Slicer and converted in Nifti.
    argument: ``--testingmode``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputTensor: (a pathlike object or string representing an existing
    file)
    Output DTI volume

```

76.3.3 DWIJointRicianLMMSEFilter[Link to code](#)

Wraps the executable command “DWIJointRicianLMMSEFilter”.

title: DWI Joint Rician LMMSE Filter

category: Diffusion.Diffusion Weighted Images

description: This module reduces Rician noise (or unwanted detail) on a set of diffusion weighted images. For this, it filters the image in the mean squared error sense using a Rician noise model. The N closest gradient directions to the direction being processed are filtered together to improve the results: the noise-free signal is seen as an n-dimensional vector which has to be estimated with the LMMSE method from a set of corrupted measurements. To that end, the covariance matrix of the noise-free vector and the cross covariance between this signal and the noise have to be estimated, which is done taking into account the image formation process. The noise parameter is automatically estimated from a rough segmentation of the background of the image. In this area the signal is simply 0, so that Rician statistics reduce to Rayleigh and the noise power can be easily estimated from the mode of the histogram. A complete description of the algorithm may be found in: Antonio Tristan-Vega and Santiago Aja-Fernandez, DWI filtering using joint information for DTI and HARDI, Medical Image Analysis, Volume 14, Issue 2, Pages 205-218. 2010.

version: 0.1.1.\$Revision: 1 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/JointRicianLMMSEImageFilter>

contributor: Antonio Tristan Vega (UVa), Santiago Aja Fernandez (UVa)

acknowledgements: Partially founded by grant number TEC2007-67073/TCM from the Comision Interministerial de Ciencia y Tecnologia (Spain).

Inputs:

```

[Optional]
re: (a list of items which are an integer (int or long))
    Estimation radius.
    argument: ``--re %s``
rf: (a list of items which are an integer (int or long))
    Filtering radius.
    argument: ``--rf %s``
ng: (an integer (int or long))
    The number of the closest gradients that are used to jointly filter
    a given gradient direction (0 to use all).
    argument: ``--ng %d``
inputVolume: (a pathlike object or string representing an existing

```

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```

    file)
    Input DWI volume.
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output DWI volume.
    argument: ``%s``, position: -1
compressOutput: (a boolean)
    Compress the data of the compressed file using gzip
    argument: ``--compressOutput``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Output DWI volume.

```

76.3.4 DWIRicianLMMSEFilter[Link to code](#)

Wraps the executable command “DWIRicianLMMSEFilter”.

title: DWI Rician LMMSE Filter

category: Diffusion.Diffusion Weighted Images

description: This module reduces noise (or unwanted detail) on a set of diffusion weighted images. For this, it filters the image in the mean squared error sense using a Rician noise model. Images corresponding to each gradient direction, including baseline, are processed individually. The noise parameter is automatically estimated (noise estimation improved but slower). Note that this is a general purpose filter for MRi images. The module jointLMMSE has been specifically designed for DWI volumes and shows a better performance, so its use is recommended instead. A complete description of the algorithm in this module can be found in: S. Aja-Fernandez, M. Niethammer, M. Kubicki, M. Shenton, and C.-F. Westin. Restoration of DWI data using a Rician LMMSE estimator. IEEE Transactions on Medical Imaging, 27(10): pp. 1389-1403, Oct. 2008.

version: 0.1.1.\$Revision: 1 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/RicianLMMSEImageFilter>

contributor: Antonio Tristan Vega (UVa), Santiago Aja Fernandez (UVa), Marc Niethammer (UNC)

acknowledgements: Partially founded by grant number TEC2007-67073/TCM from the Comision Interministerial de Ciencia y Tecnologia (Spain).

Inputs:

```

[Optional]
iter: (an integer (int or long))
    Number of iterations for the noise removal filter.
    argument: ``--iter %d``
re: (a list of items which are an integer (int or long))
    Estimation radius.
    argument: ``--re %s``
rf: (a list of items which are an integer (int or long))
    Filtering radius.

```

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```

        argument: ``--rf %s``
mnvf: (an integer (int or long))
    Minimum number of voxels in kernel used for filtering.
    argument: ``--mnvf %d``
mnve: (an integer (int or long))
    Minimum number of voxels in kernel used for estimation.
    argument: ``--mnve %d``
minnstd: (an integer (int or long))
    Minimum allowed noise standard deviation.
    argument: ``--minnstd %d``
maxnstd: (an integer (int or long))
    Maximum allowed noise standard deviation.
    argument: ``--maxnstd %d``
hrf: (a float)
    How many histogram bins per unit interval.
    argument: ``--hrf %f``
uav: (a boolean)
    Use absolute value in case of negative square.
    argument: ``--uav ``
inputVolume: (a pathlike object or string representing an existing
    file)
    Input DWI volume.
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output DWI volume.
    argument: ``%s``, position: -1
compressOutput: (a boolean)
    Compress the data of the compressed file using gzip
    argument: ``--compressOutput ``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Output DWI volume.

```

76.3.5 DWIToDTIEstimation[Link to code](#)

Wraps the executable command “DWIToDTIEstimation”.

title: DWI to DTI Estimation

category: Diffusion.Diffusion Weighted Images

description: Performs a tensor model estimation from diffusion weighted images.

There are three estimation methods available: least squares, weighted least squares and non-linear estimation. The first method is the traditional method for tensor estimation and the fastest one. Weighted least squares takes into account the noise characteristics of the MRI images to weight the DWI samples used in the estimation based on its intensity magnitude. The last method is the more complex.

version: 0.1.0.\$Revision: 1892 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/DiffusionTensorEstimation>

license: slicer3

contributor: Raul San Jose (SPL, BWH)

acknowledgements: This command module is based on the estimation functionality provided by the Teem library. This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Input DWI volume
              argument: ``%s``, position: -3
mask: (a pathlike object or string representing an existing file)
      Mask where the tensors will be computed
      argument: ``--mask %s``
outputTensor: (a boolean or a pathlike object or string representing
               a file)
               Estimated DTI volume
               argument: ``%s``, position: -2
outputBaseline: (a boolean or a pathlike object or string
                 representing a file)
                 Estimated baseline volume
                 argument: ``%s``, position: -1
enumeration: ('LS' or 'WLS')
              LS: Least Squares, WLS: Weighted Least Squares
              argument: ``--enumeration %s``
shiftNeg: (a boolean)
           Shift eigenvalues so all are positive (accounts for bad tensors
           related to noise or acquisition error)
           argument: ``--shiftNeg ``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputTensor: (a pathlike object or string representing an existing
               file)
               Estimated DTI volume
outputBaseline: (a pathlike object or string representing an existing
                 file)
                 Estimated baseline volume
```

76.3.6 DiffusionTensorScalarMeasurements

[Link to code](#)

Wraps the executable command “DiffusionTensorScalarMeasurements”.

title: Diffusion Tensor Scalar Measurements

category: Diffusion.Diffusion Tensor Images

description: Compute a set of different scalar measurements from a tensor field, specially oriented for Diffusion Tensors where some rotationally invariant measurements, like Fractional Anisotropy, are highly used to describe the anisotropic behaviour of the tensor.

version: 0.1.0.\$Revision: 1892 \$(alpha)
documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/DiffusionTensorMathematics>
contributor: Raul San Jose (SPL, BWH)
acknowledgements: LMI
Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Input DTI volume
              argument: ``%s``, position: -3
outputScalar: (a boolean or a pathlike object or string representing
               a file)
               Scalar volume derived from tensor
               argument: ``%s``, position: -1
enumeration: ('Trace' or 'Determinant' or 'RelativeAnisotropy' or
              'FractionalAnisotropy' or 'Mode' or 'LinearMeasure' or
              'PlanarMeasure' or 'SphericalMeasure' or 'MinEigenvalue' or
              'MidEigenvalue' or 'MaxEigenvalue' or 'MaxEigenvalueProjectionX'
              or 'MaxEigenvalueProjectionY' or 'MaxEigenvalueProjectionZ' or
              'RAIMaxEigenvecX' or 'RAIMaxEigenvecY' or 'RAIMaxEigenvecZ' or
              'MaxEigenvecX' or 'MaxEigenvecY' or 'MaxEigenvecZ' or 'D11' or
              'D22' or 'D33' or 'ParallelDiffusivity' or
              'PerpendicularDffusivity')
              An enumeration of strings
              argument: ``--enumeration %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables
```

Outputs:

```
outputScalar: (a pathlike object or string representing an existing
               file)
               Scalar volume derived from tensor
```

76.3.7 DiffusionWeightedVolumeMasking

[Link to code](#)

Wraps the executable command “DiffusionWeightedVolumeMasking”.

title: Diffusion Weighted Volume Masking

category: Diffusion.Diffusion Weighted Images

description: <p>Performs a mask calculation from a diffusion weighted (DW) image.</p><p>Starting from a dw image, this module computes the baseline image averaging all the images without diffusion weighting and then applies the otsu segmentation algorithm in order to produce a mask. this mask can then be used when estimating the diffusion tensor (dt) image, not to estimate tensors all over the volume.</p>

version: 0.1.0.\$Revision: 1892 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/DiffusionWeightedMasking>

license: slicer3

contributor: Demian Wassermann (SPL, BWH)

Inputs:

```
[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Input DWI volume
              argument: ``%s``, position: -4
outputBaseline: (a boolean or a pathlike object or string
                 representing a file)
                 Estimated baseline volume
                 argument: ``%s``, position: -2
thresholdMask: (a boolean or a pathlike object or string representing
                a file)
                Otsu Threshold Mask
                argument: ``%s``, position: -1
otsuomegathreshold: (a float)
                    Control the sharpness of the threshold in the Otsu computation. 0:
                    lower threshold, 1: higher threshold
                    argument: ``--otsuomegathreshold %f``
removeislands: (a boolean)
               Remove Islands in Threshold Mask?
               argument: ``--removeislands``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputBaseline: (a pathlike object or string representing an existing
                 file)
                 Estimated baseline volume
thresholdMask: (a pathlike object or string representing an existing
                file)
                Otsu Threshold Mask
```

76.3.8 ResampleDTIVolume[Link to code](#)

Wraps the executable command “ResampleDTIVolume”.

title: Resample DTI Volume

category: Diffusion.Diffusion Tensor Images

description: Resampling an image is a very important task in image analysis. It is especially important in the frame of image registration. This module implements DT image resampling through the use of itk Transforms. The resampling is controlled by the Output Spacing. “Resampling” is performed in space coordinates, not pixel/grid coordinates. It is quite important to ensure that image spacing is properly set on the images involved. The interpolator is required since the mapping from one space to the other will often require evaluation of the intensity of the image at non-grid positions.

version: 0.1

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/ResampleDTI>

contributor: Francois Budin (UNC)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149. Information on the National Centers for Biomedical Computing can be obtained from <http://nihroadmap.nih.gov/bioinformatics>

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
              file)
              Input volume to be resampled
              argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              Resampled Volume
              argument: ``%s``, position: -1
Reference: (a pathlike object or string representing an existing
            file)
            Reference Volume (spacing,size,orientation,origin)
            argument: ``--Reference %s``
transformationFile: (a pathlike object or string representing an
                    existing file)
                    argument: ``--transformationFile %s``
defField: (a pathlike object or string representing an existing file)
           File containing the deformation field (3D vector image containing
           vectors with 3 components)
           argument: ``--defField %s``
hfieldtype: ('displacement' or 'h-Field')
            Set if the deformation field is an -Field
            argument: ``--hfieldtype %s``
interpolation: ('linear' or 'nn' or 'ws' or 'bs')
               Sampling algorithm (linear , nn (nearest neighborhood), ws
               (WindowedSinc), bs (BSpline) )
               argument: ``--interpolation %s``
correction: ('zero' or 'none' or 'abs' or 'nearest')
            Correct the tensors if computed tensor is not semi-definite positive
            argument: ``--correction %s``
transform_tensor_method: ('PPD' or 'FS')
                        Chooses between 2 methods to transform the tensors: Finite Strain
                        (FS), faster but less accurate, or Preservation of the Principal
                        Direction (PPD)
                        argument: ``--transform_tensor_method %s``
transform_order: ('input-to-output' or 'output-to-input')
                Select in what order the transforms are read
                argument: ``--transform_order %s``
notbulk: (a boolean)
         The transform following the BSpline transform is not set as a bulk
         transform for the BSpline transform
         argument: ``--notbulk ``
spaceChange: (a boolean)
             Space Orientation between transform and image is different (RAS/LPS)
             (warning: if the transform is a Transform Node in Slicer3, do not
             select)
             argument: ``--spaceChange ``
rotation_point: (a list of items which are any value)
               Center of rotation (only for rigid and affine transforms)
               argument: ``--rotation_point %s``
centered_transform: (a boolean)
                   Set the center of the transformation to the center of the input
                   image (only for rigid and affine transforms)
                   argument: ``--centered_transform ``
image_center: ('input' or 'output')
              Image to use to center the transform (used only if 'Centered
              Transform' is selected)

```

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```

        argument: ``--image_center %s``
Inverse_ITK_Transformation: (a boolean)
    Inverse the transformation before applying it from output image to
    input image (only for rigid and affine transforms)
    argument: ``--Inverse_ITK_Transformation``
spacing: (a list of items which are a float)
    Spacing along each dimension (0 means use input spacing)
    argument: ``--spacing %s``
size: (a list of items which are a float)
    Size along each dimension (0 means use input size)
    argument: ``--size %s``
origin: (a list of items which are any value)
    Origin of the output Image
    argument: ``--origin %s``
direction_matrix: (a list of items which are a float)
    9 parameters of the direction matrix by rows (ijk to LPS if LPS
    transform, ijk to RAS if RAS transform)
    argument: ``--direction_matrix %s``
number_of_thread: (an integer (int or long))
    Number of thread used to compute the output image
    argument: ``--number_of_thread %d``
default_pixel_value: (a float)
    Default pixel value for samples falling outside of the input region
    argument: ``--default_pixel_value %f``
window_function: ('h' or 'c' or 'w' or 'l' or 'b')
    Window Function , h = Hamming , c = Cosine , w = Welch , l = Lanczos
    , b = Blackman
    argument: ``--window_function %s``
spline_order: (an integer (int or long))
    Spline Order (Spline order may be from 0 to 5)
    argument: ``--spline_order %d``
transform_matrix: (a list of items which are a float)
    12 parameters of the transform matrix by rows ( --last 3 being
    translation-- )
    argument: ``--transform_matrix %s``
transform: ('rt' or 'a')
    Transform algorithm, rt = Rigid Transform, a = Affine Transform
    argument: ``--transform %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Resampled Volume

```

76.3.9 TractographyLabelMapSeeding[Link to code](#)

Wraps the executable command “TractographyLabelMapSeeding”.

title: Tractography Label Map Seeding

category: Diffusion.Diffusion Tensor Images

description: Seed tracts on a Diffusion Tensor Image (DT) from a label map

version: 0.1.0.\$Revision: 1892 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/Seeding>

license: slicer3

contributor: Raul San Jose (SPL, BWH), Demian Wassermann (SPL, BWH)

acknowledgements: Laboratory of Mathematics in Imaging. This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
InputVolume: (a pathlike object or string representing an existing
              file)
              Input DTI volume
              argument: ``%s``, position: -2
inputroi: (a pathlike object or string representing an existing file)
           Label map with seeding ROIs
           argument: ``--inputroi %s``
OutputFibers: (a boolean or a pathlike object or string representing
               a file)
               Tractography result
               argument: ``%s``, position: -1
useindexspace: (a boolean)
                Seed at IJK voxel grid
                argument: ``--useindexspace``
seedspacing: (a float)
              Spacing (in mm) between seed points, only matters if use Use Index
              Space is off
              argument: ``--seedspacing %f``
randomgrid: (a boolean)
             Enable random placing of seeds
             argument: ``--randomgrid``
clthreshold: (a float)
              Minimum Linear Measure for the seeding to start.
              argument: ``--clthreshold %f``
minimumlength: (a float)
                Minimum length of the fibers (in mm)
                argument: ``--minimumlength %f``
maximumlength: (a float)
                Maximum length of fibers (in mm)
                argument: ``--maximumlength %f``
stoppingmode: ('LinearMeasure' or 'FractionalAnisotropy')
               Tensor measurement used to stop the tractography
               argument: ``--stoppingmode %s``
stoppingvalue: (a float)
                Tractography will stop when the stopping measurement drops below
                this value
                argument: ``--stoppingvalue %f``
stoppingcurvature: (a float)
                    Tractography will stop if radius of curvature becomes smaller than
                    this number units are degrees per mm
                    argument: ``--stoppingcurvature %f``
integrationsteplength: (a float)
                        Distance between points on the same fiber in mm
                        argument: ``--integrationsteplength %f``
label: (an integer (int or long))
```

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```

        Label value that defines seeding region.
        argument: ``--label %d``
writetofile: (a boolean)
        Write fibers to disk or create in the scene?
        argument: ``--writetofile``
outputdirectory: (a boolean or a pathlike object or string
        representing a directory)
        Directory in which to save fiber(s)
        argument: ``--outputdirectory %s``
name: (a unicode string)
        Name to use for fiber files
        argument: ``--name %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

OutputFibers: (a pathlike object or string representing an existing
        file)
        Tractography result
outputdirectory: (a pathlike object or string representing an
        existing directory)
        Directory in which to save fiber(s)

```

76.4 interfaces.slicer.filtering.arithmetic

76.4.1 AddScalarVolumes

Link to code

Wraps the executable command “AddScalarVolumes”.

title: Add Scalar Volumes

category: Filtering.Arithmetic

description: Adds two images. Although all image types are supported on input, only signed types are produced. The two images do not have to have the same dimensions.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/Add>

contributor: Bill Lorensen (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```

[Optional]
inputVolume1: (a pathlike object or string representing an existing
        file)
        Input volume 1
        argument: ``%s``, position: -3
inputVolume2: (a pathlike object or string representing an existing
        file)
        Input volume 2
        argument: ``%s``, position: -2

```

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```

outputVolume: (a boolean or a pathlike object or string representing
               a file)
               Volume1 + Volume2
               argument: ``%s``, position: -1
order: ('0' or '1' or '2' or '3')
       Interpolation order if two images are in different coordinate frames
       or have different sampling.
       argument: ``--order %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})
          Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
               file)
               Volume1 + Volume2

```

76.4.2 CastScalarVolume[Link to code](#)

Wraps the executable command “CastScalarVolume”.

title: Cast Scalar Volume

category: Filtering.Arithmetic

description: Cast a volume to a given data type. Use at your own risk when casting an input volume into a lower precision type! Allows casting to the same type as the input volume.

version: 0.1.0.\$Revision: 2104 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/Cast>

contributor: Nicole Aucoin (SPL, BWH), Ron Kikinis (SPL, BWH)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```

[Optional]
InputVolume: (a pathlike object or string representing an existing
              file)
              Input volume, the volume to cast.
              argument: ``%s``, position: -2
OutputVolume: (a boolean or a pathlike object or string representing
               a file)
               Output volume, cast to the new type.
               argument: ``%s``, position: -1
type: ('Char' or 'UnsignedChar' or 'Short' or 'UnsignedShort' or
       'Int' or 'UnsignedInt' or 'Float' or 'Double')
       Type for the new output volume.
       argument: ``--type %s``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipype default value: {})

```

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Environment variables

Outputs:

OutputVolume: (a pathlike `object` or string representing an existing file)
 Output volume, cast to the new `type`.

76.4.3 MaskScalarVolume[Link to code](#)

Wraps the executable command “MaskScalarVolume”.

title: Mask Scalar Volume

category: Filtering.Arithmetic

description: Masks two images. The output image is set to 0 everywhere except where the chosen label from the mask volume is present, at which point it will retain it’s original values. Although all image types are supported on input, only signed types are produced. The two images do not have to have the same dimensions.

version: 0.1.0.\$Revision: 8595 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/Mask>

contributor: Nicole Aucoin (SPL, BWH), Ron Kikinis (SPL, BWH)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
InputVolume: (a pathlike object or string representing an existing
              file)
              Input volume to be masked
              argument: ``%s``, position: -3
MaskVolume: (a pathlike object or string representing an existing
             file)
             Label volume containing the mask
             argument: ``%s``, position: -2
OutputVolume: (a boolean or a pathlike object or string representing
              a file)
              Output volume: Input Volume masked by label value from Mask Volume
              argument: ``%s``, position: -1
label: (an integer (int or long))
       Label value in the Mask Volume to use as the mask
       argument: ``--label %d``
replace: (an integer (int or long))
         Value to use for the output volume outside of the mask
         argument: ``--replace %d``
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

OutputVolume: (a pathlike `object` or string representing an existing file)
 Output volume: Input Volume masked by label value `from Mask` Volume

76.4.4 MultiplyScalarVolumes

[Link to code](#)

Wraps the executable command “MultiplyScalarVolumes”.

title: Multiply Scalar Volumes

category: Filtering.Arithmetic

description: Multiplies two images. Although all image types are supported on input, only signed types are produced. The two images do not have to have the same dimensions.

version: 0.1.0.\$Revision: 8595 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/Multiply>

contributor: Bill Lorensen (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
inputVolume1: (a pathlike object or string representing an existing
               file)
               Input volume 1
               argument: ``%s``, position: -3
inputVolume2: (a pathlike object or string representing an existing
               file)
               Input volume 2
               argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
               a file)
               Volume1 * Volume2
               argument: ``%s``, position: -1
order: ('0' or '1' or '2' or '3')
         Interpolation order if two images are in different coordinate frames
         or have different sampling.
         argument: ``--order %s``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               Volume1 * Volume2
```

76.4.5 SubtractScalarVolumes

[Link to code](#)

Wraps the executable command “SubtractScalarVolumes”.

title: Subtract Scalar Volumes

category: Filtering.Arithmetic

description: Subtracts two images. Although all image types are supported on input, only signed types are produced. The two images do not have to have the same dimensions.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/Subtract>

contributor: Bill Lorensen (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
inputVolume1: (a pathlike object or string representing an existing
               file)
               Input volume 1
               argument: ``%s``, position: -3
inputVolume2: (a pathlike object or string representing an existing
               file)
               Input volume 2
               argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
               a file)
               Volume1 - Volume2
               argument: ``%s``, position: -1
order: ('0' or '1' or '2' or '3')
         Interpolation order if two images are in different coordinate frames
         or have different sampling.
         argument: ``--order %s``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               Volume1 - Volume2
```

76.5 interfaces.slicer.filtering.checkerboardfilter

76.5.1 CheckerBoardFilter

[Link to code](#)

Wraps the executable command “CheckerBoardFilter”.

title: CheckerBoard Filter

category: Filtering

description: Create a checkerboard volume of two volumes. The output volume will show the two inputs alternating according to the user supplied checkerPattern. This filter is often used to compare the results of image registration. Note that the second input is resampled to the same origin, spacing and direction before it is composed with the first input. The scalar type of the output volume will be the same as the input image scalar type.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/CheckerBoard>

contributor: Bill Lorensen (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
checkerPattern: (a list of items which are an integer (int or long))
    The pattern of input 1 and input 2 in the output image. The user can
    specify the number of checkers in each dimension. A checkerPattern
    of 2,2,1 means that images will alternate in every other checker in
    the first two dimensions. The same pattern will be used in the 3rd
    dimension.
    argument: ``--checkerPattern %s``
inputVolume1: (a pathlike object or string representing an existing
    file)
    First Input volume
    argument: ``%s``, position: -3
inputVolume2: (a pathlike object or string representing an existing
    file)
    Second Input volume
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output filtered
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
    file)
    Output filtered
```

76.6 interfaces.slicer.filtering.denoising

76.6.1 CurvatureAnisotropicDiffusion

Link to code

Wraps the executable command “CurvatureAnisotropicDiffusion”.

title: Curvature Anisotropic Diffusion

category: Filtering.Denoising

description: Performs anisotropic diffusion on an image using a modified curvature diffusion equation (MCDE). MCDE does not exhibit the edge enhancing properties of classic anisotropic diffusion, which can under certain conditions undergo a ‘negative’ diffusion, which enhances the contrast of edges. Equations of the form of MCDE always undergo positive diffusion, with the conductance term only varying the strength of that diffusion.

Qualitatively, MCDE compares well with other non-linear diffusion techniques. It is less sensitive to contrast than classic Perona-Malik style diffusion, and preserves finer detailed structures in images. There is a potential speed trade-off for using this function in place of Gradient Anisotropic Diffusion. Each iteration of the solution takes roughly twice as long. Fewer iterations, however, may be required to reach an acceptable solution.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/CurvatureAnisotropicDiffusion>

contributor: Bill Lorensen (GE)

acknowledgements: This command module was derived from Insight/Examples (copyright) Insight Software

Consortium**Inputs:**

```
[Optional]
conductance: (a float)
    Conductance controls the sensitivity of the conductance term. As a
    general rule, the lower the value, the more strongly the filter
    preserves edges. A high value will cause diffusion (smoothing)
    across edges. Note that the number of iterations controls how much
    smoothing is done within regions bounded by edges.
    argument: ``--conductance %f``
iterations: (an integer (int or long))
    The more iterations, the more smoothing. Each iteration takes the
    same amount of time. If it takes 10 seconds for one iteration, then
    it will take 100 seconds for 10 iterations. Note that the
    conductance controls how much each iteration smooths across edges.
    argument: ``--iterations %d``
timeStep: (a float)
    The time step depends on the dimensionality of the image. In Slicer
    the images are 3D and the default (.0625) time step will provide a
    stable solution.
    argument: ``--timeStep %f``
inputVolume: (a pathlike object or string representing an existing
    file)
    Input volume to be filtered
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output filtered
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
    file)
    Output filtered
```

76.6.2 GaussianBlurImageFilter**Link to code**

Wraps the executable command “GaussianBlurImageFilter”.

title: Gaussian Blur Image Filter

category: Filtering.Denoising

description: Apply a gaussian blurr to an image

version: 0.1.0.\$Revision: 1.1 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/GaussianBlurImageFilter>

contributor: Julien Jomier (Kitware), Stephen Aylward (Kitware)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
sigma: (a float)
    Sigma value in physical units (e.g., mm) of the Gaussian kernel
    argument: ``--sigma %f``
inputVolume: (a pathlike object or string representing an existing
    file)
    Input volume
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Blurred Volume
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
    file)
    Blurred Volume
```

76.6.3 GradientAnisotropicDiffusion

[Link to code](#)

Wraps the executable command “GradientAnisotropicDiffusion”.

title: Gradient Anisotropic Diffusion

category: Filtering.Denoising

description: Runs gradient anisotropic diffusion on a volume.

Anisotropic diffusion methods reduce noise (or unwanted detail) in images while preserving specific image features, like edges. For many applications, there is an assumption that light-dark transitions (edges) are interesting. Standard isotropic diffusion methods move and blur light-dark boundaries. Anisotropic diffusion methods are formulated to specifically preserve edges. The conductance term for this implementation is a function of the gradient magnitude of the image at each point, reducing the strength of diffusion at edges. The numerical implementation of this equation is similar to that described in the Perona-Malik paper, but uses a more robust technique for gradient magnitude estimation and has been generalized to N-dimensions.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/GradientAnisotropicDiffusion>

contributor: Bill Lorensen (GE)

acknowledgements: This command module was derived from Insight/Examples (copyright) Insight Software Consortium

Inputs:

```
[Optional]
conductance: (a float)
    Conductance controls the sensitivity of the conductance term. As a
    general rule, the lower the value, the more strongly the filter
    preserves edges. A high value will cause diffusion (smoothing)
    across edges. Note that the number of iterations controls how much
    smoothing is done within regions bounded by edges.
    argument: ``--conductance %f``
```

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```

iterations: (an integer (int or long))
    The more iterations, the more smoothing. Each iteration takes the
    same amount of time. If it takes 10 seconds for one iteration, then
    it will take 100 seconds for 10 iterations. Note that the
    conductance controls how much each iteration smooths across edges.
    argument: ``--iterations %d``
timeStep: (a float)
    The time step depends on the dimensionality of the image. In Slicer
    the images are 3D and the default (.0625) time step will provide a
    stable solution.
    argument: ``--timeStep %f``
inputVolume: (a pathlike object or string representing an existing
    file)
    Input volume to be filtered
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output filtered
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Output filtered

```

76.6.4 MedianImageFilter[Link to code](#)

Wraps the executable command “MedianImageFilter”.

title: Median Image Filter

category: Filtering.Denoising

description: The MedianImageFilter is commonly used as a robust approach for noise reduction. This filter is particularly efficient against “salt-and-pepper” noise. In other words, it is robust to the presence of gray-level outliers. MedianImageFilter computes the value of each output pixel as the statistical median of the neighborhood of values around the corresponding input pixel.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/MedianImageFilter>

contributor: Bill Lorensen (GE)

acknowledgements: This command module was derived from Insight/Examples/Filtering/MedianImageFilter (copyright) Insight Software Consortium

Inputs:

```

[Optional]
neighborhood: (a list of items which are an integer (int or long))
    The size of the neighborhood in each dimension
    argument: ``--neighborhood %s``
inputVolume: (a pathlike object or string representing an existing

```

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```

    file)
    Input volume to be filtered
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output filtered
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Output filtered

```

76.7 interfaces.slicer.filtering.extractskelton

76.7.1 ExtractSkeleton

[Link to code](#)

Wraps the executable command “ExtractSkeleton”.

title: Extract Skeleton

category: Filtering

description: Extract the skeleton of a binary object. The skeleton can be limited to being a 1D curve or allowed to be a full 2D manifold. The branches of the skeleton can be pruned so that only the maximal center skeleton is returned.

version: 0.1.0.\$Revision: 2104 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/ExtractSkeleton>

contributor: Pierre Seroul (UNC), Martin Styner (UNC), Guido Gerig (UNC), Stephen Aylward (Kitware)

acknowledgements: The original implementation of this method was provided by ETH Zurich, Image Analysis Laboratory of Profs Olaf Kuebler, Gabor Szekely and Guido Gerig. Martin Styner at UNC, Chapel Hill made enhancements. Wrapping for Slicer was provided by Pierre Seroul and Stephen Aylward at Kitware, Inc.

Inputs:

```

[Optional]
InputImageFileName: (a pathlike object or string representing an
    existing file)
    Input image
    argument: ``%s``, position: -2
OutputImageFileName: (a boolean or a pathlike object or string
    representing a file)
    Skeleton of the input image
    argument: ``%s``, position: -1
type: ('1D' or '2D')
    Type of skeleton to create
    argument: ``--type %s``
dontPrune: (a boolean)
    Return the full skeleton, not just the maximal skeleton
    argument: ``--dontPrune ``

```

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```

numPoints: (an integer (int or long))
    Number of points used to represent the skeleton
    argument: ``--numPoints %d``
pointsFile: (a unicode string)
    Name of the file to store the coordinates of the central (1D)
    skeleton points
    argument: ``--pointsFile %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

OutputImageFileName: (a pathlike object or string representing an
    existing file)
    Skeleton of the input image

```

76.8 interfaces.slicer.filtering.histogrammatching

76.8.1 HistogramMatching

[Link to code](#)

Wraps the executable command “HistogramMatching”.

title: Histogram Matching

category: Filtering

description: Normalizes the grayscale values of a source image based on the grayscale values of a reference image. This filter uses a histogram matching technique where the histograms of the two images are matched only at a specified number of quantile values.

The filter was originally designed to normalize MR images of the sameMR protocol and same body part. The algorithm works best if background pixels are excluded from both the source and reference histograms. A simple background exclusion method is to exclude all pixels whose grayscale values are smaller than the mean grayscale value. ThresholdAtMeanIntensity switches on this simple background exclusion method.

Number of match points governs the number of quantile values to be matched.

The filter assumes that both the source and reference are of the same type and that the input and output image type have the same number of dimension and have scalar pixel types.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/HistogramMatching>

contributor: Bill Lorensen (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```

[Optional]
numberOfHistogramLevels: (an integer (int or long))
    The number of hisogram levels to use
    argument: ``--numberOfHistogramLevels %d``
numberOfMatchPoints: (an integer (int or long))
    The number of match points to use
    argument: ``--numberOfMatchPoints %d``

```

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```

threshold: (a boolean)
    If on, only pixels above the mean in each volume are thresholded.
    argument: ``--threshold``
inputVolume: (a pathlike object or string representing an existing
    file)
    Input volume to be filtered
    argument: ``%s``, position: -3
referenceVolume: (a pathlike object or string representing an
    existing file)
    Input volume whose histogram will be matched
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output volume. This is the input volume with intensities matched to
    the reference volume.
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Output volume. This is the input volume with intensities matched to
    the reference volume.

```

76.9 interfaces.slicer.filtering.imagelabelcombine

76.9.1 ImageLabelCombine

[Link to code](#)

Wraps the executable command “ImageLabelCombine”.

title: Image Label Combine

category: Filtering

description: Combine two label maps into one

version: 0.1.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/ImageLabelCombine>

contributor: Alex Yarmarkovich (SPL, BWH)

Inputs:

```

[Optional]
InputLabelMap_A: (a pathlike object or string representing an
    existing file)
    Label map image
    argument: ``%s``, position: -3
InputLabelMap_B: (a pathlike object or string representing an
    existing file)
    Label map image
    argument: ``%s``, position: -2

```

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```

OutputLabelMap: (a boolean or a pathlike object or string
    representing a file)
    Resulting Label map image
    argument: ``%s``, position: -1
first_overwrites: (a boolean)
    Use first or second label when both are present
    argument: ``--first_overwrites``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

OutputLabelMap: (a pathlike object or string representing an existing
    file)
    Resulting Label map image

```

76.10 interfaces.slicer.filtering.morphology

76.10.1 GrayscaleFillHoleImageFilter

Link to code

Wraps the executable command “GrayscaleFillHoleImageFilter”.

title: Grayscale Fill Hole Image Filter

category: Filtering.Morphology

description: GrayscaleFillholeImageFilter fills holes in a grayscale image. Holes are local minima in the grayscale topography that are not connected to boundaries of the image. Gray level values adjacent to a hole are extrapolated across the hole.

This filter is used to smooth over local minima without affecting the values of local maxima. If you take the difference between the output of this filter and the original image (and perhaps threshold the difference above a small value), you’ll obtain a map of the local minima.

This filter uses the itkGrayscaleGeodesicErodeImageFilter. It provides its own input as the “mask” input to the geodesic erosion. The “marker” image for the geodesic erosion is constructed such that boundary pixels match the boundary pixels of the input image and the interior pixels are set to the maximum pixel value in the input image.

Geodesic morphology and the Fillhole algorithm is described in Chapter 6 of Pierre Soille’s book “Morphological Image Analysis: Principles and Applications”, Second Edition, Springer, 2003.

A companion filter, Grayscale Grind Peak, removes peaks in grayscale images.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/GrayscaleFillHoleImageFilter>

contributor: Bill Lorensen (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    Input volume to be filtered

```

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```

        argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
               a file)
               Output filtered
        argument: ``%s``, position: -1
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
               file)
               Output filtered

```

76.10.2 GrayscaleGrindPeakImageFilter[Link to code](#)

Wraps the executable command “GrayscaleGrindPeakImageFilter”.

title: Grayscale Grind Peak Image Filter

category: Filtering.Morphology

description: GrayscaleGrindPeakImageFilter removes peaks in a grayscale image. Peaks are local maxima in the grayscale topography that are not connected to boundaries of the image. Gray level values adjacent to a peak are extrapolated through the peak.

This filter is used to smooth over local maxima without affecting the values of local minima. If you take the difference between the output of this filter and the original image (and perhaps threshold the difference above a small value), you’ll obtain a map of the local maxima.

This filter uses the GrayscaleGeodesicDilateImageFilter. It provides its own input as the “mask” input to the geodesic erosion. The “marker” image for the geodesic erosion is constructed such that boundary pixels match the boundary pixels of the input image and the interior pixels are set to the minimum pixel value in the input image.

This filter is the dual to the GrayscaleFillholeImageFilter which implements the Fillhole algorithm. Since it is a dual, it is somewhat superfluous but is provided as a convenience.

Geodesic morphology and the Fillhole algorithm is described in Chapter 6 of Pierre Soille’s book “Morphological Image Analysis: Principles and Applications”, Second Edition, Springer, 2003.

A companion filter, Grayscale Fill Hole, fills holes in grayscale images.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/GrayscaleGrindPeakImageFilter>

contributor: Bill Lorensen (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
               file)
               Input volume to be filtered
               argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing

```

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```

    a file)
    Output filtered
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Output filtered

```

76.11 interfaces.slicer.filtering.n4itkbiasfieldcorrection**76.11.1 N4ITKBiasFieldCorrection**[Link to code](#)

Wraps the executable command “N4ITKBiasFieldCorrection”.

title: N4ITK MRI Bias correction

category: Filtering

description: Performs image bias correction using N4 algorithm. This module is based on the ITK filters contributed in the following publication: Tustison N, Gee J “N4ITK: Nick’s N3 ITK Implementation For MRI Bias Field Correction”, The Insight Journal 2009 January-June, <http://hdl.handle.net/10380/3053>

version: 9

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/N4ITKBiasFieldCorrection>

contributor: Nick Tustison (UPenn), Andrey Fedorov (SPL, BWH), Ron Kikinis (SPL, BWH)

acknowledgements: The development of this module was partially supported by NIH grants R01 AA016748-01, R01 CA111288 and U01 CA151261 as well as by NA-MIC, NAC, NCIGT and the Slicer community.

Inputs:

```

[Optional]
inputimage: (a pathlike object or string representing an existing
    file)
    Input image where you observe signal inhomogeneity
    argument: ``--inputimage %s``
maskimage: (a pathlike object or string representing an existing
    file)
    Binary mask that defines the structure of your interest. NOTE: This
    parameter is OPTIONAL. If the mask is not specified, the module will
    use internally Otsu thresholding to define this mask. Better
    processing results can often be obtained when a meaningful mask is
    defined.
    argument: ``--maskimage %s``
outputimage: (a boolean or a pathlike object or string representing a
    file)
    Result of processing
    argument: ``--outputimage %s``
outputbiasfield: (a boolean or a pathlike object or string
    representing a file)

```

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```

    Recovered bias field (OPTIONAL)
    argument: ``--outputbiasfield %s``
iterations: (a list of items which are an integer (int or long))
    Maximum number of iterations at each level of resolution. Larger
    values will increase execution time, but may lead to better results.
    argument: ``--iterations %s``
convergencythreshold: (a float)
    Stopping criterion for the iterative bias estimation. Larger values
    will lead to smaller execution time.
    argument: ``--convergencythreshold %f``
meshresolution: (a list of items which are a float)
    Resolution of the initial bspline grid defined as a sequence of
    three numbers. The actual resolution will be defined by adding the
    bspline order (default is 3) to the resolution in each dimension
    specified here. For example, 1,1,1 will result in a 4x4x4 grid of
    control points. This parameter may need to be adjusted based on your
    input image. In the multi-resolution N4 framework, the resolution of
    the bspline grid at subsequent iterations will be doubled. The
    number of resolutions is implicitly defined by Number of iterations
    parameter (the size of this list is the number of resolutions)
    argument: ``--meshresolution %s``
splinedistance: (a float)
    An alternative means to define the spline grid, by setting the
    distance between the control points. This parameter is used only if
    the grid resolution is not specified.
    argument: ``--splinedistance %f``
shrinkfactor: (an integer (int or long))
    Defines how much the image should be upsampled before estimating the
    inhomogeneity field. Increase if you want to reduce the execution
    time. 1 corresponds to the original resolution. Larger values will
    significantly reduce the computation time.
    argument: ``--shrinkfactor %d``
bsplineorder: (an integer (int or long))
    Order of B-spline used in the approximation. Larger values will lead
    to longer execution times, may result in overfitting and poor
    result.
    argument: ``--bsplineorder %d``
weightimage: (a pathlike object or string representing an existing
    file)
    Weight Image
    argument: ``--weightimage %s``
histogramsharpening: (a list of items which are a float)
    A vector of up to three values. Non-zero values correspond to Bias
    Field Full Width at Half Maximum, Wiener filter noise, and Number of
    histogram bins.
    argument: ``--histogramsharpening %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputimage: (a pathlike object or string representing an existing

```

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```

    file)
    Result of processing
outputbiasfield: (a pathlike object or string representing an
    existing file)
    Recovered bias field (OPTIONAL)

```

76.12 interfaces.slicer.filtering.resamplescalarvectordwivolume

76.12.1 ResampleScalarVectorDWIVolume

[Link to code](#)

Wraps the executable command “ResampleScalarVectorDWIVolume”.

title: Resample Scalar/Vector/DWI Volume

category: Filtering

description: This module implements image and vector-image resampling through the use of itk Transforms. It can also handle diffusion weighted MRI image resampling. “Resampling” is performed in space coordinates, not pixel/grid coordinates. It is quite important to ensure that image spacing is properly set on the images involved. The interpolator is required since the mapping from one space to the other will often require evaluation of the intensity of the image at non-grid positions.

Warning: To resample DWMR Images, use nrrd input and output files.

Warning: Do not use to resample Diffusion Tensor Images, tensors would not be reoriented

version: 0.1

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/ResampleScalarVectorDWIVolume>

contributor: Francois Budin (UNC)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149. Information on the National Centers for Biomedical Computing can be obtained from <http://nihroadmap.nih.gov/bioinformatics>

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    Input Volume to be resampled
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Resampled Volume
    argument: ``%s``, position: -1
Reference: (a pathlike object or string representing an existing
    file)
    Reference Volume (spacing, size, orientation, origin)
    argument: ``--Reference %s``
transformationFile: (a pathlike object or string representing an
    existing file)
    argument: ``--transformationFile %s``
defField: (a pathlike object or string representing an existing file)
    File containing the deformation field (3D vector image containing
    vectors with 3 components)
    argument: ``--defField %s``
hfieldtype: ('displacement' or 'h-Field')
    Set if the deformation field is an h-Field

```

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```

        argument: ``--hfieldtype %s``
interpolation: ('linear' or 'nn' or 'ws' or 'bs')
    Sampling algorithm (linear or nn (nearest neighborhood), ws
    (WindowedSinc), bs (BSpline) )
    argument: ``--interpolation %s``
transform_order: ('input-to-output' or 'output-to-input')
    Select in what order the transforms are read
    argument: ``--transform_order %s``
notbulk: (a boolean)
    The transform following the BSpline transform is not set as a bulk
    transform for the BSpline transform
    argument: ``--notbulk ``
spaceChange: (a boolean)
    Space Orientation between transform and image is different (RAS/LPS)
    (warning: if the transform is a Transform Node in Slicer3, do not
    select)
    argument: ``--spaceChange ``
rotation_point: (a list of items which are any value)
    Rotation Point in case of rotation around a point (otherwise
    useless)
    argument: ``--rotation_point %s``
centered_transform: (a boolean)
    Set the center of the transformation to the center of the input
    image
    argument: ``--centered_transform ``
image_center: ('input' or 'output')
    Image to use to center the transform (used only if 'Centered
    Transform' is selected)
    argument: ``--image_center %s``
Inverse_ITK_Transformation: (a boolean)
    Inverse the transformation before applying it from output image to
    input image
    argument: ``--Inverse_ITK_Transformation ``
spacing: (a list of items which are a float)
    Spacing along each dimension (0 means use input spacing)
    argument: ``--spacing %s``
size: (a list of items which are a float)
    Size along each dimension (0 means use input size)
    argument: ``--size %s``
origin: (a list of items which are any value)
    Origin of the output Image
    argument: ``--origin %s``
direction_matrix: (a list of items which are a float)
    9 parameters of the direction matrix by rows (ijk to LPS if LPS
    transform, ijk to RAS if RAS transform)
    argument: ``--direction_matrix %s``
number_of_thread: (an integer (int or long))
    Number of thread used to compute the output image
    argument: ``--number_of_thread %d``
default_pixel_value: (a float)
    Default pixel value for samples falling outside of the input region
    argument: ``--default_pixel_value %f``
window_function: ('h' or 'c' or 'w' or 'l' or 'b')
    Window Function , h = Hamming , c = Cosine , w = Welch , l = Lanczos
    , b = Blackman
    argument: ``--window_function %s``
spline_order: (an integer (int or long))

```

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```

    Spline Order
    argument: ``--spline_order %d``
transform_matrix: (a list of items which are a float)
    12 parameters of the transform matrix by rows ( --last 3 being
    translation-- )
    argument: ``--transform_matrix %s``
transform: ('rt' or 'a')
    Transform algorithm, rt = Rigid Transform, a = Affine Transform
    argument: ``--transform %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Resampled Volume

```

76.13 interfaces.slicer.filtering.thresholdscalervolume

76.13.1 ThresholdScalarVolume

Link to code

Wraps the executable command “ThresholdScalarVolume”.

title: Threshold Scalar Volume

category: Filtering

description: <p>Threshold an image.</p><p>Set image values to a user-specified outside value if they are below, above, or between simple threshold values.</p><p>ThresholdAbove: The values greater than or equal to the threshold value are set to OutsideValue.</p><p>ThresholdBelow: The values less than or equal to the threshold value are set to OutsideValue.</p><p>ThresholdOutside: The values outside the range Lower-Upper are set to OutsideValue.</p><p>Although all image types are supported on input, only signed types are produced.</p><p>

version: 0.1.0.\$Revision: 2104 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/Threshold>

contributor: Nicole Aucoin (SPL, BWH), Ron Kikinis (SPL, BWH)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```

[Optional]
InputVolume: (a pathlike object or string representing an existing
    file)
    Input volume
    argument: ``%s``, position: -2
OutputVolume: (a boolean or a pathlike object or string representing
    a file)
    Thresholded input volume
    argument: ``%s``, position: -1
threshold: (an integer (int or long))

```

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```

    Threshold value
    argument: ``--threshold %d``
lower: (an integer (int or long))
    Lower threshold value
    argument: ``--lower %d``
upper: (an integer (int or long))
    Upper threshold value
    argument: ``--upper %d``
outsidevalue: (an integer (int or long))
    Set the voxels to this value if they fall outside the threshold
    range
    argument: ``--outsidevalue %d``
thresholdtype: ('Below' or 'Above' or 'Outside')
    What kind of threshold to perform. If Outside is selected, uses
    Upper and Lower values. If Below is selected, uses the
    ThresholdValue, if Above is selected, uses the ThresholdValue.
    argument: ``--thresholdtype %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables

```

Outputs:

```

OutputVolume: (a pathlike object or string representing an existing
    file)
    Thresholded input volume

```

76.14 interfaces.slicer.filtering.votingbinaryholefillingimagefilter

76.14.1 VotingBinaryHoleFillingImageFilter

[Link to code](#)

Wraps the executable command “VotingBinaryHoleFillingImageFilter”.

title: Voting Binary Hole Filling Image Filter

category: Filtering

description: Applies a voting operation in order to fill-in cavities. This can be used for smoothing contours and for filling holes in binary images. This technique is used frequently when segmenting complete organs that may have ducts or vasculature that may not have been included in the initial segmentation, e.g. lungs, kidneys, liver.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/VotingBinaryHoleFillingImageFilter>

contributor: Bill Lorensen (GE)

acknowledgements: This command module was derived from Insight/Examples/Filtering/VotingBinaryHoleFillingImageFilter (copyright) Insight Software Consortium

Inputs:

```

[Optional]
radius: (a list of items which are an integer (int or long))
    The radius of a hole to be filled
    argument: ``--radius %s``
majorityThreshold: (an integer (int or long))

```

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```

The number of pixels over 50% that will decide whether an OFF pixel
will become ON or not. For example, if the neighborhood of a pixel
has 124 pixels (excluding itself), the 50% will be 62, and if you
set a Majority threshold of 5, that means that the filter will
require 67 or more neighbor pixels to be ON in order to switch the
current OFF pixel to ON.
argument: ``--majorityThreshold %d``
background: (an integer (int or long))
The value associated with the background (not object)
argument: ``--background %d``
foreground: (an integer (int or long))
The value associated with the foreground (object)
argument: ``--foreground %d``
inputVolume: (a pathlike object or string representing an existing
file)
Input volume to be filtered
argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
a file)
Output filtered
argument: ``%s``, position: -1
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
file)
Output filtered

```

76.15 interfaces.slicer.legacy.converters**76.15.1 BSplineToDeformationField**[Link to code](#)

Wraps the executable command “BSplineToDeformationField”.

title: BSpline to deformation field

category: Legacy.Converters

description: Create a dense deformation field from a bspline+bulk transform.

version: 0.1.0.\$Revision: 2104 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/BSplineToDeformationField>

contributor: Andrey Fedorov (SPL, BWH)

acknowledgements: This work is funded by NIH grants R01 CA111288 and U01 CA151261.

Inputs:

```

[Optional]
tfm: (a pathlike object or string representing an existing file)
argument: ``--tfm %s``
refImage: (a pathlike object or string representing an existing file)

```

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```

    argument: ``--refImage %s``
defImage: (a boolean or a pathlike object or string representing a
    file)
    argument: ``--defImage %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```
defImage: (a pathlike object or string representing an existing file)
```

76.16 interfaces.slicer.legacy.diffusion.denoising

76.16.1 DWIUnbiasedNonLocalMeansFilter

[Link to code](#)

Wraps the executable command “DWIUnbiasedNonLocalMeansFilter”.

title: DWI Unbiased Non Local Means Filter

category: Legacy.Diffusion.Denoising

description: This module reduces noise (or unwanted detail) on a set of diffusion weighted images. For this, it filters the images using a Unbiased Non Local Means for Rician noise algorithm. It exploits not only the spatial redundancy, but the redundancy in similar gradient directions as well; it takes into account the N closest gradient directions to the direction being processed (a maximum of 5 gradient directions is allowed to keep a reasonable computational load, since we do not use neither similarity maps nor block-wise implementation). The noise parameter is automatically estimated in the same way as in the jointLMMSE module. A complete description of the algorithm may be found in: Antonio Tristan-Vega and Santiago Aja-Fernandez, DWI filtering using joint information for DTI and HARDI, Medical Image Analysis, Volume 14, Issue 2, Pages 205-218. 2010. Please, note that the execution of this filter is extremely slow, son only very conservative parameters (block size and search size as small as possible) should be used. Even so, its execution may take several hours. The advantage of this filter over joint LMMSE is its better preservation of edges and fine structures.

version: 0.0.1.\$Revision: 1 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/UnbiasedNonLocalMeansFilterForDWI>

contributor: Antonio Tristan Vega (UVa), Santiago Aja Fernandez (UVa)

acknowledgements: Partially founded by grant number TEC2007-67073/TCM from the Comision Interministerial de Ciencia y Tecnologia (Spain).

Inputs:

```

[Optional]
rs: (a list of items which are an integer (int or long))
    The algorithm search for similar voxels in a neighborhood of this
    size (larger sizes than the default one are extremely slow).
    argument: ``--rs %s``
rc: (a list of items which are an integer (int or long))
    Similarity between blocks is measured using windows of this size.
    argument: ``--rc %s``
hp: (a float)
    This parameter is related to noise; the larger the parameter, the
    more aggressive the filtering. Should be near 1, and only values

```

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```

        between 0.8 and 1.2 are allowed
        argument: ``--hp %f``
ng: (an integer (int or long))
    The number of the closest gradients that are used to jointly filter
    a given gradient direction (a maximum of 5 is allowed).
    argument: ``--ng %d``
re: (a list of items which are an integer (int or long))
    A neighborhood of this size is used to compute the statistics for
    noise estimation.
    argument: ``--re %s``
inputVolume: (a pathlike object or string representing an existing
    file)
    Input DWI volume.
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output DWI volume.
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Output DWI volume.

```

76.17 interfaces.slicer.legacy.filtering

76.17.1 OtsuThresholdImageFilter

[Link to code](#)

Wraps the executable command “OtsuThresholdImageFilter”.

title: Otsu Threshold Image Filter

category: Legacy.Filtering

description: This filter creates a binary thresholded image that separates an image into foreground and background components. The filter calculates the optimum threshold separating those two classes so that their combined spread (intra-class variance) is minimal (see http://en.wikipedia.org/wiki/Otsu%27s_method). Then the filter applies that threshold to the input image using the itkBinaryThresholdImageFilter. The numberOfHistogram bins can be set for the Otsu Calculator. The insideValue and outsideValue can be set for the BinaryThresholdImageFilter. The filter produces a labeled volume.

The original reference is:

N.Otsu, A threshold selection method from gray level histograms, IEEE Trans.Syst.ManCybern.SMC-9,62–66 1979.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/OtsuThresholdImageFilter>

contributor: Bill Lorensen (GE)

acknowledgements: This command module was derived from Insight/Examples (copyright) Insight Software Consortium

Inputs:

```
[Optional]
insideValue: (an integer (int or long))
    The value assigned to pixels that are inside the computed threshold
    argument: ``--insideValue %d``
outsideValue: (an integer (int or long))
    The value assigned to pixels that are outside the computed threshold
    argument: ``--outsideValue %d``
numberOfBins: (an integer (int or long))
    This is an advanced parameter. The number of bins in the histogram
    used to model the probability mass function of the two intensity
    distributions. Small numbers of bins may result in a more
    conservative threshold. The default should suffice for most
    applications. Experimentation is the only way to see the effect of
    varying this parameter.
    argument: ``--numberOfBins %d``
inputVolume: (a pathlike object or string representing an existing
    file)
    Input volume to be filtered
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output filtered
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
    file)
    Output filtered
```

76.17.2 ResampleScalarVolume

[Link to code](#)

Wraps the executable command “ResampleScalarVolume”.

title: Resample Scalar Volume

category: Legacy.Filtering

description: Resampling an image is an important task in image analysis. It is especially important in the frame of image registration. This module implements image resampling through the use of itk Transforms. This module uses an Identity Transform. The resampling is controlled by the Output Spacing. “Resampling” is performed in space coordinates, not pixel/grid coordinates. It is quite important to ensure that image spacing is properly set on the images involved. The interpolator is required since the mapping from one space to the other will often require evaluation of the intensity of the image at non-grid positions. Several interpolators are available: linear, nearest neighbor, bspline and five flavors of sinc. The sinc interpolators, although more precise, are much slower than the linear and nearest neighbor interpolator. To resample label volumes, nearest neighbor interpolation should be used exclusively.

version: 0.1.0.\$Revision: 20594 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/ResampleVolume>

contributor: Bill Lorensen (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
spacing: (a list of items which are a float)
    Spacing along each dimension (0 means use input spacing)
    argument: ``--spacing %s``
interpolation: ('linear' or 'nearestNeighbor' or 'bspline' or
    'hamming' or 'cosine' or 'welch' or 'lanczos' or 'blackman')
    Sampling algorithm (linear, nearest neighbor, bspline(cubic) or
    windowed sinc). There are several sinc algorithms available as
    described in the following publication: Erik H. W. Meijering, Wiro
    J. Niessen, Josien P. W. Pluim, Max A. Viergever: Quantitative
    Comparison of Sinc-Approximating Kernels for Medical Image
    Interpolation. MICCAI 1999, pp. 210-217. Each window has a radius of
    3;
    argument: ``--interpolation %s``
InputVolume: (a pathlike object or string representing an existing
    file)
    Input volume to be resampled
    argument: ``%s``, position: -2
OutputVolume: (a boolean or a pathlike object or string representing
    a file)
    Resampled Volume
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
OutputVolume: (a pathlike object or string representing an existing
    file)
    Resampled Volume
```

76.18 interfaces.slicer.legacy.registration

76.18.1 AffineRegistration

[Link to code](#)

Wraps the executable command “AffineRegistration”.

title: Affine Registration

category: Legacy.Registration

description: Registers two images together using an affine transform and mutual information. This module is often used to align images of different subjects or images of the same subject from different modalities.

This module can smooth images prior to registration to mitigate noise and improve convergence. Many of the registration parameters require a working knowledge of the algorithm although the default parameters are sufficient for many registration tasks.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/AffineRegistration>

contributor: Daniel Blezek (GE)

acknowledgements: This module was developed by Daniel Blezek while at GE Research with contributions from Jim Miller.

This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
fixedsmoothingfactor: (an integer (int or long))
    Amount of smoothing applied to fixed image prior to registration.
    Default is 0 (none). Range is 0-5 (unitless). Consider smoothing the
    input data if there is considerable amounts of noise or the noise
    pattern in the fixed and moving images is very different.
    argument: ``--fixedsmoothingfactor %d``
movingsmoothingfactor: (an integer (int or long))
    Amount of smoothing applied to moving image prior to registration.
    Default is 0 (none). Range is 0-5 (unitless). Consider smoothing the
    input data if there is considerable amounts of noise or the noise
    pattern in the fixed and moving images is very different.
    argument: ``--movingsmoothingfactor %d``
histogrambins: (an integer (int or long))
    Number of histogram bins to use for Mattes Mutual Information.
    Reduce the number of bins if a registration fails. If the number of
    bins is too large, the estimated PDFs will be a field of impulses
    and will inhibit reliable registration estimation.
    argument: ``--histogrambins %d``
spatialsamples: (an integer (int or long))
    Number of spatial samples to use in estimating Mattes Mutual
    Information. Larger values yield more accurate PDFs and improved
    registration quality.
    argument: ``--spatialsamples %d``
iterations: (an integer (int or long))
    Number of iterations
    argument: ``--iterations %d``
translationscale: (a float)
    Relative scale of translations to rotations, i.e. a value of 100
    means 10mm = 1 degree. (Actual scale used is
    1/(TranslationScale^2)). This parameter is used to 'weight' or
    'standardized' the transform parameters and their effect on the
    registration objective function.
    argument: ``--translationscale %f``
initialtransform: (a pathlike object or string representing an
    existing file)
    Initial transform for aligning the fixed and moving image. Maps
    positions in the fixed coordinate frame to positions in the moving
    coordinate frame. Optional.
    argument: ``--initialtransform %s``
FixedImageFileName: (a pathlike object or string representing an
    existing file)
    Fixed image to which to register
    argument: ``%s``, position: -2
MovingImageFileName: (a pathlike object or string representing an
    existing file)
    Moving image
    argument: ``%s``, position: -1
outputtransform: (a boolean or a pathlike object or string
    representing a file)
    Transform calculated that aligns the fixed and moving image. Maps
    positions in the fixed coordinate frame to the moving coordinate
```

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```

    frame. Optional (specify an output transform or an output volume or
    both).
    argument: ``--outputtransform %s``
resampledmovingfilename: (a boolean or a pathlike object or string
    representing a file)
    Resampled moving image to the fixed image coordinate frame. Optional
    (specify an output transform or an output volume or both).
    argument: ``--resampledmovingfilename %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

outputtransform: (a pathlike object or string representing an
    existing file)
    Transform calculated that aligns the fixed and moving image. Maps
    positions in the fixed coordinate frame to the moving coordinate
    frame. Optional (specify an output transform or an output volume or
    both).
resampledmovingfilename: (a pathlike object or string representing an
    existing file)
    Resampled moving image to the fixed image coordinate frame. Optional
    (specify an output transform or an output volume or both).

```

76.18.2 BSplineDeformableRegistration**Link to code**

Wraps the executable command “BSplineDeformableRegistration”.

title: BSpline Deformable Registration

category: Legacy.Registration

description: Registers two images together using BSpline transform and mutual information.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/BSplineDeformableRegistration>

contributor: Bill Lorensen (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```

[Optional]
iterations: (an integer (int or long))
    Number of iterations
    argument: ``--iterations %d``
gridSize: (an integer (int or long))
    Number of grid points on interior of the fixed image. Larger grid
    sizes allow for finer registrations.
    argument: ``--gridSize %d``
histogrambins: (an integer (int or long))
    Number of histogram bins to use for Mattes Mutual Information.
    Reduce the number of bins if a deformable registration fails. If the
    number of bins is too large, the estimated PDFs will be a field of

```

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```

        impulses and will inhibit reliable registration estimation.
        argument: ``--histogrambins %d``
spatialsamples: (an integer (int or long))
        Number of spatial samples to use in estimating Mattes Mutual
        Information. Larger values yield more accurate PDFs and improved
        registration quality.
        argument: ``--spatialsamples %d``
constrain: (a boolean)
        Constrain the deformation to the amount specified in Maximum
        Deformation
        argument: ``--constrain ``
maximumDeformation: (a float)
        If Constrain Deformation is checked, limit the deformation to this
        amount.
        argument: ``--maximumDeformation %f``
default: (an integer (int or long))
        Default pixel value used if resampling a pixel outside of the
        volume.
        argument: ``--default %d``
initialtransform: (a pathlike object or string representing an
        existing file)
        Initial transform for aligning the fixed and moving image. Maps
        positions in the fixed coordinate frame to positions in the moving
        coordinate frame. This transform should be an affine or rigid
        transform. It is used as a bulk transform for the BSpline. Optional.
        argument: ``--initialtransform %s``
FixedImageFileName: (a pathlike object or string representing an
        existing file)
        Fixed image to which to register
        argument: ``%s``, position: -2
MovingImageFileName: (a pathlike object or string representing an
        existing file)
        Moving image
        argument: ``%s``, position: -1
outputtransform: (a boolean or a pathlike object or string
        representing a file)
        Transform calculated that aligns the fixed and moving image. Maps
        positions from the fixed coordinate frame to the moving coordinate
        frame. Optional (specify an output transform or an output volume or
        both).
        argument: ``--outputtransform %s``
outputwarp: (a boolean or a pathlike object or string representing a
        file)
        Vector field that applies an equivalent warp as the BSpline. Maps
        positions from the fixed coordinate frame to the moving coordinate
        frame. Optional.
        argument: ``--outputwarp %s``
resampledmovingfilename: (a boolean or a pathlike object or string
        representing a file)
        Resampled moving image to fixed image coordinate frame. Optional
        (specify an output transform or an output volume or both).
        argument: ``--resampledmovingfilename %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a

```

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```
value of class 'str', nipy default value: {}  
Environment variables
```

Outputs:

```
outputtransform: (a pathlike object or string representing an  
existing file)  
Transform calculated that aligns the fixed and moving image. Maps  
positions from the fixed coordinate frame to the moving coordinate  
frame. Optional (specify an output transform or an output volume or  
both).  
outputwarp: (a pathlike object or string representing an existing  
file)  
Vector field that applies an equivalent warp as the BSpline. Maps  
positions from the fixed coordinate frame to the moving coordinate  
frame. Optional.  
resampledmovingfilename: (a pathlike object or string representing an  
existing file)  
Resampled moving image to fixed image coordinate frame. Optional  
(specify an output transform or an output volume or both).
```

76.18.3 ExpertAutomatedRegistration[Link to code](#)

Wraps the executable command “ExpertAutomatedRegistration”.

title: Expert Automated Registration

category: Legacy.Registration

description: Provides rigid, affine, and BSpline registration methods via a simple GUI

version: 0.1.0.\$Revision: 2104 \$(alpha)

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/ExpertAutomatedRegistration>

contributor: Stephen R Aylward (Kitware), Casey B Goodlett (Kitware)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]  
fixedImage: (a pathlike object or string representing an existing  
file)  
Image which defines the space into which the moving image is  
registered  
argument: ``%s``, position: -2  
movingImage: (a pathlike object or string representing an existing  
file)  
The transform goes from the fixed image's space into the moving  
image's space  
argument: ``%s``, position: -1  
resampledImage: (a boolean or a pathlike object or string  
representing a file)  
Registration results  
argument: ``--resampledImage %s``  
loadTransform: (a pathlike object or string representing an existing  
file)  
Load a transform that is immediately applied to the moving image  
argument: ``--loadTransform %s``  
saveTransform: (a boolean or a pathlike object or string representing
```

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```

    a file)
    Save the transform that results from registration
    argument: ``--saveTransform %s``
initialization: ('None' or 'Landmarks' or 'ImageCenters' or
    'CentersOfMass' or 'SecondMoments')
    Method to prime the registration process
    argument: ``--initialization %s``
registration: ('None' or 'Initial' or 'Rigid' or 'Affine' or
    'BSpline' or 'PipelineRigid' or 'PipelineAffine' or
    'PipelineBSpline')
    Method for the registration process
    argument: ``--registration %s``
metric: ('MattesMI' or 'NormCorr' or 'MeanSqr')
    Method to quantify image match
    argument: ``--metric %s``
expectedOffset: (a float)
    Expected misalignment after initialization
    argument: ``--expectedOffset %f``
expectedRotation: (a float)
    Expected misalignment after initialization
    argument: ``--expectedRotation %f``
expectedScale: (a float)
    Expected misalignment after initialization
    argument: ``--expectedScale %f``
expectedSkew: (a float)
    Expected misalignment after initialization
    argument: ``--expectedSkew %f``
verbosityLevel: ('Silent' or 'Standard' or 'Verbose')
    Level of detail of reporting progress
    argument: ``--verbosityLevel %s``
sampleFromOverlap: (a boolean)
    Limit metric evaluation to the fixed image region overlapped by the
    moving image
    argument: ``--sampleFromOverlap ``
fixedImageMask: (a pathlike object or string representing an existing
    file)
    Image which defines a mask for the fixed image
    argument: ``--fixedImageMask %s``
randomNumberSeed: (an integer (int or long))
    Seed to generate a consistent random number sequence
    argument: ``--randomNumberSeed %d``
numberOfThreads: (an integer (int or long))
    Number of CPU threads to use
    argument: ``--numberOfThreads %d``
minimizeMemory: (a boolean)
    Reduce the amount of memory required at the cost of increased
    computation time
    argument: ``--minimizeMemory ``
interpolation: ('NearestNeighbor' or 'Linear' or 'BSpline')
    Method for interpolation within the optimization process
    argument: ``--interpolation %s``
fixedLandmarks: (a list of items which are a list of from 3 to 3
    items which are a float)
    Ordered list of landmarks in the fixed image
    argument: ``--fixedLandmarks %s...``
movingLandmarks: (a list of items which are a list of from 3 to 3
    items which are a float)

```

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```

        Ordered list of landmarks in the moving image
        argument: ``--movingLandmarks %s...``
rigidMaxIterations: (an integer (int or long))
        Maximum number of rigid optimization iterations
        argument: ``--rigidMaxIterations %d``
rigidSamplingRatio: (a float)
        Portion of the image to use in computing the metric during rigid
        registration
        argument: ``--rigidSamplingRatio %f``
affineMaxIterations: (an integer (int or long))
        Maximum number of affine optimization iterations
        argument: ``--affineMaxIterations %d``
affineSamplingRatio: (a float)
        Portion of the image to use in computing the metric during affine
        registration
        argument: ``--affineSamplingRatio %f``
bsplineMaxIterations: (an integer (int or long))
        Maximum number of bspline optimization iterations
        argument: ``--bsplineMaxIterations %d``
bsplineSamplingRatio: (a float)
        Portion of the image to use in computing the metric during BSpline
        registration
        argument: ``--bsplineSamplingRatio %f``
controlPointSpacing: (an integer (int or long))
        Number of pixels between control points
        argument: ``--controlPointSpacing %d``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

resampledImage: (a pathlike object or string representing an existing
        file)
        Registration results
saveTransform: (a pathlike object or string representing an existing
        file)
        Save the transform that results from registration

```

76.18.4 LinearRegistration[Link to code](#)

Wraps the executable command “LinearRegistration”.

title: Linear Registration

category: Legacy.Registration

description: Registers two images together using a rigid transform and mutual information.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/LinearRegistration>

contributor: Daniel Blezek (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
fixedsmoothingfactor: (an integer (int or long))
    Amount of smoothing applied to fixed image prior to registration.
    Default is 0 (none). Range is 0-5 (unitless). Consider smoothing the
    input data if there is considerable amounts of noise or the noise
    pattern in the fixed and moving images is very different.
    argument: ``--fixedsmoothingfactor %d``
movingsmoothingfactor: (an integer (int or long))
    Amount of smoothing applied to moving image prior to registration.
    Default is 0 (none). Range is 0-5 (unitless). Consider smoothing the
    input data if there is considerable amounts of noise or the noise
    pattern in the fixed and moving images is very different.
    argument: ``--movingsmoothingfactor %d``
histogrambins: (an integer (int or long))
    Number of histogram bins to use for Mattes Mutual Information.
    Reduce the number of bins if a registration fails. If the number of
    bins is too large, the estimated PDFs will be a field of impulses
    and will inhibit reliable registration estimation.
    argument: ``--histogrambins %d``
spatialsamples: (an integer (int or long))
    Number of spatial samples to use in estimating Mattes Mutual
    Information. Larger values yield more accurate PDFs and improved
    registration quality.
    argument: ``--spatialsamples %d``
iterations: (a list of items which are an integer (int or long))
    Comma separated list of iterations. Must have the same number of
    elements as the learning rate.
    argument: ``--iterations %s``
learningrate: (a list of items which are a float)
    Comma separated list of learning rates. Learning rate is a scale
    factor on the gradient of the registration objective function
    (gradient with respect to the parameters of the transformation) used
    to update the parameters of the transformation during optimization.
    Smaller values cause the optimizer to take smaller steps through the
    parameter space. Larger values are typically used early in the
    registration process to take large jumps in parameter space followed
    by smaller values to home in on the optimum value of the
    registration objective function. Default is: 0.01, 0.005, 0.0005,
    0.0002. Must have the same number of elements as iterations.
    argument: ``--learningrate %s``
translationscale: (a float)
    Relative scale of translations to rotations, i.e. a value of 100
    means 10mm = 1 degree. (Actual scale used  $1/(\text{TranslationScale}^2)$ ).
    This parameter is used to 'weight' or 'standardized' the transform
    parameters and their effect on the registration objective function.
    argument: ``--translationscale %f``
initialtransform: (a pathlike object or string representing an
    existing file)
    Initial transform for aligning the fixed and moving image. Maps
    positions in the fixed coordinate frame to positions in the moving
    coordinate frame. Optional.
    argument: ``--initialtransform %s``
FixedImageFileName: (a pathlike object or string representing an
    existing file)
    Fixed image to which to register
    argument: ``%s``, position: -2
MovingImageFileName: (a pathlike object or string representing an
```

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```

    existing file)
    Moving image
    argument: ``%s``, position: -1
outputtransform: (a boolean or a pathlike object or string
    representing a file)
    Transform calculated that aligns the fixed and moving image. Maps
    positions in the fixed coordinate frame to the moving coordinate
    frame. Optional (specify an output transform or an output volume or
    both).
    argument: ``--outputtransform %s``
resampledmovingfilename: (a boolean or a pathlike object or string
    representing a file)
    Resampled moving image to the fixed image coordinate frame. Optional
    (specify an output transform or an output volume or both).
    argument: ``--resampledmovingfilename %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputtransform: (a pathlike object or string representing an
    existing file)
    Transform calculated that aligns the fixed and moving image. Maps
    positions in the fixed coordinate frame to the moving coordinate
    frame. Optional (specify an output transform or an output volume or
    both).
resampledmovingfilename: (a pathlike object or string representing an
    existing file)
    Resampled moving image to the fixed image coordinate frame. Optional
    (specify an output transform or an output volume or both).

```

76.18.5 MultiResolutionAffineRegistration**Link to code**

Wraps the executable command “MultiResolutionAffineRegistration”.

title: Robust Multiresolution Affine Registration

category: Legacy.Registration

description: Provides affine registration using multiple resolution levels and decomposed affine transforms.

version: 0.1.0.\$Revision: 2104 \$(alpha)

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/MultiResolutionAffineRegistration>

contributor: Casey B Goodlett (Utah)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```

[Optional]
fixedImage: (a pathlike object or string representing an existing
    file)
    Image which defines the space into which the moving image is
    registered

```

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```

    argument: ``%s``, position: -2
movingImage: (a pathlike object or string representing an existing
    file)
    The transform goes from the fixed image's space into the moving
    image's space
    argument: ``%s``, position: -1
resampledImage: (a boolean or a pathlike object or string
    representing a file)
    Registration results
    argument: ``--resampledImage %s``
saveTransform: (a boolean or a pathlike object or string representing
    a file)
    Save the output transform from the registration
    argument: ``--saveTransform %s``
fixedImageMask: (a pathlike object or string representing an existing
    file)
    Label image which defines a mask of interest for the fixed image
    argument: ``--fixedImageMask %s``
fixedImageROI: (a list of items which are any value)
    Label image which defines a ROI of interest for the fixed image
    argument: ``--fixedImageROI %s``
numIterations: (an integer (int or long))
    Number of iterations to run at each resolution level.
    argument: ``--numIterations %d``
numLineIterations: (an integer (int or long))
    Number of iterations to run at each resolution level.
    argument: ``--numLineIterations %d``
stepSize: (a float)
    The maximum step size of the optimizer in voxels
    argument: ``--stepSize %f``
stepTolerance: (a float)
    The maximum step size of the optimizer in voxels
    argument: ``--stepTolerance %f``
metricTolerance: (a float)
    argument: ``--metricTolerance %f``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

resampledImage: (a pathlike object or string representing an existing
    file)
    Registration results
saveTransform: (a pathlike object or string representing an existing
    file)
    Save the output transform from the registration

```

76.18.6 RigidRegistration[Link to code](#)

Wraps the executable command “RigidRegistration”.

title: Rigid Registration

category: Legacy.Registration

description: Registers two images together using a rigid transform and mutual information.

This module was originally distributed as “Linear registration” but has been renamed to eliminate confusion with the “Affine registration” module.

This module is often used to align images of different subjects or images of the same subject from different modalities.

This module can smooth images prior to registration to mitigate noise and improve convergence. Many of the registration parameters require a working knowledge of the algorithm although the default parameters are sufficient for many registration tasks.

version: 0.1.0.\$Revision: 19608 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/RigidRegistration>

contributor: Daniel Blezek (GE)

acknowledgements: This module was developed by Daniel Blezek while at GE Research with contributions from Jim Miller.

This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
fixedsmoothingfactor: (an integer (int or long))
    Amount of smoothing applied to fixed image prior to registration.
    Default is 0 (none). Range is 0-5 (unitless). Consider smoothing the
    input data if there is considerable amounts of noise or the noise
    pattern in the fixed and moving images is very different.
    argument: ``--fixedsmoothingfactor %d``
movingsmoothingfactor: (an integer (int or long))
    Amount of smoothing applied to moving image prior to registration.
    Default is 0 (none). Range is 0-5 (unitless). Consider smoothing the
    input data if there is considerable amounts of noise or the noise
    pattern in the fixed and moving images is very different.
    argument: ``--movingsmoothingfactor %d``
testingmode: (a boolean)
    Enable testing mode. Input transform will be used to construct
    floating image. The floating image will be ignored if passed.
    argument: ``--testingmode``
histogrambins: (an integer (int or long))
    Number of histogram bins to use for Mattes Mutual Information.
    Reduce the number of bins if a registration fails. If the number of
    bins is too large, the estimated PDFs will be a field of impulses
    and will inhibit reliable registration estimation.
    argument: ``--histogrambins %d``
spatialsamples: (an integer (int or long))
    Number of spatial samples to use in estimating Mattes Mutual
    Information. Larger values yield more accurate PDFs and improved
    registration quality.
    argument: ``--spatialsamples %d``
iterations: (a list of items which are an integer (int or long))
    Comma separated list of iterations. Must have the same number of
    elements as the learning rate.
    argument: ``--iterations %s``
learningrate: (a list of items which are a float)
    Comma separated list of learning rates. Learning rate is a scale
    factor on the gradient of the registration objective function
    (gradient with respect to the parameters of the transformation) used
    to update the parameters of the transformation during optimization.
    Smaller values cause the optimizer to take smaller steps through the
    parameter space. Larger values are typically used early in the
```

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```

registration process to take large jumps in parameter space followed
by smaller values to home in on the optimum value of the
registration objective function. Default is: 0.01, 0.005, 0.0005,
0.0002. Must have the same number of elements as iterations.
argument: ``--learningrate %s``
translationscale: (a float)
    Relative scale of translations to rotations, i.e. a value of 100
    means 10mm = 1 degree. (Actual scale used 1/(TranslationScale^2)).
    This parameter is used to 'weight' or 'standardized' the transform
    parameters and their effect on the registration objective function.
    argument: ``--translationscale %f``
initialtransform: (a pathlike object or string representing an
    existing file)
    Initial transform for aligning the fixed and moving image. Maps
    positions in the fixed coordinate frame to positions in the moving
    coordinate frame. Optional.
    argument: ``--initialtransform %s``
FixedImageFileName: (a pathlike object or string representing an
    existing file)
    Fixed image to which to register
    argument: ``%s``, position: -2
MovingImageFileName: (a pathlike object or string representing an
    existing file)
    Moving image
    argument: ``%s``, position: -1
outputtransform: (a boolean or a pathlike object or string
    representing a file)
    Transform calculated that aligns the fixed and moving image. Maps
    positions in the fixed coordinate frame to the moving coordinate
    frame. Optional (specify an output transform or an output volume or
    both).
    argument: ``--outputtransform %s``
resampledmovingfilename: (a boolean or a pathlike object or string
    representing a file)
    Resampled moving image to the fixed image coordinate frame. Optional
    (specify an output transform or an output volume or both).
    argument: ``--resampledmovingfilename %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputtransform: (a pathlike object or string representing an
    existing file)
    Transform calculated that aligns the fixed and moving image. Maps
    positions in the fixed coordinate frame to the moving coordinate
    frame. Optional (specify an output transform or an output volume or
    both).
resampledmovingfilename: (a pathlike object or string representing an
    existing file)
    Resampled moving image to the fixed image coordinate frame. Optional
    (specify an output transform or an output volume or both).

```

76.19 interfaces.slicer.legacy.segmentation

76.19.1 OtsuThresholdSegmentation

[Link to code](#)

Wraps the executable command “OtsuThresholdSegmentation”.

title: Otsu Threshold Segmentation

category: Legacy.Segmentation

description: This filter creates a labeled image from a grayscale image. First, it calculates an optimal threshold that separates the image into foreground and background. This threshold separates those two classes so that their intra-class variance is minimal (see http://en.wikipedia.org/wiki/Otsu%27s_method). Then the filter runs a connected component algorithm to generate unique labels for each connected region of the foreground. Finally, the resulting image is relabeled to provide consecutive numbering.

version: 1.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/OtsuThresholdSegmentation>

contributor: Bill Lorensen (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
brightObjects: (a boolean)
    Segmenting bright objects on a dark background or dark objects on a
    bright background.
    argument: ``--brightObjects ``
numberOfBins: (an integer (int or long))
    This is an advanced parameter. The number of bins in the histogram
    used to model the probability mass function of the two intensity
    distributions. Small numbers of bins may result in a more
    conservative threshold. The default should suffice for most
    applications. Experimentation is the only way to see the effect of
    varying this parameter.
    argument: ``--numberOfBins %d``
faceConnected: (a boolean)
    This is an advanced parameter. Adjacent voxels are face connected.
    This affects the connected component algorithm. If this parameter is
    false, more regions are likely to be identified.
    argument: ``--faceConnected ``
minimumObjectSize: (an integer (int or long))
    Minimum size of object to retain. This parameter can be used to get
    rid of small regions in noisy images.
    argument: ``--minimumObjectSize %d``
inputVolume: (a pathlike object or string representing an existing
    file)
    Input volume to be segmented
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output filtered
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
```

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```

    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
               file)
               Output filtered

```

76.20 interfaces.slicer.quantification.changequantification

76.20.1 IntensityDifferenceMetric

[Link to code](#)

Wraps the executable command “IntensityDifferenceMetric”.

title: Intensity Difference Change Detection (FAST)

category: Quantification.ChangeQuantification

description: Quantifies the changes between two spatially aligned images based on the pixel-wise difference of image intensities.

version: 0.1

contributor: Andrey Fedorov

acknowledgements:

Inputs:

```

[Optional]
sensitivityThreshold: (a float)
    This parameter should be between 0 and 1, and defines how sensitive
    the metric should be to the intensity changes.
    argument: ``--sensitivityThreshold %f``
changingBandSize: (an integer (int or long))
    How far (in mm) from the boundary of the segmentation should the
    intensity changes be considered.
    argument: ``--changingBandSize %d``
baselineVolume: (a pathlike object or string representing an existing
                file)
    Baseline volume to be compared to
    argument: ``%s``, position: -4
baselineSegmentationVolume: (a pathlike object or string representing
                             an existing file)
    Label volume that contains segmentation of the structure of interest
    in the baseline volume.
    argument: ``%s``, position: -3
followupVolume: (a pathlike object or string representing an existing
                file)
    Followup volume to be compare to the baseline
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
               a file)
    Output volume to keep the results of change quantification.
    argument: ``%s``, position: -1
reportFileName: (a boolean or a pathlike object or string
                 representing a file)
    Report file name
    argument: ``--reportFileName %s``
args: (a unicode string)

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```

Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
               file)
               Output volume to keep the results of change quantification.
reportFileName: (a pathlike object or string representing an existing
                 file)
                 Report file name

```

76.21 interfaces.slicer.quantification.petstandarduptakevaluecomputation

76.21.1 PETStandardUptakeValueComputation

Link to code

Wraps the executable command “PETStandardUptakeValueComputation”.

title: PET Standard Uptake Value Computation

category: Quantification

description: Computes the standardized uptake value based on body weight. Takes an input PET image in DICOM and NRRD format (DICOM header must contain Radiopharmaceutical parameters). Produces a CSV file that contains patientID, studyDate, dose, labelID, suvmin, suvmax, suvmean, labelName for each volume of interest. It also displays some of the information as output strings in the GUI, the CSV file is optional in that case. The CSV file is appended to on each execution of the CLI.

version: 0.1.0.\$Revision: 8595 \$(alpha)

documentation-url: [http://www.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/](http://www.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/ComputeSUVBodyWeight)

ComputeSUVBodyWeight

contributor: Wendy Plesniak (SPL, BWH), Nicole Aucoin (SPL, BWH), Ron Kikinis (SPL, BWH)

acknowledgements: This work is funded by the Harvard Catalyst, and the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```

[Optional]
petDICOMPath: (a pathlike object or string representing an existing
               directory)
               Input path to a directory containing a PET volume containing DICOM
               header information for SUV computation
               argument: ``--petDICOMPath %s``
petVolume: (a pathlike object or string representing an existing
            file)
            Input PET volume for SUVbw computation (must be the same volume as
            pointed to by the DICOM path!).
            argument: ``--petVolume %s``
labelMap: (a pathlike object or string representing an existing file)
           Input label volume containing the volumes of interest
           argument: ``--labelMap %s``
color: (a pathlike object or string representing an existing file)
        Color table to to map labels to colors and names

```

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        argument: ``--color %s``
csvFile: (a boolean or a pathlike object or string representing a
        file)
        A file holding the output SUV values in comma separated lines, one
        per label. Optional.
        argument: ``--csvFile %s``
OutputLabel: (a unicode string)
        List of labels for which SUV values were computed
        argument: ``--OutputLabel %s``
OutputLabelValue: (a unicode string)
        List of label values for which SUV values were computed
        argument: ``--OutputLabelValue %s``
SUVMax: (a unicode string)
        SUV max for each label
        argument: ``--SUVMax %s``
SUVMean: (a unicode string)
        SUV mean for each label
        argument: ``--SUVMean %s``
SUVMin: (a unicode string)
        SUV minimum for each label
        argument: ``--SUVMin %s``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

csvFile: (a pathlike object or string representing an existing file)
        A file holding the output SUV values in comma separated lines, one
        per label. Optional.

```

76.22 interfaces.slicer.registration.brainsfit**76.22.1 BRAINSFit**[Link to code](#)

Wraps the executable command “BRAINSFit”.

title: General Registration (BRAINS)

category: Registration

description: Register a three-dimensional volume to a reference volume (Mattes Mutual Information by default). Described in BRAINSFit: Mutual Information Registrations of Whole-Brain 3D Images, Using the Insight Toolkit, Johnson H.J., Harris G., Williams K., The Insight Journal, 2007. <http://hdl.handle.net/1926/1291>

version: 3.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:BRAINSFit>license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>contributor: Hans J. Johnson, hans-johnson -at- uiowa.edu, <http://www.psychiatry.uiowa.edu>

acknowledgements: Hans Johnson(1,3,4); Kent Williams(1); Gregory Harris(1), Vincent Magnotta(1,2,3); Andriy Fedorov(5) 1=University of Iowa Department of Psychiatry, 2=University of Iowa Department of Radiology, 3=University of Iowa Department of Biomedical Engineering, 4=University of Iowa Department of Electrical and Computer Engineering, 5=Surgical Planning Lab, Harvard

Inputs:

```
[Optional]
fixedVolume: (a pathlike object or string representing an existing
              file)
              The fixed image for registration by mutual information optimization.
              argument: ``--fixedVolume %s``
movingVolume: (a pathlike object or string representing an existing
              file)
              The moving image for registration by mutual information
              optimization.
              argument: ``--movingVolume %s``
bsplineTransform: (a boolean or a pathlike object or string
                  representing a file)
                  (optional) Filename to which save the estimated transform. NOTE: You
                  must set at least one output object (either a deformed image or a
                  transform. NOTE: USE THIS ONLY IF THE FINAL TRANSFORM IS BSpline
                  argument: ``--bsplineTransform %s``
linearTransform: (a boolean or a pathlike object or string
                  representing a file)
                  (optional) Filename to which save the estimated transform. NOTE: You
                  must set at least one output object (either a deformed image or a
                  transform. NOTE: USE THIS ONLY IF THE FINAL TRANSFORM IS ---NOT---
                  BSpline
                  argument: ``--linearTransform %s``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              (optional) Output image for registration. NOTE: You must select
              either the outputTransform or the outputVolume option.
              argument: ``--outputVolume %s``
initialTransform: (a pathlike object or string representing an
                  existing file)
                  Filename of transform used to initialize the registration. This CAN
                  NOT be used with either CenterOfHeadLAlign, MomentsAlign,
                  GeometryAlign, or initialTransform file.
                  argument: ``--initialTransform %s``
initializeTransformMode: ('Off' or 'useMomentsAlign' or
                          'useCenterOfHeadAlign' or 'useGeometryAlign' or
                          'useCenterOfROIALign')
                          Determine how to initialize the transform center. GeometryAlign on
                          assumes that the center of the voxel lattice of the images represent
                          similar structures. MomentsAlign assumes that the center of mass of
                          the images represent similar structures. useCenterOfHeadAlign
                          attempts to use the top of head and shape of neck to drive a center
                          of mass estimate. Off assumes that the physical space of the images
                          are close, and that centering in terms of the image Origins is a
                          good starting point. This flag is mutually exclusive with the
                          initialTransform flag.
                          argument: ``--initializeTransformMode %s``
useRigid: (a boolean)
          Perform a rigid registration as part of the sequential registration
          steps. This family of options superceeds the use of transformType if
          any of them are set.
          argument: ``--useRigid``
useScaleVersor3D: (a boolean)
                  Perform a ScaleVersor3D registration as part of the sequential
                  registration steps. This family of options superceeds the use of
                  transformType if any of them are set.
                  argument: ``--useScaleVersor3D``
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useScaleSkewVersor3D: (a boolean)
    Perform a ScaleSkewVersor3D registration as part of the sequential
    registration steps. This family of options superceeds the use of
    transformType if any of them are set.
    argument: ``--useScaleSkewVersor3D``

useAffine: (a boolean)
    Perform an Affine registration as part of the sequential
    registration steps. This family of options superceeds the use of
    transformType if any of them are set.
    argument: ``--useAffine``

useBSpline: (a boolean)
    Perform a BSpline registration as part of the sequential
    registration steps. This family of options superceeds the use of
    transformType if any of them are set.
    argument: ``--useBSpline``

numberOfSamples: (an integer (int or long))
    The number of voxels sampled for mutual information computation.
    Increase this for a slower, more careful fit. You can also limit the
    sampling focus with ROI masks and ROIAUTO mask generation.
    argument: ``--numberOfSamples %d``

splineGridSize: (a list of items which are an integer (int or long))
    The number of subdivisions of the BSpline Grid to be centered on the
    image space. Each dimension must have at least 3 subdivisions for
    the BSpline to be correctly computed.
    argument: ``--splineGridSize %s``

numberOfIterations: (a list of items which are an integer (int or
    long))
    The maximum number of iterations to try before failing to converge.
    Use an explicit limit like 500 or 1000 to manage risk of divergence
    argument: ``--numberOfIterations %s``

maskProcessingMode: ('NOMASK' or 'ROIAUTO' or 'ROI')
    What mode to use for using the masks. If ROIAUTO is choosen, then
    the mask is implicitly defined using a otsu forground and hole
    filling algorithm. The Region Of Interest mode (choose ROI) uses the
    masks to define what parts of the image should be used for computing
    the transform.
    argument: ``--maskProcessingMode %s``

fixedBinaryVolume: (a pathlike object or string representing an
    existing file)
    Fixed Image binary mask volume, ONLY FOR MANUAL ROI mode.
    argument: ``--fixedBinaryVolume %s``

movingBinaryVolume: (a pathlike object or string representing an
    existing file)
    Moving Image binary mask volume, ONLY FOR MANUAL ROI mode.
    argument: ``--movingBinaryVolume %s``

outputFixedVolumeROI: (a boolean or a pathlike object or string
    representing a file)
    The ROI automatically found in fixed image, ONLY FOR ROIAUTO mode.
    argument: ``--outputFixedVolumeROI %s``

outputMovingVolumeROI: (a boolean or a pathlike object or string
    representing a file)
    The ROI automatically found in moving image, ONLY FOR ROIAUTO mode.
    argument: ``--outputMovingVolumeROI %s``

outputVolumePixelType: ('float' or 'short' or 'ushort' or 'int' or
    'uint' or 'uchar')
    The output image Pixel Type is the scalar datatype for
    representation of the Output Volume.

```

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        argument: ``--outputVolumePixelType %s``
backgroundFillValue: (a float)
    Background fill value for output image.
    argument: ``--backgroundFillValue %f``
maskInferiorCutOffFromCenter: (a float)
    For use with --useCenterOfHeadAlign (and --maskProcessingMode
    ROIAUTO): the cut-off below the image centers, in millimeters,
    argument: ``--maskInferiorCutOffFromCenter %f``
scaleOutputValues: (a boolean)
    If true, and the voxel values do not fit within the minimum and
    maximum values of the desired outputVolumePixelType, then linearly
    scale the min/max output image voxel values to fit within the
    min/max range of the outputVolumePixelType.
    argument: ``--scaleOutputValues ``
interpolationMode: ('NearestNeighbor' or 'Linear' or
    'ResampleInPlace' or 'BSpline' or 'WindowedSinc' or 'Hamming' or
    'Cosine' or 'Welch' or 'Lanczos' or 'Blackman')
    Type of interpolation to be used when applying transform to moving
    volume. Options are Linear, NearestNeighbor, BSpline, WindowedSinc,
    or ResampleInPlace. The ResampleInPlace option will create an image
    with the same discrete voxel values and will adjust the origin and
    direction of the physical space interpretation.
    argument: ``--interpolationMode %s``
minimumStepLength: (a list of items which are a float)
    Each step in the optimization takes steps at least this big. When
    none are possible, registration is complete.
    argument: ``--minimumStepLength %s``
translationScale: (a float)
    How much to scale up changes in position compared to unit rotational
    changes in radians -- decrease this to put more rotation in the
    search pattern.
    argument: ``--translationScale %f``
reproportionScale: (a float)
    ScaleVersor3D 'Scale' compensation factor. Increase this to put more
    rescaling in a ScaleVersor3D or ScaleSkewVersor3D search pattern.
    1.0 works well with a translationScale of 1000.0
    argument: ``--reproportionScale %f``
skewScale: (a float)
    ScaleSkewVersor3D Skew compensation factor. Increase this to put
    more skew in a ScaleSkewVersor3D search pattern. 1.0 works well with
    a translationScale of 1000.0
    argument: ``--skewScale %f``
maxBSplineDisplacement: (a float)
    Sets the maximum allowed displacements in image physical
    coordinates for BSpline control grid along each axis. A value of 0.0
    indicates that the problem should be unbounded. NOTE: This only
    constrains the BSpline portion, and does not limit the displacement
    from the associated bulk transform. This can lead to a substantial
    reduction in computation time in the BSpline optimizer.,
    argument: ``--maxBSplineDisplacement %f``
histogramMatch: (a boolean)
    Histogram Match the input images. This is suitable for images of the
    same modality that may have different absolute scales, but the same
    overall intensity profile. Do NOT use if registering images from
    different modalities.
    argument: ``--histogramMatch ``
numberOfHistogramBins: (an integer (int or long))

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    The number of histogram levels
    argument: ``--numberOfHistogramBins %d``
numberOfMatchPoints: (an integer (int or long))
    the number of match points
    argument: ``--numberOfMatchPoints %d``
strippedOutputTransform: (a boolean or a pathlike object or string
    representing a file)
    File name for the rigid component of the estimated affine transform.
    Can be used to rigidly register the moving image to the fixed image.
    NOTE: This value is overwritten if either bsplineTransform or
    linearTransform is set.
    argument: ``--strippedOutputTransform %s``
transformType: (a list of items which are a unicode string)
    Specifies a list of registration types to be used. The valid types
    are, Rigid, ScaleVersor3D, ScaleSkewVersor3D, Affine, and BSpline.
    Specifiying more than one in a comma separated list will initialize
    the next stage with the previous results. If registrationClass flag
    is used, it overrides this parameter setting.
    argument: ``--transformType %s``
outputTransform: (a boolean or a pathlike object or string
    representing a file)
    (optional) Filename to which save the (optional) estimated
    transform. NOTE: You must select either the outputTransform or the
    outputVolume option.
    argument: ``--outputTransform %s``
fixedVolumeTimeIndex: (an integer (int or long))
    The index in the time series for the 3D fixed image to fit, if
    4-dimensional.
    argument: ``--fixedVolumeTimeIndex %d``
movingVolumeTimeIndex: (an integer (int or long))
    The index in the time series for the 3D moving image to fit, if
    4-dimensional.
    argument: ``--movingVolumeTimeIndex %d``
medianFilterSize: (a list of items which are an integer (int or
    long))
    The radius for the optional MedianImageFilter preprocessing in all 3
    directions.
    argument: ``--medianFilterSize %s``
removeIntensityOutliers: (a float)
    The half percentage to decide outliers of image intensities. The
    default value is zero, which means no outlier removal. If the value
    of 0.005 is given, the moduel will throw away 0.005 % of both tails,
    so 0.01% of intensities in total would be ignored in its statistic
    calculation.
    argument: ``--removeIntensityOutliers %f``
useCachingOfBSplineWeightsMode: ('ON' or 'OFF')
    This is a 5x speed advantage at the expense of requiring much more
    memory. Only relevant when transformType is BSpline.
    argument: ``--useCachingOfBSplineWeightsMode %s``
useExplicitPDFDerivativesMode: ('AUTO' or 'ON' or 'OFF')
    Using mode AUTO means OFF for BSplineDeformableTransforms and ON for
    the linear transforms. The ON alternative uses more memory to
    sometimes do a better job.
    argument: ``--useExplicitPDFDerivativesMode %s``
ROIAutoDilateSize: (a float)
    This flag is only relavent when using ROIAUTO mode for initializing
    masks. It defines the final dilation size to capture a bit of

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background outside the tissue region. At setting of 10mm has been
shown to help regularize a BSpline registration type so that there
is some background constraints to match the edges of the head
better.
argument: ``--ROIAutoDilateSize %f``
ROIAutoClosingSize: (a float)
    This flag is only relevant when using ROIAUTO mode for initializing
    masks. It defines the hole closing size in mm. It is rounded up to
    the nearest whole pixel size in each direction. The default is to
    use a closing size of 9mm. For mouse data this value may need to be
    reset to 0.9 or smaller.
    argument: ``--ROIAutoClosingSize %f``
relaxationFactor: (a float)
    Internal debugging parameter, and should probably never be used from
    the command line. This will be removed in the future.
    argument: ``--relaxationFactor %f``
maximumStepLength: (a float)
    Internal debugging parameter, and should probably never be used from
    the command line. This will be removed in the future.
    argument: ``--maximumStepLength %f``
failureExitCode: (an integer (int or long))
    If the fit fails, exit with this status code. (It can be used to
    force a successful exit status of (0) if the registration fails due
    to reaching the maximum number of iterations.
    argument: ``--failureExitCode %d``
writeTransformOnFailure: (a boolean)
    Flag to save the final transform even if the numberOfIterations are
    reached without convergence. (Intended for use when
    --failureExitCode 0 )
    argument: ``--writeTransformOnFailure ``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use. (default is
    auto-detected)
    argument: ``--numberOfThreads %d``
forceMINumberOfThreads: (an integer (int or long))
    Force the the maximum number of threads to use for non thread safe
    MI metric. CAUTION: Inconsistent results may arise!
    argument: ``--forceMINumberOfThreads %d``
debugLevel: (an integer (int or long))
    Display debug messages, and produce debug intermediate results.
    0=OFF, 1=Minimal, 10=Maximum debugging.
    argument: ``--debugLevel %d``
costFunctionConvergenceFactor: (a float)
    From itkLBFGSBOptimizer.h: Set/Get the
    CostFunctionConvergenceFactor. Algorithm terminates when the
    reduction in cost function is less than (factor * epsmcj) where
    epsmcj is the machine precision. Typical values for factor: 1e+12
    for low accuracy; 1e+7 for moderate accuracy and 1e+1 for extremely
    high accuracy. 1e+9 seems to work well.,
    argument: ``--costFunctionConvergenceFactor %f``
projectedGradientTolerance: (a float)
    From itkLBFGSBOptimizer.h: Set/Get the ProjectedGradientTolerance.
    Algorithm terminates when the project gradient is below the
    tolerance. Default lbfgsb value is 1e-5, but 1e-4 seems to work
    well.,
    argument: ``--projectedGradientTolerance %f``
gui: (a boolean)

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    Display intermediate image volumes for debugging. NOTE: This is not
    part of the standard build sytem, and probably does nothing on your
    installation.
    argument: ``--gui ``
promptUser: (a boolean)
    Prompt the user to hit enter each time an image is sent to the
    DebugImageViewer
    argument: ``--promptUser ``
NEVER_USE_THIS_FLAG_IT_IS_OUTDATED_00: (a boolean)
    DO NOT USE THIS FLAG
    argument: ``--NEVER_USE_THIS_FLAG_IT_IS_OUTDATED_00 ``
NEVER_USE_THIS_FLAG_IT_IS_OUTDATED_01: (a boolean)
    DO NOT USE THIS FLAG
    argument: ``--NEVER_USE_THIS_FLAG_IT_IS_OUTDATED_01 ``
NEVER_USE_THIS_FLAG_IT_IS_OUTDATED_02: (a boolean)
    DO NOT USE THIS FLAG
    argument: ``--NEVER_USE_THIS_FLAG_IT_IS_OUTDATED_02 ``
permitParameterVariation: (a list of items which are an integer (int
    or long))
    A bit vector to permit linear transform parameters to vary under
    optimization. The vector order corresponds with transform
    parameters, and beyond the end ones fill in as a default. For
    instance, you can choose to rotate only in x (pitch) with 1,0,0;
    this is mostly for expert use in turning on and off individual
    degrees of freedom in rotation, translation or scaling without
    multiplying the number of transform representations; this trick is
    probably meaningless when tried with the general affine transform.
    argument: ``--permitParameterVariation %s``
costMetric: ('MMI' or 'MSE' or 'NC' or 'MC')
    The cost metric to be used during fitting. Defaults to MMI. Options
    are MMI (Mattes Mutual Information), MSE (Mean Square Error), NC
    (Normalized Correlation), MC (Match Cardinality for binary images)
    argument: ``--costMetric %s``
writeOutputTransformInFloat: (a boolean)
    By default, the output registration transforms (either the output
    composite transform or each transform component) are written to the
    disk in double precision. If this flag is ON, the output transforms
    will be written in single (float) precision. It is especially
    important if the output transform is a displacement field transform,
    or it is a composite transform that includes several displacement
    fields.
    argument: ``--writeOutputTransformInFloat ``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables

```

Outputs:

```

bsplineTransform: (a pathlike object or string representing an
    existing file)
    (optional) Filename to which save the estimated transform. NOTE: You
    must set at least one output object (either a deformed image or a
    transform. NOTE: USE THIS ONLY IF THE FINAL TRANSFORM IS BSpline

```

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```

linearTransform: (a pathlike object or string representing an
    existing file)
    (optional) Filename to which save the estimated transform. NOTE: You
    must set at least one output object (either a deformed image or a
    transform. NOTE: USE THIS ONLY IF THE FINAL TRANSFORM IS ---NOT---
    BSpline
outputVolume: (a pathlike object or string representing an existing
    file)
    (optional) Output image for registration. NOTE: You must select
    either the outputTransform or the outputVolume option.
outputFixedVolumeROI: (a pathlike object or string representing an
    existing file)
    The ROI automatically found in fixed image, ONLY FOR ROIAUTO mode.
outputMovingVolumeROI: (a pathlike object or string representing an
    existing file)
    The ROI automatically found in moving image, ONLY FOR ROIAUTO mode.
strippedOutputTransform: (a pathlike object or string representing an
    existing file)
    File name for the rigid component of the estimated affine transform.
    Can be used to rigidly register the moving image to the fixed image.
    NOTE: This value is overwritten if either bsplineTransform or
    linearTransform is set.
outputTransform: (a pathlike object or string representing an
    existing file)
    (optional) Filename to which save the (optional) estimated
    transform. NOTE: You must select either the outputTransform or the
    outputVolume option.

```

76.23 interfaces.slicer.registration.brainsresample

76.23.1 BRAINSResample

[Link to code](#)

Wraps the executable command “BRAINSResample”.

title: Resample Image (BRAINS)

category: Registration

description: This program resamples an image image using a deformation field or a transform (BSpline, Affine, Rigid, etc.).

version: 3.0.0

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Modules:BRAINSResample>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Vincent Magnotta, Greg Harris, and Hans Johnson.

acknowledgements: The development of this tool was supported by funding from grants NS050568 and NS40068 from the National Institute of Neurological Disorders and Stroke and grants MH31593, MH40856, from the National Institute of Mental Health.

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)
    Image To Warp
    argument: ``--inputVolume %s``
referenceVolume: (a pathlike object or string representing an
    existing file)

```

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```

Reference image used only to define the output space. If not
specified, the warping is done in the same space as the image to
warp.
argument: ``--referenceVolume %s``
outputVolume: (a boolean or a pathlike object or string representing
a file)
Resulting deformed image
argument: ``--outputVolume %s``
pixelType: ('float' or 'short' or 'ushort' or 'int' or 'uint' or
'uchar' or 'binary')
Specifies the pixel type for the input/output images. The 'binary'
pixel type uses a modified algorithm whereby the image is read in as
unsigned char, a signed distance map is created, signed distance map
is resampled, and then a thresholded image of type unsigned char is
written to disk.
argument: ``--pixelType %s``
deformationVolume: (a pathlike object or string representing an
existing file)
Displacement Field to be used to warp the image
argument: ``--deformationVolume %s``
warpTransform: (a pathlike object or string representing an existing
file)
Filename for the BRAINSFit transform used in place of the
deformation field
argument: ``--warpTransform %s``
interpolationMode: ('NearestNeighbor' or 'Linear' or
'ResampleInPlace' or 'BSpline' or 'WindowedSinc' or 'Hamming' or
'Cosine' or 'Welch' or 'Lanczos' or 'Blackman')
Type of interpolation to be used when applying transform to moving
volume. Options are Linear, ResampleInPlace, NearestNeighbor,
BSpline, or WindowedSinc
argument: ``--interpolationMode %s``
inverseTransform: (a boolean)
True/False is to compute inverse of given transformation. Default is
false
argument: ``--inverseTransform ``
defaultValue: (a float)
Default voxel value
argument: ``--defaultValue %f``
gridSpacing: (a list of items which are an integer (int or long))
Add warped grid to output image to help show the deformation that
occured with specified spacing. A spacing of 0 in a dimension
indicates that grid lines should be rendered to fall exactly (i.e.
do not allow displacements off that plane). This is useful for
making a 2D image of grid lines from the 3D space
argument: ``--gridSpacing %s``
numberOfThreads: (an integer (int or long))
Explicitly specify the maximum number of threads to use.
argument: ``--numberOfThreads %d``
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables

```

Outputs:

```
outputVolume: (a pathlike object or string representing an existing
               file)
               Resulting deformed image
```

76.24 interfaces.slicer.registration.specialized

76.24.1 ACPCTransform

[Link to code](#)

Wraps the executable command “ACPCTransform”.

title: ACPC Transform

category: Registration.Specialized

description: <p>Calculate a transformation from two lists of fiducial points.</p><p>ACPC line is two fiducial points, one at the anterior commissure and one at the posterior commissure. The resulting transform will bring the line connecting them to horizontal to the AP axis.</p><p>The midline is a series of points defining the division between the hemispheres of the brain (the mid sagittal plane). The resulting transform will put the output volume with the mid sagittal plane lined up with the AS plane.</p><p>Use the Filtering moduleResample Scalar/Vector/DWI Volume to apply the transformation to a volume.</p>

version: 1.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/ACPCTransform>

license: slicer3

contributor: Nicole Aucoin (SPL, BWH), Ron Kikinis (SPL, BWH)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
acpc: (a list of items which are a list of from 3 to 3 items which
      are a float)
      ACPC line, two fiducial points, one at the anterior commissure and
      one at the posterior commissure.
      argument: ``--acpc %s...``
midline: (a list of items which are a list of from 3 to 3 items which
          are a float)
          The midline is a series of points defining the division between the
          hemispheres of the brain (the mid sagittal plane).
          argument: ``--midline %s...``
outputTransform: (a boolean or a pathlike object or string
                  representing a file)
                  A transform filled in from the ACPC and Midline registration
                  calculation
                  argument: ``--outputTransform %s``
debugSwitch: (a boolean)
              Click if wish to see debugging output
              argument: ``--debugSwitch ``
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
outputTransform: (a pathlike object or string representing an
                  existing file)
                  A transform filled in from the ACPC and Midline registration
                  calculation
```

76.24.2 BRAINSDemonWarp

[Link to code](#)

Wraps the executable command “BRAINSDemonWarp”.

title: Demon Registration (BRAINS)

category: Registration.Specialized

description: This program finds a deformation field to warp a moving image onto a fixed image. The images must be of the same signal kind, and contain an image of the same kind of object. This program uses the Thirion Demons warp software in ITK, the Insight Toolkit. Additional information is available at: <http://www.nitrc.org/projects/brainsdemonwarp>.

version: 3.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:BRAINSDemonWarp>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Hans J. Johnson and Greg Harris.

acknowledgements: The development of this tool was supported by funding from grants NS050568 and NS40068 from the National Institute of Neurological Disorders and Stroke and grants MH31593, MH40856, from the National Institute of Mental Health.

Inputs:

```
[Optional]
movingVolume: (a pathlike object or string representing an existing
              file)
              Required: input moving image
              argument: ``--movingVolume %s``
fixedVolume: (a pathlike object or string representing an existing
             file)
             Required: input fixed (target) image
             argument: ``--fixedVolume %s``
inputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
                Input volumes will be typecast to this format:
                float|short|ushort|int|uchar
                argument: ``--inputPixelType %s``
outputVolume: (a boolean or a pathlike object or string representing
              a file)
              Required: output resampled moving image (will have the same physical
              space as the fixedVolume).
              argument: ``--outputVolume %s``
outputDisplacementFieldVolume: (a boolean or a pathlike object or
                               string representing a file)
                               Output deformation field vector image (will have the same physical
                               space as the fixedVolume).
                               argument: ``--outputDisplacementFieldVolume %s``
outputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
                 outputVolume will be typecast to this format:
                 float|short|ushort|int|uchar
                 argument: ``--outputPixelType %s``
interpolationMode: ('NearestNeighbor' or 'Linear' or
                   'ResampleInPlace' or 'BSpline' or 'WindowedSinc' or 'Hamming' or
                   'Cosine' or 'Welch' or 'Lanczos' or 'Blackman')
                   Type of interpolation to be used when applying transform to moving
```

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```

    volume. Options are Linear, ResampleInPlace, NearestNeighbor,
    BSpline, or WindowedSinc
    argument: ``--interpolationMode %s``
registrationFilterType: ('Demons' or 'FastSymmetricForces' or
    'Diffeomorphic')
    Registration Filter Type: Demons|FastSymmetricForces|Diffeomorphic
    argument: ``--registrationFilterType %s``
smoothDisplacementFieldSigma: (a float)
    A gaussian smoothing value to be applied to the deformation feild at
    each iteration.
    argument: ``--smoothDisplacementFieldSigma %f``
numberOfPyramidLevels: (an integer (int or long))
    Number of image pyramid levels to use in the multi-resolution
    registration.
    argument: ``--numberOfPyramidLevels %d``
minimumFixedPyramid: (a list of items which are an integer (int or
    long))
    The shrink factor for the first level of the fixed image pyramid.
    (i.e. start at 1/16 scale, then 1/8, then 1/4, then 1/2, and finally
    full scale)
    argument: ``--minimumFixedPyramid %s``
minimumMovingPyramid: (a list of items which are an integer (int or
    long))
    The shrink factor for the first level of the moving image pyramid.
    (i.e. start at 1/16 scale, then 1/8, then 1/4, then 1/2, and finally
    full scale)
    argument: ``--minimumMovingPyramid %s``
arrayOfPyramidLevelIterations: (a list of items which are an integer
    (int or long))
    The number of iterations for each pyramid level
    argument: ``--arrayOfPyramidLevelIterations %s``
histogramMatch: (a boolean)
    Histogram Match the input images. This is suitable for images of the
    same modality that may have different absolute scales, but the same
    overall intense.
    argument: ``--histogramMatch ``
numberOfHistogramBins: (an integer (int or long))
    The number of histogram levels
    argument: ``--numberOfHistogramBins %d``
numberOfMatchPoints: (an integer (int or long))
    The number of match points for histogramMatch
    argument: ``--numberOfMatchPoints %d``
medianFilterSize: (a list of items which are an integer (int or
    long))
    Median filter radius in all 3 directions. When images have a lot of
    salt and pepper noise, this step can improve the registration.
    argument: ``--medianFilterSize %s``
initializeWithDisplacementField: (a pathlike object or string
    representing an existing file)
    Initial deformation field vector image file name
    argument: ``--initializeWithDisplacementField %s``
initializeWithTransform: (a pathlike object or string representing an
    existing file)
    Initial Transform filename
    argument: ``--initializeWithTransform %s``
maskProcessingMode: ('NOMASK' or 'ROIAUTO' or 'ROI' or 'BOBF')
    What mode to use for using the masks: NOMASK|ROIAUTO|ROI|BOBF. If

```

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ROIAUTO is choosen, then the mask is implicitly defined using a otsu foreground and hole filling algorithm. Where the Region Of Interest mode uses the masks to define what parts of the image should be used for computing the deformation field. Brain Only Background Fill uses the masks to pre-process the input images by clipping and filling in the background with a predefined value.

argument: ``--maskProcessingMode %s``

fixedBinaryVolume: (a pathlike object or string representing an existing file)

Mask filename for desired region of interest in the Fixed image.

argument: ``--fixedBinaryVolume %s``

movingBinaryVolume: (a pathlike object or string representing an existing file)

Mask filename for desired region of interest in the Moving image.

argument: ``--movingBinaryVolume %s``

lowerThresholdForBOBF: (an integer (int or long))

Lower threshold for performing BOBF

argument: ``--lowerThresholdForBOBF %d``

upperThresholdForBOBF: (an integer (int or long))

Upper threshold for performing BOBF

argument: ``--upperThresholdForBOBF %d``

backgroundFillValue: (an integer (int or long))

Replacement value to overwrite background when performing BOBF

argument: ``--backgroundFillValue %d``

seedForBOBF: (a list of items which are an integer (int or long))

coordinates in all 3 directions for Seed when performing BOBF

argument: ``--seedForBOBF %s``

neighborhoodForBOBF: (a list of items which are an integer (int or long))

neighborhood in all 3 directions to be included when performing BOBF

argument: ``--neighborhoodForBOBF %s``

outputDisplacementFieldPrefix: (a unicode string)

Displacement field filename prefix for writing separate x, y, and z component images

argument: ``--outputDisplacementFieldPrefix %s``

outputCheckerboardVolume: (a boolean or a pathlike object or string representing a file)

Genete a checkerboard image volume between the fixedVolume and the deformed movingVolume.

argument: ``--outputCheckerboardVolume %s``

checkerboardPatternSubdivisions: (a list of items which are an integer (int or long))

Number of Checkerboard subdivisions in all 3 directions

argument: ``--checkerboardPatternSubdivisions %s``

outputNormalized: (a boolean)

Flag to warp and write the normalized images to output. In normalized images the image values are fit-scaled to be between 0 and the maximum storage type value.

argument: ``--outputNormalized ``

outputDebug: (a boolean)

Flag to write debugging images after each step.

argument: ``--outputDebug ``

gradient_type: ('0' or '1' or '2')

Type of gradient used for computing the demons force (0 is symmetrized, 1 is fixed image, 2 is moving image)

argument: ``--gradient_type %s``

upFieldSmoothing: (a float)

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```

        Smoothing sigma for the update field at each iteration
        argument: ``--upFieldSmoothing %f``
max_step_length: (a float)
        Maximum length of an update vector (0: no restriction)
        argument: ``--max_step_length %f``
use_vanilla_dem: (a boolean)
        Run vanilla demons algorithm
        argument: ``--use_vanilla_dem ``
gui: (a boolean)
        Display intermediate image volumes for debugging
        argument: ``--gui ``
promptUser: (a boolean)
        Prompt the user to hit enter each time an image is sent to the
        DebugImageViewer
        argument: ``--promptUser ``
numberOfBCHApproximationTerms: (an integer (int or long))
        Number of terms in the BCH expansion
        argument: ``--numberOfBCHApproximationTerms %d``
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        argument: ``--numberOfThreads %d``
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
        file)
        Required: output resampled moving image (will have the same physical
        space as the fixedVolume).
outputDisplacementFieldVolume: (a pathlike object or string
        representing an existing file)
        Output deformation field vector image (will have the same physical
        space as the fixedVolume).
outputCheckerboardVolume: (a pathlike object or string representing
        an existing file)
        Genete a checkerboard image volume between the fixedVolume and the
        deformed movingVolume.

```

76.24.3 FiducialRegistration[Link to code](#)

Wraps the executable command “FiducialRegistration”.

title: Fiducial Registration

category: Registration.Specialized

description: Computes a rigid, similarity or affine transform from a matched list of fiducials

version: 0.1.0.\$Revision\$

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/TransformFromFiducials>

contributor: Casey B Goodlett (Kitware), Dominik Meier (SPL, BWH)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded

by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.
Inputs:

```
[Optional]
fixedLandmarks: (a list of items which are a list of from 3 to 3
    items which are a float)
    Ordered list of landmarks in the fixed image
    argument: ``--fixedLandmarks %s...``
movingLandmarks: (a list of items which are a list of from 3 to 3
    items which are a float)
    Ordered list of landmarks in the moving image
    argument: ``--movingLandmarks %s...``
saveTransform: (a boolean or a pathlike object or string representing
    a file)
    Save the transform that results from registration
    argument: ``--saveTransform %s``
transformType: ('Translation' or 'Rigid' or 'Similarity')
    Type of transform to produce
    argument: ``--transformType %s``
rms: (a float)
    Display RMS Error.
    argument: ``--rms %f``
outputMessage: (a unicode string)
    Provides more information on the output
    argument: ``--outputMessage %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables
```

Outputs:

```
saveTransform: (a pathlike object or string representing an existing
    file)
    Save the transform that results from registration
```

76.24.4 VBRAINSDemonWarp

[Link to code](#)

Wraps the executable command “VBRAINSDemonWarp”.

title: Vector Demon Registration (BRAINS)

category: Registration.Specialized

description: This program finds a deformation field to warp a moving image onto a fixed image. The images must be of the same signal kind, and contain an image of the same kind of object. This program uses the Thirion Demons warp software in ITK, the Insight Toolkit. Additional information is available at: <http://www.nitrc.org/projects/brainsdemonwarp>.

version: 3.0.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Modules:BRAINSDemonWarp>

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>

contributor: This tool was developed by Hans J. Johnson and Greg Harris.

acknowledgements: The development of this tool was supported by funding from grants NS050568 and NS40068 from the National Institute of Neurological Disorders and Stroke and grants MH31593, MH40856, from the National Institute of Mental Health.

Inputs:

```

[Optional]
movingVolume: (a list of items which are a pathlike object or string
    representing an existing file)
    Required: input moving image
    argument: ``--movingVolume %s...``
fixedVolume: (a list of items which are a pathlike object or string
    representing an existing file)
    Required: input fixed (target) image
    argument: ``--fixedVolume %s...``
inputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
    Input volumes will be typecast to this format:
    float|short|ushort|int|uchar
    argument: ``--inputPixelType %s``
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Required: output resampled moving image (will have the same physical
    space as the fixedVolume).
    argument: ``--outputVolume %s``
outputDisplacementFieldVolume: (a boolean or a pathlike object or
    string representing a file)
    Output deformation field vector image (will have the same physical
    space as the fixedVolume).
    argument: ``--outputDisplacementFieldVolume %s``
outputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
    outputVolume will be typecast to this format:
    float|short|ushort|int|uchar
    argument: ``--outputPixelType %s``
interpolationMode: ('NearestNeighbor' or 'Linear' or
    'ResampleInPlace' or 'BSpline' or 'WindowedSinc' or 'Hamming' or
    'Cosine' or 'Welch' or 'Lanczos' or 'Blackman')
    Type of interpolation to be used when applying transform to moving
    volume. Options are Linear, ResampleInPlace, NearestNeighbor,
    BSpline, or WindowedSinc
    argument: ``--interpolationMode %s``
registrationFilterType: ('Demons' or 'FastSymmetricForces' or
    'Diffeomorphic' or 'LogDemons' or 'SymmetricLogDemons')
    Registration Filter Type: Demons|FastSymmetricForces|Diffeomorphic|L
    ogDemons|SymmetricLogDemons
    argument: ``--registrationFilterType %s``
smoothDisplacementFieldSigma: (a float)
    A gaussian smoothing value to be applied to the deformation feild at
    each iteration.
    argument: ``--smoothDisplacementFieldSigma %f``
numberOfPyramidLevels: (an integer (int or long))
    Number of image pyramid levels to use in the multi-resolution
    registration.
    argument: ``--numberOfPyramidLevels %d``
minimumFixedPyramid: (a list of items which are an integer (int or
    long))
    The shrink factor for the first level of the fixed image pyramid.
    (i.e. start at 1/16 scale, then 1/8, then 1/4, then 1/2, and finally
    full scale)
    argument: ``--minimumFixedPyramid %s``
minimumMovingPyramid: (a list of items which are an integer (int or
    long))
    The shrink factor for the first level of the moving image pyramid.
    (i.e. start at 1/16 scale, then 1/8, then 1/4, then 1/2, and finally

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    full scale)
    argument: ``--minimumMovingPyramid %s``
arrayOfPyramidLevelIterations: (a list of items which are an integer
    (int or long))
    The number of iterations for each pyramid level
    argument: ``--arrayOfPyramidLevelIterations %s``
histogramMatch: (a boolean)
    Histogram Match the input images. This is suitable for images of the
    same modality that may have different absolute scales, but the same
    overall intensity profile.
    argument: ``--histogramMatch ``
numberOfHistogramBins: (an integer (int or long))
    The number of histogram levels
    argument: ``--numberOfHistogramBins %d``
numberOfMatchPoints: (an integer (int or long))
    The number of match points for histogramMatch
    argument: ``--numberOfMatchPoints %d``
medianFilterSize: (a list of items which are an integer (int or
    long))
    Median filter radius in all 3 directions. When images have a lot of
    salt and pepper noise, this step can improve the registration.
    argument: ``--medianFilterSize %s``
initializeWithDisplacementField: (a pathlike object or string
    representing an existing file)
    Initial deformation field vector image file name
    argument: ``--initializeWithDisplacementField %s``
initializeWithTransform: (a pathlike object or string representing an
    existing file)
    Initial Transform filename
    argument: ``--initializeWithTransform %s``
makeBOBF: (a boolean)
    Flag to make Brain-Only Background-Filled versions of the input and
    target volumes.
    argument: ``--makeBOBF ``
fixedBinaryVolume: (a pathlike object or string representing an
    existing file)
    Mask filename for desired region of interest in the Fixed image.
    argument: ``--fixedBinaryVolume %s``
movingBinaryVolume: (a pathlike object or string representing an
    existing file)
    Mask filename for desired region of interest in the Moving image.
    argument: ``--movingBinaryVolume %s``
lowerThresholdForBOBF: (an integer (int or long))
    Lower threshold for performing BOBF
    argument: ``--lowerThresholdForBOBF %d``
upperThresholdForBOBF: (an integer (int or long))
    Upper threshold for performing BOBF
    argument: ``--upperThresholdForBOBF %d``
backgroundFillValue: (an integer (int or long))
    Replacement value to overwrite background when performing BOBF
    argument: ``--backgroundFillValue %d``
seedForBOBF: (a list of items which are an integer (int or long))
    coordinates in all 3 directions for Seed when performing BOBF
    argument: ``--seedForBOBF %s``
neighborhoodForBOBF: (a list of items which are an integer (int or
    long))
    neighborhood in all 3 directions to be included when performing BOBF

```

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```

    argument: ``--neighborhoodForBOBF %s``
outputDisplacementFieldPrefix: (a unicode string)
    Displacement field filename prefix for writing separate x, y, and z
    component images
    argument: ``--outputDisplacementFieldPrefix %s``
outputCheckerboardVolume: (a boolean or a pathlike object or string
    representing a file)
    Genete a checkerboard image volume between the fixedVolume and the
    deformed movingVolume.
    argument: ``--outputCheckerboardVolume %s``
checkerboardPatternSubdivisions: (a list of items which are an
    integer (int or long))
    Number of Checkerboard subdivisions in all 3 directions
    argument: ``--checkerboardPatternSubdivisions %s``
outputNormalized: (a boolean)
    Flag to warp and write the normalized images to output. In
    normalized images the image values are fit-scaled to be between 0
    and the maximum storage type value.
    argument: ``--outputNormalized ``
outputDebug: (a boolean)
    Flag to write debugging images after each step.
    argument: ``--outputDebug ``
weightFactors: (a list of items which are a float)
    Weight fatctors for each input images
    argument: ``--weightFactors %s``
gradient_type: ('0' or '1' or '2')
    Type of gradient used for computing the demons force (0 is
    symmetrized, 1 is fixed image, 2 is moving image)
    argument: ``--gradient_type %s``
upFieldSmoothing: (a float)
    Smoothing sigma for the update field at each iteration
    argument: ``--upFieldSmoothing %f``
max_step_length: (a float)
    Maximum length of an update vector (0: no restriction)
    argument: ``--max_step_length %f``
use_vanilla_dem: (a boolean)
    Run vanilla demons algorithm
    argument: ``--use_vanilla_dem ``
gui: (a boolean)
    Display intermediate image volumes for debugging
    argument: ``--gui ``
promptUser: (a boolean)
    Prompt the user to hit enter each time an image is sent to the
    DebugImageViewer
    argument: ``--promptUser ``
numberOfBCHApproximationTerms: (an integer (int or long))
    Number of terms in the BCH expansion
    argument: ``--numberOfBCHApproximationTerms %d``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})

```

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Environment variables

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
               file)
               Required: output resampled moving image (will have the same physical
               space as the fixedVolume).
outputDisplacementFieldVolume: (a pathlike object or string
                                representing an existing file)
                                Output deformation field vector image (will have the same physical
                                space as the fixedVolume).
outputCheckerboardVolume: (a pathlike object or string representing
                           an existing file)
                           Generate a checkerboard image volume between the fixedVolume and the
                           deformed movingVolume.

```

76.25 interfaces.slicer.segmentation.simpleregiongrowingsegmentation

76.25.1 SimpleRegionGrowingSegmentation

[Link to code](#)

Wraps the executable command “SimpleRegionGrowingSegmentation”.

title: Simple Region Growing Segmentation

category: Segmentation

description: A simple region growing segmentation algorithm based on intensity statistics. To create a list of fiducials (Seeds) for this algorithm, click on the tool bar icon of an arrow pointing to a starburst fiducial to enter the ‘place a new object mode’ and then use the fiducials module. This module uses the Slicer Command Line Interface (CLI) and the ITK filters CurvatureFlowImageFilter and ConfidenceConnectedImageFilter.

version: 0.1.0.\$Revision: 19904 \$(alpha)

documentation-url: <http://www.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/SimpleRegionGrowingSegmentation>

contributor: Jim Miller (GE)

acknowledgements: This command module was derived from Insight/Examples (copyright) Insight Software Consortium

Inputs:

```

[Optional]
smoothingIterations: (an integer (int or long))
                    Number of smoothing iterations
                    argument: ``--smoothingIterations %d``
timestep: (a float)
          Timestep for curvature flow
          argument: ``--timestep %f``
iterations: (an integer (int or long))
            Number of iterations of region growing
            argument: ``--iterations %d``
multiplier: (a float)
            Number of standard deviations to include in intensity model
            argument: ``--multiplier %f``
neighborhood: (an integer (int or long))
              The radius of the neighborhood over which to calculate intensity
              model
              argument: ``--neighborhood %d``

```

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```

labelvalue: (an integer (int or long))
    The integer value (0-255) to use for the segmentation results. This
    will determine the color of the segmentation that will be generated
    by the Region growing algorithm
    argument: ``--labelvalue %d``
seed: (a list of items which are a list of from 3 to 3 items which
    are a float)
    Seed point(s) for region growing
    argument: ``--seed %s...``
inputVolume: (a pathlike object or string representing an existing
    file)
    Input volume to be filtered
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Output filtered
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Output filtered

```

76.26 interfaces.slicer.segmentation.specialized

76.26.1 BRAINSROIAuto

Link to code

Wraps the executable command “BRAINSROIAuto”.

title: Foreground masking (BRAINS)

category: Segmentation.Specialized

description: This tool uses a combination of otsu thresholding and a closing operations to identify the most prominent foreground region in an image.

version: 2.4.1

license: <https://www.nitrc.org/svn/brains/BuildScripts/trunk/License.txt>contributor: Hans J. Johnson, hans-johnson -at- uiowa.edu, <http://www.psychiatry.uiowa.edu>

acknowledgements: Hans Johnson(1,3,4); Kent Williams(1); Gregory Harris(1), Vincent Magnotta(1,2,3); Andriy Fedorov(5), fedorov -at- bwh.harvard.edu (Slicer integration); (1=University of Iowa Department of Psychiatry, 2=University of Iowa Department of Radiology, 3=University of Iowa Department of Biomedical Engineering, 4=University of Iowa Department of Electrical and Computer Engineering, 5=Surgical Planning Lab, Harvard)

Inputs:

```

[Optional]
inputVolume: (a pathlike object or string representing an existing
    file)

```

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```

    The input image for finding the largest region filled mask.
    argument: ``--inputVolume %s``
outputROIMaskVolume: (a boolean or a pathlike object or string
    representing a file)
    The ROI automatically found from the input image.
    argument: ``--outputROIMaskVolume %s``
outputClippedVolumeROI: (a boolean or a pathlike object or string
    representing a file)
    The inputVolume clipped to the region of the brain mask.
    argument: ``--outputClippedVolumeROI %s``
otsuPercentileThreshold: (a float)
    Parameter to the Otsu threshold algorithm.
    argument: ``--otsuPercentileThreshold %f``
thresholdCorrectionFactor: (a float)
    A factor to scale the Otsu algorithm's result threshold, in case
    clipping mangles the image.
    argument: ``--thresholdCorrectionFactor %f``
closingSize: (a float)
    The Closing Size (in millimeters) for largest connected filled mask.
    This value is divided by image spacing and rounded to the next
    largest voxel number.
    argument: ``--closingSize %f``
ROIAutoDilateSize: (a float)
    This flag is only relavent when using ROIAUTO mode for initializing
    masks. It defines the final dilation size to capture a bit of
    background outside the tissue region. At setting of 10mm has been
    shown to help regularize a BSpline registration type so that there
    is some background constraints to match the edges of the head
    better.
    argument: ``--ROIAutoDilateSize %f``
outputVolumePixelType: ('float' or 'short' or 'ushort' or 'int' or
    'uint' or 'uchar')
    The output image Pixel Type is the scalar datatype for
    representation of the Output Volume.
    argument: ``--outputVolumePixelType %s``
numberOfThreads: (an integer (int or long))
    Explicitly specify the maximum number of threads to use.
    argument: ``--numberOfThreads %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputROIMaskVolume: (a pathlike object or string representing an
    existing file)
    The ROI automatically found from the input image.
outputClippedVolumeROI: (a pathlike object or string representing an
    existing file)
    The inputVolume clipped to the region of the brain mask.

```

76.26.2 EMSegmentCommandLine

[Link to code](#)

Wraps the executable command “EMSegmentCommandLine”.

title: EMSegment Command-line

category: Segmentation.Specialized

description: This module is used to simplify the process of segmenting large collections of images by providing a command line interface to the EMSegment algorithm for script and batch processing.

documentation-url: http://www.slicer.org/slicerWiki/index.php/Documentation/4.0/EMSegment_Command-line

contributor: Sebastien Barre, Brad Davis, Kilian Pohl, Polina Golland, Yumin Yuan, Daniel Haehn

acknowledgements: Many people and organizations have contributed to the funding, design, and development of the EMSegment algorithm and its various implementations.

Inputs:

```
[Optional]
mrmlSceneFileName: (a pathlike object or string representing an
    existing file)
    Active MRML scene that contains EMSegment algorithm parameters.
    argument: ``--mrmlSceneFileName %s``
resultVolumeFileName: (a boolean or a pathlike object or string
    representing a file)
    The file name that the segmentation result volume will be written
    to.
    argument: ``--resultVolumeFileName %s``
targetVolumeFileNames: (a list of items which are a pathlike object
    or string representing an existing file)
    File names of target volumes (to be segmented). The number of target
    images must be equal to the number of target images specified in the
    parameter set, and these images must be spatially aligned.
    argument: ``--targetVolumeFileNames %s...``
intermediateResultsDirectory: (a pathlike object or string
    representing an existing directory)
    Directory where EMSegmenter will write intermediate data (e.g.,
    aligned atlas data).
    argument: ``--intermediateResultsDirectory %s``
parametersMRMLNodeName: (a unicode string)
    The name of the EMSegment parameters node within the active MRML
    scene. Leave blank for default.
    argument: ``--parametersMRMLNodeName %s``
disableMultithreading: (an integer (int or long))
    Disable multithreading for the EMSegmenter algorithm only!
    Preprocessing might still run in multi-threaded mode. -1: Do not
    overwrite default value. 0: Disable. 1: Enable.
    argument: ``--disableMultithreading %d``
dontUpdateIntermediateData: (an integer (int or long))
    Disable update of intermediate results. -1: Do not overwrite default
    value. 0: Disable. 1: Enable.
    argument: ``--dontUpdateIntermediateData %d``
verbose: (a boolean)
    Enable verbose output.
    argument: ``--verbose ``
loadTargetCentered: (a boolean)
    Read target files centered.
    argument: ``--loadTargetCentered ``
loadAtlasNonCentered: (a boolean)
    Read atlas files non-centered.
```

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```

        argument: ``--loadAtlasNonCentered ``
taskPreProcessingSetting: (a unicode string)
    Specifies the different task parameter. Leave blank for default.
    argument: ``--taskPreProcessingSetting %s``
keepTempFiles: (a boolean)
    If flag is set then at the end of command the temporary files are
    not removed
    argument: ``--keepTempFiles ``
resultStandardVolumeFileName: (a pathlike object or string
    representing an existing file)
    Used for testing. Compare segmentation results to this image and
    return EXIT_FAILURE if they do not match.
    argument: ``--resultStandardVolumeFileName %s``
dontWriteResults: (a boolean)
    Used for testing. Don't actually write the resulting labelmap to
    disk.
    argument: ``--dontWriteResults ``
generateEmptyMRMLSceneAndQuit: (a boolean or a pathlike object or
    string representing a file)
    Used for testing. Only write a scene with default mrml parameters.
    argument: ``--generateEmptyMRMLSceneAndQuit %s``
resultMRMLSceneFileName: (a boolean or a pathlike object or string
    representing a file)
    Write out the MRML scene after command line substitutions have been
    made.
    argument: ``--resultMRMLSceneFileName %s``
disableCompression: (a boolean)
    Don't use compression when writing result image to disk.
    argument: ``--disableCompression ``
atlasVolumeFileNames: (a list of items which are a pathlike object or
    string representing an existing file)
    Use an alternative atlas to the one that is specified by the mrml
    file - note the order matters !
    argument: ``--atlasVolumeFileNames %s...``
registrationPackage: (a unicode string)
    specify the registration package for preprocessing (CMTK or BRAINS
    or PLASTIMATCH or DEMONS)
    argument: ``--registrationPackage %s``
registrationAffineType: (an integer (int or long))
    specify the accuracy of the affine registration. -2: Do not
    overwrite default, -1: Test, 0: Disable, 1: Fast, 2: Accurate
    argument: ``--registrationAffineType %d``
registrationDeformableType: (an integer (int or long))
    specify the accuracy of the deformable registration. -2: Do not
    overwrite default, -1: Test, 0: Disable, 1: Fast, 2: Accurate
    argument: ``--registrationDeformableType %d``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

resultVolumeFileName: (a pathlike object or string representing an

```

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```

    existing file)
    The file name that the segmentation result volume will be written
    to.
generateEmptyMRMLSceneAndQuit: (a pathlike object or string
    representing an existing file)
    Used for testing. Only write a scene with default mrml parameters.
resultMRMLSceneFileName: (a pathlike object or string representing an
    existing file)
    Write out the MRML scene after command line substitutions have been
    made.

```

76.26.3 RobustStatisticsSegmenter

[Link to code](#)

Wraps the executable command “RobustStatisticsSegmenter”.

title: Robust Statistics Segmenter

category: Segmentation.Specialized

description: Active contour segmentation using robust statistic.

version: 1.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/RobustStatisticsSegmenter>

contributor: Yi Gao (gatech), Allen Tannenbaum (gatech), Ron Kikinis (SPL, BWH)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health

Inputs:

```

[Optional]
expectedVolume: (a float)
    The approximate volume of the object, in mL.
    argument: ``--expectedVolume %f``
intensityHomogeneity: (a float)
    What is the homogeneity of intensity within the object? Given
    constant intensity at 1.0 score and extreme fluctuating intensity at
    0.
    argument: ``--intensityHomogeneity %f``
curvatureWeight: (a float)
    Given sphere 1.0 score and extreme rough bounday/surface 0 score,
    what is the expected smoothness of the object?
    argument: ``--curvatureWeight %f``
labelValue: (an integer (int or long))
    Label value of the output image
    argument: ``--labelValue %d``
maxRunningTime: (a float)
    The program will stop if this time is reached.
    argument: ``--maxRunningTime %f``
originalImageFileName: (a pathlike object or string representing an
    existing file)
    Original image to be segmented
    argument: ``%s``, position: -3
labelImageFileName: (a pathlike object or string representing an
    existing file)
    Label image for initialization
    argument: ``%s``, position: -2
segmentedImageFileName: (a boolean or a pathlike object or string
    representing a file)

```

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```

        Segmented image
        argument: ``%s``, position: -1
args: (a unicode string)
        Additional parameters to the command
        argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
        of class 'str' and with values which are a bytes or None or a
        value of class 'str', nipy default value: {})
        Environment variables

```

Outputs:

```

segmentedImageFileName: (a pathlike object or string representing an
        existing file)
        Segmented image

```

76.27 interfaces.slicer.surface

76.27.1 GrayscaleModelMaker

[Link to code](#)

Wraps the executable command “GrayscaleModelMaker”.

title: Grayscale Model Maker

category: Surface Models

description: Create 3D surface models from grayscale data. This module uses Marching Cubes to create an isosurface at a given threshold. The resulting surface consists of triangles that separate a volume into regions below and above the threshold. The resulting surface can be smoothed and decimated. This model works on continuous data while the module Model Maker works on labeled (or discrete) data.

version: 3.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/GrayscaleModelMaker>

license: slicer3

contributor: Nicole Aucoin (SPL, BWH), Bill Lorensen (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```

[Optional]
InputVolume: (a pathlike object or string representing an existing
        file)
        Volume containing the input grayscale data.
        argument: ``%s``, position: -2
OutputGeometry: (a boolean or a pathlike object or string
        representing a file)
        Output that contains geometry model.
        argument: ``%s``, position: -1
threshold: (a float)
        Grayscale threshold of isosurface. The resulting surface of
        triangles separates the volume into voxels that lie above (inside)
        and below (outside) the threshold.
        argument: ``--threshold %f``
name: (a unicode string)
        Name to use for this model.
        argument: ``--name %s``

```

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```

smooth: (an integer (int or long))
    Number of smoothing iterations. If 0, no smoothing will be done.
    argument: ``--smooth %d``
decimate: (a float)
    Target reduction during decimation, as a decimal percentage
    reduction in the number of polygons. If 0, no decimation will be
    done.
    argument: ``--decimate %f``
splitnormals: (a boolean)
    Splitting normals is useful for visualizing sharp features. However
    it creates holes in surfaces which affect measurements
    argument: ``--splitnormals``
pointnormals: (a boolean)
    Calculate the point normals? Calculated point normals make the
    surface appear smooth. Without point normals, the surface will
    appear faceted.
    argument: ``--pointnormals``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

OutputGeometry: (a pathlike object or string representing an existing
    file)
    Output that contains geometry model.

```

76.27.2 LabelMapSmoothing[Link to code](#)

Wraps the executable command “LabelMapSmoothing”.

title: Label Map Smoothing

category: Surface Models

description: This filter smoothes a binary label map. With a label map as input, this filter runs an anti-aliasing algorithm followed by a Gaussian smoothing algorithm. The output is a smoothed label map.

version: 1.0

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/LabelMapSmoothing>

contributor: Dirk Padfield (GE), Josh Cates (Utah), Ross Whitaker (Utah)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149. This filter is based on work developed at the University of Utah, and implemented at GE Research.

Inputs:

```

[Optional]
labelToSmooth: (an integer (int or long))
    The label to smooth. All others will be ignored. If no label is
    selected by the user, the maximum label in the image is chosen by
    default.
    argument: ``--labelToSmooth %d``
numberOfIterations: (an integer (int or long))

```

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```

    The number of iterations of the level set AntiAliasing algorithm
    argument: ``--numberOfIterations %d``
maxRMSError: (a float)
    The maximum RMS error.
    argument: ``--maxRMSError %f``
gaussianSigma: (a float)
    The standard deviation of the Gaussian kernel
    argument: ``--gaussianSigma %f``
inputVolume: (a pathlike object or string representing an existing
    file)
    Input label map to smooth
    argument: ``%s``, position: -2
outputVolume: (a boolean or a pathlike object or string representing
    a file)
    Smoothed label map
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

outputVolume: (a pathlike object or string representing an existing
    file)
    Smoothed label map

```

76.27.3 MergeModels[Link to code](#)

Wraps the executable command “MergeModels”.

title: Merge Models

category: Surface Models

description: Merge the polydata from two input models and output a new model with the added polydata. Uses the vtkAppendPolyData filter. Works on .vtp and .vtk surface files.

version: \$Revision\$

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/MergeModels>

contributor: Nicole Aucoin (SPL, BWH), Ron Kikinis (SPL, BWH), Daniel Haehn (SPL, BWH)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```

[Optional]
Model1: (a pathlike object or string representing an existing file)
    Model
    argument: ``%s``, position: -3
Model2: (a pathlike object or string representing an existing file)
    Model
    argument: ``%s``, position: -2
ModelOutput: (a boolean or a pathlike object or string representing a
    file)
    Model
    argument: ``%s``, position: -1

```

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```
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
ModelOutput: (a pathlike object or string representing an existing
    file)
    Model
```

76.27.4 ModelMaker[Link to code](#)

Wraps the executable command “ModelMaker”.

title: Model Maker

category: Surface Models

description: Create 3D surface models from segmented data.<p>Models are imported into Slicer under a model hierarchy node in a MRML scene. The model colors are set by the color table associated with the input volume (these colours will only be visible if you load the model scene file).</p><p>Create Multiple:</p><p>If you specify a list of Labels, it will over ride any start/end label settings.</p><p>If you click<i>Generate All</i>it will over ride the list of lables and any start/end label settings.</p><p>Model Maker Settings:</p><p>You can set the number of smoothing iterations, target reduction in number of polygons (decimal percentage). Use 0 and 1 if you wish no smoothing nor decimation.
You can set the flags to split normals or generate point normals in this pane as well.
You can save a copy of the models after intermediate steps (marching cubes, smoothing, and decimation if not joint smoothing, otherwise just after decimation); these models are not saved in the mrml file, turn off deleting temporary files first in the python window:
<i>slicer.modules.modelmaker.cliModuleLogic().DeleteTemporaryFilesOff()</i></p>

version: 4.1

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/ModelMaker>

license: slicer4

contributor: Nicole Aucoin (SPL, BWH), Ron Kikinis (SPL, BWH), Bill Lorensen (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
InputVolume: (a pathlike object or string representing an existing
    file)
    Input label map. The Input Volume drop down menu is populated with
    the label map volumes that are present in the scene, select one from
    which to generate models.
    argument: ``%s``, position: -1
color: (a pathlike object or string representing an existing file)
    Color table to make labels to colors and objects
    argument: ``--color %s``
modelSceneFile: (a boolean or a list of items which are a pathlike
    object or string representing a file)
    Generated models, under a model hierarchy node. Models are imported
    into Slicer under a model hierarchy node, and their colors are set
    by the color table associated with the input label map volume. The
    model hierarchy node must be created before running the model maker,
```

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```

    by selecting Create New ModelHierarchy from the Models drop down
    menu. If you're running from the command line, a model hierarchy
    node in a new mrml scene will be created for you.
    argument: ``--modelSceneFile %s...``

name: (a unicode string)
    Name to use for this model. Any text entered in the entry box will
    be the starting string for the created model file names. The label
    number and the color name will also be part of the file name. If
    making multiple models, use this as a prefix to the label and color
    name.
    argument: ``--name %s``

generateAll: (a boolean)
    Generate models for all labels in the input volume. select this
    option if you want to create all models that correspond to all
    values in a labelmap volume (using the Joint Smoothing option below
    is useful with this option). Ignores Labels, Start Label, End Label
    settings. Skips label 0.
    argument: ``--generateAll``

labels: (a list of items which are an integer (int or long))
    A comma separated list of label values from which to make models. f
    you specify a list of Labels, it will override any start/end label
    settings. If you click Generate All Models it will override the list
    of labels and any start/end label settings.
    argument: ``--labels %s``

start: (an integer (int or long))
    If you want to specify a continuous range of labels from which to
    generate models, enter the lower label here. Voxel value from which
    to start making models. Used instead of the label list to specify a
    range (make sure the label list is empty or it will over ride this).
    argument: ``--start %d``

end: (an integer (int or long))
    If you want to specify a continuous range of labels from which to
    generate models, enter the higher label here. Voxel value up to
    which to continue making models. Skip any values with zero voxels.
    argument: ``--end %d``

skipUnNamed: (a boolean)
    Select this to not generate models from labels that do not have
    names defined in the color look up table associated with the input
    label map. If true, only models which have an entry in the color
    table will be generated. If false, generate all models that exist
    within the label range.
    argument: ``--skipUnNamed``

jointsmooth: (a boolean)
    This will ensure that all resulting models fit together smoothly,
    like jigsaw puzzle pieces. Otherwise the models will be smoothed
    independently and may overlap.
    argument: ``--jointsmooth``

smooth: (an integer (int or long))
    Here you can set the number of smoothing iterations for Laplacian
    smoothing, or the degree of the polynomial approximating the
    windowed Sinc function. Use 0 if you wish no smoothing.
    argument: ``--smooth %d``

filtertype: ('Sinc' or 'Laplacian')
    You can control the type of smoothing done on the models by
    selecting a filter type of either Sinc or Laplacian.
    argument: ``--filtertype %s``

decimate: (a float)

```

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```

    Chose the target reduction in number of polygons as a decimal
    percentage (between 0 and 1) of the number of polygons. Specifies
    the percentage of triangles to be removed. For example, 0.1 means
    10% reduction and 0.9 means 90% reduction.
    argument: ``--decimate %f``

splitnormals: (a boolean)
    Splitting normals is useful for visualizing sharp features. However
    it creates holes in surfaces which affects measurements.
    argument: ``--splitnormals``

pointnormals: (a boolean)
    Turn this flag on if you wish to calculate the normal vectors for
    the points.
    argument: ``--pointnormals``

pad: (a boolean)
    Pad the input volume with zero value voxels on all 6 faces in order
    to ensure the production of closed surfaces. Sets the origin
    translation and extent translation so that the models still line up
    with the unpadded input volume.
    argument: ``--pad``

saveIntermediateModels: (a boolean)
    You can save a copy of the models after each of the intermediate
    steps (marching cubes, smoothing, and decimation if not joint
    smoothing, otherwise just after decimation). These intermediate
    models are not saved in the mrml file, you have to load them
    manually after turning off deleting temporary files in they python
    console (View ->Python Interactor) using the following command slice
    r.modules.modelmaker.cliModuleLogic().DeleteTemporaryFilesOff().
    argument: ``--saveIntermediateModels``

debug: (a boolean)
    turn this flag on in order to see debugging output (look in the
    Error Log window that is accessed via the View menu)
    argument: ``--debug``

args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``

environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables

```

Outputs:

```

modelSceneFile: (a list of items which are a pathlike object or
    string representing an existing file)
    Generated models, under a model hierarchy node. Models are imported
    into Slicer under a model hierarchy node, and their colors are set
    by the color table associated with the input label map volume. The
    model hierarchy node must be created before running the model maker,
    by selecting Create New ModelHierarchy from the Models drop down
    menu. If you're running from the command line, a model hierarchy
    node in a new mrml scene will be created for you.

```

76.27.5 ModelToLabelMap[Link to code](#)

Wraps the executable command “ModelToLabelMap”.

title: Model To Label Map

category: Surface Models

description: Intersects an input model with an reference volume and produces an output label map.

version: 0.1.0.\$Revision: 8643 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/PolyDataToLabelMap>

contributor: Nicole Aucoin (SPL, BWH), Xiaodong Tao (GE)

acknowledgements: This work is part of the National Alliance for Medical Image Computing (NAMIC), funded by the National Institutes of Health through the NIH Roadmap for Medical Research, Grant U54 EB005149.

Inputs:

```
[Optional]
distance: (a float)
    Sample distance
    argument: ``--distance %f``
InputVolume: (a pathlike object or string representing an existing
    file)
    Input volume
    argument: ``%s``, position: -3
surface: (a pathlike object or string representing an existing file)
    Model
    argument: ``%s``, position: -2
OutputVolume: (a boolean or a pathlike object or string representing
    a file)
    The label volume
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyype default value: {})
    Environment variables
```

Outputs:

```
OutputVolume: (a pathlike object or string representing an existing
    file)
    The label volume
```

76.27.6 ProbeVolumeWithModel

[Link to code](#)

Wraps the executable command “ProbeVolumeWithModel”.

title: Probe Volume With Model

category: Surface Models

description: Paint a model by a volume (using vtkProbeFilter).

version: 0.1.0.\$Revision: 1892 \$(alpha)

documentation-url: <http://wiki.slicer.org/slicerWiki/index.php/Documentation/4.1/Modules/ProbeVolumeWithModel>

contributor: Lauren O'Donnell (SPL, BWH)

acknowledgements: BWH, NCIGT/LMI

Inputs:

```
[Optional]
InputVolume: (a pathlike object or string representing an existing
    file)
```

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```

    Volume to use to 'paint' the model
    argument: ``%s``, position: -3
InputModel: (a pathlike object or string representing an existing
    file)
    Input model
    argument: ``%s``, position: -2
OutputModel: (a boolean or a pathlike object or string representing a
    file)
    Output 'painted' model
    argument: ``%s``, position: -1
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

OutputModel: (a pathlike object or string representing an existing
    file)
    Output 'painted' model

```

76.28 interfaces.slicer.utilities

76.28.1 EMSegmentTransformToNewFormat

[Link to code](#)

Wraps the executable command “EMSegmentTransformToNewFormat”.

title: Transform MRML Files to New EMSegmenter Standard**category:** Utilities**description:** Transform MRML Files to New EMSegmenter Standard**Inputs:**

```

[Optional]
inputMRMLFileName: (a pathlike object or string representing an
    existing file)
    Active MRML scene that contains EMSegment algorithm parameters in
    the format before 3.6.3 - please include absolute file name in path.
    argument: ``--inputMRMLFileName %s``
outputMRMLFileName: (a boolean or a pathlike object or string
    representing a file)
    Write out the MRML scene after transformation to format 3.6.3 has
    been made. - has to be in the same directory as the input MRML file
    due to Slicer Core bug - please include absolute file name in path
    argument: ``--outputMRMLFileName %s``
templateFlag: (a boolean)
    Set to true if the transformed mrml file should be used as template
    file
    argument: ``--templateFlag ``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value

```

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```
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipyte default value: {}))
Environment variables
```

Outputs:

```
outputMRMLFileName: (a pathlike object or string representing an
existing file)
Write out the MRML scene after transformation to format 3.6.3 has
been made. - has to be in the same directory as the input MRML file
due to Slicer Core bug - please include absolute file name in path
```


77.1 interfaces.spm.model

77.1.1 EstimateContrast

[Link to code](#)

Use `spm_contrasts` to estimate contrasts of interest

Examples

```
>>> import nipy.interfaces.spm as spm
>>> est = spm.EstimateContrast()
>>> est.inputs.spm_mat_file = 'SPM.mat'
>>> cont1 = ('Task>Baseline', 'T', ['Task-Odd', 'Task-Even'], [0.5, 0.5])
>>> cont2 = ('Task-Odd>Task-Even', 'T', ['Task-Odd', 'Task-Even'], [1, -1])
>>> contrasts = [cont1, cont2]
>>> est.inputs.contrasts = contrasts
>>> est.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
spm_mat_file: (a pathlike object or string representing an existing
               file)
               Absolute path to SPM.mat
contrasts: (a list of items which are a tuple of the form: (a unicode
                 string, 'T', a list of items which are a unicode string, a list of
                 items which are a float) or a tuple of the form: (a unicode
                 string, 'T', a list of items which are a unicode string, a list of
                 items which are a float, a list of items which are a float) or a
                 tuple of the form: (a unicode string, 'F', a list of items which
                 are a tuple of the form: (a unicode string, 'T', a list of items
                 which are a unicode string, a list of items which are a float) or
                 a tuple of the form: (a unicode string, 'T', a list of items which
                 are a unicode string, a list of items which are a float, a list of
                 items which are a float)))
               List of contrasts with each contrast being a list of the form:
```

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```
[('name', 'stat', [condition list], [weight list], [session list])]
If session list is None or not provided, all sessions are used. For
F contrasts, the condition list should contain previously defined
T-contrasts.
beta_images: (a list of items which are a pathlike object or string
    representing an existing file)
    Parameter estimates of the design matrix
residual_image: (a pathlike object or string representing an existing
    file)
    Mean-squared image of the residuals

[Optional]
use_derivs: (a boolean)
    use derivatives for estimation
    mutually_exclusive: group_contrast
group_contrast: (a boolean)
    higher level contrast
    mutually_exclusive: use_derivs
matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
    representing a directory)
    Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
    Generate SPM8 and higher compatible jobs
```

Outputs:

```
con_images: (a list of items which are a pathlike object or string
    representing an existing file)
    contrast images from a t-contrast
spmT_images: (a list of items which are a pathlike object or string
    representing an existing file)
    stat images from a t-contrast
ess_images: (a list of items which are a pathlike object or string
    representing an existing file)
    contrast images from an F-contrast
spmF_images: (a list of items which are a pathlike object or string
    representing an existing file)
    stat images from an F-contrast
spm_mat_file: (a pathlike object or string representing an existing
    file)
    Updated SPM mat file
```

References:

None

77.1.2 EstimateModel[Link to code](#)Use `spm_spm` to estimate the parameters of a model<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=69>

Examples

```

>>> est = EstimateModel()
>>> est.inputs.spm_mat_file = 'SPM.mat'
>>> est.inputs.estimate_method = {'Classical': 1}
>>> est.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
spm_mat_file: (a pathlike object or string representing an existing
               file)
               Absolute path to SPM.mat
estimate_method: (a dictionary with keys which are 'Classical' or
                  'Bayesian2' or 'Bayesian' and with values which are any value)
                  Dictionary of either Classical: 1, Bayesian: 1, or Bayesian2: 1
                  (dict)

[Optional]
write_residuals: (a boolean)
                  Write individual residual images
flags: (a dictionary with keys which are any value and with values
        which are any value)
        Additional arguments
matlab_cmd: (a unicode string)
             matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
          Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
               Generate SPM8 and higher compatible jobs

```

Outputs:

```

mask_image: (a pathlike object or string representing an existing
             file)
             binary mask to constrain estimation
beta_images: (a list of items which are a pathlike object or string
              representing an existing file)
              design parameter estimates
residual_image: (a pathlike object or string representing an existing
                 file)
                 Mean-squared image of the residuals
residual_images: (a list of items which are a pathlike object or
                  string representing an existing file)
                  individual residual images (requires `write_residuals`)
RPVimage: (a pathlike object or string representing an existing file)
           Resels per voxel image
spm_mat_file: (a pathlike object or string representing an existing
               file)
               Updated SPM mat file
labels: (a pathlike object or string representing an existing file)
         label file
SDerror: (a list of items which are a pathlike object or string
          representing an existing file)

```

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```

    Images of the standard deviation of the error
ARcoef: (a list of items which are a pathlike object or string
        representing an existing file)
    Images of the AR coefficient
Cbetas: (a list of items which are a pathlike object or string
        representing an existing file)
    Images of the parameter posteriors
SDBetas: (a list of items which are a pathlike object or string
        representing an existing file)
    Images of the standard deviation of parameter posteriors

```

References:

None

77.1.3 FactorialDesign[Link to code](#)

Base class for factorial designs

<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=77>

Inputs:

```

[Optional]
spm_mat_dir: (a pathlike object or string representing an existing
    directory)
    directory to store SPM.mat file (opt)
covariates: (a list of items which are a dictionary with keys which
    are 'vector' or 'name' or 'interaction' or 'centering' and with
    values which are any value)
    covariate dictionary {vector, name, interaction, centering}
threshold_mask_none: (a boolean)
    do not use threshold masking
    mutually_exclusive: threshold_mask_absolute, threshold_mask_relative
threshold_mask_absolute: (a float)
    use an absolute threshold
    mutually_exclusive: threshold_mask_none, threshold_mask_relative
threshold_mask_relative: (a float)
    threshold using a proportion of the global value
    mutually_exclusive: threshold_mask_absolute, threshold_mask_none
use_implicit_threshold: (a boolean)
    use implicit mask NaNs or zeros to threshold
explicit_mask_file: (a pathlike object or string representing a file)
    use an implicit mask file to threshold
global_calc_omit: (a boolean)
    omit global calculation
    mutually_exclusive: global_calc_mean, global_calc_values
global_calc_mean: (a boolean)
    use mean for global calculation
    mutually_exclusive: global_calc_omit, global_calc_values
global_calc_values: (a list of items which are a float)
    omit global calculation
    mutually_exclusive: global_calc_mean, global_calc_omit
no_grand_mean_scaling: (a boolean)
    do not perform grand mean scaling
global_normalization: (1 or 2 or 3)
    global normalization None-1, Proportional-2, ANCOVA-3

```

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```

matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
    representing a directory)
    Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```

spm_mat_file: (a pathlike object or string representing an existing
    file)
    SPM mat file

```

References:

None

77.1.4 Level1Design[Link to code](#)

Generate an SPM design matrix

<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=59>**Examples**

```

>>> level1design = Level1Design()
>>> level1design.inputs.timing_units = 'secs'
>>> level1design.inputs.interscan_interval = 2.5
>>> level1design.inputs.bases = {'hrf':{'derivs': [0,0]}}
>>> level1design.inputs.session_info = 'session_info.npz'
>>> level1design.inputs.flags = {'mthresh': 0.4}
>>> level1design.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
timing_units: ('secs' or 'scans')
    units for specification of onsets
interscan_interval: (a float)
    Interscan interval in secs
session_info: (any value)
    Session specific information generated by ``modelgen.SpecifyModel``
bases: (a dictionary with keys which are 'hrf' or 'fourier' or
    'fourier_han' or 'gamma' or 'fir' and with values which are any
    value)
    dict {'name':{'basesparam1':val,...}}
    name : string
    Name of basis function (hrf, fourier, fourier_han,
    gamma, fir)
    hrf :
    derivs : 2-element list

```

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```

    Model HRF Derivatives. No derivatives: [0,0],
    Time derivatives : [1,0], Time and Dispersion
    derivatives: [1,1]
    fourier, fourier_han, gamma, fir:
    length : int
    Post-stimulus window length (in seconds)
    order : int
    Number of basis functions

[Optional]
spm_mat_dir: (a pathlike object or string representing an existing
    directory)
    directory to store SPM.mat file (opt)
microtime_resolution: (an integer (int or long))
    Number of time-bins per scan in secs (opt)
microtime_onset: (a float)
    The onset/time-bin in seconds for alignment (opt)
factor_info: (a list of items which are a dictionary with keys which
    are 'name' or 'levels' and with values which are any value)
    Factor specific information file (opt)
volterra_expansion_order: (1 or 2)
    Model interactions - yes:1, no:2
global_intensity_normalization: ('none' or 'scaling')
    Global intensity normalization - scaling or none
mask_image: (a pathlike object or string representing an existing
    file)
    Image for explicitly masking the analysis
mask_threshold: ('-Inf' or a float, nipy default value: -Inf)
    Thresholding for the mask
model_serial_correlations: ('AR(1)' or 'FAST' or 'none')
    Model serial correlations AR(1), FAST or none. FAST is available in
    SPM12
flags: (a dictionary with keys which are any value and with values
    which are any value)
    Additional arguments to the job, e.g., a common SPM operation is to
    modify the default masking threshold (mthresh)
matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
    representing a directory)
    Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```

spm_mat_file: (a pathlike object or string representing an existing
    file)
    SPM mat file

```

References:

None

77.1.5 MultipleRegressionDesign

[Link to code](#)

Create SPM design for multiple regression

Examples

```
>>> mreg = MultipleRegressionDesign()
>>> mreg.inputs.in_files = ['cont1.nii', 'cont2.nii']
>>> mreg.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_files: (a list of at least 2 items which are a pathlike object or
          string representing an existing file)
          List of files

[Optional]
include_intercept: (a boolean, nipy default value: True)
                   Include intercept in design
user_covariates: (a list of items which are a dictionary with keys
                  which are 'vector' or 'name' or 'centering' and with values which
                  are any value)
                  covariate dictionary {vector, name, centering}
spm_mat_dir: (a pathlike object or string representing an existing
              directory)
              directory to store SPM.mat file (opt)
covariates: (a list of items which are a dictionary with keys which
             are 'vector' or 'name' or 'interaction' or 'centering' and with
             values which are any value)
             covariate dictionary {vector, name, interaction, centering}
threshold_mask_none: (a boolean)
                     do not use threshold masking
                     mutually_exclusive: threshold_mask_absolute, threshold_mask_relative
threshold_mask_absolute: (a float)
                          use an absolute threshold
                          mutually_exclusive: threshold_mask_none, threshold_mask_relative
threshold_mask_relative: (a float)
                          threshold using a proportion of the global value
                          mutually_exclusive: threshold_mask_absolute, threshold_mask_none
use_implicit_threshold: (a boolean)
                        use implicit mask NaNs or zeros to threshold
explicit_mask_file: (a pathlike object or string representing a file)
                    use an implicit mask file to threshold
global_calc_omit: (a boolean)
                  omit global calculation
                  mutually_exclusive: global_calc_mean, global_calc_values
global_calc_mean: (a boolean)
                  use mean for global calculation
                  mutually_exclusive: global_calc_omit, global_calc_values
global_calc_values: (a list of items which are a float)
                    omit global calculation
                    mutually_exclusive: global_calc_mean, global_calc_omit
no_grand_mean_scaling: (a boolean)
                       do not perform grand mean scaling
global_normalization: (1 or 2 or 3)
                       global normalization None-1, Proportional-2, ANCOVA-3
```

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```

matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
    representing a directory)
    Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```

spm_mat_file: (a pathlike object or string representing an existing
    file)
    SPM mat file

```

References:

None

77.1.6 OneSampleTTestDesign[Link to code](#)

Create SPM design for one sample t-test

Examples

```

>>> ttest = OneSampleTTestDesign()
>>> ttest.inputs.in_files = ['cont1.nii', 'cont2.nii']
>>> ttest.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a list of at least 2 items which are a pathlike object or
    string representing an existing file)
    input files

[Optional]
spm_mat_dir: (a pathlike object or string representing an existing
    directory)
    directory to store SPM.mat file (opt)
covariates: (a list of items which are a dictionary with keys which
    are 'vector' or 'name' or 'interaction' or 'centering' and with
    values which are any value)
    covariate dictionary {vector, name, interaction, centering}
threshold_mask_none: (a boolean)
    do not use threshold masking
    mutually_exclusive: threshold_mask_absolute, threshold_mask_relative
threshold_mask_absolute: (a float)
    use an absolute threshold
    mutually_exclusive: threshold_mask_none, threshold_mask_relative
threshold_mask_relative: (a float)
    threshold using a proportion of the global value

```

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```

        mutually_exclusive: threshold_mask_absolute, threshold_mask_none
use_implicit_threshold: (a boolean)
    use implicit mask NaNs or zeros to threshold
explicit_mask_file: (a pathlike object or string representing a file)
    use an implicit mask file to threshold
global_calc_omit: (a boolean)
    omit global calculation
    mutually_exclusive: global_calc_mean, global_calc_values
global_calc_mean: (a boolean)
    use mean for global calculation
    mutually_exclusive: global_calc_omit, global_calc_values
global_calc_values: (a list of items which are a float)
    omit global calculation
    mutually_exclusive: global_calc_mean, global_calc_omit
no_grand_mean_scaling: (a boolean)
    do not perform grand mean scaling
global_normalization: (1 or 2 or 3)
    global normalization None-1, Proportional-2, ANCOVA-3
matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
    representing a directory)
    Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```

spm_mat_file: (a pathlike object or string representing an existing
    file)
    SPM mat file

```

References:

None

77.1.7 PairedTTestDesign[Link to code](#)

Create SPM design for paired t-test

Examples

```

>>> ptttest = PairedTTestDesign()
>>> ptttest.inputs.paired_files = [['cont1.nii', 'cont1a.nii'], ['cont2.nii', 'cont2a.
↪nii']]
>>> ptttest.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
paired_files: (a list of at least 2 items which are a list of from 2

```

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```

        to 2 items which are a pathlike object or string representing an
        existing file)
    List of paired files

[Optional]
grand_mean_scaling: (a boolean)
    Perform grand mean scaling
ancova: (a boolean)
    Specify ancova-by-factor regressors
spm_mat_dir: (a pathlike object or string representing an existing
    directory)
    directory to store SPM.mat file (opt)
covariates: (a list of items which are a dictionary with keys which
    are 'vector' or 'name' or 'interaction' or 'centering' and with
    values which are any value)
    covariate dictionary {vector, name, interaction, centering}
threshold_mask_none: (a boolean)
    do not use threshold masking
    mutually_exclusive: threshold_mask_absolute, threshold_mask_relative
threshold_mask_absolute: (a float)
    use an absolute threshold
    mutually_exclusive: threshold_mask_none, threshold_mask_relative
threshold_mask_relative: (a float)
    threshold using a proportion of the global value
    mutually_exclusive: threshold_mask_absolute, threshold_mask_none
use_implicit_threshold: (a boolean)
    use implicit mask NaNs or zeros to threshold
explicit_mask_file: (a pathlike object or string representing a file)
    use an implicit mask file to threshold
global_calc_omit: (a boolean)
    omit global calculation
    mutually_exclusive: global_calc_mean, global_calc_values
global_calc_mean: (a boolean)
    use mean for global calculation
    mutually_exclusive: global_calc_omit, global_calc_values
global_calc_values: (a list of items which are a float)
    omit global calculation
    mutually_exclusive: global_calc_mean, global_calc_omit
no_grand_mean_scaling: (a boolean)
    do not perform grand mean scaling
global_normalization: (1 or 2 or 3)
    global normalization None-1, Proportional-2, ANCOVA-3
matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
    representing a directory)
    Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```
spm_mat_file: (a pathlike object or string representing an existing
```

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```
file)
SPM mat file
```

References:

None

77.1.8 Threshold[Link to code](#)

Topological FDR thresholding based on cluster extent/size. Smoothness is estimated from GLM residuals but is assumed to be the same for all of the voxels.

Examples

```
>>> thresh = Threshold()
>>> thresh.inputs.spm_mat_file = 'SPM.mat'
>>> thresh.inputs.stat_image = 'spmT_0001.img'
>>> thresh.inputs.contrast_index = 1
>>> thresh.inputs.extent_fdr_p_threshold = 0.05
>>> thresh.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
spm_mat_file: (a pathlike object or string representing an existing
file)
    absolute path to SPM.mat
stat_image: (a pathlike object or string representing an existing
file)
    stat image
contrast_index: (an integer (int or long))
    which contrast in the SPM.mat to use

[Optional]
use_fwe_correction: (a boolean, nipyne default value: True)
    whether to use FWE (Bonferroni) correction for initial threshold
    (height_threshold_type has to be set to p-value)
use_topo_fdr: (a boolean, nipyne default value: True)
    whether to use FDR over cluster extent probabilities
height_threshold: (a float, nipyne default value: 0.05)
    value for initial thresholding (defining clusters)
height_threshold_type: ('p-value' or 'stat', nipyne default value:
p-value)
    Is the cluster forming threshold a stat value or p-value?
extent_fdr_p_threshold: (a float, nipyne default value: 0.05)
    p threshold on FDR corrected cluster size probabilities
extent_threshold: (an integer (int or long), nipyne default value: 0)
    Minimum cluster size in voxels
force_activation: (a boolean, nipyne default value: False)
    In case no clusters survive the topological inference step this will
    pick a cluster with the highest sum of t-values. Use with care.
matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
```

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```

        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
        Generate SPM8 and higher compatible jobs

```

Outputs:

```

thresholded_map: (a pathlike object or string representing an
                  existing file)
n_clusters: (an integer (int or long))
pre_topo_fdr_map: (a pathlike object or string representing an
                  existing file)
pre_topo_n_clusters: (an integer (int or long))
activation_forced: (a boolean)
cluster_forming_thr: (a float)

```

References:

None

77.1.9 ThresholdStatistics[Link to code](#)

Given height and cluster size threshold calculate theoretical probabilities concerning false positives

Examples

```

>>> thresh = ThresholdStatistics()
>>> thresh.inputs.spm_mat_file = 'SPM.mat'
>>> thresh.inputs.stat_image = 'spmT_0001.img'
>>> thresh.inputs.contrast_index = 1
>>> thresh.inputs.height_threshold = 4.56
>>> thresh.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
spm_mat_file: (a pathlike object or string representing an existing
              file)
              absolute path to SPM.mat
stat_image: (a pathlike object or string representing an existing
            file)
            stat image
contrast_index: (an integer (int or long))
               which contrast in the SPM.mat to use
height_threshold: (a float)
                 stat value for initial thresholding (defining clusters)

[Optional]
extent_threshold: (an integer (int or long), nipy default value: 0)
                 Minimum cluster size in voxels
matlab_cmd: (a unicode string)

```

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```

        matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipyte default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipyte default value: True)
        Generate SPM8 and higher compatible jobs

```

Outputs:

```

voxelwise_P_Bonf: (a float)
voxelwise_P_RF: (a float)
voxelwise_P_uncor: (a float)
voxelwise_P_FDR: (a float)
clusterwise_P_RF: (a float)
clusterwise_P_FDR: (a float)

```

References:

None

77.1.10 TwoSampleTTestDesign[Link to code](#)

Create SPM design for two sample t-test

Examples

```

>>> ttest = TwoSampleTTestDesign()
>>> ttest.inputs.group1_files = ['cont1.nii', 'cont2.nii']
>>> ttest.inputs.group2_files = ['cont1a.nii', 'cont2a.nii']
>>> ttest.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
group1_files: (a list of at least 2 items which are a pathlike object
              or string representing an existing file)
              Group 1 input files
group2_files: (a list of at least 2 items which are a pathlike object
              or string representing an existing file)
              Group 2 input files

[Optional]
dependent: (a boolean)
            Are the measurements dependent between levels
unequal_variance: (a boolean)
                  Are the variances equal or unequal between groups
spm_mat_dir: (a pathlike object or string representing an existing
             directory)
             directory to store SPM.mat file (opt)
covariates: (a list of items which are a dictionary with keys which
            are 'vector' or 'name' or 'interaction' or 'centering' and with

```

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```

        values which are any value)
        covariate dictionary {vector, name, interaction, centering}
threshold_mask_none: (a boolean)
    do not use threshold masking
    mutually_exclusive: threshold_mask_absolute, threshold_mask_relative
threshold_mask_absolute: (a float)
    use an absolute threshold
    mutually_exclusive: threshold_mask_none, threshold_mask_relative
threshold_mask_relative: (a float)
    threshold using a proportion of the global value
    mutually_exclusive: threshold_mask_absolute, threshold_mask_none
use_implicit_threshold: (a boolean)
    use implicit mask NaNs or zeros to threshold
explicit_mask_file: (a pathlike object or string representing a file)
    use an implicit mask file to threshold
global_calc_omit: (a boolean)
    omit global calculation
    mutually_exclusive: global_calc_mean, global_calc_values
global_calc_mean: (a boolean)
    use mean for global calculation
    mutually_exclusive: global_calc_omit, global_calc_values
global_calc_values: (a list of items which are a float)
    omit global calculation
    mutually_exclusive: global_calc_mean, global_calc_omit
no_grand_mean_scaling: (a boolean)
    do not perform grand mean scaling
global_normalization: (1 or 2 or 3)
    global normalization None-1, Proportional-2, ANCOVA-3
matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
    representing a directory)
    Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```

spm_mat_file: (a pathlike object or string representing an existing
    file)
    SPM mat file

```

References:

None

77.2 interfaces.spm.preprocess**77.2.1 ApplyDeformations**[Link to code](#)**Inputs:**

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
           representing an existing file)
deformation_field: (a pathlike object or string representing an
                    existing file)
reference_volume: (a pathlike object or string representing an
                  existing file)

[Optional]
interp: (0 <= a long integer <= 7)
        degree of b-spline used for interpolation
matlab_cmd: (a unicode string)
            matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
              Generate SPM8 and higher compatible jobs
```

Outputs:

```
out_files: (a list of items which are a pathlike object or string
            representing an existing file)
```

References:

None

77.2.2 Coregister[Link to code](#)Use `spm_coreg` for estimating cross-modality rigid body alignment<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=39>**Examples**

```
>>> import nipy.interfaces.spm as spm
>>> coreg = spm.Coregister()
>>> coreg.inputs.target = 'functional.nii'
>>> coreg.inputs.source = 'structural.nii'
>>> coreg.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
target: (a pathlike object or string representing an existing file)
        reference file to register to
source: (a list of items which are a pathlike object or string
        representing an existing file)
        file to register to target

[Optional]
jobtype: ('estwrite' or 'estimate' or 'write', nipy default value:
```

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```

        estwrite)
    one of: estimate, write, estwrite
apply_to_files: (a list of items which are a pathlike object or
    string representing an existing file)
    files to apply transformation to
cost_function: ('mi' or 'nmi' or 'ecc' or 'ncc')
    cost function, one of:
    'mi' - Mutual Information,
    'nmi' - Normalised Mutual Information,
    'ecc' - Entropy Correlation Coefficient,
    'ncc' - Normalised Cross Correlation
fwhm: (a list of from 2 to 2 items which are a float)
    gaussian smoothing kernel width (mm)
separation: (a list of items which are a float)
    sampling separation in mm
tolerance: (a list of items which are a float)
    acceptable tolerance for each of 12 params
write_interp: (0 <= a long integer <= 7)
    degree of b-spline used for interpolation
write_wrap: (a list of from 3 to 3 items which are an integer (int or
    long))
    Check if interpolation should wrap in [x,y,z]
write_mask: (a boolean)
    True/False mask output image
out_prefix: (a string, nipy default value: r)
    coregistered output prefix
matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
    representing a directory)
    Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```

coregistered_source: (a list of items which are a pathlike object or
    string representing an existing file)
    Coregistered source files
coregistered_files: (a list of items which are a pathlike object or
    string representing an existing file)
    Coregistered other files

```

References:

None

77.2.3 CreateWarped[Link to code](#)

Apply a flow field estimated by DARTEL to create warped images

<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=190>

Examples

```
>>> import nipyre.interfaces.spm as spm
>>> create_warped = spm.CreateWarped()
>>> create_warped.inputs.image_files = ['rcls1.nii', 'rcls2.nii']
>>> create_warped.inputs.flowfield_files = ['u_rcls1_Template.nii', 'u_rcls2_
↳Template.nii']
>>> create_warped.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
image_files: (a list of items which are a pathlike object or string
              representing an existing file)
              A list of files to be warped
flowfield_files: (a list of items which are a pathlike object or
                  string representing an existing file)
                  DARTEL flow fields u_rcl*

[Optional]
iterations: (0 <= a long integer <= 9)
              The number of iterations: log2(number of time steps)
interp: (0 <= a long integer <= 7)
          degree of b-spline used for interpolation
modulate: (a boolean)
            Modulate images
matlab_cmd: (a unicode string)
             matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipyre default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
          Run m-code using SPM MCR
use_v8struct: (a boolean, nipyre default value: True)
               Generate SPM8 and higher compatible jobs
```

Outputs:

```
warped_files: (a list of items which are a pathlike object or string
               representing an existing file)
```

References:

None

77.2.4 DARTEL

[Link to code](#)

Use spm DARTEL to create a template and flow fields

<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=185>

Examples

```
>>> import nipyre.interfaces.spm as spm
>>> dartel = spm.DARTEL()
```

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```
>>> dartel.inputs.image_files = [['rc1s1.nii', 'rc1s2.nii'], ['rc2s1.nii', 'rc2s2.
↪nii']]
>>> dartel.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
image_files: (a list of items which are a list of items which are a
              pathlike object or string representing an existing file)
              A list of files to be segmented

[Optional]
template_prefix: (a unicode string, nipy default value: Template)
                 Prefix for template
regularization_form: ('Linear' or 'Membrane' or 'Bending')
                     Form of regularization energy term
iteration_parameters: (a list of from 3 to 12 items which are a tuple
                      of the form: (1 <= a long integer <= 10, a tuple of the form: (a
                      float, a float, a float), 1 or 2 or 4 or 8 or 16 or 32 or 64 or
                      128 or 256 or 512, 0 or 0.5 or 1 or 2 or 4 or 8 or 16 or 32))
                      List of tuples for each iteration
                      - Inner iterations
                      - Regularization parameters
                      - Time points for deformation model
                      - smoothing parameter
optimization_parameters: (a tuple of the form: (a float, 1 <= a long
                      integer <= 8, 1 <= a long integer <= 8))
                      Optimization settings a tuple
                      - LM regularization
                      - cycles of multigrid solver
                      - relaxation iterations
matlab_cmd: (a unicode string)
             matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
          Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
               Generate SPM8 and higher compatible jobs
```

Outputs:

```
final_template_file: (a pathlike object or string representing an
                     existing file)
                     final DARTEL template
template_files: (a list of items which are a pathlike object or
                 string representing an existing file)
                 Templates from different stages of iteration
dartel_flow_fields: (a list of items which are a pathlike object or
                    string representing an existing file)
                    DARTEL flow fields
```

References:

None

77.2.5 DARTELNorm2MNI

[Link to code](#)

Use `spm` DARTEL to normalize data to MNI space

<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=188>

Examples

```
>>> import nipy.interfaces.spm as spm
>>> nm = spm.DARTELNorm2MNI()
>>> nm.inputs.template_file = 'Template_6.nii'
>>> nm.inputs.flowfield_files = ['u_rcls1_Template.nii', 'u_rcls3_Template.nii']
>>> nm.inputs.apply_to_files = ['cls1.nii', 'cls3.nii']
>>> nm.inputs.modulate = True
>>> nm.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
template_file: (a pathlike object or string representing an existing
               file)
               DARTEL template
flowfield_files: (a list of items which are a pathlike object or
                 string representing an existing file)
                 DARTEL flow fields u_rcl*
apply_to_files: (a list of items which are a pathlike object or
                string representing an existing file)
                Files to apply the transform to

[Optional]
voxel_size: (a tuple of the form: (a float, a float, a float))
            Voxel sizes for output file
bounding_box: (a tuple of the form: (a float, a float, a float, a
                                     float, a float, a float))
              Voxel sizes for output file
modulate: (a boolean)
           Modulate out images - no modulation preserves concentrations
fwhm: (a list of from 3 to 3 items which are a float or a float)
      3-list of fwhm for each dimension
matlab_cmd: (a unicode string)
            matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
          Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
              Generate SPM8 and higher compatible jobs
```

Outputs:

```
normalized_files: (a list of items which are a pathlike object or
                  string representing an existing file)
                  Normalized files in MNI space
normalization_parameter_file: (a pathlike object or string
                              representing an existing file)
                              Transform parameters to MNI space
```

References:

None

77.2.6 FieldMap

[Link to code](#)

Use the fieldmap toolbox from spm to calculate the voxel displacement map (VDM).

<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=173>

To do

Deal with real/imag magnitude images and with the two phase files case.

Examples

```
>>> from nipyype.interfaces.spm import FieldMap
>>> fm = FieldMap()
>>> fm.inputs.phase_file = 'phase.nii'
>>> fm.inputs.magnitude_file = 'magnitude.nii'
>>> fm.inputs.echo_times = (5.19, 7.65)
>>> fm.inputs.blip_direction = 1
>>> fm.inputs.total_readout_time = 15.6
>>> fm.inputs.epi_file = 'epi.nii'
>>> fm.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
phase_file: (a pathlike object or string representing an existing
            file)
            presubtracted phase file
magnitude_file: (a pathlike object or string representing an existing
                file)
                presubtracted magnitude file
echo_times: (a tuple of the form: (a float, a float))
            short and long echo times
blip_direction: (1 or -1)
               polarity of the phase-encode blips
total_readout_time: (a float)
                   total EPI readout time
epi_file: (a pathlike object or string representing an existing file)
          EPI to unwarp

[Optional]
jobtype: ('calculatevdm' or 'applyvdm', nipyype default value:
         calculatevdm)
         one of: calculatevdm, applyvdm
maskbrain: (a boolean, nipyype default value: True)
           masking or no masking of the brain
epifm: (a boolean, nipyype default value: False)
       epi-based field map
jacobian_modulation: (a boolean, nipyype default value: False)
                    jacobian modulation
method: ('Mark3D' or 'Mark2D' or 'Huttonish', nipyype default value:
        Mark3D)
        One of: Mark3D, Mark2D, Huttonish
unwarp_fwhm: (a long integer >= 0, nipyype default value: 10)
```

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```

        gaussian smoothing kernel width
pad: (a long integer >= 0, nipy default value: 0)
    padding kernel width
ws: (a boolean, nipy default value: True)
    weighted smoothing
template: (a pathlike object or string representing an existing file)
    template image for brain masking
mask_fwhm: (a long integer >= 0, nipy default value: 5)
    gaussian smoothing kernel width
nerode: (a long integer >= 0, nipy default value: 2)
    number of erosions
ndilate: (a long integer >= 0, nipy default value: 4)
    number of erosions
thresh: (a float, nipy default value: 0.5)
    threshold used to create brain mask from segmented data
reg: (a float, nipy default value: 0.02)
    regularization value used in the segmentation
matchvdm: (a boolean, nipy default value: True)
    match VDM to EPI
sessname: (a unicode string, nipy default value: _run-)
    VDM filename extension
writeunwarped: (a boolean, nipy default value: False)
    write unwarped EPI
anat_file: (a pathlike object or string representing an existing
    file)
    anatomical image for comparison
matchanat: (a boolean, nipy default value: True)
    match anatomical image to EPI
matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
    representing a directory)
    Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```

vdm: (a pathlike object or string representing an existing file)
    voxel difference map

```

References:

None

77.2.7 NewSegment[Link to code](#)

Use `spm_preproc8` (New Segment) to separate structural images into different tissue classes. Supports multiple modalities.

NOTE: This interface currently supports single channel input only

<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=43>

Examples

```
>>> import nipy.interfaces.spm as spm
>>> seg = spm.NewSegment()
>>> seg.inputs.channel_files = 'structural.nii'
>>> seg.inputs.channel_info = (0.0001, 60, (True, True))
>>> seg.run() # doctest: +SKIP
```

For VBM pre-processing [<http://www.fil.ion.ucl.ac.uk/~john/misc/VBMclass10.pdf>], TPM.nii should be replaced by /path/to/spm8/toolbox/Seg/TPM.nii

```
>>> seg = NewSegment()
>>> seg.inputs.channel_files = 'structural.nii'
>>> tissue1 = (('TPM.nii', 1), 2, (True, True), (False, False))
>>> tissue2 = (('TPM.nii', 2), 2, (True, True), (False, False))
>>> tissue3 = (('TPM.nii', 3), 2, (True, False), (False, False))
>>> tissue4 = (('TPM.nii', 4), 2, (False, False), (False, False))
>>> tissue5 = (('TPM.nii', 5), 2, (False, False), (False, False))
>>> seg.inputs.tissues = [tissue1, tissue2, tissue3, tissue4, tissue5]
>>> seg.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
channel_files: (a list of items which are a pathlike object or string
               representing an existing file)
               A list of files to be segmented

[Optional]
channel_info: (a tuple of the form: (a float, a float, a tuple of the
               form: (a boolean, a boolean)))
               A tuple with the following fields:
               - bias regularisation (0-10)
               - FWHM of Gaussian smoothness of bias
               - which maps to save (Field, Corrected) - a tuple of two boolean
                 values
tissues: (a list of items which are a tuple of the form: (a tuple of
               the form: (a pathlike object or string representing an existing
               file, an integer (int or long)), an integer (int or long), a tuple
               of the form: (a boolean, a boolean), a tuple of the form: (a
               boolean, a boolean)))
               A list of tuples (one per tissue) with the following fields:
               - tissue probability map (4D), 1-based index to frame
               - number of gaussians
               - which maps to save [Native, DARTEL] - a tuple of two boolean
                 values
               - which maps to save [Unmodulated, Modulated] - a tuple of two
                 boolean values
affine_regularization: ('mni' or 'eastern' or 'subj' or 'none')
                       mni, eastern, subj, none
warping_regularization: (a list of from 5 to 5 items which are a
                        float or a float)
                        Warping regularization parameter(s). Accepts float or list of floats
                        (the latter is required by SPM12)
sampling_distance: (a float)
                   Sampling distance on data for parameter estimation
write_deformation_fields: (a list of from 2 to 2 items which are a
                          boolean)
```

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```

        Which deformation fields to write:[Inverse, Forward]
matlab_cmd: (a unicode string)
            matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
        Generate SPM8 and higher compatible jobs

```

Outputs:

```

native_class_images: (a list of items which are a list of items which
                    are a pathlike object or string representing an existing file)
                    native space probability maps
dartel_input_images: (a list of items which are a list of items which
                    are a pathlike object or string representing an existing file)
                    dartel imported class images
normalized_class_images: (a list of items which are a list of items
                        which are a pathlike object or string representing an existing
                        file)
                        normalized class images
modulated_class_images: (a list of items which are a list of items
                        which are a pathlike object or string representing an existing
                        file)
                        modulated+normalized class images
transformation_mat: (a list of items which are a pathlike object or
                    string representing an existing file)
                    Normalization transformation
bias_corrected_images: (a list of items which are a pathlike object
                        or string representing an existing file)
                        bias corrected images
bias_field_images: (a list of items which are a pathlike object or
                    string representing an existing file)
                    bias field images
forward_deformation_field: (a list of items which are a pathlike
                            object or string representing an existing file)
inverse_deformation_field: (a list of items which are a pathlike
                            object or string representing an existing file)

```

References:

None

77.2.8 Normalize[Link to code](#)use `spm_normalise` for warping an image to a template<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=203>

Examples

```
>>> import nipy.interfaces.spm as spm
>>> norm = spm.Normalize()
>>> norm.inputs.source = 'functional.nii'
>>> norm.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
template: (a pathlike object or string representing an existing file)
    template file to normalize to
    mutually_exclusive: parameter_file
source: (a list of items which are a pathlike object or string
    representing an existing file)
    file to normalize to template
    mutually_exclusive: parameter_file
parameter_file: (a pathlike object or string representing a file)
    normalization parameter file*_sn.mat
    mutually_exclusive: source, template

[Optional]
jobtype: ('estwrite' or 'est' or 'write', nipy default value:
    estwrite)
    Estimate, Write or do both
apply_to_files: (a list of items which are a pathlike object or
    string representing an existing file or a list of items which are
    a pathlike object or string representing an existing file)
    files to apply transformation to
source_weight: (a pathlike object or string representing a file)
    name of weighting image for source
template_weight: (a pathlike object or string representing a file)
    name of weighting image for template
source_image_smoothing: (a float)
    source smoothing
template_image_smoothing: (a float)
    template smoothing
affine_regularization_type: ('mni' or 'size' or 'none')
    mni, size, none
DCT_period_cutoff: (a float)
    Cutoff of for DCT bases
nonlinear_iterations: (an integer (int or long))
    Number of iterations of nonlinear warping
nonlinear_regularization: (a float)
    the amount of the regularization for the nonlinear part of the
    normalization
write_preserve: (a boolean)
    True/False warped images are modulated
write_bounding_box: (a list of from 2 to 2 items which are a list of
    from 3 to 3 items which are a float)
    3x2-element list of lists
write_voxel_sizes: (a list of from 3 to 3 items which are a float)
    3-element list
write_interp: (0 <= a long integer <= 7)
    degree of b-spline used for interpolation
write_wrap: (a list of items which are an integer (int or long))
    Check if interpolation should wrap in [x,y,z] - list of bools
out_prefix: (a string, nipy default value: w)
```

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```

        normalized output prefix
matlab_cmd: (a unicode string)
            matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
        Generate SPM8 and higher compatible jobs

```

Outputs:

```

normalization_parameters: (a list of items which are a pathlike
                           object or string representing an existing file)
                           MAT files containing the normalization parameters
normalized_source: (a list of items which are a pathlike object or
                   string representing an existing file)
                   Normalized source files
normalized_files: (a list of items which are a pathlike object or
                  string representing an existing file)
                  Normalized other files

```

References:

None

77.2.9 Normalize12**Link to code**

uses SPM12's new Normalise routine for warping an image to a template. Spatial normalisation is now done via the segmentation routine (which was known as New Segment in SPM8). Note that the normalisation in SPM12 is done towards a file containing multiple tissue probability maps, which was not the case in SPM8. <http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=49>

Examples

```

>>> import nipy.interfaces.spm as spm
>>> norm12 = spm.Normalize12()
>>> norm12.inputs.image_to_align = 'structural.nii'
>>> norm12.inputs.apply_to_files = 'functional.nii'
>>> norm12.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
image_to_align: (a pathlike object or string representing an existing
                file)
                file to estimate normalization parameters with
                mutually_exclusive: deformation_file
deformation_file: (a pathlike object or string representing a file)
                  file y_*.nii containing 3 deformation fields for the deformation in
                  x, y and z dimension
                  mutually_exclusive: image_to_align, tpm

```

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```

[Optional]
apply_to_files: (a list of items which are a pathlike object or
                 string representing an existing file or a list of items which are
                 a pathlike object or string representing an existing file)
                 files to apply transformation to
jobtype: ('estwrite' or 'est' or 'write', nipy default value:
          estwrite)
          Estimate, Write or do Both
bias_regularization: (0 or 1e-05 or 0.0001 or 0.001 or 0.01 or 0.1 or
                      1 or 10)
                      no(0) - extremely heavy (10)
bias_fwhm: (30 or 40 or 50 or 60 or 70 or 80 or 90 or 100 or 110 or
            120 or 130 or 140 or 150 or 'Inf')
            FWHM of Gaussian smoothness of bias
tpm: (a pathlike object or string representing an existing file)
      template in form of tissue probability maps to normalize to
      mutually_exclusive: deformation_file
affine_regularization_type: ('mni' or 'size' or 'none')
                             mni, size, none
warping_regularization: (a list of from 5 to 5 items which are a
                         float)
                         controls balance between parameters and data
smoothness: (a float)
              value (in mm) to smooth the data before normalization
sampling_distance: (a float)
                   Sampling distance on data for parameter estimation
write_bounding_box: (a list of from 2 to 2 items which are a list of
                    from 3 to 3 items which are a float)
                    3x2-element list of lists representing the bounding box (in mm) to
                    be written
write_voxel_sizes: (a list of from 3 to 3 items which are a float)
                   3-element list representing the voxel sizes (in mm) of the written
                   normalised images
write_interp: (0 <= a long integer <= 7)
              degree of b-spline used for interpolation
out_prefix: (a string, nipy default value: w)
            Normalized output prefix
matlab_cmd: (a unicode string)
            matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
          Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
              Generate SPM8 and higher compatible jobs

```

Outputs:

```

deformation_field: (a list of items which are a pathlike object or
                   string representing an existing file)
                   NIfTI file containing 3 deformation fields for the deformation in x,
                   y and z dimension
normalized_image: (a list of items which are a pathlike object or

```

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```

        string representing an existing file)
        Normalized file that needed to be aligned
normalized_files: (a list of items which are a pathlike object or
        string representing an existing file)
        Normalized other files

```

References:

None

77.2.10 Realign[Link to code](#)Use `spm_realign` for estimating within modality rigid body alignment<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=25>**Examples**

```

>>> import nipy.interfaces.spm as spm
>>> realign = spm.Realign()
>>> realign.inputs.in_files = 'functional.nii'
>>> realign.inputs.register_to_mean = True
>>> realign.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string
        representing an existing file or a list of items which are a
        pathlike object or string representing an existing file)
        list of filenames to realign

[Optional]
jobtype: ('estwrite' or 'estimate' or 'write', nipy default value:
        estwrite)
        one of: estimate, write, estwrite
quality: (0.0 <= a floating point number <= 1.0)
        0.1 = fast, 1.0 = precise
fwhm: (a floating point number >= 0.0)
        gaussian smoothing kernel width
separation: (a floating point number >= 0.0)
        sampling separation in mm
register_to_mean: (a boolean)
        Indicate whether realignment is done to the mean image
weight_img: (a pathlike object or string representing an existing
        file)
        filename of weighting image
interp: (0 <= a long integer <= 7)
        degree of b-spline used for interpolation
wrap: (a list of from 3 to 3 items which are an integer (int or
        long))
        Check if interpolation should wrap in [x,y,z]
write_which: (a list of items which are a value of class 'int',
        nipy default value: [2, 1])
        determines which images to reslice

```

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```

write_interp: (0 <= a long integer <= 7)
    degree of b-spline used for interpolation
write_wrap: (a list of from 3 to 3 items which are an integer (int or
    long))
    Check if interpolation should wrap in [x,y,z]
write_mask: (a boolean)
    True/False mask output image
out_prefix: (a string, nipy default value: r)
    realigned output prefix
matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
    representing a directory)
    Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```

mean_image: (a pathlike object or string representing an existing
    file)
    Mean image file from the realignment
modified_in_files: (a list of items which are a list of items which
    are a pathlike object or string representing an existing file or a
    pathlike object or string representing an existing file)
    Copies of all files passed to in_files. Headers will have been
    modified to align all images with the first, or optionally to first
    do that, extract a mean image, and re-align to that mean image.
realigned_files: (a list of items which are a list of items which are
    a pathlike object or string representing an existing file or a
    pathlike object or string representing an existing file)
    If jobtype is write or estwrite, these will be the resliced files.
    Otherwise, they will be copies of in_files that have had their
    headers rewritten.
realignment_parameters: (a list of items which are a pathlike object
    or string representing an existing file)
    Estimated translation and rotation parameters

```

References:

None

77.2.11 RealignUnwarp**Link to code**

Use `spm_uw_estimate` for estimating within subject registration and unwarping of time series. Function accepts only one single field map. If `in_files` is a list of files they will be treated as separate sessions but associated to the same fieldmap.

<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=31>

Examples

```
>>> import nipy.interfaces.spm as spm
>>> realignUnwarp = spm.RealignUnwarp()
>>> realignUnwarp.inputs.in_files = ['functional.nii', 'functional2.nii']
>>> realignUnwarp.inputs.phase_map = 'voxeldisplacemap.vdm'
>>> realignUnwarp.inputs.register_to_mean = True
>>> realignUnwarp.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
           representing an existing file or a list of items which are a
           pathlike object or string representing an existing file)
           list of filenames to realign and unwarp

[Optional]
phase_map: (a pathlike object or string representing a file)
            Voxel displacement map to use in unwarping. Unlike SPM standard
            behaviour, the same map will be used for all sessions
quality: (0.0 <= a floating point number <= 1.0)
          0.1 = fast, 1.0 = precise
fwhm: (a floating point number >= 0.0)
       gaussian smoothing kernel width
separation: (a floating point number >= 0.0)
             sampling separation in mm
register_to_mean: (a boolean)
                  Indicate whether realignment is done to the mean image
weight_img: (a pathlike object or string representing an existing
             file)
             filename of weighting image
interp: (0 <= a long integer <= 7)
         degree of b-spline used for interpolation
wrap: (a list of from 3 to 3 items which are an integer (int or
       long))
       Check if interpolation should wrap in [x,y,z]
est_basis_func: (a list of from 2 to 2 items which are an integer
                 (int or long))
                 Number of basis functions to use for each dimension
est_reg_order: (0 <= a long integer <= 3)
                This parameter determines how to balance the compromise between
                likelihood maximization and smoothness maximization of the estimated
                field.
est_reg_factor: (a list of items which are a value of class 'int',
                 nipy default value: [100000])
                 Regularisation factor. Default: 100000 (medium).
est_jacobian_deformations: (a boolean)
                            Jacobian deformations. In theory a good idea to include them, in
                            practice a bad idea. Default: No.
est_first_order_effects: (a list of from 1 to 6 items which are an
                           integer (int or long))
                           First order effects should only depend on pitch and roll, i.e. [4 5]
est_second_order_effects: (a list of from 1 to 6 items which are an
                            integer (int or long))
                            List of second order terms to model second derivatives of.
est_unwarp_fwhm: (a floating point number >= 0.0)
                  gaussian smoothing kernel width for unwarp
```

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```

est_re_est_mov_par: (a boolean)
    Re-estimate movement parameters at each unwarping iteration.
est_num_of_iterations: (a list of items which are a value of class
    'int', nipyne default value: [5])
    Number of iterations.
est_taylor_expansion_point: (a string, nipyne default value: Average)
    Point in position space to perform Taylor-expansion around.
reslice_which: (a list of items which are a value of class 'int',
    nipyne default value: [2, 1])
    determines which images to reslice
reslice_interp: (0 <= a long integer <= 7)
    degree of b-spline used for interpolation
reslice_wrap: (a list of from 3 to 3 items which are an integer (int
    or long))
    Check if interpolation should wrap in [x,y,z]
reslice_mask: (a boolean)
    True/False mask output image
out_prefix: (a string, nipyne default value: u)
    realigned and unwrapped output prefix
matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
    representing a directory)
    Paths to add to matlabpath
mfile: (a boolean, nipyne default value: True)
    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipyne default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```

mean_image: (a pathlike object or string representing an existing
    file)
    Mean image file from the realignment & unwarping
modified_in_files: (a list of items which are a list of items which
    are a pathlike object or string representing an existing file or a
    pathlike object or string representing an existing file)
    Copies of all files passed to in_files. Headers will have been
    modified to align all images with the first, or optionally to first
    do that, extract a mean image, and re-align to that mean image.
realigned_unwarped_files: (a list of items which are a list of items
    which are a pathlike object or string representing an existing
    file or a pathlike object or string representing an existing file)
    Realigned and unwrapped files written to disc.
realignment_parameters: (a list of items which are a pathlike object
    or string representing an existing file)
    Estimated translation and rotation parameters

```

References:

None

77.2.12 Segment[Link to code](#)

use `spm_segment` to separate structural images into different tissue classes.
<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=209>

Examples

```
>>> import nipy.interfaces.spm as spm
>>> seg = spm.Segment()
>>> seg.inputs.data = 'structural.nii'
>>> seg.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
data: (a list of items which are a pathlike object or string
      representing an existing file)
      one scan per subject

[Optional]
gm_output_type: (a list of from 3 to 3 items which are a boolean)
Options to produce grey matter images: c1*.img, wcl*.img and
mwc1*.img.
None: [False, False, False],
Native Space: [False, False, True],
Unmodulated Normalised: [False, True, False],
Modulated Normalised: [True, False, False],
Native + Unmodulated Normalised: [False, True, True],
Native + Modulated Normalised: [True, False, True],
Native + Modulated + Unmodulated: [True, True, True],
Modulated + Unmodulated Normalised: [True, True, False]
wm_output_type: (a list of from 3 to 3 items which are a boolean)
Options to produce white matter images: c2*.img, wc2*.img and
mwc2*.img.
None: [False, False, False],
Native Space: [False, False, True],
Unmodulated Normalised: [False, True, False],
Modulated Normalised: [True, False, False],
Native + Unmodulated Normalised: [False, True, True],
Native + Modulated Normalised: [True, False, True],
Native + Modulated + Unmodulated: [True, True, True],
Modulated + Unmodulated Normalised: [True, True, False]
csf_output_type: (a list of from 3 to 3 items which are a boolean)
Options to produce CSF images: c3*.img, wc3*.img and mwc3*.img.
None: [False, False, False],
Native Space: [False, False, True],
Unmodulated Normalised: [False, True, False],
Modulated Normalised: [True, False, False],
Native + Unmodulated Normalised: [False, True, True],
Native + Modulated Normalised: [True, False, True],
Native + Modulated + Unmodulated: [True, True, True],
Modulated + Unmodulated Normalised: [True, True, False]
save_bias_corrected: (a boolean)
True/False produce a bias corrected image
clean_masks: ('no' or 'light' or 'thorough')
clean using estimated brain mask ('no', 'light', 'thorough')
tissue_prob_maps: (a list of items which are a pathlike object or
string representing an existing file)
list of gray, white & csf prob. (opt,)
gaussians_per_class: (a list of items which are an integer (int or
```

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```

        long))
        num Gaussians capture intensity distribution
    affine_regularization: ('mni' or 'eastern' or 'subj' or 'none' or '')
        Possible options: "mni", "eastern", "subj", "none" (no
        regularisation), "" (no affine registration)
    warping_regularization: (a float)
        Controls balance between parameters and data
    warp_frequency_cutoff: (a float)
        Cutoff of DCT bases
    bias_regularization: (0 or 1e-05 or 0.0001 or 0.001 or 0.01 or 0.1 or
        1 or 10)
        no(0) - extremely heavy (10)
    bias_fwhm: (30 or 40 or 50 or 60 or 70 or 80 or 90 or 100 or 110 or
        120 or 130 or 'Inf')
        FWHM of Gaussian smoothness of bias
    sampling_distance: (a float)
        Sampling distance on data for parameter estimation
    mask_image: (a pathlike object or string representing an existing
        file)
        Binary image to restrict parameter estimation
    matlab_cmd: (a unicode string)
        matlab command to use
    paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
    mfile: (a boolean, nipy default value: True)
        Run m-code using m-file
    use_mcr: (a boolean)
        Run m-code using SPM MCR
    use_v8struct: (a boolean, nipy default value: True)
        Generate SPM8 and higher compatible jobs

```

Outputs:

```

native_gm_image: (a pathlike object or string representing a file)
    native space grey probability map
normalized_gm_image: (a pathlike object or string representing a
    file)
    normalized grey probability map
modulated_gm_image: (a pathlike object or string representing a file)
    modulated, normalized grey probability map
native_wm_image: (a pathlike object or string representing a file)
    native space white probability map
normalized_wm_image: (a pathlike object or string representing a
    file)
    normalized white probability map
modulated_wm_image: (a pathlike object or string representing a file)
    modulated, normalized white probability map
native_csf_image: (a pathlike object or string representing a file)
    native space csf probability map
normalized_csf_image: (a pathlike object or string representing a
    file)
    normalized csf probability map
modulated_csf_image: (a pathlike object or string representing a
    file)
    modulated, normalized csf probability map
modulated_input_image: (a pathlike object or string representing a

```

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```

        file)
        bias-corrected version of input image
bias_corrected_image: (a pathlike object or string representing a
        file)
        bias-corrected version of input image
transformation_mat: (a pathlike object or string representing an
        existing file)
        Normalization transformation
inverse_transformation_mat: (a pathlike object or string representing
        an existing file)
        Inverse normalization info

```

References:

None

77.2.13 SliceTiming[Link to code](#)Use `spm` to perform slice timing correction.<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=19>**Examples**

```

>>> from nipy.interfaces.spm import SliceTiming
>>> st = SliceTiming()
>>> st.inputs.in_files = 'functional.nii'
>>> st.inputs.num_slices = 32
>>> st.inputs.time_repetition = 6.0
>>> st.inputs.time_acquisition = 6. - 6./32.
>>> st.inputs.slice_order = list(range(32,0,-1))
>>> st.inputs.ref_slice = 1
>>> st.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a list of items which are a
        pathlike object or string representing an existing file or a
        pathlike object or string representing an existing file)
        list of filenames to apply slice timing
num_slices: (an integer (int or long))
        number of slices in a volume
time_repetition: (a float)
        time between volume acquisitions(start to start time)
time_acquisition: (a float)
        time of volume acquisition. usuallycalculated as TR-(TR/num_slices)
slice_order: (a list of items which are a float)
        1-based order or onset (in ms) in which slices are acquired
ref_slice: (an integer (int or long))
        1-based Number of the reference slice or reference time point if
        slice_order is in onsets (ms)

[Optional]
out_prefix: (a string, nipy default value: a)

```

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```

    slicetimed output prefix
matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
    representing a directory)
    Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```

timecorrected_files: (a list of items which are a list of items which
    are a pathlike object or string representing an existing file or a
    pathlike object or string representing an existing file)
    slice time corrected files

```

References:

None

77.2.14 Smooth[Link to code](#)Use `spm_smooth` for 3D Gaussian smoothing of image volumes.<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=55>**Examples**

```

>>> import nipy.interfaces.spm as spm
>>> smooth = spm.Smooth()
>>> smooth.inputs.in_files = 'functional.nii'
>>> smooth.inputs.fwhm = [4, 4, 4]
>>> smooth.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string
    representing an existing file)
    list of files to smooth

[Optional]
fwhm: (a list of from 3 to 3 items which are a float or a float)
    3-list of fwhm for each dimension
data_type: (an integer (int or long))
    Data type of the output images
implicit_masking: (a boolean)
    A mask implied by a particular voxel value
out_prefix: (a string, nipy default value: s)
    smoothed output prefix
matlab_cmd: (a unicode string)
    matlab command to use

```

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```

paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipyne default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipyne default value: True)
        Generate SPM8 and higher compatible jobs

```

Outputs:

```

smoothed_files: (a list of items which are a pathlike object or
                 string representing an existing file)
                 smoothed files

```

References:

None

77.2.15 VBMSegment[Link to code](#)

Use VBM8 toolbox to separate structural images into different tissue classes.

Example

```

>>> import nipyne.interfaces.spm as spm
>>> seg = spm.VBMSegment()
>>> seg.inputs.tissues = 'TPM.nii'
>>> seg.inputs.dartel_template = 'Template_1_IXI550_MNI152.nii'
>>> seg.inputs.bias_corrected_native = True
>>> seg.inputs.gm_native = True
>>> seg.inputs.wm_native = True
>>> seg.inputs.csf_native = True
>>> seg.inputs.pve_label_native = True
>>> seg.inputs.deformation_field = (True, False)
>>> seg.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string
           representing an existing file)
           A list of files to be segmented

[Optional]
tissues: (a pathlike object or string representing an existing file)
          tissue probability map
gaussians_per_class: (a tuple of the form: (an integer (int or long),
          an integer (int or long), an integer (int or long), an integer
          (int or long), an integer (int or long), an integer (int or
          long)), nipyne default value: (2, 2, 2, 3, 4, 2))
          number of gaussians for each tissue class
bias_regularization: (0 or 1e-05 or 0.0001 or 0.001 or 0.01 or 0.1 or
          1 or 10, nipyne default value: 0.0001)

```

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```

no(0) - extremely heavy (10)
bias_fwhm: (30 or 40 or 50 or 60 or 70 or 80 or 90 or 100 or 110 or
120 or 130 or 'Inf', nipy default value: 60)
FWHM of Gaussian smoothness of bias
sampling_distance: (a float, nipy default value: 3)
Sampling distance on data for parameter estimation
warping_regularization: (a float, nipy default value: 4)
Controls balance between parameters and data
spatial_normalization: ('high' or 'low', nipy default value: high)
dartel_template: (a pathlike object or string representing an
existing file)
use_sanlm_denoising_filter: (0 <= a long integer <= 2, nipy default
value: 2)
0=No denoising, 1=denoising, 2=denoising multi-threaded
mrf_weighting: (a float, nipy default value: 0.15)
cleanup_partitions: (an integer (int or long), nipy default value:
1)
0=None, 1=light, 2=thorough
display_results: (a boolean, nipy default value: True)
gm_native: (a boolean, nipy default value: False)
gm_normalized: (a boolean, nipy default value: False)
gm_modulated_normalized: (0 <= a long integer <= 2, nipy default
value: 2)
0=none, 1=affine+non-linear(SPM8 default), 2=non-linear only
gm_dartel: (0 <= a long integer <= 2, nipy default value: 0)
0=None, 1=rigid(SPM8 default), 2=affine
wm_native: (a boolean, nipy default value: False)
wm_normalized: (a boolean, nipy default value: False)
wm_modulated_normalized: (0 <= a long integer <= 2, nipy default
value: 2)
0=none, 1=affine+non-linear(SPM8 default), 2=non-linear only
wm_dartel: (0 <= a long integer <= 2, nipy default value: 0)
0=None, 1=rigid(SPM8 default), 2=affine
csf_native: (a boolean, nipy default value: False)
csf_normalized: (a boolean, nipy default value: False)
csf_modulated_normalized: (0 <= a long integer <= 2, nipy default
value: 2)
0=none, 1=affine+non-linear(SPM8 default), 2=non-linear only
csf_dartel: (0 <= a long integer <= 2, nipy default value: 0)
0=None, 1=rigid(SPM8 default), 2=affine
bias_corrected_native: (a boolean, nipy default value: False)
bias_corrected_normalized: (a boolean, nipy default value: True)
bias_corrected_affine: (a boolean, nipy default value: False)
pve_label_native: (a boolean, nipy default value: False)
pve_label_normalized: (a boolean, nipy default value: False)
pve_label_dartel: (0 <= a long integer <= 2, nipy default value: 0)
0=None, 1=rigid(SPM8 default), 2=affine
jacobian_determinant: (a boolean, nipy default value: False)
deformation_field: (a tuple of the form: (a boolean, a boolean),
nipy default value: (0, 0))
forward and inverse field
matlab_cmd: (a unicode string)
matlab command to use
paths: (a list of items which are a pathlike object or string
representing a directory)
Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)

```

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```

    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```

native_class_images: (a list of items which are a list of items which
    are a pathlike object or string representing an existing file)
    native space probability maps
dartel_input_images: (a list of items which are a list of items which
    are a pathlike object or string representing an existing file)
    dartel imported class images
normalized_class_images: (a list of items which are a list of items
    which are a pathlike object or string representing an existing
    file)
    normalized class images
modulated_class_images: (a list of items which are a list of items
    which are a pathlike object or string representing an existing
    file)
    modulated+normalized class images
transformation_mat: (a list of items which are a pathlike object or
    string representing an existing file)
    Normalization transformation
bias_corrected_images: (a list of items which are a pathlike object
    or string representing an existing file)
    bias corrected images
normalized_bias_corrected_images: (a list of items which are a
    pathlike object or string representing an existing file)
    bias corrected images
pve_label_native_images: (a list of items which are a pathlike object
    or string representing an existing file)
pve_label_normalized_images: (a list of items which are a pathlike
    object or string representing an existing file)
pve_label_registered_images: (a list of items which are a pathlike
    object or string representing an existing file)
forward_deformation_field: (a list of items which are a pathlike
    object or string representing an existing file)
inverse_deformation_field: (a list of items which are a pathlike
    object or string representing an existing file)
jacobian_determinant_images: (a list of items which are a pathlike
    object or string representing an existing file)

```

References:

None

77.3 interfaces.spm.utils**77.3.1 Analyze2nii**[Link to code](#)

Inputs:

```
[Mandatory]
analyze_file: (a pathlike object or string representing an existing
              file)

[Optional]
matlab_cmd: (a unicode string)
            matlab command to use
paths: (a list of items which are a pathlike object or string
       representing a directory)
       Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
       Run m-code using m-file
use_mcr: (a boolean)
         Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
              Generate SPM8 and higher compatible jobs
```

Outputs:

```
nifti_file: (a pathlike object or string representing an existing
            file)
matlab_cmd: (a unicode string)
            matlab command to use
paths: (a list of items which are a pathlike object or string
       representing a directory)
       Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
       Run m-code using m-file
use_mcr: (a boolean)
         Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
              Generate SPM8 and higher compatible jobs
```

References:

None

77.3.2 ApplyInverseDeformation[Link to code](#)

Uses spm to apply inverse deformation stored in a .mat file or a deformation field to a given file

Examples

```
>>> import nipy.interfaces.spm.utils as spmu
>>> inv = spmu.ApplyInverseDeformation()
>>> inv.inputs.in_files = 'functional.nii'
>>> inv.inputs.deformation = 'struct_to_func.mat'
>>> inv.inputs.target = 'structural.nii'
>>> inv.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a pathlike object or string
          representing an existing file)
          Files on which deformation is applied
```

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```

[Optional]
target: (a pathlike object or string representing an existing file)
        File defining target space
deformation: (a pathlike object or string representing an existing
              file)
              SN SPM deformation file
              mutually_exclusive: deformation_field
deformation_field: (a pathlike object or string representing an
                   existing file)
                   SN SPM deformation file
                   mutually_exclusive: deformation
interpolation: (0 <= a long integer <= 7)
               degree of b-spline used for interpolation
bounding_box: (a list of from 6 to 6 items which are a float)
              6-element list (opt)
voxel_sizes: (a list of from 3 to 3 items which are a float)
             3-element list (opt)
matlab_cmd: (a unicode string)
            matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
       Run m-code using m-file
use_mcr: (a boolean)
         Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
              Generate SPM8 and higher compatible jobs

```

Outputs:

```

out_files: (a list of items which are a pathlike object or string
            representing an existing file)
            Transformed files

```

References:

None

77.3.3 ApplyTransform[Link to code](#)

Uses SPM to apply transform stored in a .mat file to given file

Examples

```

>>> import nipy.interfaces.spm.utils as spmu
>>> applymat = spmu.ApplyTransform()
>>> applymat.inputs.in_file = 'functional.nii'
>>> applymat.inputs.mat = 'func_to_struct.mat'
>>> applymat.run() # doctest: +SKIP

```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        file to apply transform to, (only updates header)
mat: (a pathlike object or string representing an existing file)
     file holding transform to apply

[Optional]
out_file: (a pathlike object or string representing a file)
          output file name for transformed data
matlab_cmd: (a unicode string)
            matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
          Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
              Generate SPM8 and higher compatible jobs
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          Transformed image file
```

References:

None

77.3.4 CalcCoregAffine[Link to code](#)

Uses SPM (spm_coreg) to calculate the transform mapping moving to target. Saves Transform in mat (matlab binary file) Also saves inverse transform

Examples

```
>>> import nipy.interfaces.spm.utils as spmu
>>> coreg = spmu.CalcCoregAffine(matlab_cmd='matlab-spm8')
>>> coreg.inputs.target = 'structural.nii'
>>> coreg.inputs.moving = 'functional.nii'
>>> coreg.inputs.mat = 'func_to_struct.mat'
>>> coreg.run() # doctest: +SKIP
```

Note:

- the output file mat is saves as a matlab binary file
- calculating the transforms does NOT change either input image it does not **move** the moving image, only calculates the transform that can be used to move it

Inputs:

```
[Mandatory]
target: (a pathlike object or string representing an existing file)
        target for generating affine transform
```

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```

moving: (a pathlike object or string representing an existing file)
        volume transform can be applied to register with target

[Optional]
mat: (a pathlike object or string representing a file)
     Filename used to store affine matrix
invmat: (a pathlike object or string representing a file)
        Filename used to store inverse affine matrix
matlab_cmd: (a unicode string)
            matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
          Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
              Generate SPM8 and higher compatible jobs

```

Outputs:

```

mat: (a pathlike object or string representing an existing file)
     Matlab file holding transform
invmat: (a pathlike object or string representing a file)
        Matlab file holding inverse transform

```

References:

None

77.3.5 DicomImport[Link to code](#)

Uses spm to convert DICOM files to nii or img+hdr.

Examples

```

>>> import nipy.interfaces.spm.utils as spmu
>>> di = spmu.DicomImport()
>>> di.inputs.in_files = ['functional_1.dcm', 'functional_2.dcm']
>>> di.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string
          representing an existing file)
          dicom files to be converted

[Optional]
output_dir_struct: ('flat' or 'series' or 'patname' or 'patid_date'
                   or 'patid' or 'date_time', nipy default value: flat)
                  directory structure for the output.
output_dir: (a unicode string, nipy default value:
            ./converted_dicom)

```

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```

        output directory.
format: ('nii' or 'img', nipy default value: nii)
        output format.
icedims: (a boolean, nipy default value: False)
        If image sorting fails, one can try using the additional SIEMENS
        ICEDims information to create unique filenames. Use this only if
        there would be multiple volumes with exactly the same file names.
matlab_cmd: (a unicode string)
        matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
        Run m-code using m-file
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipy default value: True)
        Generate SPM8 and higher compatible jobs

```

Outputs:

```

out_files: (a list of items which are a pathlike object or string
            representing an existing file)
            converted files

```

References:

None

77.3.6 Reslice[Link to code](#)uses `spm_reslice` to resample `in_file` into space of `space_defining`**Inputs:**

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        file to apply transform to, (only updates header)
space_defining: (a pathlike object or string representing an existing
                file)
                Volume defining space to slice in_file into

[Optional]
interp: (0 <= a long integer <= 7, nipy default value: 0)
        degree of b-spline used for interpolation0 is nearest neighbor
        (default)
out_file: (a pathlike object or string representing a file)
        Optional file to save resliced volume
matlab_cmd: (a unicode string)
        matlab command to use
paths: (a list of items which are a pathlike object or string
        representing a directory)
        Paths to add to matlabpath
mfile: (a boolean, nipy default value: True)
        Run m-code using m-file
use_mcr: (a boolean)

```

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```

    Run m-code using SPM MCR
    use_v8struct: (a boolean, nipyte default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    resliced volume

```

References:

None

77.3.7 ResliceToReference[Link to code](#)

Uses spm to reslice a volume to a target image space or to a provided voxel size and bounding box

Examples

```

>>> import nipyte.interfaces.spm.utils as spmu
>>> r2ref = spmu.ResliceToReference()
>>> r2ref.inputs.in_files = 'functional.nii'
>>> r2ref.inputs.target = 'structural.nii'
>>> r2ref.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_files: (a list of items which are a pathlike object or string
    representing an existing file)
    Files on which deformation is applied

[Optional]
target: (a pathlike object or string representing an existing file)
    File defining target space
interpolation: (0 <= a long integer <= 7)
    degree of b-spline used for interpolation
bounding_box: (a list of from 6 to 6 items which are a float)
    6-element list (opt)
voxel_sizes: (a list of from 3 to 3 items which are a float)
    3-element list (opt)
matlab_cmd: (a unicode string)
    matlab command to use
paths: (a list of items which are a pathlike object or string
    representing a directory)
    Paths to add to matlabpath
mfile: (a boolean, nipyte default value: True)
    Run m-code using m-file
use_mcr: (a boolean)
    Run m-code using SPM MCR
use_v8struct: (a boolean, nipyte default value: True)
    Generate SPM8 and higher compatible jobs

```

Outputs:

```
out_files: (a list of items which are a pathlike object or string
            representing an existing file)
            Transformed files
```

References:

None

78.1 interfaces.utility.base

78.1.1 AssertEqual

[Link to code](#)

Inputs:

```
[Mandatory]
volume1: (a pathlike object or string representing an existing file)
volume2: (a pathlike object or string representing an existing file)
```

Outputs:

```
None
```

78.1.2 IdentityInterface

[Link to code](#)

Basic interface class generates identity mappings

Examples

```
>>> from nipy.interfaces.utility import IdentityInterface
>>> ii = IdentityInterface(fields=['a', 'b'], mandatory_inputs=False)
>>> ii.inputs.a
<undefined>
```

```
>>> ii.inputs.a = 'foo'
>>> out = ii._outputs()
>>> out.a
<undefined>
```

```
>>> out = ii.run()
>>> out.outputs.a
'foo'
```

```
>>> ii2 = IdentityInterface(fields=['a', 'b'], mandatory_inputs=True)
>>> ii2.inputs.a = 'foo'
>>> out = ii2.run() # doctest: +SKIP
ValueError: IdentityInterface requires a value for input 'b' because it was_
↳ listed in 'fields' Interface IdentityInterface failed to run.
```

Inputs:

None

Outputs:

None

78.1.3 Merge

[Link to code](#)

Basic interface class to merge inputs into a single list

Merge (1) will merge a list of lists

Examples

```
>>> from nipyne.interfaces.utility import Merge
>>> mi = Merge(3)
>>> mi.inputs.in1 = 1
>>> mi.inputs.in2 = [2, 5]
>>> mi.inputs.in3 = 3
>>> out = mi.run()
>>> out.outputs.out
[1, 2, 5, 3]
```

```
>>> merge = Merge(1)
>>> merge.inputs.in1 = [1, [2, 5], 3]
>>> out = merge.run()
>>> out.outputs.out
[1, [2, 5], 3]
```

```
>>> merge = Merge(1)
>>> merge.inputs.in1 = [1, [2, 5], 3]
>>> merge.inputs.ravel_inputs = True
>>> out = merge.run()
>>> out.outputs.out
[1, 2, 5, 3]
```

```
>>> merge = Merge(1)
>>> merge.inputs.in1 = [1, [2, 5], 3]
>>> merge.inputs.no_flatten = True
>>> out = merge.run()
>>> out.outputs.out
[[1, [2, 5], 3]]
```

Inputs:

[Optional]
axis: ('vstack' or 'hstack', nipyne default value: vstack)
direction in which to merge, hstack requires same number of elements

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```

    in each input
no_flatten: (a boolean, nipyte default value: False)
    append to outlist instead of extending in vstack mode
ravel_inputs: (a boolean, nipyte default value: False)
    ravel inputs when no_flatten is False

```

Outputs:

```

out: (a list of items which are any value)
    Merged output

```

78.1.4 Rename

[Link to code](#)

Change the name of a file based on a mapped format string.

To use additional inputs that will be defined at run-time, the class constructor must be called with the format template, and the fields identified will become inputs to the interface.

Additionally, you may set the parse_string input, which will be run over the input filename with a regular expressions search, and will fill in additional input fields from matched groups. Fields set with inputs have precedence over fields filled in with the regexp match.

Examples

```

>>> from nipyte.interfaces.utility import Rename
>>> rename1 = Rename()
>>> rename1.inputs.in_file = os.path.join(datadir, "zstat1.nii.gz") # datadir is
↳ a directory with exemplary files, defined in conftest.py
>>> rename1.inputs.format_string = "Faces-Scenes.nii.gz"
>>> res = rename1.run() # doctest: +SKIP
>>> res.outputs.out_file # doctest: +SKIP
'Faces-Scenes.nii.gz' # doctest: +SKIP

```

```

>>> rename2 = Rename(format_string="% (subject_id) s_func_run%(run) 02d")
>>> rename2.inputs.in_file = os.path.join(datadir, "functional.nii")
>>> rename2.inputs.keep_ext = True
>>> rename2.inputs.subject_id = "subj_201"
>>> rename2.inputs.run = 2
>>> res = rename2.run() # doctest: +SKIP
>>> res.outputs.out_file # doctest: +SKIP
'subj_201_func_run02.nii' # doctest: +SKIP

```

```

>>> rename3 = Rename(format_string="% (subject_id) s_%(seq) s_run%(run) 02d.nii")
>>> rename3.inputs.in_file = os.path.join(datadir, "func_epi_1_1.nii")
>>> rename3.inputs.parse_string = "func_(?P<seq>\w*)_.*"
>>> rename3.inputs.subject_id = "subj_201"
>>> rename3.inputs.run = 2
>>> res = rename3.run() # doctest: +SKIP
>>> res.outputs.out_file # doctest: +SKIP
'subj_201_epi_run02.nii' # doctest: +SKIP

```

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    file to rename

```

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```

format_string: (a unicode string)
    Python formatting string for output template

[Optional]
keep_ext: (a boolean)
    Keep in_file extension, replace non-extension component of name
parse_string: (a unicode string)
    Python regexp parse string to define replacement inputs
use_fullpath: (a boolean, nipy default value: False)
    Use full path as input to regex parser

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    softlink to original file with new name

```

78.1.5 Select[Link to code](#)

Basic interface class to select specific elements from a list

Examples

```

>>> from nipy.interfaces.utility import Select
>>> sl = Select()
>>> _ = sl.inputs.trait_set(inlist=[1, 2, 3, 4, 5], index=[3])
>>> out = sl.run()
>>> out.outputs.out
~

```

```

>>> _ = sl.inputs.trait_set(inlist=[1, 2, 3, 4, 5], index=[3, 4])
>>> out = sl.run()
>>> out.outputs.out
[4, 5]

```

Inputs:

```

[Mandatory]
inlist: (a list of items which are any value)
    list of values to choose from
index: (a list of items which are an integer (int or long))
    0-based indices of values to choose

```

Outputs:

```

out: (a list of items which are any value)
    list of selected values

```

78.1.6 Split[Link to code](#)

Basic interface class to split lists into multiple outputs

Examples

```
>>> from nipyype.interfaces.utility import Split
>>> sp = Split()
>>> _ = sp.inputs.trait_set(inlist=[1, 2, 3], splits=[2, 1])
>>> out = sp.run()
>>> out.outputs.out1
[1, 2]
```

Inputs:

```
[Mandatory]
inlist: (a list of items which are any value)
        list of values to split
splits: (a list of items which are an integer (int or long))
        Number of outputs in each split - should add to number of inputs

[Optional]
squeeze: (a boolean, nipyype default value: False)
        unfold one-element splits removing the list
```

Outputs:

None

78.2 interfaces.utility.csv

78.2.1 CSVReader

[Link to code](#)

Examples

```
>>> reader = CSVReader() # doctest: +SKIP
>>> reader.inputs.in_file = 'noHeader.csv' # doctest: +SKIP
>>> out = reader.run() # doctest: +SKIP
>>> out.outputs.column_0 == ['foo', 'bar', 'baz'] # doctest: +SKIP
True
>>> out.outputs.column_1 == ['hello', 'world', 'goodbye'] # doctest: +SKIP
True
>>> out.outputs.column_2 == ['300.1', '5', '0.3'] # doctest: +SKIP
True
```

```
>>> reader = CSVReader() # doctest: +SKIP
>>> reader.inputs.in_file = 'header.csv' # doctest: +SKIP
>>> reader.inputs.header = True # doctest: +SKIP
>>> out = reader.run() # doctest: +SKIP
>>> out.outputs.files == ['foo', 'bar', 'baz'] # doctest: +SKIP
True
>>> out.outputs.labels == ['hello', 'world', 'goodbye'] # doctest: +SKIP
True
>>> out.outputs.erosion == ['300.1', '5', '0.3'] # doctest: +SKIP
True
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        Input comma-seperated value (CSV) file

[Optional]
header: (a boolean, nipyre default value: False)
        True if the first line is a column header
```

Outputs:

```
None
```

78.3 interfaces.utility.wrappers

78.3.1 Function

[Link to code](#)

Runs arbitrary function as an interface

Examples

```
>>> func = 'def func(arg1, arg2=5): return arg1 + arg2'
>>> fi = Function(input_names=['arg1', 'arg2'], output_names=['out'])
>>> fi.inputs.function_str = func
>>> res = fi.run(arg1=1)
>>> res.outputs.out
~
```

Inputs:

```
[Mandatory]
function_str: (a unicode string)
              code for function
```

Outputs:

```
None
```


79.1 interfaces.vista.vista

79.1.1 Vnifti2Image

[Link to code](#)

Wraps the executable command `vnifti2image`.

Convert a nifti file into a vista file.

Example

```
>>> vimage = Vnifti2Image()
>>> vimage.inputs.in_file = 'image.nii'
>>> vimage.cmdline
'vnifti2image -in image.nii -out image.v'
>>> vimage.run()                                     # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         in file
         argument: ``-in %s``, position: 1

[Optional]
attributes: (a pathlike object or string representing an existing
            file)
            attribute file
            argument: ``-attr %s``, position: 2
out_file: (a pathlike object or string representing a file)
          output data file
          argument: ``-out %s``, position: -1
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
```

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```
value of class 'str', nipy default value: {})  
Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)  
Output vista file
```

79.1.2 VtoMat[Link to code](#)Wraps the executable command `vtomat`.

Convert a nifti file into a vista file.

Example

```
>>> vimage = VtoMat()  
>>> vimage.inputs.in_file = 'image.v'  
>>> vimage.cmdline  
'vtomat -in image.v -out image.mat'  
>>> vimage.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]  
in_file: (a pathlike object or string representing an existing file)  
in file  
argument: ``-in %s``, position: 1  
  
[Optional]  
out_file: (a pathlike object or string representing a file)  
output mat file  
argument: ``-out %s``, position: -1  
args: (a unicode string)  
Additional parameters to the command  
argument: ``%s``  
environ: (a dictionary with keys which are a bytes or None or a value  
of class 'str' and with values which are a bytes or None or a  
value of class 'str', nipy default value: {})  
Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)  
Output mat file
```

80.1 interfaces.workbench.base

80.1.1 WBCommand

[Link to code](#)

Base support for workbench commands.

Inputs:

```
[Optional]
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipype default value: {})
    Environment variables
```

Outputs:

None

80.2 interfaces.workbench.cifti

80.2.1 CiftiSmooth

[Link to code](#)

Wraps the executable command `wb_command -cifti-smoothing`.

Smooth a CIFTI file

The input cifti file must have a brain models mapping on the chosen dimension, columns for .dtseries, and either for .dconn. By default, data in different structures is smoothed independently (i.e., “parcel constrained” smoothing), so volume structures that touch do not smooth across this boundary. Specify `merged_volume` to ignore these boundaries. Surface smoothing uses the `GEO_GAUSS_AREA` smoothing method.

The `*_corrected_areas` options are intended for when it is unavoidable to smooth on group average surfaces, it is only an approximate correction for the reduction of structure in a group average surface. It is better to smooth the data on individuals before averaging, when feasible.

The `fix_zeros_*` options will treat values of zero as lack of data, and not use that value when generating the smoothed values, but will fill zeros with extrapolated values. The ROI should have a brain models mapping along columns, exactly matching the mapping of the chosen direction in the input file. Data outside the ROI is ignored.

```
>>> from nipy.interfaces.workbench import CiftiSmooth
>>> smooth = CiftiSmooth()
>>> smooth.inputs.in_file = 'sub-01_task-rest.dtseries.nii'
>>> smooth.inputs.sigma_surf = 4
>>> smooth.inputs.sigma_vol = 4
>>> smooth.inputs.direction = 'COLUMN'
>>> smooth.inputs.right_surf = 'sub-01.R.midthickness.32k_fs_LR.surf.gii'
>>> smooth.inputs.left_surf = 'sub-01.L.midthickness.32k_fs_LR.surf.gii'
>>> smooth.cmdline
'wb_command -cifti-smoothing sub-01_task-rest.dtseries.nii 4.0 4.0 COLUMN
↳smoothed_sub-01_task-rest.dtseries.nii -left-surface sub-01.L.midthickness.
↳32k_fs_LR.surf.gii -right-surface sub-01.R.midthickness.32k_fs_LR.surf.gii'
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    The input CIFTI file
    argument: ``%s``, position: 0
sigma_surf: (a float)
    the sigma for the gaussian surface smoothing kernel, in mm
    argument: ``%s``, position: 1
sigma_vol: (a float)
    the sigma for the gaussian volume smoothing kernel, in mm
    argument: ``%s``, position: 2
direction: ('ROW' or 'COLUMN')
    which dimension to smooth along, ROW or COLUMN
    argument: ``%s``, position: 3
left_surf: (a pathlike object or string representing an existing
    file)
    Specify the left surface to use
    argument: ``-left-surface %s``, position: 5
right_surf: (a pathlike object or string representing an existing
    file)
    Specify the right surface to use
    argument: ``-right-surface %s``, position: 7

[Optional]
out_file: (a pathlike object or string representing a file)
    The output CIFTI
    argument: ``%s``, position: 4
left_corrected_areas: (a pathlike object or string representing an
    existing file)
    vertex areas (as a metric) to use instead of computing them from the
    left surface.
    argument: ``-left-corrected-areas %s``, position: 6
right_corrected_areas: (a pathlike object or string representing an
    existing file)
    vertex areas (as a metric) to use instead of computing them from the
    right surface
    argument: ``-right-corrected-areas %s``, position: 8
cerebellum_surf: (a pathlike object or string representing an
    existing file)
```

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```

        specify the cerebellum surface to use
        argument: ``-cerebellum-surface %s``, position: 9
cerebellum_corrected_areas: (a pathlike object or string representing
    an existing file)
    vertex areas (as a metric) to use instead of computing them from the
    cerebellum surface
    argument: ``-cerebellum-corrected-areas %s``, position: 10
    requires: cerebellum_surf
cifti_roi: (a pathlike object or string representing an existing
    file)
    CIFTI file for ROI smoothing
    argument: ``-cifti-roi %s``, position: 11
fix_zeros_vol: (a boolean)
    treat values of zero in the volume as missing data
    argument: ``-fix-zeros-volume``, position: 12
fix_zeros_surf: (a boolean)
    treat values of zero on the surface as missing data
    argument: ``-fix-zeros-surface``, position: 13
merged_volume: (a boolean)
    smooth across subcortical structure boundaries
    argument: ``-merged-volume``, position: 14
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing an existing file)
    output CIFTI file

```

80.3 interfaces.workbench.metric

80.3.1 MetricResample

[Link to code](#)

Wraps the executable command `wb_command -metric-resample`.

Resample a metric file to a different mesh

Resamples a metric file, given two spherical surfaces that are in register. If `ADAP_BARY_AREA` is used, exactly one of `-area-surfs` or `-area-metrics` must be specified.

The `ADAP_BARY_AREA` method is recommended for ordinary metric data, because it should use all data while downsampling, unlike `BARYCENTRIC`. The recommended areas option for most data is individual midthicknesses for individual data, and averaged vertex area metrics from individual midthicknesses for group average data.

The `-current-roi` option only masks the input, the output may be slightly dilated in comparison, consider using `-metric-mask` on the output when using `-current-roi`.

The `-largest` option results in nearest vertex behavior when used with `BARYCENTRIC`. When resampling a binary metric, consider thresholding at 0.5 after resampling rather than using `-largest`.

```

>>> from nipy.interfaces.workbench import MetricResample
>>> metres = MetricResample()
>>> metres.inputs.in_file = 'sub-01_task-rest_bold_space-fsaverage5.L.func.gii'

```

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```

>>> metres.inputs.method = 'ADAP_BARY_AREA'
>>> metres.inputs.current_sphere = 'fsaverage5_std_sphere.L.10k_fsavg_L.surf.gii'
>>> metres.inputs.new_sphere = 'fs_LR-deformed_to-fsaverage.L.sphere.32k_fs_LR.
↳surf.gii'
>>> metres.inputs.area_metrics = True
>>> metres.inputs.current_area = 'fsaverage5.L.midthickness_va_avg.10k_fsavg_L.
↳shape.gii'
>>> metres.inputs.new_area = 'fs_LR.L.midthickness_va_avg.32k_fs_LR.shape.gii'
>>> metres.cmdline
'wb_command -metric-resample sub-01_task-rest_bold_space-fsaverage5.L.func.gii
↳ fsaverage5_std_sphere.L.10k_fsavg_L.surf.gii fs_LR-deformed_to-fsaverage.L.
↳ sphere.32k_fs_LR.surf.gii ADAP_BARY_AREA fs_LR-deformed_to-fsaverage.L.
↳ sphere.32k_fs_LR.surf.out -area-metrics fsaverage5.L.midthickness_va_avg.
↳ 10k_fsavg_L.shape.gii fs_LR.L.midthickness_va_avg.32k_fs_LR.shape.gii'

```

Inputs:

[Mandatory]

in_file: (a pathlike object or string representing an existing file)
 The metric file to resample
 argument: ``%s``, position: 0

current_sphere: (a pathlike object or string representing an existing file)
 A sphere surface with the mesh that the metric is currently on
 argument: ``%s``, position: 1

new_sphere: (a pathlike object or string representing an existing file)
 A sphere surface that is in register with <current-sphere> and has the desired output mesh
 argument: ``%s``, position: 2

method: ('ADAP_BARY_AREA' or 'BARYCENTRIC')
 The method name - ADAP_BARY_AREA method is recommended for ordinary metric data, because it should use all data while downsampling, unlike BARYCENTRIC. If ADAP_BARY_AREA is used, exactly one of area_surfs or area_metrics must be specified
 argument: ``%s``, position: 3

[Optional]

out_file: (a pathlike object or string representing a file)
 The output metric
 argument: ``%s``, position: 4

area_surfs: (a boolean)
 Specify surfaces to do vertex area correction based on
 argument: ``-area-surfs``, position: 5
 mutually_exclusive: area_metrics

area_metrics: (a boolean)
 Specify vertex area metrics to do area correction based on
 argument: ``-area-metrics``, position: 5
 mutually_exclusive: area_surfs

current_area: (a pathlike object or string representing an existing file)
 A relevant anatomical surface with <current-sphere> mesh OR a metric file with vertex areas for <current-sphere> mesh
 argument: ``%s``, position: 6

new_area: (a pathlike object or string representing an existing file)
 A relevant anatomical surface with <current-sphere> mesh OR a metric file with vertex areas for <current-sphere> mesh

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```
    argument: ``%s``, position: 7
roi_metric: (a pathlike object or string representing an existing
    file)
    Input roi on the current mesh used to exclude non-data vertices
    argument: ``-current-roi %s``, position: 8
valid_roi_out: (a boolean)
    Output the ROI of vertices that got data from valid source vertices
    argument: ``-valid-roi-out``, position: 9
largest: (a boolean)
    Use only the value of the vertex with the largest weight
    argument: ``-largest``, position: 10
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipy default value: {})
    Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
    the output metric
roi_file: (a pathlike object or string representing a file)
    ROI of vertices that got data from valid source vertices
```


81.1 Bru2

[Link to code](#)

Wraps the executable command Bru2.

Uses bru2nii's Bru2 to convert Bruker files

81.1.1 Examples

```
>>> from nipy.interfaces.bru2nii import Bru2
>>> converter = Bru2()
>>> converter.inputs.input_dir = "brukerdir"
>>> converter.cmdline # doctest: +ELLIPSIS
'Bru2 -o .../data/brukerdir brukerdir'
```

Inputs:

```
[Mandatory]
input_dir: (a pathlike object or string representing an existing
           directory)
           Input Directory
           argument: ``%s``, position: -1

[Optional]
actual_size: (a boolean)
             Keep actual size - otherwise x10 scale so animals match human.
             argument: ``-a``
force_conversion: (a boolean)
                  Force conversion of localizers images (multiple slice orientations).
                  argument: ``-f``
compress: (a boolean)
           gz compress images (".nii.gz").
           argument: ``-z``
append_protocol_name: (a boolean)
                      Append protocol name to output filename.
                      argument: ``-p``
output_filename: (a unicode string)
```

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```
Output filename (".nii" will be appended, or ".nii.gz" if the "-z"
compress option is selected)
argument: ``-o %s``
args: (a unicode string)
Additional parameters to the command
argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
of class 'str' and with values which are a bytes or None or a
value of class 'str', nipy default value: {})
Environment variables
```

Outputs:

```
nii_file: (a pathlike object or string representing an existing file)
```

82.1 C3d

[Link to code](#)

Wraps the executable command `c3d`.

Convert3d is a command-line tool for converting 3D (or 4D) images between common file formats. The tool also includes a growing list of commands for image manipulation, such as thresholding and resampling. The tool can also be used to obtain information about image files. More information on Convert3d can be found at: <https://sourceforge.net/p/c3d/git/ci/master/tree/doc/c3d.md>

82.1.1 Example

```

>>> from nipy.interfaces.c3 import C3d
>>> c3 = C3d()
>>> c3.inputs.in_file = "T1.nii"
>>> c3.inputs.pix_type = "short"
>>> c3.inputs.out_file = "T1.img"
>>> c3.cmdline
'c3d T1.nii -type short -o T1.img'
>>> c3.inputs.is_4d = True
>>> c3.inputs.in_file = "epi.nii"
>>> c3.inputs.out_file = "epi.img"
>>> c3.cmdline
'c4d epi.nii -type short -o epi.img'

```

Inputs:

```

[Mandatory]
in_file: (a list of items which are a pathlike object or string
         representing a file)
         Input file (wildcard and multiple are supported).
         argument: ``%s``, position: 1

[Optional]
out_file: (a pathlike object or string representing a file)
         Output file of last image on the stack.

```

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```

        argument: ``-o %s``, position: -1
        mutually_exclusive: out_files
out_files: (a list of items which are a pathlike object or string
            representing a file)
            Write all images on the convert3d stack as multiple files. Supports
            both list of output files or a pattern for the output filenames
            (using %d substitution).
            argument: ``-oo %s``, position: -1
            mutually_exclusive: out_file
pix_type: ('float' or 'char' or 'uchar' or 'short' or 'ushort' or
            'int' or 'uint' or 'double')
            Specifies the pixel type for the output image. By default, images
            are written in floating point (float) format
            argument: ``-type %s``
scale: (an integer (int or long) or a float)
            Multiplies the intensity of each voxel in the last image on the
            stack by the given factor.
            argument: ``-scale %s``
shift: (an integer (int or long) or a float)
            Adds the given constant to every voxel.
            argument: ``-shift %s``
interp: ('Linear' or 'NearestNeighbor' or 'Cubic' or 'Sinc' or
            'Gaussian')
            Specifies the interpolation used with -resample and other commands.
            Default is Linear.
            argument: ``-interpolation %s``
resample: (a unicode string)
            Resamples the image, keeping the bounding box the same, but changing
            the number of voxels in the image. The dimensions can be specified
            as a percentage, for example to double the number of voxels in each
            direction. The -interpolation flag affects how sampling is
            performed.
            argument: ``-resample %s``
smooth: (a unicode string)
            Applies Gaussian smoothing to the image. The parameter vector
            specifies the standard deviation of the Gaussian kernel.
            argument: ``-smooth %s``
multicomp_split: (a boolean, nipy default value: False)
            Enable reading of multi-component images.
            argument: ``-mcr``, position: 0
is_4d: (a boolean, nipy default value: False)
            Changes command to support 4D file operations (default is false).
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
            of class 'str' and with values which are a bytes or None or a
            value of class 'str', nipy default value: {})
            Environment variables

```

Outputs:

```

out_files: (a list of items which are a pathlike object or string
            representing a file)

```

82.2 C3dAffineTool

[Link to code](#)

Wraps the executable command `c3d_affine_tool`.

Converts fsl-style Affine registration into ANTS compatible itk format

82.2.1 Example

```
>>> from nipy.interfaces.c3 import C3dAffineTool
>>> c3 = C3dAffineTool()
>>> c3.inputs.source_file = 'cmatrix.mat'
>>> c3.inputs.itk_transform = 'affine.txt'
>>> c3.inputs.fsl2ras = True
>>> c3.cmdline
'c3d_affine_tool -src cmatrix.mat -fsl2ras -oitk affine.txt'
```

Inputs:

```
[Optional]
reference_file: (a pathlike object or string representing an existing
                file)
                argument: ``-ref %s``, position: 1
source_file: (a pathlike object or string representing an existing
              file)
              argument: ``-src %s``, position: 2
transform_file: (a pathlike object or string representing an existing
                 file)
                 argument: ``%s``, position: 3
itk_transform: (a boolean or a pathlike object or string representing
                a file)
                Export ITK transform.
                argument: ``-oitk %s``, position: 5
fsl2ras: (a boolean)
          argument: ``-fsl2ras``, position: 4
args: (a unicode string)
       Additional parameters to the command
       argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
          of class 'str' and with values which are a bytes or None or a
          value of class 'str', nipy default value: {})
          Environment variables
```

Outputs:

```
itk_transform: (a pathlike object or string representing an existing
                file)
```


83.1 Dcm2nii

[Link to code](#)

Wraps the executable command dcm2nii.

Uses MRICron's dcm2nii to convert dicom files

83.1.1 Examples

```
>>> from nipy.interfaces.dcm2nii import Dcm2nii
>>> converter = Dcm2nii()
>>> converter.inputs.source_names = ['functional_1.dcm', 'functional_2.dcm']
>>> converter.inputs.gzip_output = True
>>> converter.inputs.output_dir = '.'
>>> converter.cmdline # doctest: +ELLIPSIS
'dcm2nii -a y -c y -b config.ini -v y -d y -e y -g y -i n -n y -o . -p y -x n -f_
↪n functional_1.dcm'
```

Inputs:

```
[Mandatory]
source_names: (a list of items which are a pathlike object or string
               representing an existing file)
               argument: ``%s``, position: -1
               mutually_exclusive: source_dir
source_dir: (a pathlike object or string representing an existing
             directory)
             argument: ``%s``, position: -1
             mutually_exclusive: source_names

[Optional]
anonymize: (a boolean, nipy default value: True)
            Remove identifying information
            argument: ``-a``
config_file: (a pathlike object or string representing an existing
             file)
             Load settings from specified inifile
```

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```

        argument: ``-b %s``
collapse_folders: (a boolean, nipyte default value: True)
    Collapse input folders
    argument: ``-c``
date_in_filename: (a boolean, nipyte default value: True)
    Date in filename
    argument: ``-d``
events_in_filename: (a boolean, nipyte default value: True)
    Events (series/acq) in filename
    argument: ``-e``
source_in_filename: (a boolean, nipyte default value: False)
    Source filename
    argument: ``-f``
gzip_output: (a boolean, nipyte default value: False)
    Gzip output (.gz)
    argument: ``-g``
id_in_filename: (a boolean, nipyte default value: False)
    ID in filename
    argument: ``-i``
nii_output: (a boolean, nipyte default value: True)
    Save as .nii - if no, create .hdr/.img pair
    argument: ``-n``
output_dir: (a pathlike object or string representing an existing
    directory)
    Output dir - if unspecified, source directory is used
    argument: ``-o %s``
protocol_in_filename: (a boolean, nipyte default value: True)
    Protocol in filename
    argument: ``-p``
reorient: (a boolean)
    Reorient image to nearest orthogonal
    argument: ``-r``
spm_analyze: (a boolean)
    SPM2/Analyze not SPM5/NIfTI
    argument: ``-s``
    mutually_exclusive: nii_output
convert_all_pars: (a boolean, nipyte default value: True)
    Convert every image in directory
    argument: ``-v``
reorient_and_crop: (a boolean, nipyte default value: False)
    Reorient and crop 3D images
    argument: ``-x``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyte default value: {})
    Environment variables

```

Outputs:

```

converted_files: (a list of items which are a pathlike object or
    string representing an existing file)
reoriented_files: (a list of items which are a pathlike object or
    string representing an existing file)
reoriented_and_cropped_files: (a list of items which are a pathlike

```

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```

    object or string representing an existing file)
bvecs: (a list of items which are a pathlike object or string
        representing an existing file)
bvals: (a list of items which are a pathlike object or string
        representing an existing file)

```

83.2 Dcm2niix

[Link to code](#)

Wraps the executable command dcm2niix.

Uses Chris Rorden's dcm2niix to convert dicom files

83.2.1 Examples

```

>>> from nipy.interfaces.dcm2nii import Dcm2niix
>>> converter = Dcm2niix()
>>> converter.inputs.source_dir = 'dicomdir'
>>> converter.inputs.compression = 5
>>> converter.inputs.output_dir = 'ds005'
>>> converter.cmdline
'dcm2niix -b y -z y -5 -x n -t n -m n -o ds005 -s n -v n dicomdir'
>>> converter.run() # doctest: +SKIP

```

In the example below, we note that the current version of dcm2niix converts any files in the directory containing the files in the list. We also do not support nested filenames with this option. **Thus all files must have a common root directory.**

```

>>> converter = Dcm2niix()
>>> converter.inputs.source_names = ['functional_1.dcm', 'functional_2.dcm']
>>> converter.inputs.compression = 5
>>> converter.inputs.output_dir = 'ds005'
>>> converter.cmdline
'dcm2niix -b y -z y -5 -x n -t n -m n -o ds005 -s n -v n .'
>>> converter.run() # doctest: +SKIP

```

Inputs:

```

[Mandatory]
source_names: (a list of items which are a pathlike object or string
               representing an existing file)
               A set of filenames to be converted. Note that the current version
               (1.0.20180328) of dcm2niix converts any files in the directory. To
               only convert specific files they should be in an isolated directory
               argument: ``%s``, position: -1
               mutually_exclusive: source_dir
source_dir: (a pathlike object or string representing an existing
             directory)
             A directory containing dicom files to be converted
             argument: ``%s``, position: -1
             mutually_exclusive: source_names

[Optional]
out_filename: (a unicode string)
               Output filename template (%a=antenna (coil) number, %c=comments,
               %d=description, %e=echo number, %f=folder name, %i=ID of patient,

```

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```

        %j=seriesInstanceUID, %k=studyInstanceUID, %m=manufacturer, %n=name
        of patient, %p=protocol, %s=series number, %t=time, %u=acquisition
        number, %v=vendor, %x=study ID; %z=sequence name)
        argument: ``-f %s``
output_dir: (a pathlike object or string representing an existing
            directory, nipy default value: .)
            Output directory
            argument: ``-o %s``
bids_format: (a boolean, nipy default value: True)
            Create a BIDS sidecar file
            argument: ``-b``
anon_bids: (a boolean)
            Anonymize BIDS
            argument: ``-ba``
            requires: bids_format
compress: ('y' or 'i' or 'n' or '3', nipy default value: y)
            Gzip compress images - [y=pigz, i=internal, n=no, 3=no,3D]
            argument: ``-z %s``
merge_imgs: (a boolean, nipy default value: False)
            merge 2D slices from same series
            argument: ``-m``
single_file: (a boolean, nipy default value: False)
            Single file mode
            argument: ``-s``
verbose: (a boolean, nipy default value: False)
            Verbose output
            argument: ``-v``
crop: (a boolean, nipy default value: False)
            Crop 3D T1 acquisitions
            argument: ``-x``
has_private: (a boolean, nipy default value: False)
            Flag if text notes include private patient details
            argument: ``-t``
compression: (1 or 2 or 3 or 4 or 5 or 6 or 7 or 8 or 9)
            Gz compression level (1=fastest, 9=smallest)
            argument: ``-%d``
comment: (a unicode string)
            Comment stored as NIfTI aux_file
            argument: ``-c %s``
ignore_deriv: (a boolean)
            Ignore derived, localizer and 2D images
            argument: ``-i``
series_numbers: (a list of items which are a unicode string)
            Selectively convert by series number - can be used up to 16 times
            argument: ``-n %s...``
philips_float: (a boolean)
            Philips precise float (not display) scaling
            argument: ``-p``
args: (a unicode string)
            Additional parameters to the command
            argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
            of class 'str' and with values which are a bytes or None or a
            value of class 'str', nipy default value: {})
            Environment variables

```

Outputs:

```
converted_files: (a list of items which are a pathlike object or
                  string representing an existing file)
bvecs: (a list of items which are a pathlike object or string
        representing an existing file)
bvals: (a list of items which are a pathlike object or string
        representing an existing file)
bids: (a list of items which are a pathlike object or string
       representing an existing file)
```


84.1 CopyMeta

[Link to code](#)

Copy meta data from one Nifti file to another. Useful for preserving meta data after some processing steps.

Inputs:

```
[Mandatory]
src_file: (a pathlike object or string representing an existing file)
dest_file: (a pathlike object or string representing an existing
            file)

[Optional]
include_classes: (a list of items which are any value)
                  List of specific meta data classifications to include. If not
                  specified include everything.
exclude_classes: (a list of items which are any value)
                  List of meta data classifications to exclude
```

Outputs:

```
dest_file: (a pathlike object or string representing an existing
            file)
```

84.2 DcmStack

[Link to code](#)

Create one Nifti file from a set of DICOM files. Can optionally embed meta data.

84.2.1 Example

```
>>> from nipy.interfaces.dcmstack import DcmStack
>>> stacker = DcmStack()
>>> stacker.inputs.dicom_files = 'path/to/series/'
>>> stacker.run() # doctest: +SKIP
```

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```
>>> result.outputs.out_file # doctest: +SKIP
'/path/to/cwd/sequence.nii.gz'
```

Inputs:

```
[Mandatory]
dicom_files: (a list of items which are a pathlike object or string
              representing an existing file or a pathlike object or string
              representing an existing directory or a unicode string)

[Optional]
embed_meta: (a boolean)
              Embed DICOM meta data into result
exclude_regexes: (a list of items which are any value)
                  Meta data to exclude, supplementing any default exclude filters
include_regexes: (a list of items which are any value)
                  Meta data to include, overriding any exclude filters
force_read: (a boolean, nipy default value: True)
              Force reading files without DICM marker
out_format: (a unicode string)
              String which can be formatted with meta data to create the output
              filename(s)
out_ext: (a unicode string, nipy default value: .nii.gz)
           Determines output file type
out_path: (a pathlike object or string representing a directory)
           output path, current working directory if not set
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
```

84.3 GroupAndStack

[Link to code](#)

Create (potentially) multiple Nifti files for a set of DICOM files.

Inputs:

```
[Mandatory]
dicom_files: (a list of items which are a pathlike object or string
              representing an existing file or a pathlike object or string
              representing an existing directory or a unicode string)

[Optional]
embed_meta: (a boolean)
              Embed DICOM meta data into result
exclude_regexes: (a list of items which are any value)
                  Meta data to exclude, supplementing any default exclude filters
include_regexes: (a list of items which are any value)
                  Meta data to include, overriding any exclude filters
force_read: (a boolean, nipy default value: True)
              Force reading files without DICM marker
out_format: (a unicode string)
              String which can be formatted with meta data to create the output
              filename(s)
out_ext: (a unicode string, nipy default value: .nii.gz)
           Determines output file type
```

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```
out_path: (a pathlike object or string representing a directory)
          output path, current working directory if not set
```

Outputs:

```
out_list: (a list of items which are any value)
          List of output nifti files
```

84.4 LookupMeta

[Link to code](#)

Lookup meta data values from a Nifti with embedded meta data.

84.4.1 Example

```
>>> from nipy.interfaces import dcmstack
>>> lookup = dcmstack.LookupMeta()
>>> lookup.inputs.in_file = 'functional.nii'
>>> lookup.inputs.meta_keys = {'RepetitionTime' : 'TR',
    ↪      'EchoTime' : 'TE'}
>>> result = lookup.run() # doctest: +SKIP
>>> result.outputs.TR # doctest: +SKIP
9500.0
>>> result.outputs.TE # doctest: +SKIP
95.0
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
          The input Nifti file
meta_keys: (a list of items which are any value or a dictionary with
            keys which are any value and with values which are any value)
            List of meta data keys to lookup, or a dict where keys specify the
            meta data keys to lookup and the values specify the output names
```

Outputs:

```
None
```

84.5 MergeNifti

[Link to code](#)

Merge multiple Nifti files into one. Merges together meta data extensions as well.

Inputs:

```
[Mandatory]
in_files: (a list of items which are any value)
          List of Nifti files to merge

[Optional]
sort_order: (a unicode string or a list of items which are any value)
            One or more meta data keys to sort files by.
merge_dim: (an integer (int or long))
```

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```

        Dimension to merge along. If not specified, the last singular or
        non-existent dimension is used.
    out_format: (a unicode string)
        String which can be formatted with meta data to create the output
        filename(s)
    out_ext: (a unicode string, nipy default value: .nii.gz)
        Determines output file type
    out_path: (a pathlike object or string representing a directory)
        output path, current working directory if not set

```

Outputs:

```

    out_file: (a pathlike object or string representing an existing file)
        Merged Nifti file

```

84.6 NiftiGeneratorBase

[Link to code](#)

Base class for interfaces that produce Nifti files, potentially with embedded meta data.

Inputs:**None****Outputs:****None**

84.7 SplitNifti

[Link to code](#)

Split one Nifti file into many along the specified dimension. Each result has an updated meta data extension as well.

Inputs:

```

[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        Nifti file to split

[Optional]
split_dim: (an integer (int or long))
        Dimension to split along. If not specified, the last dimension is
        used.
out_format: (a unicode string)
        String which can be formatted with meta data to create the output
        filename(s)
out_ext: (a unicode string, nipy default value: .nii.gz)
        Determines output file type
out_path: (a pathlike object or string representing a directory)
        output path, current working directory if not set

```

Outputs:

```

    out_list: (a list of items which are a pathlike object or string
        representing an existing file)
        Split Nifti files

```


84.8 `make_key_func()`

[Link to code](#)

84.9 `sanitize_path_comp()`

[Link to code](#)

85.1 SlicerCommandLine

[Link to code](#)

Wraps the executable command `Slicer3`.

Experimental Slicer wrapper. Work in progress.

Inputs:

```
[Optional]
module: (a unicode string)
        name of the Slicer command line module you want to use
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

None

86.1 Reorient

[Link to code](#)

Conform an image to a given orientation

Flips and reorder the image data array so that the axes match the directions indicated in `orientation`. The default RAS orientation corresponds to the first axis being ordered from left to right, the second axis from posterior to anterior, and the third axis from inferior to superior.

For oblique images, the original orientation is considered to be the closest plumb orientation.

No resampling is performed, and thus the output image is not de-obliques or registered to any other image or template.

The effective transform is calculated from the original affine matrix to the reoriented affine matrix.

86.1.1 Examples

If an image is not reoriented, the original file is not modified

```
>>> import numpy as np
>>> from nipy.interfaces.image import Reorient
>>> reorient = Reorient(orientation='LPS')
>>> reorient.inputs.in_file = 'segmentation0.nii.gz'
>>> res = reorient.run()
>>> res.outputs.out_file
'segmentation0.nii.gz'
```

```
>>> print_affine(np.loadtxt(res.outputs.transform))
1.  0.  0.  0.
0.  1.  0.  0.
0.  0.  1.  0.
0.  0.  0.  1.
```

```
>>> reorient.inputs.orientation = 'RAS'
>>> res = reorient.run()
>>> res.outputs.out_file # doctest: +ELLIPSIS
'.../segmentation0_ras.nii.gz'
```

```
>>> print_affine(np.loadtxt(res.outputs.transform))
-1.  0.  0.  60.
 0. -1.  0.  72.
 0.  0.  1.   0.
 0.  0.  0.   1.
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
        Input image

[Optional]
orientation: ('RAS' or 'RAI' or 'RPS' or 'RPI' or 'LAS' or 'LAI' or
              'LPS' or 'LPI' or 'RSA' or 'RSP' or 'RIA' or 'RIP' or 'LSA' or
              'LSP' or 'LIA' or 'LIP' or 'ARS' or 'ARI' or 'ALS' or 'ALI' or
              'PRS' or 'PRI' or 'PLS' or 'PLI' or 'ASR' or 'ASL' or 'AIR' or
              'AIL' or 'PSR' or 'PSL' or 'PIR' or 'PIL' or 'SRA' or 'SRP' or
              'SLA' or 'SLP' or 'IRA' or 'IRP' or 'ILA' or 'ILP' or 'SAR' or
              'SAL' or 'SPR' or 'SPL' or 'IAR' or 'IAL' or 'IPR' or 'IPL',
              nipy default value: RAS)
        Target axis orientation
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
          Reoriented image
transform: (a pathlike object or string representing an existing
          file)
          Affine transform from input orientation to output
```

86.2 Rescale

[Link to code](#)**Rescale an image**

Rescales the non-zero portion of `in_file` to match the bounds of the non-zero portion of `ref_file`. Reference values in the input and reference images are defined by the `percentile` parameter, and the reference values in each image are identified and the remaining values are scaled accordingly. In the case of `percentile == 0`, the reference values are the maxima and minima of each image. If the `invert` parameter is set, the input file is inverted prior to rescaling.

86.2.1 Examples

To use a high-resolution T1w image as a registration target for a T2* image, it may be useful to invert the T1w image and rescale to the T2* range. Using the 1st and 99th percentiles may reduce the impact of outlier voxels.

```
>>> from nipy.interfaces.image import Rescale
>>> invert_t1w = Rescale(invert=True)
>>> invert_t1w.inputs.in_file = 'structural.nii'
>>> invert_t1w.inputs.ref_file = 'functional.nii'
>>> invert_t1w.inputs.percentile = 1.
>>> res = invert_t1w.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
```

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```
Skull-stripped image to rescale
ref_file: (a pathlike object or string representing an existing file)
Skull-stripped reference image

[Optional]
invert: (a boolean)
    Invert contrast of rescaled image
percentile: (0.0 <= a floating point number <= 50.0, nipyte default
    value: 0.0)
    Percentile to use for reference to allow for outliers - 1 indicates
    the 1st and 99th percentiles in the input file will be mapped to the
    99th and 1st percentiles in the reference; 0 indicates minima and
    maxima will be mapped
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
Rescaled image
```


87.1 BIDSDataGrabber

[Link to code](#)

BIDS datagrabber module that wraps around pybids to allow arbitrary querying of BIDS datasets.

87.1.1 Examples

By default, the BIDSDataGrabber fetches anatomical and functional images from a project, and makes BIDS entities (e.g. subject) available for filtering outputs.

```
>>> bg = BIDSDataGrabber()
>>> bg.inputs.base_dir = 'ds005/'
>>> bg.inputs.subject = '01'
>>> results = bg.run() # doctest: +SKIP
```

Dynamically created, user-defined output fields can also be defined to return different types of outputs from the same project. All outputs are filtered on common entities, which can be explicitly defined as infields.

```
>>> bg = BIDSDataGrabber(infields = ['subject'])
>>> bg.inputs.base_dir = 'ds005/'
>>> bg.inputs.subject = '01'
>>> bg.inputs.output_query['dwi'] = dict(datatype='dwi')
>>> results = bg.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
base_dir: (a pathlike object or string representing an existing
          directory)
          Path to BIDS Directory.
index_derivatives: (a boolean, nipype default value: False)
                   Index derivatives/ sub-directory

[Optional]
output_query: (a dictionary with keys which are a unicode string and
              with values which are a dictionary with keys which are any value
              and with values which are any value)
```

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```

    Queries for outfield outputs
    raise_on_empty: (a boolean, nipyne default value: True)
        Generate exception if list is empty for a given field
    extra_derivatives: (a list of items which are a pathlike object or
        string representing an existing directory)
        Additional derivative directories to index

```

Outputs:

None

87.2 DataFinder

[Link to code](#)

Search for paths that match a given regular expression. Allows a less proscriptive approach to gathering input files compared to DataGrabber. Will recursively search any subdirectories by default. This can be limited with the min/max depth options. Matched paths are available in the output 'out_paths'. Any named groups of captured text from the regular expression are also available as outputs of the same name.

87.2.1 Examples

```

>>> from nipyne.interfaces.io import DataFinder
>>> df = DataFinder()
>>> df.inputs.root_paths = '.'
>>> df.inputs.match_regex = '.*/(?P<series_dir>.*(qT1|ep2d_fid_T1).+)/(?P
↳<basename>.+)\.nii.gz'
>>> result = df.run() # doctest: +SKIP
>>> result.outputs.out_paths # doctest: +SKIP
['./027-ep2d_fid_T1_Gd4/acquisition.nii.gz',
 './018-ep2d_fid_T1_Gd2/acquisition.nii.gz',
 './016-ep2d_fid_T1_Gd1/acquisition.nii.gz',
 './013-ep2d_fid_T1_pre/acquisition.nii.gz']
>>> result.outputs.series_dir # doctest: +SKIP
['027-ep2d_fid_T1_Gd4',
 '018-ep2d_fid_T1_Gd2',
 '016-ep2d_fid_T1_Gd1',
 '013-ep2d_fid_T1_pre']
>>> result.outputs.basename # doctest: +SKIP
['acquisition',
 'acquisition',
 'acquisition',
 'acquisition']

```

Inputs:

```

[Mandatory]
root_paths: (a list of items which are any value or a unicode string)

[Optional]
match_regex: (a unicode string, nipyne default value: (.+))
    Regular expression for matching paths.
ignore_regexes: (a list of items which are any value)
    List of regular expressions, if any match the path it will be
    ignored.
max_depth: (an integer (int or long))

```

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```

        The maximum depth to search beneath the root_paths
min_depth: (an integer (int or long))
        The minimum depth to search beneath the root paths
unpack_single: (a boolean, nipy default value: False)
        Unpack single results from list

```

Outputs:

None

87.3 DataGrabber

[Link to code](#)

Generic datagrabber module that wraps around glob in an intelligent way for neuroimaging tasks to grab files

Attention: Doesn't support directories currently

87.3.1 Examples

```
>>> from nipy.interfaces.io import DataGrabber
```

Pick all files from current directory

```
>>> dg = DataGrabber()
>>> dg.inputs.template = '*'
```

Pick file foo/foo.nii from current directory

```
>>> dg.inputs.template = '%s/%s.dcm'
>>> dg.inputs.template_args['outfiles'] = [['dicomdir', '123456-1-1.dcm']]
```

Same thing but with dynamically created fields

```
>>> dg = DataGrabber(infields=['arg1', 'arg2'])
>>> dg.inputs.template = '%s/%s.nii'
>>> dg.inputs.arg1 = 'foo'
>>> dg.inputs.arg2 = 'foo'
```

however this latter form can be used with iterables and iterfield in a pipeline.

Dynamically created, user-defined input and output fields

```
>>> dg = DataGrabber(infields=['sid'], outfields=['func', 'struct', 'ref'])
>>> dg.inputs.base_directory = '.'
>>> dg.inputs.template = '%s/%s.nii'
>>> dg.inputs.template_args['func'] = [['sid', ['f3', 'f5']]]
>>> dg.inputs.template_args['struct'] = [['sid', ['struct']]]
>>> dg.inputs.template_args['ref'] = [['sid', 'ref']]
>>> dg.inputs.sid = 's1'
```

Change the template only for output field struct. The rest use the general template

```
>>> dg.inputs.field_template = dict(struct='%s/struct.nii')
>>> dg.inputs.template_args['struct'] = [['sid']]
```

Inputs:

```
[Mandatory]
sort_filelist: (a boolean)
    Sort the filelist that matches the template
template: (a unicode string)
    Layout used to get files. relative to base directory if defined

[Optional]
base_directory: (a pathlike object or string representing an existing
    directory)
    Path to the base directory consisting of subject data.
raise_on_empty: (a boolean, nipyne default value: True)
    Generate exception if list is empty for a given field
drop_blank_outputs: (a boolean, nipyne default value: False)
    Remove ``None`` entries from output lists
template_args: (a dictionary with keys which are a unicode string and
    with values which are a list of items which are a list of items
    which are any value)
    Information to plug into template
```

Outputs:

None

87.4 DataSink

[Link to code](#)

Generic datasink module to store structured outputs

Primarily for use within a workflow. This interface allows arbitrary creation of input attributes. The names of these attributes define the directory structure to create for storage of the files or directories.

The attributes take the following form:

```
string[.[@]]string[.[@]]string[.[@]]...
```

where parts between [] are optional.

An attribute such as contrasts.@con will create a 'contrasts' directory to store the results linked to the attribute.

If the @ is left out, such as in 'contrasts.con', a subdirectory 'con' will be created under 'contrasts'.

the general form of the output is:

```
'base_directory/container/parameterization/destloc/filename'
```

```
destloc = string[.[@]]string[.[@]]string[.[@]] and
filename comes from the input to the connect statement.
```

Warning: This is not a thread-safe node because it can write to a common shared location. It will not complain when it overwrites a file.

Note: If both substitutions and regexp_substitutions are used, then substitutions are applied first followed by regexp_substitutions.

This interface **cannot** be used in a MapNode as the inputs are defined only when the connect statement is executed.

87.4.1 Examples

```
>>> ds = DataSink()
>>> ds.inputs.base_directory = 'results_dir'
>>> ds.inputs.container = 'subject'
>>> ds.inputs.structural = 'structural.nii'
>>> setattr(ds.inputs, 'contrasts.@con', ['cont1.nii', 'cont2.nii'])
>>> setattr(ds.inputs, 'contrasts.alt', ['cont1a.nii', 'cont2a.nii'])
>>> ds.run() # doctest: +SKIP
```

To use DataSink in a MapNode, its inputs have to be defined at the time the interface is created.

```
>>> ds = DataSink(infields=['contrasts.@con'])
>>> ds.inputs.base_directory = 'results_dir'
>>> ds.inputs.container = 'subject'
>>> ds.inputs.structural = 'structural.nii'
>>> setattr(ds.inputs, 'contrasts.@con', ['cont1.nii', 'cont2.nii'])
>>> setattr(ds.inputs, 'contrasts.alt', ['cont1a.nii', 'cont2a.nii'])
>>> ds.run() # doctest: +SKIP
```

Inputs:

```
[Optional]
base_directory: (a pathlike object or string representing a
    directory)
    Path to the base directory for storing data.
container: (a unicode string)
    Folder within base directory in which to store output
parameterization: (a boolean, nipy default value: True)
    store output in parametrized structure
strip_dir: (a pathlike object or string representing a directory)
    path to strip out of filename
substitutions: (a list of items which are a tuple of the form: (a
    unicode string, a unicode string))
    List of 2-tuples reflecting string to substitute and string to
    replace it with
regexp_substitutions: (a list of items which are a tuple of the form:
    (a unicode string, a unicode string))
    List of 2-tuples reflecting a pair of a Python regexp pattern and a
    replacement string. Invoked after string `substitutions`
_outputs: (a dictionary with keys which are a unicode string and with
    values which are any value, nipy default value: {})
remove_dest_dir: (a boolean, nipy default value: False)
    remove dest directory when copying dirs
creds_path: (a unicode string)
    Filepath to AWS credentials file for S3 bucket access; if not
    specified, the credentials will be taken from the AWS_ACCESS_KEY_ID
    and AWS_SECRET_ACCESS_KEY environment variables
encrypt_bucket_keys: (a boolean)
    Flag indicating whether to use S3 server-side AES-256 encryption
bucket: (any value)
    Boto3 S3 bucket for manual override of bucket
local_copy: (a unicode string)
    Copy files locally as well as to S3 bucket
```

Outputs:

```
out_file: (any value)
    datasink output
```

87.5 FreeSurferSource

[Link to code](#)

Generates freesurfer subject info from their directories

87.5.1 Examples

```
>>> from nipy.interfaces.io import FreeSurferSource
>>> fs = FreeSurferSource()
>>> #fs.inputs.subjects_dir = '.'
>>> fs.inputs.subject_id = 'PWS04'
>>> res = fs.run() # doctest: +SKIP
```

```
>>> fs.inputs.hemi = 'lh'
>>> res = fs.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
subjects_dir: (a pathlike object or string representing an existing
               directory)
               Freesurfer subjects directory.
subject_id: (a unicode string)
             Subject name for whom to retrieve data

[Optional]
hemi: ('both' or 'lh' or 'rh', nipy default value: both)
       Selects hemisphere specific outputs
```

Outputs:

```
T1: (a pathlike object or string representing an existing file)
     Intensity normalized whole-head volume
aseg: (a pathlike object or string representing an existing file)
       Volumetric map of regions from automatic segmentation
brain: (a pathlike object or string representing an existing file)
        Intensity normalized brain-only volume
brainmask: (a pathlike object or string representing an existing
            file)
            Skull-stripped (brain-only) volume
filled: (a pathlike object or string representing an existing file)
         Subcortical mass volume
norm: (a pathlike object or string representing an existing file)
        Normalized skull-stripped volume
nu: (a pathlike object or string representing an existing file)
     Non-uniformity corrected whole-head volume
orig: (a pathlike object or string representing an existing file)
        Base image conformed to Freesurfer space
rawavg: (a pathlike object or string representing an existing file)
          Volume formed by averaging input images
ribbon: (a list of items which are a pathlike object or string
          representing an existing file)
          Volumetric maps of cortical ribbons
wm: (a pathlike object or string representing an existing file)
     Segmented white-matter volume
wmparc: (a pathlike object or string representing an existing file)
          Aparc parcellation projected into subcortical white matter
```

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```

curv: (a list of items which are a pathlike object or string
      representing an existing file)
      Maps of surface curvature
avg_curv: (a list of items which are a pathlike object or string
          representing an existing file)
          Average atlas curvature, sampled to subject
inflated: (a list of items which are a pathlike object or string
          representing an existing file)
          Inflated surface meshes
pial: (a list of items which are a pathlike object or string
      representing an existing file)
      Gray matter/pia mater surface meshes
area_pial: (a list of items which are a pathlike object or string
           representing an existing file)
           Mean area of triangles each vertex on the pial surface is associated
           with
curv_pial: (a list of items which are a pathlike object or string
           representing an existing file)
           Curvature of pial surface
smoothwm: (a list of items which are a pathlike object or string
          representing an existing file)
          Smoothed original surface meshes
sphere: (a list of items which are a pathlike object or string
        representing an existing file)
        Spherical surface meshes
sulc: (a list of items which are a pathlike object or string
      representing an existing file)
      Surface maps of sulcal depth
thickness: (a list of items which are a pathlike object or string
          representing an existing file)
          Surface maps of cortical thickness
volume: (a list of items which are a pathlike object or string
        representing an existing file)
        Surface maps of cortical volume
white: (a list of items which are a pathlike object or string
       representing an existing file)
       White/gray matter surface meshes
jacobian_white: (a list of items which are a pathlike object or
               string representing an existing file)
               Distortion required to register to spherical atlas
graymid: (a list of items which are a pathlike object or string
         representing an existing file)
         Graymid/midthickness surface meshes
label: (a list of items which are a pathlike object or string
       representing an existing file)
       Volume and surface label files
annot: (a list of items which are a pathlike object or string
      representing an existing file)
      Surface annotation files
aparc_aseg: (a list of items which are a pathlike object or string
            representing an existing file)
            Aparc parcellation projected into aseg volume
sphere_reg: (a list of items which are a pathlike object or string
            representing an existing file)
            Spherical registration file
aseg_stats: (a list of items which are a pathlike object or string
            representing an existing file)

```

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```

Automated segmentation statistics file
wmparc_stats: (a list of items which are a pathlike object or string
               representing an existing file)
White matter parcellation statistics file
aparc_stats: (a list of items which are a pathlike object or string
              representing an existing file)
Aparc parcellation statistics files
BA_stats: (a list of items which are a pathlike object or string
           representing an existing file)
Brodmann Area statistics files
aparc_a2009s_stats: (a list of items which are a pathlike object or
                    string representing an existing file)
Aparc a2009s parcellation statistics files
curv_stats: (a list of items which are a pathlike object or string
             representing an existing file)
Curvature statistics files
entorhinal_exvivo_stats: (a list of items which are a pathlike object
                          or string representing an existing file)
Entorhinal exvivo statistics files

```

87.6 IOBase

[Link to code](#)

Inputs:

None

Outputs:

None

87.7 JSONFileGrabber

[Link to code](#)

Datagrabber interface that loads a json file and generates an output for every first-level object

87.7.1 Example

```

>>> import pprint
>>> from nipy.interfaces.io import JSONFileGrabber
>>> jsonSource = JSONFileGrabber()
>>> jsonSource.inputs.defaults = {'param1': 'overrideMe', 'param3': 1.0}
>>> res = jsonSource.run()
>>> pprint.pprint(res.outputs.get())
{'param1': 'overrideMe', 'param3': 1.0}
>>> jsonSource.inputs.in_file = os.path.join(datadir, 'jsongrabber.txt')
>>> res = jsonSource.run()
>>> pprint.pprint(res.outputs.get()) # doctest:, +ELLIPSIS
{'param1': 'exampleStr', 'param2': 4, 'param3': 1.0}

```

Inputs:


```
[Optional]
in_file: (a pathlike object or string representing an existing file)
        JSON source file
defaults: (a dictionary with keys which are any value and with values
           which are any value)
           JSON dictionary that sets default outputvalues, overridden by values
           found in in_file
```

Outputs:

None

87.8 JSONFileSink

[Link to code](#)

Very simple frontend for storing values into a JSON file. Entries already existing in in_dict will be overridden by matching entries dynamically added as inputs.

Warning: This is not a thread-safe node because it can write to a common shared location. It will not complain when it overwrites a file.

```
>>> jsonsink = JSONFileSink(input_names=['subject_id',
...                               'some_measurement'])
>>> jsonsink.inputs.subject_id = 's1'
>>> jsonsink.inputs.some_measurement = 11.4
>>> jsonsink.run() # doctest: +SKIP
```

Using a dictionary as input:

```
>>> dictsink = JSONFileSink()
>>> dictsink.inputs.in_dict = {'subject_id': 's1',
...                             'some_measurement': 11.4}
>>> dictsink.run() # doctest: +SKIP
```

Inputs:

```
[Optional]
out_file: (a pathlike object or string representing a file)
        JSON sink file
in_dict: (a dictionary with keys which are any value and with values
         which are any value, nipype default value: {})
         input JSON dictionary
_outputs: (a dictionary with keys which are any value and with values
         which are any value, nipype default value: {})
```

Outputs:

```
out_file: (a pathlike object or string representing a file)
        JSON sink file
```

87.9 MySQLSink

[Link to code](#)

Very simple frontend for storing values into MySQL database.

87.9.1 Examples

```
>>> sql = MySQLSink(input_names=['subject_id', 'some_measurement'])
>>> sql.inputs.database_name = 'my_database'
>>> sql.inputs.table_name = 'experiment_results'
>>> sql.inputs.username = 'root'
>>> sql.inputs.password = 'secret'
>>> sql.inputs.subject_id = 's1'
>>> sql.inputs.some_measurement = 11.4
>>> sql.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
host: (a unicode string, nipy default value: localhost)
      mutually_exclusive: config
      requires: username, password
config: (a pathlike object or string representing a file)
        MySQL Options File (same format as my.cnf)
        mutually_exclusive: host
database_name: (a unicode string)
               Otherwise known as the schema name
table_name: (a unicode string)

[Optional]
username: (a unicode string)
password: (a unicode string)
```

Outputs:

None

87.10 S3DataGrabber

[Link to code](#)

Generic datagrabber module that wraps around glob in an intelligent way for neuroimaging tasks to grab files from Amazon S3

Works exactly like DataGrabber, except, you must specify an S3 “bucket” and “bucket_path” to search for your data and a “local_directory” to store the data. “local_directory” should be a location on HDFS for Spark jobs. Additionally, “template” uses regex style formatting, rather than the glob-style found in the original DataGrabber.

87.10.1 Examples

```
>>> s3grab = S3DataGrabber(infields=['subj_id'], outfields=["func", "anat"])
>>> s3grab.inputs.bucket = 'openneuro'
>>> s3grab.inputs.sort_filelist = True
>>> s3grab.inputs.template = '*'
>>> s3grab.inputs.anon = True
>>> s3grab.inputs.bucket_path = 'ds000101/ds000101_R2.0.0/uncompressed/'
>>> s3grab.inputs.local_directory = '/tmp'
>>> s3grab.inputs.field_template = {'anat': '%s/anat/%s_T1w.nii.gz',
...                               'func': '%s/func/%s_task-simon_run-1_bold.nii.
→gz'}
>>> s3grab.inputs.template_args = {'anat': [['subj_id', 'subj_id']],
```

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```
...                                     'func': [['subj_id', 'subj_id']]}
>>> s3grab.inputs.subj_id = 'sub-01'
>>> s3grab.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
bucket: (a unicode string)
    Amazon S3 bucket where your data is stored
sort_filelist: (a boolean)
    Sort the filelist that matches the template
template: (a unicode string)
    Layout used to get files. Relative to bucket_path if defined. Uses
    regex rather than glob style formatting.

[Optional]
anon: (a boolean, nipy default value: False)
    Use anonymous connection to s3. If this is set to True, boto may
    print a urlopen error, but this does not prevent data from being
    downloaded.
region: (a unicode string, nipy default value: us-east-1)
    Region of s3 bucket
bucket_path: (a unicode string, nipy default value: )
    Location within your bucket for subject data.
local_directory: (a pathlike object or string representing an
    existing directory)
    Path to the local directory for subject data to be downloaded and
    accessed. Should be on HDFS for Spark jobs.
raise_on_empty: (a boolean, nipy default value: True)
    Generate exception if list is empty for a given field
template_args: (a dictionary with keys which are a unicode string and
    with values which are a list of items which are a list of items
    which are any value)
    Information to plug into template
```

Outputs:

```
None
```

87.11 SQLiteSink

[Link to code](#)

Very simple frontend for storing values into SQLite database.

Warning: This is not a thread-safe node because it can write to a common shared location. It will not complain when it overwrites a file.

87.11.1 Examples

```
>>> sql = SQLiteSink(input_names=['subject_id', 'some_measurement'])
>>> sql.inputs.database_file = 'my_database.db'
>>> sql.inputs.table_name = 'experiment_results'
>>> sql.inputs.subject_id = 's1'
```

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```
>>> sql.inputs.some_measurement = 11.4
>>> sql.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
database_file: (a pathlike object or string representing an existing
               file)
table_name: (a unicode string)
```

Outputs:

```
None
```

87.12 SSHDataGrabber

[Link to code](#)

Extension of DataGrabber module that downloads the file list and optionally the files from a SSH server. The SSH operation must not need user and password so an SSH agent must be active in where this module is being run.

Attention: Doesn't support directories currently

87.12.1 Examples

```
>>> from nipyne.interfaces.io import SSHDataGrabber
>>> dg = SSHDataGrabber()
>>> dg.inputs.hostname = 'test.rebex.net'
>>> dg.inputs.user = 'demo'
>>> dg.inputs.password = 'password'
>>> dg.inputs.base_directory = 'pub/example'
```

Pick all files from the base directory

```
>>> dg.inputs.template = '*'
```

Pick all files starting with “s” and a number from current directory

```
>>> dg.inputs.template_expression = 'regexp'
>>> dg.inputs.template = 'pop[0-9].*'
```

Same thing but with dynamically created fields

```
>>> dg = SSHDataGrabber(infields=['arg1', 'arg2'])
>>> dg.inputs.hostname = 'test.rebex.net'
>>> dg.inputs.user = 'demo'
>>> dg.inputs.password = 'password'
>>> dg.inputs.base_directory = 'pub'
>>> dg.inputs.template = '%s/%s.txt'
>>> dg.inputs.arg1 = 'example'
>>> dg.inputs.arg2 = 'foo'
```

however this latter form can be used with iterables and iterfield in a pipeline.
Dynamically created, user-defined input and output fields

```
>>> dg = SSHDataGrabber(infields=['sid'], outfields=['func', 'struct', 'ref'])
>>> dg.inputs.hostname = 'myhost.com'
>>> dg.inputs.base_directory = '/main_folder/my_remote_dir'
>>> dg.inputs.template_args['func'] = [['sid'], ['f3', 'f5']]
>>> dg.inputs.template_args['struct'] = [['sid'], ['struct']]
>>> dg.inputs.template_args['ref'] = [['sid', 'ref']]
>>> dg.inputs.sid = 's1'
```

Change the template only for output field struct. The rest use the general template

```
>>> dg.inputs.field_template = dict(struct='%s/struct.nii')
>>> dg.inputs.template_args['struct'] = [['sid']]
```

Inputs:

```
[Mandatory]
hostname: (a unicode string)
    Server hostname.
base_directory: (a unicode string)
    Path to the base directory consisting of subject data.
sort_filelist: (a boolean)
    Sort the filelist that matches the template
template: (a unicode string)
    Layout used to get files. relative to base directory if defined

[Optional]
username: (a unicode string)
    Server username.
password: (a string)
    Server password.
download_files: (a boolean, nipyne default value: True)
    If false it will return the file names without downloading them
template_expression: ('fnmatch' or 'regex', nipyne default value:
    fnmatch)
    Use either fnmatch or regex to express templates
ssh_log_to_file: (a unicode string, nipyne default value: )
    If set SSH commands will be logged to the given file
raise_on_empty: (a boolean, nipyne default value: True)
    Generate exception if list is empty for a given field
drop_blank_outputs: (a boolean, nipyne default value: False)
    Remove ``None`` entries from output lists
template_args: (a dictionary with keys which are a unicode string and
    with values which are a list of items which are a list of items
    which are any value)
    Information to plug into template
```

Outputs:

None

87.13 SelectFiles

[Link to code](#)

Flexibly collect data from disk to feed into workflows.

This interface uses the {}-based string formatting syntax to plug values (possibly known only at workflow execution time) into string templates and collect files from persistent storage. These templates can also be combined with glob wildcards. The field names in the formatting template (i.e. the terms in braces) will become inputs fields on the interface, and the keys in the templates dictionary will form the output fields.

87.13.1 Examples

```
>>> import pprint
>>> from nipy import SelectFiles, Node
>>> templates={"T1": "{subject_id}/struct/T1.nii",
...           "epi": "{subject_id}/func/f[0, 1].nii"}
>>> dg = Node(SelectFiles(templates), "selectfiles")
>>> dg.inputs.subject_id = "subj1"
>>> pprint.pprint(dg.outputs.get()) # doctest:
{'T1': <undefined>, 'epi': <undefined>}
```

The same thing with dynamic grabbing of specific files:

```
>>> templates["epi"] = "{subject_id}/func/f{run!s}.nii"
>>> dg = Node(SelectFiles(templates), "selectfiles")
>>> dg.inputs.subject_id = "subj1"
>>> dg.inputs.run = [2, 4]
```

Inputs:

```
[Optional]
base_directory: (a pathlike object or string representing an existing
                 directory)
                 Root path common to templates.
sort_filelist: (a boolean, nipy default value: True)
                 When matching mutliple files, return them in sorted order.
raise_on_empty: (a boolean, nipy default value: True)
                 Raise an exception if a template pattern matches no files.
force_lists: (a boolean or a list of items which are a unicode
              string, nipy default value: False)
              Whether to return outputs as a list even when only one file matches
              the template. Either a boolean that applies to all output fields or
              a list of output field names to coerce to a list
```

Outputs:

None

87.14 XNATSink

[Link to code](#)

Generic datasink module that takes a directory containing a list of nifti files and provides a set of structured output fields.

Inputs:

```
[Mandatory]
server: (a unicode string)
        mutually_exclusive: config
        requires: user, pwd
config: (a pathlike object or string representing a file)
        mutually_exclusive: server
project_id: (a unicode string)
            Project in which to store the outputs
subject_id: (a unicode string)
            Set to subject id
experiment_id: (a unicode string)
               Set to workflow name
```

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```
[Optional]
_outputs: (a dictionary with keys which are a unicode string and with
          values which are any value, nipy default value: {})
user: (a unicode string)
pwd: (a string)
cache_dir: (a pathlike object or string representing a directory)
assessor_id: (a unicode string)
    Option to customize outputs representation in XNAT - assessor level
    will be used with specified id
    mutually_exclusive: reconstruction_id
reconstruction_id: (a unicode string)
    Option to customize outputs representation in XNAT - reconstruction
    level will be used with specified id
    mutually_exclusive: assessor_id
share: (a boolean, nipy default value: False)
    Option to share the subjects from the original project instead of
    creating new ones when possible - the created experiments are then
    shared back to the original project
```

Outputs:

None

87.15 XNATSource

[Link to code](#)

Generic XNATSource module that wraps around the pyxnat module in an intelligent way for neuroimaging tasks to grab files and data from an XNAT server.

87.15.1 Examples

```
>>> from nipy.interfaces.io import XNATSource
```

Pick all files from current directory

```
>>> dg = XNATSource()
>>> dg.inputs.template = '*'
```

```
>>> dg = XNATSource(infields=['project', 'subject', 'experiment', 'assessor', 'inout
↪'])
>>> dg.inputs.query_template = '/projects/%s/subjects/%s/experiments/%s'
↪ '/assessors/%s/%s_resources/files'
>>> dg.inputs.project = 'IMAGEN'
>>> dg.inputs.subject = 'IMAGEN_000000001274'
>>> dg.inputs.experiment = '*SessionA*'
>>> dg.inputs.assessor = '*ADNI_MPRAGE_nii'
>>> dg.inputs.inout = 'out'
```

```
>>> dg = XNATSource(infields=['sid'], outfields=['struct', 'func'])
>>> dg.inputs.query_template = '/projects/IMAGEN/subjects/%s/experiments/
↪ *SessionA*'
>>> dg.inputs.query_template_args['struct'] = [['sid', 'ADNI_MPRAGE']]
>>> dg.inputs.query_template_args['func'] = [['sid', 'EPI_faces']]
>>> dg.inputs.sid = 'IMAGEN_000000001274'
```

Inputs:

```
[Mandatory]
query_template: (a unicode string)
    Layout used to get files. Relative to base directory if defined
server: (a unicode string)
    mutually_exclusive: config
    requires: user, pwd
config: (a pathlike object or string representing a file)
    mutually_exclusive: server

[Optional]
query_template_args: (a dictionary with keys which are a unicode
    string and with values which are a list of items which are a list
    of items which are any value, nipyre default value: {'outfiles':
    []})
    Information to plug into template
user: (a unicode string)
pwd: (a string)
cache_dir: (a pathlike object or string representing a directory)
    Cache directory
```

Outputs:

```
None
```

87.16 add_traits()

[Link to code](#)

Add traits to a traitled class.

All traits are set to Undefined by default

87.17 copytree()

[Link to code](#)

Recursively copy a directory tree using `nipyre.utils.filemanip.copyfile()`

This is not a thread-safe routine. However, in the case of creating new directories, it checks to see if a particular directory has already been created by another process.

87.18 push_file()

[Link to code](#)

87.19 quote_id()

[Link to code](#)

87.20 unquote_id()

[Link to code](#)

88.1 MeshFix

[Link to code](#)

Wraps the executable command `meshfix`.

MeshFix v1.2-alpha - by Marco Attene, Mirko Windhoff, Axel Thielscher.

See also:

<http://jmeshlib.sourceforge.net> Sourceforge page

<http://simnibs.de/installation/meshfixandgetfem> Ubuntu installation instructions

If MeshFix is used for research purposes, please cite the following paper: M. Attene - A lightweight approach to repairing digitized polygon meshes. The Visual Computer, 2010. (c) Springer.

Accepted input formats are OFF, PLY and STL. Other formats (like .msh for gmsh) are supported only partially.

88.1.1 Example

```
>>> import nipy.interfaces.meshfix as mf
>>> fix = mf.MeshFix()
>>> fix.inputs.in_file1 = 'lh-pial.stl'
>>> fix.inputs.in_file2 = 'rh-pial.stl'
>>> fix.run()                                     # doctest: +SKIP
>>> fix.cmdline
'meshfix lh-pial.stl rh-pial.stl -o lh-pial_fixed.off'
```

Inputs:

```
[Mandatory]
in_file1: (a pathlike object or string representing an existing file)
          argument: ``%s``, position: 1

[Optional]
number_of_biggest_shells: (an integer (int or long))
                          Only the N biggest shells are kept
                          argument: ``--shells %d``
epsilon_angle: (0.0 <= a floating point number <= 2.0)
                Epsilon angle in degrees (must be between 0 and 2)
                argument: ``-a %f``
```

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```

join_overlapping_largest_components: (a boolean)
    Join 2 biggest components if they overlap, remove the rest.
    argument: ``-j``
    mutually_exclusive: join_closest_components
join_closest_components: (a boolean)
    Join the closest pair of components.
    argument: ``-jc``
    mutually_exclusive: join_closest_components
quiet_mode: (a boolean)
    Quiet mode, don't write much to stdout.
    argument: ``-q``
dont_clean: (a boolean)
    Don't Clean
    argument: ``--no-clean``
save_as_stl: (a boolean)
    Result is saved in stereolithographic format (.stl)
    argument: ``--stl``
    mutually_exclusive: save_as_vrml, save_as_freesurfer_mesh
save_as_vrml: (a boolean)
    Result is saved in VRML1.0 format (.wrl)
    argument: ``--wrl``
    mutually_exclusive: save_as_stl, save_as_freesurfer_mesh
save_as_freesurfer_mesh: (a boolean)
    Result is saved in freesurfer mesh format
    argument: ``--fsmesh``
    mutually_exclusive: save_as_vrml, save_as_stl
remove_handles: (a boolean)
    Remove handles
    argument: ``--remove-handles``
uniform_remeshing_steps: (an integer (int or long))
    Number of steps for uniform remeshing of the whole mesh
    argument: ``-u %d``
    requires: uniform_remeshing_vertices
uniform_remeshing_vertices: (an integer (int or long))
    Constrains the number of vertices. Must be used with
    uniform_remeshing_steps
    argument: ``--vertices %d``
    requires: uniform_remeshing_steps
laplacian_smoothing_steps: (an integer (int or long))
    The number of laplacian smoothing steps to apply
    argument: ``--smooth %d``
x_shift: (an integer (int or long))
    Shifts the coordinates of the vertices when saving. Output must be
    in FreeSurfer format
    argument: ``--smooth %d``
cut_outer: (an integer (int or long))
    Remove triangles of 1st that are outside of the 2nd shell.
    argument: ``--cut-outer %d``
cut_inner: (an integer (int or long))
    Remove triangles of 1st that are inside of the 2nd shell. Dilate 2nd
    by N; Fill holes and keep only 1st afterwards.
    argument: ``--cut-inner %d``
decouple_inin: (an integer (int or long))
    Treat 1st file as inner, 2nd file as outer component. Resolve
    overlaps by moving inners triangles inwards. Constrain the min
    distance between the components > d.
    argument: ``--decouple-inin %d``

```

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```

decouple_outin: (an integer (int or long))
    Treat 1st file as outer, 2nd file as inner component. Resolve
    overlaps by moving outers triangles inwards. Constrain the min
    distance between the components > d.
    argument: ``--decouple-outin %d``
decouple_outout: (an integer (int or long))
    Treat 1st file as outer, 2nd file as inner component. Resolve
    overlaps by moving outers triangles outwards. Constrain the min
    distance between the components > d.
    argument: ``--decouple-outout %d``
finetuning_inwards: (a boolean)
    Used to fine-tune the minimal distance between surfaces.
    argument: ``--fineTuneIn``, position: -3
    requires: finetuning_distance, finetuning_substeps
finetuning_outwards: (a boolean)
    Similar to finetuning_inwards, but ensures minimal distance in the
    other direction
    argument: ``--fineTuneOut``, position: -3
    mutually_exclusive: finetuning_inwards
    requires: finetuning_distance, finetuning_substeps
finetuning_distance: (a float)
    Used to fine-tune the minimal distance between surfaces. A minimal
    distance d is ensured, and reached in n substeps. When using the
    surfaces for subsequent volume meshing by gmsh, this step prevent
    too flat tetrahedra2)
    argument: ``%f``, position: -2
    requires: finetuning_substeps
finetuning_substeps: (an integer (int or long))
    Used to fine-tune the minimal distance between surfaces. A minimal
    distance d is ensured, and reached in n substeps. When using the
    surfaces for subsequent volume meshing by gmsh, this step prevent
    too flat tetrahedra2)
    argument: ``%d``, position: -1
    requires: finetuning_distance
dilation: (an integer (int or long))
    Dilate the surface by d. d < 0 means shrinking.
    argument: ``--dilate %d``
set_intersections_to_one: (a boolean)
    If the mesh contains intersections, return value = 1. If saved in
    gmsh format, intersections will be highlighted.
    argument: ``--intersect``
in_file2: (a pathlike object or string representing an existing file)
    argument: ``%s``, position: 2
output_type: ('stl' or 'msh' or 'wrl' or 'vrml' or 'fs' or 'off',
    nipyre default value: off)
    The output type to save the file as.
out_filename: (a pathlike object or string representing a file)
    The output filename for the fixed mesh file
    argument: ``-o %s``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyre default value: {})
    Environment variables

```

Outputs:

```
mesh_file: (a pathlike object or string representing an existing
            file)
            The output mesh file
```

89.1 NilearnBaseInterface

[Link to code](#)

Inputs:

None

Outputs:

None

89.2 SignalExtraction

[Link to code](#)

Extracts signals over tissue classes or brain regions

```
>>> seinterface = SignalExtraction()
>>> seinterface.inputs.in_file = 'functional.nii'
>>> seinterface.inputs.label_files = 'segmentation0.nii.gz'
>>> seinterface.inputs.out_file = 'means.tsv'
>>> segments = ['CSF', 'GrayMatter', 'WhiteMatter']
>>> seinterface.inputs.class_labels = segments
>>> seinterface.inputs.detrrend = True
>>> seinterface.inputs.include_global = True
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         4-D fMRI nii file
label_files: (a list of items which are a pathlike object or string
              representing an existing file)
              a 3-D label image, with 0 denoting background, or a list of 3-D
              probability maps (one per label) or the equivalent 4D file.
class_labels: (a list of items which are any value)
               Human-readable labels for each segment in the label file, in order.
```

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The length of `class_labels` must be equal to the number of segments (background excluded). This `list` corresponds to the `class labels in label_file` in ascending order

[Optional]

`out_file`: (a pathlike `object` or string representing a file, nipy default value: `signals.tsv`)

The name of the file to output to. `signals.tsv` by default

`incl_shared_variance`: (a boolean, nipy default value: `True`)

By default (`True`), returns simple time series calculated from each region independently (e.g., for noise regression). If `False`, returns unique signals for each region, discarding shared variance (e.g., for connectivity. Only has effect with 4D probability maps.

`include_global`: (a boolean, nipy default value: `False`)

If `True`, include an extra column labeled "`GlobalSignal`", with values calculated from the entire brain (instead of just regions).

`detrend`: (a boolean, nipy default value: `False`)

If `True`, perform detrending using `nilearn`.

Outputs:

`out_file`: (a pathlike `object` or string representing an existing file)
tsv file containing the computed signals, with as many columns as there are labels and as many rows as there are timepoints in `in_file`, plus a header row with values from `class_labels`

90.1 PETPVC

[Link to code](#)

Wraps the executable command `petpvc`.

Use PETPVC for partial volume correction of PET images.

PETPVC is a software from the Nuclear Medicine Department of the UCL University Hospital, London, UK.

Its source code is here: <https://github.com/UCL/PETPVC>

The methods that it implement are explained here: K. Erlandsson, I. Buvat, P. H. Pretorius, B. A. Thomas, and B. F. Hutton, “A review of partial volume correction techniques for emission tomography and their applications in neurology, cardiology and oncology,” *Phys. Med. Biol.*, vol. 57, no. 21, p. R119, 2012.

Its command line help shows this:

```
-i -input < filename > = PET image file
-o -output < filename > = Output file
[-m -mask < filename > ] = Mask image file
-p -pvc < keyword > = Desired PVC method
    -x < X >           = The full-width at half maximum in mm along x-axis
    -y < Y >           = The full-width at half maximum in mm along y-axis
    -z < Z >           = The full-width at half maximum in mm along z-axis
[-d -debug ] = Prints debug information
[-n -iter [ Val ] ]
    = Number of iterations With: Val (Default = 10)
[-k [ Val ] ]
    = Number of deconvolution iterations With: Val (Default = 10)
[-a -alpha [ aval ] ]
    = Alpha value With: aval (Default = 1.5)
[-s -stop [ stopval ] ]
    = Stopping criterion With: stopval (Default = 0.01)
```

90.1.1 Technique - keyword

- Geometric transfer matrix - “GTM”
- Labbe approach - “LABBE”
- Richardson-Lucy - “RL”
- Van-Cittert - “VC”

- Region-based voxel-wise correction - “RBV”
- RBV with Labbe - “LABBE+RBV”
- RBV with Van-Cittert - “RBV+VC”
- RBV with Richardson-Lucy - “RBV+RL”
- RBV with Labbe and Van-Cittert - “LABBE+RBV+VC”
- RBV with Labbe and Richardson-Lucy- “LABBE+RBV+RL”
- Multi-target correction - “MTC”
- MTC with Labbe - “LABBE+MTC”
- MTC with Van-Cittert - “MTC+VC”
- MTC with Richardson-Lucy - “MTC+RL”
- MTC with Labbe and Van-Cittert - “LABBE+MTC+VC”
- MTC with Labbe and Richardson-Lucy- “LABBE+MTC+RL”
- Iterative Yang - “IY”
- Iterative Yang with Van-Cittert - “IY+VC”
- Iterative Yang with Richardson-Lucy - “IY+RL”
- Muller Gartner - “MG”
- Muller Gartner with Van-Cittert - “MG+VC”
- Muller Gartner with Richardson-Lucy - “MG+RL”

90.1.2 Examples

```
>>> from ..testing import example_data
>>> #TODO get data for PETPVC
>>> pvc = PETPVC()
>>> pvc.inputs.in_file = 'pet.nii.gz'
>>> pvc.inputs.mask_file = 'tissues.nii.gz'
>>> pvc.inputs.out_file = 'pet_pvc_rbv.nii.gz'
>>> pvc.inputs.pvc = 'RBV'
>>> pvc.inputs.fwhm_x = 2.0
>>> pvc.inputs.fwhm_y = 2.0
>>> pvc.inputs.fwhm_z = 2.0
>>> outs = pvc.run() #doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
    PET image file
    argument: ``-i %s``
mask_file: (a pathlike object or string representing an existing
    file)
    Mask image file
    argument: ``-m %s``
pvc: ('GTM' or 'IY' or 'IY+RL' or 'IY+VC' or 'LABBE' or 'LABBE+MTC'
    or 'LABBE+MTC+RL' or 'LABBE+MTC+VC' or 'LABBE+RBV' or
    'LABBE+RBV+RL' or 'LABBE+RBV+VC' or 'MG' or 'MG+RL' or 'MG+VC' or
    'MTC' or 'MTC+RL' or 'MTC+VC' or 'RBV' or 'RBV+RL' or 'RBV+VC' or
    'RL' or 'VC')
    Desired PVC method
    argument: ``-p %s``
fwhm_x: (a float)
    The full-width at half maximum in mm along x-axis
    argument: ``-x %.4f``
fwhm_y: (a float)
    The full-width at half maximum in mm along y-axis
    argument: ``-y %.4f``
```

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```

fwhm_z: (a float)
    The full-width at half maximum in mm along z-axis
    argument: ``-z %.4f``

[Optional]
out_file: (a pathlike object or string representing a file)
    Output file
    argument: ``-o %s``
debug: (a boolean, nipyne default value: False)
    Prints debug information
    argument: ``-d``
n_iter: (an integer (int or long), nipyne default value: 10)
    Number of iterations
    argument: ``-n %d``
n_deconv: (an integer (int or long), nipyne default value: 10)
    Number of deconvolution iterations
    argument: ``-k %d``
alpha: (a float, nipyne default value: 1.5)
    Alpha value
    argument: ``-a %.4f``
stop_crit: (a float, nipyne default value: 0.01)
    Stopping criterion
    argument: ``-s %.4f``
args: (a unicode string)
    Additional parameters to the command
    argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
    of class 'str' and with values which are a bytes or None or a
    value of class 'str', nipyne default value: {})
    Environment variables

```

Outputs:

```

out_file: (a pathlike object or string representing a file)
    Output file

```

90.1.3 References:

None

91.1 Quickshear

[Link to code](#)

Wraps the executable command `quickshear`.

Quickshear is a simple geometric defacing algorithm

Given an anatomical image and a reasonable brainmask, Quickshear estimates a shearing plane with the brain mask on one side and the face on the other, zeroing out the face side.

```
>>> from nipy.interfaces.quickshear import Quickshear
>>> qs = Quickshear(in_file='T1.nii', mask_file='brain_mask.nii')
>>> qs.cmdline
'quickshear T1.nii brain_mask.nii T1_defaced.nii'
```

In the absence of a precomputed mask, a simple pipeline can be generated with any tool that generates brain masks:

```
>>> from nipy.pipeline import engine as pe
>>> from nipy.interfaces import utility as niu
>>> from nipy.interfaces.fsl import BET
>>> deface_wf = pe.Workflow('deface_wf')
>>> inputnode = pe.Node(niu.IdentityInterface(['in_file']),
...                      name='inputnode')
>>> outputnode = pe.Node(niu.IdentityInterface(['out_file']),
...                       name='outputnode')
>>> bet = pe.Node(BET(mask=True), name='bet')
>>> quickshear = pe.Node(Quickshear(), name='quickshear')
>>> deface_wf.connect([
...     (inputnode, bet, [('in_file', 'in_file')]),
...     (inputnode, quickshear, [('in_file', 'in_file')]),
...     (bet, quickshear, [('mask_file', 'mask_file')]),
...     (quickshear, outputnode, [('out_file', 'out_file')]),
... ])
>>> inputnode.inputs.in_file = 'T1.nii'
>>> res = deface_wf.run() # doctest: +SKIP
```

Inputs:

```
[Mandatory]
in_file: (a pathlike object or string representing an existing file)
         neuroimage to deface
         argument: ``%s``, position: 1
mask_file: (a pathlike object or string representing an existing
            file)
            brain mask
            argument: ``%s``, position: 2

[Optional]
out_file: (a pathlike object or string representing a file)
         defaced output image
         argument: ``%s``, position: 3
buff: (an integer (int or long))
      buffer size (in voxels) between shearing plane and the brain
      argument: ``%d``, position: 4
args: (a unicode string)
      Additional parameters to the command
      argument: ``%s``
environ: (a dictionary with keys which are a bytes or None or a value
         of class 'str' and with values which are a bytes or None or a
         value of class 'str', nipy default value: {})
         Environment variables
```

Outputs:

```
out_file: (a pathlike object or string representing an existing file)
         defaced output image
```

91.1.1 References:

None

92.1 `configure_input_data()`

[Link to code](#)

Configure the input data for vtk pipeline object obj. Copied from latest version of mayavi

92.2 `vtk_old()`

[Link to code](#)

Checks if VTK uses the old-style pipeline (VTK<6.0)

92.3 `vtk_output()`

[Link to code](#)

Configure the input data for vtk pipeline object obj.

Developer Guides

- API

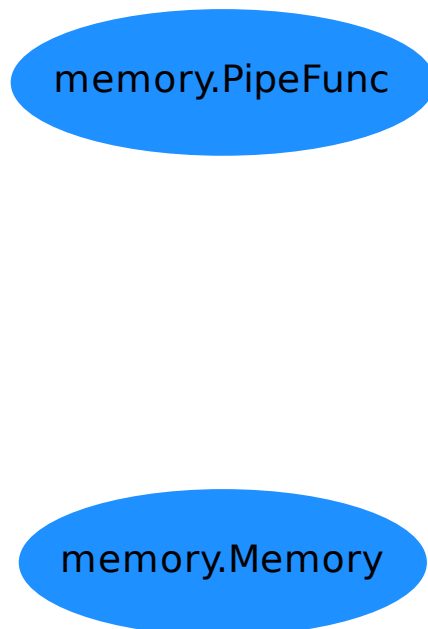
Release 1.2.2

Date September 09, 2019, 18:24 PDT

93.1 caching.memory

93.1.1 Module: `caching.memory`

Inheritance diagram for `nipype.caching.memory`:



Using nipype with persistence and lazy recompu-

tation but without explicit name-steps pipeline: getting back scope in command-line based programming.

93.1.2 Classes

Memory

class `nipyype.caching.memory.Memory` (*base_dir*)

Bases: `object`

Memory context to provide caching for interfaces

Parameters

base_dir: `string` The directory name of the location for the caching

Methods

<code>cache(self, interface)</code>	Returns a callable that caches the output of an interface
<code>clear_previous_runs(self[, warn])</code>	Remove all the cache that where not used in the latest run of the memory object: i.e.
<code>clear_previous_runs(self[, warn])</code>	Remove all the cache that where not used in the latest run of the memory object: i.e.

__init__ (*self, base_dir*)

Initialize self. See `help(type(self))` for accurate signature.

cache (*self, interface*)

Returns a callable that caches the output of an interface

Parameters

interface: `nipyype interface` The nipyype interface class to be wrapped and cached

Returns

pipe_func: `a PipeFunc callable object` An object that can be used as a function to apply the interface to arguments. Inputs of the interface are given as keyword arguments, bearing the same name as the name in the inputs specs of the interface.

Examples

```
>>> from tempfile import mkdtemp
>>> mem = Memory(mkdtemp())
>>> from nipyype.interfaces import fsl
```

Here we create a callable that can be used to apply an `fsl.Merge` interface to files

```
>>> fsl_merge = mem.cache(fsl.Merge)
```

Now we apply it to a list of files. We need to specify the list of input files and the dimension along which the files should be merged.

```
>>> results = fsl_merge(in_files=['a.nii', 'b.nii'],
...                      dimension='t') # doctest: +SKIP
```

We can retrieve the resulting file from the outputs: `>>> results.outputs.merged_file` # doctest: +SKIP
'...'

clear_previous_runs (*self, warn=True*)

Remove all the cache that where not used in the latest run of the memory object: i.e. since the corresponding Python object was created.

Parameters

warn: `boolean, optional` If true, echoes warning messages for all directory removed

clear_runs_since (*self*, *day=None*, *month=None*, *year=None*, *warn=True*)

Remove all the cache that where not used since the given date

Parameters

day, month, year: integers, optional The integers specifying the latest day (in localtime) that a node should have been accessed to be kept. If not given, the current date is used.

warn: boolean, optional If true, echoes warning messages for all directory removed

PipeFunc

class nipyte.caching.memory.**PipeFunc** (*interface*, *base_dir*, *callback=None*)

Bases: object

Callable interface to nipyte.interface objects

Use this to wrap nipyte.interface object and call them specifying their input with keyword arguments:

```
fsl_merge = PipeFunc(fsl.Merge, base_dir='.')
out = fsl_merge(in_files=files, dimension='t')
```

Methods

<code>__call__(self, **kwargs)</code>	Call self as a function.
---------------------------------------	--------------------------

`__init__(self, interface, base_dir, callback=None)`

Parameters

interface: a nipyte interface class The interface class to wrap

base_dir: a string The directory in which the computation will be stored

callback: a callable An optional callable called each time after the function is called.

93.1.3 Functions

nipyte.caching.memory.**read_log** (*filename*, *run_dict=None*)

nipyte.caching.memory.**rm_all_but** (*base_dir*, *dirs_to_keep*, *warn=False*)

Remove all the sub-directories of *base_dir*, but those listed

Parameters

base_dir: string The base directory

dirs_to_keep: set The names of the directories to keep

93.2 conftest

93.2.1 Module: conftest

93.2.2 Functions

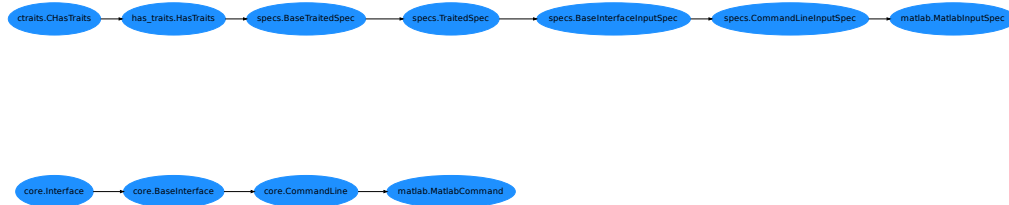
nipyte.conftest.**add_np** (*doctest_namespace*)

nipyte.conftest.**pytest_unconfigure** (*config*)

93.3 interfaces.matlab

93.3.1 Module: interfaces.matlab

Inheritance diagram for nipyte.interfaces.matlab:



General matlab interface code

93.3.2 Classes

MatlabCommand

class `nipyne.interfaces.matlab.MatlabCommand` (*matlab_cmd=None, **inputs*)

Bases: `nipyne.interfaces.base.core.CommandLine`

Interface that runs matlab code

```
>>> import nipyne.interfaces.matlab as matlab
>>> mlab = matlab.MatlabCommand(mfile=False) # don't write script file
>>> mlab.inputs.script = "which('who') "
>>> out = mlab.run() # doctest: +SKIP
```

Attributes

always_run Should the interface be always run even if the inputs were not changed?

Only applies to interfaces being run within a workflow context.

can_resume Defines if the interface can reuse partial results after interruption.

cmd sets base command, immutable

cmdline *command* plus any arguments (*args*)

output_spec

terminal_output

version interfaces should implement a version property

Methods

<code>aggregate_outputs(self[, runtime, ...])</code>	Collate expected outputs and apply output traits validation.
<code>help([returnhelp])</code>	Prints class help
<code>input_spec</code>	alias of <code>MatlabInputSpec</code>
<code>load_inputs_from_json(self, json_file[, ...])</code>	A convenient way to load pre-set inputs from a JSON file.
<code>run(self[, cwd, ignore_exception])</code>	Execute this interface.
<code>save_inputs_to_json(self, json_file)</code>	A convenient way to save current inputs to a JSON file.
<code>set_default_matlab_cmd(matlab_cmd)</code>	Set the default MATLAB command line for MATLAB classes.
<code>set_default_mfile(mfile)</code>	Set the default MATLAB script file format for MATLAB classes.
<code>set_default_paths(paths)</code>	Set the default MATLAB paths for MATLAB classes.

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Table 3 – continued from previous page

`set_default_terminal_output(output_type)` Set the default terminal output for CommandLine Interfaces.

raise_exception	
version_from_command	

__init__ (*self*, *matlab_cmd=None*, ***inputs*)
initializes interface to matlab (default ‘matlab -nodesktop -nosplash’)

aggregate_outputs (*self*, *runtime=None*, *needed_outputs=None*)
Collate expected outputs and apply output traits validation.

always_run
Should the interface be always run even if the inputs were not changed? Only applies to interfaces being run within a workflow context.

can_resume
Defines if the interface can reuse partial results after interruption. Only applies to interfaces being run within a workflow context.

cmd
sets base command, immutable

cmdline
command plus any arguments (*args*) validates arguments and generates command line

classmethod help (*returnhelp=False*)
Prints class help

input_spec
alias of *MatlabInputSpec*

load_inputs_from_json (*self*, *json_file*, *overwrite=True*)
A convenient way to load pre-set inputs from a JSON file.

output_spec = None

raise_exception (*self*, *runtime*)

references_ = []

resource_monitor = True

run (*self*, *cwd=None*, *ignore_exception=None*, ***inputs*)
Execute this interface.
This interface will not raise an exception if runtime.returncode is non-zero.

Parameters
cwd [specify a folder where the interface should be run]
inputs [allows the interface settings to be updated]

Returns
results [an InterfaceResult object containing a copy of the instance]
that was executed, provenance information and, if successful, results

save_inputs_to_json (*self*, *json_file*)
A convenient way to save current inputs to a JSON file.

classmethod set_default_matlab_cmd (*matlab_cmd*)
Set the default MATLAB command line for MATLAB classes.
This method is used to set values for all MATLAB subclasses. However, setting this will not update the output type for any existing instances. For these, assign the <instance>.inputs.matlab_cmd.

classmethod set_default_mfile (*mfile*)
Set the default MATLAB script file format for MATLAB classes.
This method is used to set values for all MATLAB subclasses. However, setting this will not update the output type for any existing instances. For these, assign the <instance>.inputs.mfile.

classmethod set_default_paths (*paths*)
Set the default MATLAB paths for MATLAB classes.
This method is used to set values for all MATLAB subclasses. However, setting this will not update the output type for any existing instances. For these, assign the <instance>.inputs.paths.

classmethod `set_default_terminal_output` (*output_type*)

Set the default terminal output for CommandLine Interfaces.

This method is used to set default terminal output for CommandLine Interfaces. However, setting this will not update the output type for any existing instances. For these, assign the <instance>.terminal_output.

terminal_output

version

interfaces should implement a version property

version_from_command (*self*, *flag*=' -v', *cmd*=None)

MatlabInputSpec

class `nipyte.interfaces.matlab.MatlabInputSpec` (**kwargs)

Bases: `nipyte.interfaces.base.specs.CommandLineInputSpec`

Basic expected inputs to Matlab interface

Methods

<code>add_class_trait</code> (name, *trait)	Adds a named trait attribute to this class.
<code>add_trait</code> (self, name, *trait)	Adds a trait attribute to this object.
<code>add_trait_category</code> (category)	Adds a trait category to a class.
<code>all_trait_names</code> (self)	Returns the list of all trait names, including implicitly defined traits.
<code>base_trait</code> (self, name)	Returns the base trait definition for a trait attribute.
<code>class_default_traits_view</code> ()	Returns the name of the default traits view for the class.
<code>class_editable_traits</code> ()	Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current class.
<code>class_trait_names</code> (**metadata)	Returns a list of the names of all trait attributes whose definitions match the set of <i>metadata</i> criteria specified.
<code>class_trait_view_elements</code> ()	Returns the ViewElements object associated with the class.
<code>class_traits</code> (**metadata)	Returns a dictionary containing the definitions of all of the trait attributes of the class that match the set of <i>metadata</i> criteria.
<code>class_visible_traits</code> ()	Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current class, that should be GUI visible
<code>clone_traits</code> (self[, traits, memo, copy])	Clones a new object from this one, optionally copying only a specified set of traits.
<code>configure_traits</code> (self[, filename, view, ...])	Creates and displays a dialog box for editing values of trait attributes, as if it were a complete, self-contained GUI application.
<code>copy_traits</code> (self, other[, traits, memo, copy])	Copies another object's trait attributes into this one.
<code>copyable_trait_names</code> (self, **metadata)	Returns the list of trait names to copy or clone by default.
<code>default_traits_view</code> (self)	Returns the name of the default traits view for the object's class.

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Table 4 – continued from previous page

<code>edit_traits(self[, view, parent, kind, ...])</code>	Displays a user interface window for editing trait attribute values.
<code>editable_traits(self)</code>	Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current object.
<code>get(self, **kwargs)</code>	Returns traitled class as a dict
<code>get_hashval(self[, hash_method])</code>	Return a dictionary of our items with hashes for each file.
<code>get_traitsfree(self, **kwargs)</code>	Returns traitled class as a dict
<code>has_metadata(self, name, metadata[, value, ...])</code>	Return <code>has_metadata</code> for the requested trait name in this interface
<code>has_traits_interface(self, **interfaces)</code>	Returns whether the object implements a specified traits interface.
<code>items(self)</code>	Name, trait generator for user modifiable traits
<code>on_trait_change(self, handler[, name, ...])</code>	Causes the object to invoke a handler whenever a trait attribute matching a specified pattern is modified, or removes the association.
<code>on_trait_event(self, handler[, name, ...])</code>	Causes the object to invoke a handler whenever a trait attribute matching a specified pattern is modified, or removes the association.
<code>print_traits(self[, show_help])</code>	Prints the values of all explicitly-defined, non-event trait attributes on the current object, in an easily readable format.
<code>remove_trait(self, name)</code>	Removes a trait attribute from this object.
<code>reset_traits(self[, traits])</code>	Resets some or all of an object’s trait attributes to their default values.
<code>set(self[, trait_change_notify])</code>	Shortcut for setting object trait attributes.
<code>set_trait_dispatch_handler(name, klass[, ...])</code>	Sets a trait notification dispatch handler.
<code>sync_trait(self, trait_name, object[, ...])</code>	Synchronizes the value of a trait attribute on this object with a trait attribute on another object.
<code>trait(self, name[, force, copy])</code>	Returns the trait definition for the <i>name</i> trait attribute.
<code>trait_context(self)</code>	Returns the default context to use for editing or configuring traits.
<code>trait_get(self, **kwargs)</code>	Returns traitled class as a dict
<code>trait_items_event(event_trait, name, items_event)</code>	
<code>trait_monitor(handler[, remove])</code>	Adds or removes the specified <i>handler</i> from the list of active monitors.
<code>trait_names(self, **metadata)</code>	Returns a list of the names of all trait attributes whose definitions match the set of <i>metadata</i> criteria specified.
<code>trait_property_changed(...)</code>	
<code>trait_set(self[, trait_change_notify])</code>	Shortcut for setting object trait attributes.
<code>trait_setq(self, **traits)</code>	Shortcut for setting object trait attributes.
<code>trait_subclasses([all])</code>	Returns a list of the immediate (or all) subclasses of this class.
<code>trait_view(self[, name, view_element])</code>	Gets or sets a ViewElement associated with an object’s class.
<code>trait_view_elements(self)</code>	Returns the ViewElements object associated with the object’s class.

Continued on next page

Table 4 – continued from previous page

<code>trait_views(self[, klass])</code>	Returns a list of the names of all view elements associated with the current object’s class.
<code>traits(self, **metadata)</code>	Returns a dictionary containing the definitions of all of the trait attributes of this object that match the set of <i>metadata</i> criteria.
<code>traits_init()</code>	
<code>traits_inited([True])</code>	
<code>validate_trait(self, name, value)</code>	Validates whether a value is legal for a trait.
<code>visible_traits(self)</code>	Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current object, that should be GUI visible

add_trait_listener	
class_trait_view	
remove_trait_listener	

__init__(*self*, ****kwargs**)

Initialize handlers and inputs

classmethod add_class_trait(*name*, **trait*)

Adds a named trait attribute to this class.

Parameters

name [str] Name of the attribute to add.

***trait** : A trait or a value that can be converted to a trait using Trait() Trait definition of the attribute. It can be a single value or a list equivalent to an argument list for the Trait() function.

add_trait(*self*, *name*, **trait*)

Adds a trait attribute to this object.

Parameters

name [str] Name of the attribute to add.

***trait** : Trait or a value that can be converted to a trait by Trait(). Trait definition for *name*. If more than one value is specified, it is equivalent to passing the entire list of values to Trait().

classmethod add_trait_category(*category*)

Adds a trait category to a class.

add_trait_listener(*self*, *object*, *prefix*=’')

all_trait_names(*self*)

Returns the list of all trait names, including implicitly defined traits.

base_trait(*self*, *name*)

Returns the base trait definition for a trait attribute.

Parameters

name [str] Name of the attribute whose trait definition is returned.

classmethod class_default_traits_view()

Returns the name of the default traits view for the class.

classmethod class_editable_traits()

Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current class.

classmethod class_trait_names(****metadata**)

Returns a list of the names of all trait attributes whose definitions match the set of *metadata* criteria specified.

Parameters

****metadata** : Criteria for selecting trait attributes.

classmethod class_trait_view(*name*=None, *view_element*=None)

classmethod class_trait_view_elements()

Returns the ViewElements object associated with the class.

The returned object can be used to access all the view elements associated with the class.

classmethod class_traits (***metadata*)

Returns a dictionary containing the definitions of all of the trait attributes of the class that match the set of *metadata* criteria.

Parameters

****metadata** : Criteria for selecting trait attributes.

classmethod class_visible_traits ()

Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current class, that should be GUI visible

clone_traits (*self*, *traits=None*, *memo=None*, *copy=None*, ***metadata*)

Clones a new object from this one, optionally copying only a specified set of traits.

Parameters

traits [list of strings] The list of names of the trait attributes to copy.

memo [dict] A dictionary of objects that have already been copied.

copy [str] The type of copy *deep* or *shallow* to perform on any trait that does not have explicit 'copy' metadata. A value of *None* means 'copy reference'.

Returns

new : The newly cloned object.

configure_traits (*self*, *filename=None*, *view=None*, *kind=None*, *edit=True*, *context=None*, *handler=None*, *id=""*, *scrollable=None*, ***args*)

Creates and displays a dialog box for editing values of trait attributes, as if it were a complete, self-contained GUI application.

Parameters

filename [str] The name (including path) of a file that contains a pickled representation of the current object. When this parameter is specified, the method reads the corresponding file (if it exists) to restore the saved values of the object's traits before displaying them. If the user confirms the dialog box (by clicking **OK**), the new values are written to the file. If this parameter is not specified, the values are loaded from the in-memory object, and are not persisted when the dialog box is closed.

view [View or str] A View object (or its name) that defines a user interface for editing trait attribute values of the current object. If the view is defined as an attribute on this class, use the name of the attribute. Otherwise, use a reference to the view object. If this attribute is not specified, the View object returned by *trait_view()* is used.

kind [str] The type of user interface window to create. See the **traitsui.view.kind_trait** trait for values and their meanings. If *kind* is unspecified or *None*, the **kind** attribute of the View object is used.

edit [bool] Indicates whether to display a user interface. If *filename* specifies an existing file, setting *edit* to *False* loads the saved values from that file into the object without requiring user interaction.

context [object or dictionary] A single object or a dictionary of string/object pairs, whose trait attributes are to be edited. If not specified, the current object is used

handler [Handler] A handler object used for event handling in the dialog box. If *None*, the default handler for Traits UI is used.

id [str] A unique ID for persisting preferences about this user interface, such as size and position. If not specified, no user preferences are saved.

scrollable [bool] Indicates whether the dialog box should be scrollable. When set to *True*, scroll bars appear on the dialog box if it is not large enough to display all of the items in the view at one time.

Returns

True on success.

copy_traits (*self*, *other*, *traits=None*, *memo=None*, *copy=None*, ***metadata*)

Copies another object's trait attributes into this one.

Parameters

other [object] The object whose trait attribute values should be copied.

traits [list of strings] A list of names of trait attributes to copy. If None or unspecified, the set of names returned by `trait_names()` is used. If 'all' or an empty list, the set of names returned by `all_trait_names()` is used.

memo [dict] A dictionary of objects that have already been copied.

copy [None | 'deep' | 'shallow'] The type of copy to perform on any trait that does not have explicit 'copy' metadata. A value of None means 'copy reference'.

Returns

unassignable [list of strings] A list of attributes that the method was unable to copy, which is empty if all the attributes were successfully copied.

copyable_trait_names (*self*, ***metadata*)

Returns the list of trait names to copy or clone by default.

default_traits_view (*self*)

Returns the name of the default traits view for the object's class.

edit_traits (*self*, *view=None*, *parent=None*, *kind=None*, *context=None*, *handler=None*, *id=""*, *scrollable=None*, ***args*)

Displays a user interface window for editing trait attribute values.

Parameters

view [View or string] A View object (or its name) that defines a user interface for editing trait attribute values of the current object. If the view is defined as an attribute on this class, use the name of the attribute. Otherwise, use a reference to the view object. If this attribute is not specified, the View object returned by `trait_view()` is used.

parent [toolkit control] The reference to a user interface component to use as the parent window for the object's UI window.

kind [str] The type of user interface window to create. See the `traitsui.view.kind_trait` trait for values and their meanings. If *kind* is unspecified or None, the **kind** attribute of the View object is used.

context [object or dictionary] A single object or a dictionary of string/object pairs, whose trait attributes are to be edited. If not specified, the current object is used.

handler [Handler] A handler object used for event handling in the dialog box. If None, the default handler for Traits UI is used.

id [str] A unique ID for persisting preferences about this user interface, such as size and position. If not specified, no user preferences are saved.

scrollable [bool] Indicates whether the dialog box should be scrollable. When set to True, scroll bars appear on the dialog box if it is not large enough to display all of the items in the view at one time.

Returns

A UI object.

editable_traits (*self*)

Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current object.

get (*self*, ***kwargs*)

Returns traitled class as a dict

Augments the trait get function to return a dictionary without notification handles

get_hashval (*self*, *hash_method=None*)

Return a dictionary of our items with hashes for each file.

Searches through dictionary items and if an item is a file, it calculates the md5 hash of the file contents and stores the file name and hash value as the new key value.

However, the overall bunch hash is calculated only on the hash value of a file. The path and name of the file are not used in the overall hash calculation.

Returns

list_withhash [dict] Copy of our dictionary with the new file hashes included with each file.

hashvalue [str] The md5 hash value of the traitled spec

get_traitsfree (*self*, ***kwargs*)

Returns traitled class as a dict

Augments the trait get function to return a dictionary without any traits. The dictionary does not contain any attributes that were Undefined

has_metadata (*self*, *name*, *metadata*, *value=None*, *recursive=True*)

Return has_metadata for the requested trait name in this interface

has_traits_interface (*self*, **interfaces*)

Returns whether the object implements a specified traits interface.

Parameters

***interfaces** : One or more traits Interface (sub)classes.

items (*self*)

Name, trait generator for user modifiable traits

on_trait_change (*self*, *handler*, *name=None*, *remove=False*, *dispatch='same'*, *priority=False*, *deferred=False*, *target=None*)

Causes the object to invoke a handler whenever a trait attribute matching a specified pattern is modified, or removes the association.

Parameters

handler [function] A trait notification function for the *name* trait attribute, with one of the signatures described below.

name [str] The name of the trait attribute whose value changes trigger the notification. The *name* can specify complex patterns of trait changes using an extended *name* syntax, which is described below.

remove [bool] If True, removes the previously-set association between *handler* and *name*; if False (the default), creates the association.

dispatch [str] A string indicating the thread on which notifications must be run. Possible values are:

value	dispatch
same	Run notifications on the same thread as this one.
ui	Run notifications on the UI thread. If the current thread is the UI thread, the notifications are executed immediately; otherwise, they are placed on the UI event queue.
fast	Alias for ui.
new	Run notifications in a new thread.

on_trait_event (*self*, *handler*, *name=None*, *remove=False*, *dispatch='same'*, *priority=False*, *deferred=False*, *target=None*)

Causes the object to invoke a handler whenever a trait attribute matching a specified pattern is modified, or removes the association.

Parameters

handler [function] A trait notification function for the *name* trait attribute, with one of the signatures described below.

name [str] The name of the trait attribute whose value changes trigger the notification. The *name* can specify complex patterns of trait changes using an extended *name* syntax, which is described below.

remove [bool] If True, removes the previously-set association between *handler* and *name*; if False (the default), creates the association.

dispatch [str] A string indicating the thread on which notifications must be run. Possible values are:

value	dispatch
same	Run notifications on the same thread as this one.
ui	Run notifications on the UI thread. If the current thread is the UI thread, the notifications are executed immediately; otherwise, they are placed on the UI event queue.
fast	Alias for ui.
new	Run notifications in a new thread.

```
package_version = <Version('1.2.2')>
```

```
print_traits(self, show_help=False, **metadata)
```

Prints the values of all explicitly-defined, non-event trait attributes on the current object, in an easily readable format.

Parameters

show_help [bool] Indicates whether to display additional descriptive information.

```
remove_trait(self, name)
```

Removes a trait attribute from this object.

Parameters

name [str] Name of the attribute to remove.

Returns

result [bool] True if the trait was successfully removed.

```
remove_trait_listener(self, object, prefix="")
```

```
reset_traits(self, traits=None, **metadata)
```

Resets some or all of an object's trait attributes to their default values.

Parameters

traits [list of strings] Names of trait attributes to reset.

Returns

unresetable [list of strings] A list of attributes that the method was unable to reset, which is empty if all the attributes were successfully reset.

```
set(self, trait_change_notify=True, **traits)
```

Shortcut for setting object trait attributes.

Parameters

trait_change_notify [bool] If **True** (the default), then each value assigned may generate a trait change notification. If **False**, then no trait change notifications will be generated. (see also: `trait_setq`)

****traits** : Key/value pairs, the trait attributes and their values to be set

Returns

self : The method returns this object, after setting attributes.

```
classmethod set_trait_dispatch_handler(name, klass, override=False)
```

Sets a trait notification dispatch handler.

```
sync_trait(self, trait_name, object, alias=None, mutual=True, remove=False)
```

Synchronizes the value of a trait attribute on this object with a trait attribute on another object.

Parameters

name [str] Name of the trait attribute on this object.

object [object] The object with which to synchronize.

alias [str] Name of the trait attribute on *other*; if None or omitted, same as *name*.

mutual [bool or int] Indicates whether synchronization is mutual (True or non-zero) or one-way (False or zero)

remove [bool or int] Indicates whether synchronization is being added (False or zero) or removed (True or non-zero)

```
trait(self, name, force=False, copy=False)
```

Returns the trait definition for the *name* trait attribute.

Parameters

name [str] Name of the attribute whose trait definition is to be returned.

force [bool] Indicates whether to return a trait definition if *name* is not explicitly defined.

copy [bool] Indicates whether to return the original trait definition or a copy.

trait_context (*self*)
Returns the default context to use for editing or configuring traits.

trait_get (*self*, ***kwargs*)
Returns traitled class as a dict
Augments the trait get function to return a dictionary without notification handles

trait_items_event (*event_trait*, *name*, *items_event*)

classmethod trait_monitor (*handler*, *remove=False*)
Adds or removes the specified *handler* from the list of active monitors.

Parameters
handler [function] The function to add or remove as a monitor.
remove [bool] Flag indicating whether to remove (True) or add the specified handler as a monitor for this class.

trait_names (*self*, ***metadata*)
Returns a list of the names of all trait attributes whose definitions match the set of *metadata* criteria specified.

Parameters
****metadata** : Criteria for selecting trait attributes.

trait_property_changed (*name*, *old_value* [, *new_value*])

trait_set (*self*, *trait_change_notify=True*, ***traits*)
Shortcut for setting object trait attributes.

Parameters
trait_change_notify [bool] If **True** (the default), then each value assigned may generate a trait change notification. If **False**, then no trait change notifications will be generated. (see also: `trait_setq`)
****traits** : Key/value pairs, the trait attributes and their values to be set

Returns
self : The method returns this object, after setting attributes.

trait_setq (*self*, ***traits*)
Shortcut for setting object trait attributes.

Parameters
****traits** : Key/value pairs, the trait attributes and their values to be set. No trait change notifications will be generated for any values assigned (see also: `trait_set`).

Returns
self : The method returns this object, after setting attributes.

classmethod trait_subclasses (*all=False*)
Returns a list of the immediate (or all) subclasses of this class.

Parameters
all [bool] Indicates whether to return all subclasses of this class. If False, only immediate subclasses are returned.

trait_view (*self*, *name=None*, *view_element=None*)
Gets or sets a ViewElement associated with an object's class.

Parameters
name [str] Name of a view element
view_element [ViewElement] View element to associate

Returns
A view element.

trait_view_elements (*self*)
Returns the ViewElements object associated with the object's class.
The returned object can be used to access all the view elements associated with the class.

trait_views (*self*, *klass=None*)
Returns a list of the names of all view elements associated with the current object's class.

Parameters

class [class] A class, such that all returned names must correspond to instances of this class. Possible values include:

- Group
- Item
- View
- ViewElement
- ViewSubElement

traits (self, **metadata)
Returns a dictionary containing the definitions of all of the trait attributes of this object that match the set of *metadata* criteria.

Parameters

- **metadata** : Criteria for selecting trait attributes.

traits_init ()
traits_inited ([True])
validate_trait (self, name, value)
Validates whether a value is legal for a trait.
Returns the validated value if it is valid.

visible_traits (self)
Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current object, that should be GUI visible

wrappers = {'extended': <class 'traits.trait_notifiers.ExtendedTraitChangeNotifyW

93.3.3 Function

nipyype.interfaces.matlab.get_matlab_command()

93.4 pipeline.engine.base

93.4.1 Module: pipeline.engine.base

Inheritance diagram for nipyype.pipeline.engine.base:



```
graph TD;
    A([base.EngineBase])
```

Defines functionality for pipelined execution of interfaces
The *EngineBase* class implements the more general view of a task.

93.4.2 EngineBase

class nipyype.pipeline.engine.base.**EngineBase** (name=None, base_dir=None)

Bases: object

Defines common attributes and functions for workflows and nodes.

Attributes

fullname

inputs

itername Name for expanded iterable
name
outputs

Methods

<code>clone(self, name)</code>	Clone an EngineBase object
--------------------------------	----------------------------

load	
save	

__init__ (*self, name=None, base_dir=None*)

Initialize base parameters of a workflow or node

Parameters

name [string (mandatory)] Name of this node. Name must be alphanumeric and not contain any special characters (e.g., '.', '@').

base_dir [string] base output directory (will be hashed before creations) default=None, which results in the use of mkdtemp

clone (*self, name*)

Clone an EngineBase object

Parameters

name [string (mandatory)] A clone of node or workflow must have a new name

fullname

inputs

itername

Name for expanded iterable

load (*self, filename*)

name

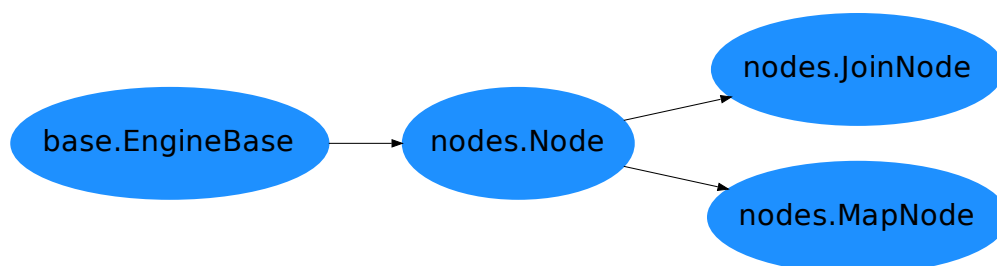
outputs

save (*self, filename=None*)

93.5 pipeline.engine.nodes

93.5.1 Module: pipeline.engine.nodes

Inheritance diagram for `nipyte.pipeline.engine.nodes`:



Defines functionality for pipelined execution of interfaces
 The *Node* class provides core functionality for batch processing.

93.5.2 Classes

JoinNode

class `nipyte.pipeline.engine.nodes.JoinNode`(*interface*, *name*, *joinsource*, *joinfield*=None, *unique*=False, ***kwargs*)

Bases: `nipyte.pipeline.engine.nodes.Node`

Wraps interface objects that join inputs into a list.

Examples

```
>>> import nipyte.pipeline.engine as pe
>>> from nipyte import Node, JoinNode, Workflow
>>> from nipyte.interfaces.utility import IdentityInterface
>>> from nipyte.interfaces import (ants, dcm2nii, fsl)
>>> wf = Workflow(name='preprocess')
>>> inputspec = Node(IdentityInterface(fields=['image']),
...                  name='inputspec')
>>> inputspec.iterables = [('image',
...                        ['img1.nii', 'img2.nii', 'img3.nii'])]
>>> img2flt = Node(fsl.ImageMaths(out_data_type='float'),
...               name='img2flt')
>>> wf.connect(inputspec, 'image', img2flt, 'in_file')
>>> average = JoinNode(ants.AverageImages(), joinsource='inputspec',
...                   joinfield='images', name='average')
>>> wf.connect(img2flt, 'out_file', average, 'images')
>>> realign = Node(fsl.FLIRT(), name='realign')
>>> wf.connect(img2flt, 'out_file', realign, 'in_file')
>>> wf.connect(average, 'output_average_image', realign, 'reference')
>>> strip = Node(fsl.BET(), name='strip')
>>> wf.connect(realign, 'out_file', strip, 'in_file')
```

Attributes

fullname

inputs The JoinNode inputs include the join field overrides.

interface Return the underlying interface object

itername Name for expanded iterable

joinsource

mem_gb Get estimated memory (GB)

n_procs Get the estimated number of processes/threads

name

needed_outputs

outputs Return the output fields of the underlying interface

result Get result from result file (do not hold it in memory)

Methods

<code>clone(self, name)</code>	Clone an EngineBase object
<code>get_output(self, parameter)</code>	Retrieve a particular output of the node
<code>hash_exists(self[, updatehash])</code>	Decorate the new <i>is_cached</i> method with hash updating to maintain backwards compatibility.
<code>help(self)</code>	Print interface help
<code>is_cached(self[, rm_outdated])</code>	Check if the interface has been run previously, and whether cached results are up-to-date.

Continued on next page

Table 6 – continued from previous page

<code>output_dir(self)</code>	Return the location of the output directory for the node
<code>run(self[, updatehash])</code>	Execute the node in its directory.
<code>set_input(self, parameter, val)</code>	Set interface input value
<code>update(self, **opts)</code>	Update inputs

load	
save	

`__init__(self, interface, name, joinsource, joinfield=None, unique=False, **kwargs)`

Parameters

interface [interface object] node specific interface (fsl.Bet(), spm.Coregister())

name [alphanumeric string] node specific name

joinsource [node name] name of the join predecessor iterable node

joinfield [string or list of strings] name(s) of list input fields that will be aggregated. The default is all of the join node input fields.

unique [flag indicating whether to ignore duplicate input values]

See Node docstring for additional keyword arguments.

`clone(self, name)`

Clone an EngineBase object

Parameters

name [string (mandatory)] A clone of node or workflow must have a new name

fullname

`get_output(self, parameter)`

Retrieve a particular output of the node

`hash_exists(self, updatehash=False)`

Decorate the new `is_cached` method with hash updating to maintain backwards compatibility.

`help(self)`

Print interface help

inputs

The JoinNode inputs include the join field overrides.

interface

Return the underlying interface object

`is_cached(self, rm_outdated=False)`

Check if the interface has been run previously, and whether cached results are up-to-date.

itername

Name for expanded iterable

joinfield = None

the fields to join

joinsource

the join predecessor iterable node

`load(self, filename)`

mem_gb

Get estimated memory (GB)

n_procs

Get the estimated number of processes/threads

name

needed_outputs

`output_dir(self)`

Return the location of the output directory for the node

outputs

Return the output fields of the underlying interface

result

Get result from result file (do not hold it in memory)

run (*self*, *updatehash=False*)

Execute the node in its directory.

Parameters

updatehash: boolean When the hash stored in the output directory as a result of a previous run does not match that calculated for this execution, updatehash=True only updates the hash without re-running.

save (*self*, *filename=None*)

set_input (*self*, *parameter*, *val*)

Set interface input value

update (*self*, ***opts*)

Update inputs

MapNode

class `nipyype.pipeline.engine.nodes.MapNode` (*interface*, *iterfield*, *name*, *serial=False*, *nested=False*, ***kwargs*)

Bases: `nipyype.pipeline.engine.nodes.Node`

Wraps interface objects that need to be iterated on a list of inputs.

Examples

```
>>> from nipyype import MapNode
>>> from nipyype.interfaces import fsl
>>> realign = MapNode(fsl.MCFLIRT(), 'in_file', 'realign')
>>> realign.inputs.in_file = ['functional.nii',
...                           'functional2.nii',
...                           'functional3.nii']
>>> realign.run() # doctest: +SKIP
```

Attributes

fullname

inputs Return the inputs of the underlying interface

interface Return the underlying interface object

itername Name for expanded iterable

mem_gb Get estimated memory (GB)

n_procs Get the estimated number of processes/threads

name

needed_outputs

outputs Return the output fields of the underlying interface

result Get result from result file (do not hold it in memory)

Methods

<code>clone</code> (<i>self</i> , <i>name</i>)	Clone an EngineBase object
<code>get_output</code> (<i>self</i> , <i>parameter</i>)	Retrieve a particular output of the node
<code>get_subnodes</code> (<i>self</i>)	Generate subnodes of a mapnode and write pre-execution report
<code>hash_exists</code> (<i>self</i> [, <i>updatehash</i>])	Decorate the new <i>is_cached</i> method with hash updating to maintain backwards compatibility.
<code>help</code> (<i>self</i>)	Print interface help
<code>is_cached</code> (<i>self</i> [, <i>rm_outdated</i>])	Check if the interface has been run previously, and whether cached results are up-to-date.

Continued on next page

Table 7 – continued from previous page

<code>num_subnodes(self)</code>	Get the number of subnodes to iterate in this MapNode
<code>output_dir(self)</code>	Return the location of the output directory for the node
<code>run(self[, updatehash])</code>	Execute the node in its directory.
<code>set_input(self, parameter, val)</code>	Set interface input value or nodewrapper attribute Priority goes to interface.
<code>update(self, **opts)</code>	Update inputs

load	
save	

`__init__(self, interface, iterfield, name, serial=False, nested=False, **kwargs)`

Parameters

- interface** [interface object] node specific interface (fsl.Bet(), spm.Coregister())
- iterfield** [string or list of strings] name(s) of input fields that will receive a list of whatever kind of input they take. the node will be run separately for each value in these lists. for more than one input, the values are paired (i.e. it does not compute a combinatorial product).
- name** [alphanumeric string] node specific name
- serial** [boolean] flag to enforce executing the jobs of the mapnode in a serial manner rather than parallel
- nested** [boolean] support for nested lists. If set, the input list will be flattened before running and the nested list structure of the outputs will be resored.

See docstring for additional keyword arguments.

`clone(self, name)`

Clone an EngineBase object

Parameters

- name** [string (mandatory)] A clone of node or workflow must have a new name

fullname

`get_output(self, parameter)`

Retrieve a particular output of the node

`get_subnodes(self)`

Generate subnodes of a mapnode and write pre-execution report

`hash_exists(self, updatehash=False)`

Decorate the new `is_cached` method with hash updating to maintain backwards compatibility.

`help(self)`

Print interface help

inputs

Return the inputs of the underlying interface

interface

Return the underlying interface object

`is_cached(self, rm_outdated=False)`

Check if the interface has been run previously, and whether cached results are up-to-date.

itername

Name for expanded iterable

`load(self, filename)`

mem_gb

Get estimated memory (GB)

n_procs

Get the estimated number of processes/threads

name

needed_outputs

num_subnodes (*self*)

Get the number of subnodes to iterate in this MapNode

output_dir (*self*)

Return the location of the output directory for the node

outputs

Return the output fields of the underlying interface

result

Get result from result file (do not hold it in memory)

run (*self*, *updatehash=False*)

Execute the node in its directory.

Parameters

updatehash: boolean When the hash stored in the output directory as a result of a previous run does not match that calculated for this execution, `updatehash=True` only updates the hash without re-running.

save (*self*, *filename=None*)

set_input (*self*, *parameter*, *val*)

Set interface input value or nodewrapper attribute Priority goes to interface.

update (*self*, ***opts*)

Update inputs

Node

```
class nipyype.pipeline.engine.nodes.Node(interface, name, iterables=None, iter-  
source=None, synchronize=False, over-  
write=None, needed_outputs=None,  
run_without_submitting=False,  
n_procs=None, mem_gb=0.2, **kwargs)
```

Bases: `nipyype.pipeline.engine.base.EngineBase`

Wraps interface objects for use in pipeline

A Node creates a sandbox-like directory for executing the underlying interface. It will copy or link inputs into this directory to ensure that input data are not overwritten. A hash of the input state is used to determine if the Node inputs have changed and whether the node needs to be re-executed.

Examples

```
>>> from nipyype import Node  
>>> from nipyype.interfaces import spm  
>>> realign = Node(spm.Realign(), 'realign')  
>>> realign.inputs.in_files = 'functional.nii'  
>>> realign.inputs.register_to_mean = True  
>>> realign.run() # doctest: +SKIP
```

Attributes

fullname

inputs Return the inputs of the underlying interface

interface Return the underlying interface object

itername Name for expanded iterable

mem_gb Get estimated memory (GB)

n_procs Get the estimated number of processes/threads

name

needed_outputs

outputs Return the output fields of the underlying interface

result Get result from result file (do not hold it in memory)

Methods

<code>clone(self, name)</code>	Clone an EngineBase object
<code>get_output(self, parameter)</code>	Retrieve a particular output of the node
<code>hash_exists(self[, updatehash])</code>	Decorate the new <code>is_cached</code> method with hash updating to maintain backwards compatibility.
<code>help(self)</code>	Print interface help
<code>is_cached(self[, rm_outdated])</code>	Check if the interface has been run previously, and whether cached results are up-to-date.
<code>output_dir(self)</code>	Return the location of the output directory for the node
<code>run(self[, updatehash])</code>	Execute the node in its directory.
<code>set_input(self, parameter, val)</code>	Set interface input value
<code>update(self, **opts)</code>	Update inputs

load	
save	

`__init__(self, interface, name, iterables=None, itersource=None, synchronize=False, overwrite=None, needed_outputs=None, run_without_submitting=False, n_procs=None, mem_gb=0.2, **kwargs)`

Parameters

interface [interface object] node specific interface (fsl.Bet(), spm.Coregister())

name [alphanumeric string] node specific name

iterables [generator] Input field and list to iterate using the pipeline engine for example to iterate over different frac values in fsl.Bet() for a single field the input can be a tuple, otherwise a list of tuples

```
node.iterables = ('frac', [0.5, 0.6, 0.7])
node.iterables = [('fwhm', [2, 4]), ('fieldx', [0.5, 0.6, 0.7])]
```

If this node has an itersource, then the iterables values is a dictionary which maps an iterable source field value to the target iterables field values, e.g.:

```
inputspec.iterables = ('images', ['img1.nii', 'img2.nii'])
node.itersource = ('inputspec', ['frac'])
node.iterables = ('frac', {'img1.nii': [0.5, 0.6],
                           'img2.nii': [0.6, 0.7]})
```

If this node's synchronize flag is set, then an alternate form of the iterables is a [fields, values] list, where fields is the list of iterated fields and values is the list of value tuples for the given fields, e.g.:

```
node.synchronize = True
node.iterables = [('frac', 'threshold'),
                  [(0.5, True),
                   (0.6, False)]]
```

itersource: tuple The (name, fields) iterables source which specifies the name of the predecessor iterable node and the input fields to use from that source node. The output field values comprise the key to the iterables parameter value mapping dictionary.

synchronize: boolean Flag indicating whether iterables are synchronized. If the iterables are synchronized, then this iterable node is expanded once per iteration over all of the iterables values. Otherwise, this iterable node is expanded once per each permutation of the iterables values.

overwrite [Boolean] Whether to overwrite contents of output directory if it already exists.

If directory exists and hash matches it assumes that process has been executed

needed_outputs [list of output_names] Force the node to keep only specific outputs. By default all outputs are kept. Setting this attribute will delete any output files and directories from the node's working directory that are not part of the *needed_outputs*.

run_without_submitting [boolean] Run the node without submitting to a job engine or to a multiprocessing pool

clone (*self*, *name*)

Clone an EngineBase object

Parameters

name [string (mandatory)] A clone of node or workflow must have a new name

fullname

get_output (*self*, *parameter*)

Retrieve a particular output of the node

hash_exists (*self*, *updatehash=False*)

Decorate the new *is_cached* method with hash updating to maintain backwards compatibility.

help (*self*)

Print interface help

inputs

Return the inputs of the underlying interface

interface

Return the underlying interface object

is_cached (*self*, *rm_outdated=False*)

Check if the interface has been run previously, and whether cached results are up-to-date.

itername

Name for expanded iterable

load (*self*, *filename*)

mem_gb

Get estimated memory (GB)

n_procs

Get the estimated number of processes/threads

name

needed_outputs

output_dir (*self*)

Return the location of the output directory for the node

outputs

Return the output fields of the underlying interface

result

Get result from result file (do not hold it in memory)

run (*self*, *updatehash=False*)

Execute the node in its directory.

Parameters

updatehash: boolean When the hash stored in the output directory as a result of a previous run does not match that calculated for this execution, updatehash=True only updates the hash without re-running.

save (*self*, *filename=None*)

set_input (*self*, *parameter*, *val*)

Set interface input value

update (*self*, ***opts*)

Update inputs

93.6 pipeline.engine.utils

93.6.1 Module: pipeline.engine.utils

Utility routines for workflow graphs

93.6.2 Functions

`nipyte.pipeline.engine.utils.clean_working_directory` (*outputs*, *cwd*, *inputs*,
needed_outputs, *con-*
fig, *files2keep=None*,
dirs2keep=None)

Removes all files not needed for further analysis from the directory

`nipyte.pipeline.engine.utils.count_iterables` (*iterables*, *synchronize=False*)

Return the number of iterable expansion nodes.

If *synchronize* is *True*, then the count is the maximum number of iterables value lists. Otherwise, the count is the product of the iterables value list sizes.

`nipyte.pipeline.engine.utils.evaluate_connect_function` (*function_source*, *args*,
first_arg)

`nipyte.pipeline.engine.utils.expand_iterables` (*iterables*, *synchronize=False*)

`nipyte.pipeline.engine.utils.export_graph` (*graph_in*, *base_dir=None*,
show=False, *use_execgraph=False*,
show_connectioninfo=False, *dotfile-*
name='graph.dot', *format='png'*,
simple_form=True)

Displays the graph layout of the pipeline

This function requires that pygraphviz and matplotlib are available on the system.

Parameters

show [boolean]

Indicate whether to generate pygraphviz output fromn
networkx. default [False]

use_execgraph [boolean]

Indicates whether to use the specification graph or the
execution graph. default [False]

show_connectioninfo [boolean]

Indicates whether to show the edge data on the graph. This
makes the graph rather cluttered. default [False]

`nipyte.pipeline.engine.utils.format_dot` (*dotfilename*, *format='png'*)

Dump a directed graph (Linux only; install via *brew* on OSX)

`nipyte.pipeline.engine.utils.format_node` (*node*, *format='python'*, *in-*
clude_config=False)

Format a node in a given output syntax.

`nipyte.pipeline.engine.utils.generate_expanded_graph` (*graph_in*)

Generates an expanded graph based on node parameterization

Parameterization is controlled using the *iterables* field of the pipeline elements. Thus if there are two nodes with iterables *a*=[1,2] and *b*=[3,4] this procedure will generate a graph with sub-graphs parameterized as (*a*=1,*b*=3), (*a*=1,*b*=4), (*a*=2,*b*=3) and (*a*=2,*b*=4).

`nipyte.pipeline.engine.utils.get_all_files` (*infile*)

`nipyte.pipeline.engine.utils.get_levels` (*G*)

`nipyte.pipeline.engine.utils.get_print_name` (*node*, *simple_form=True*)

Get the name of the node

For example, a node containing an instance of `interfaces.fsl.BET` would be called `nodename.BET.fsl`

`nipyte.pipeline.engine.utils.load_resultfile` (*results_file*, *resolve=True*)

Load InterfaceResult file from path.

Returns

result [InterfaceResult structure]

aggregate [boolean indicating whether node should aggregate_outputs]

attribute error [boolean indicating whether there was some mismatch in] versions of traits used to store result and hence node needs to rerun

nipyype.pipeline.engine.utils.**merge_bundles** (*g1*, *g2*)

nipyype.pipeline.engine.utils.**merge_dict** (*d1*, *d2*, *merge*=<function <lambda> at 0x7fbd92d91840>)

Merges two dictionaries, non-destructively, combining values on duplicate keys as defined by the optional merge function. The default behavior replaces the values in *d1* with corresponding values in *d2*. (There is no other generally applicable merge strategy, but often you'll have homogeneous types in your dicts, so specifying a merge technique can be valuable.)

Examples:

```
>>> d1 = {'a': 1, 'c': 3, 'b': 2}
>>> d2 = merge_dict(d1, d1)
>>> len(d2)
3
>>> [d2[k] for k in ['a', 'b', 'c']]
[1, 2, 3]
```

```
>>> d3 = merge_dict(d1, d1, lambda x,y: x+y)
>>> len(d3)
3
>>> [d3[k] for k in ['a', 'b', 'c']]
[2, 4, 6]
```

nipyype.pipeline.engine.utils.**modify_paths** (*object*, *relative*=*True*, *basedir*=*None*)

Convert paths in data structure to either full paths or relative paths

Supports combinations of lists, dicts, tuples, strs

Parameters

relative [boolean indicating whether paths should be set relative to the] current directory

basedir [default os.getcwd()] what base directory to use as default

nipyype.pipeline.engine.utils.**nodelist_runner** (*nodes*, *updatehash*=*False*, *stop_first*=*False*)

A generator that iterates and over a list of nodes and executes them.

nipyype.pipeline.engine.utils.**save_hashfile** (*hashfile*, *hashed_inputs*)

Store a hashfile

nipyype.pipeline.engine.utils.**save_resultfile** (*result*, *cwd*, *name*, *rebase*=*None*)

Save a result pklz file to cwd.

nipyype.pipeline.engine.utils.**strip_temp** (*files*, *wd*)

Remove temp from a list of file paths

nipyype.pipeline.engine.utils.**synchronize_iterables** (*iterables*)

Synchronize the given iterables in item-wise order.

Return: the {field: value} dictionary list

Examples

```
>>> from nipyype.pipeline.engine.utils import synchronize_iterables
>>> iterables = dict(a=lambda: [1, 2], b=lambda: [3, 4])
>>> synced = synchronize_iterables(iterables)
>>> synced == [{'a': 1, 'b': 3}, {'a': 2, 'b': 4}]
True
>>> iterables = dict(a=lambda: [1, 2], b=lambda: [3], c=lambda: [4, 5, 6])
>>> synced = synchronize_iterables(iterables)
>>> synced == [{'a': 1, 'b': 3, 'c': 4}, {'a': 2, 'c': 5}, {'c': 6}]
True
```

`nipyte.pipeline.engine.utils.topological_sort` (*graph*, *depth_first=False*)
 Returns a depth first sorted order if *depth_first* is True

`nipyte.pipeline.engine.utils.walk` (*children*, *level=0*, *path=None*, *username=True*)
 Generate all the full paths in a tree, as a dict.

Examples

```
>>> from nipyte.pipeline.engine.utils import walk
>>> iterables = [('a', lambda: [1, 2]), ('b', lambda: [3, 4])]
>>> [val['a'] for val in walk(iterables)]
[1, 1, 2, 2]
>>> [val['b'] for val in walk(iterables)]
[3, 4, 3, 4]
```

`nipyte.pipeline.engine.utils.walk_files` (*cwd*)
`nipyte.pipeline.engine.utils.walk_outputs` (*object*)
 Extract every file and directory from a python structure

`nipyte.pipeline.engine.utils.write_report` (*node*, *report_type=None*, *is_mapnode=False*)
 Write a report file for a node

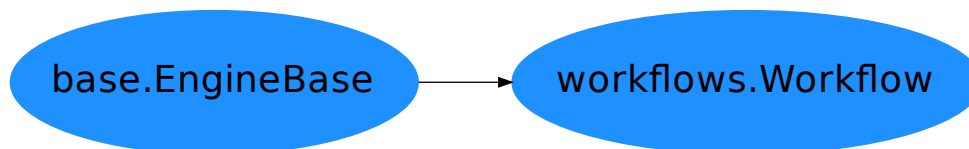
`nipyte.pipeline.engine.utils.write_workflow_prov` (*graph*, *filename=None*, *format='all'*)
 Write W3C PROV Model JSON file

`nipyte.pipeline.engine.utils.write_workflow_resources` (*graph*, *filename=None*, *append=None*)
 Generate a JSON file with profiling traces that can be loaded in a pandas DataFrame or processed with JavaScript like D3.js

93.7 pipeline.engine.workflows

93.7.1 Module: pipeline.engine.workflows

Inheritance diagram for `nipyte.pipeline.engine.workflows`:



Defines functionality for pipelined execution of interfaces
 The *Workflow* class provides core functionality for batch processing.

93.7.2 Workflow

class `nipyte.pipeline.engine.workflows.Workflow` (*name*, *base_dir=None*)
 Bases: `nipyte.pipeline.engine.base.EngineBase`
 Controls the setup and execution of a pipeline of processes.

Attributes

fullname

inputs
itername Name for expanded iterable
name
outputs

Methods

<i>add_nodes</i> (self, nodes)	Add nodes to a workflow
<i>clone</i> (self, name)	Clone a workflow
<i>connect</i> (self, <i>*args</i> , <i>**kwargs</i>)	Connect nodes in the pipeline.
<i>disconnect</i> (self, <i>*args</i>)	Disconnect nodes See the docstring for connect for format.
<i>export</i> (self[, filename, prefix, format, ...])	Export object into a different format
<i>get_node</i> (self, name)	Return an internal node by name
<i>list_node_names</i> (self)	List names of all nodes in a workflow
<i>remove_nodes</i> (self, nodes)	Remove nodes from a workflow
<i>run</i> (self[, plugin, plugin_args, updatehash])	Execute the workflow
<i>write_graph</i> (self[, dotfilename, graph2use, ...])	Generates a graphviz dot file and a png file

load	
save	
write_hierarchical_dotfile	

__init__ (self, name, base_dir=None)

Create a workflow object.

Parameters

name [alphanumeric string] unique identifier for the workflow

base_dir [string, optional] path to workflow storage

add_nodes (self, nodes)

Add nodes to a workflow

Parameters

nodes [list] A list of EngineBase-based objects

clone (self, name)

Clone a workflow

Note: Will reset attributes used for executing workflow. See `_init_runtime_fields`.

Parameters

name: alphanumeric name unique name for the workflow

connect (self, **args*, ***kwargs*)

Connect nodes in the pipeline.

This routine also checks if inputs and outputs are actually provided by the nodes that are being connected.

Creates edges in the directed graph using the nodes and edges specified in the *connection_list*. Uses the NetworkX method `DiGraph.add_edges_from`.

Parameters

args [list or a set of four positional arguments] Four positional arguments of the form:

<code>connect(source, sourceoutput, dest, destinput)</code>

source : nodewrapper node sourceoutput : string (must be in source.outputs) dest :
nodewrapper node destinput : string (must be in dest.inputs)

A list of 3-tuples of the following form:


```
[ (source, target,
    [ ('sourceoutput/attribute', 'targetinput'),
      ...]),
  ...]
```

Or:

```
[ (source, target, [ ('sourceoutput1', func, arg2, ...),
                    ('targetinput'), ...]),
  ...]
sourceoutput1 will always be the first argument to func
and func will be evaluated and the results sent to targetinput

currently func needs to define all its needed imports within the
function as we use the inspect module to get at the source code
and execute it remotely
```

disconnect (*self*, **args*)

Disconnect nodes See the docstring for connect for format.

export (*self*, *filename=None*, *prefix='output'*, *format='python'*, *include_config=False*)

Export object into a different format

Parameters

filename: string file to save the code to; overrides prefix

prefix: string prefix to use for output file

format: string one of “python”

include_config: boolean whether to include node and workflow config values

fullname

get_node (*self*, *name*)

Return an internal node by name

inputs

itername

Name for expanded iterable

list_node_names (*self*)

List names of all nodes in a workflow

load (*self*, *filename*)

name

outputs

remove_nodes (*self*, *nodes*)

Remove nodes from a workflow

Parameters

nodes [list] A list of EngineBase-based objects

run (*self*, *plugin=None*, *plugin_args=None*, *updatehash=False*)

Execute the workflow

Parameters

plugin: plugin name or object Plugin to use for execution. You can create your own plugins for execution.

plugin_args [dictionary containing arguments to be sent to plugin] constructor. see individual plugin doc strings for details.

save (*self*, *filename=None*)

write_graph (*self*, *dotfilename='graph.dot'*, *graph2use='hierarchical'*, *format='png'*, *simple_form=True*)

Generates a graphviz dot file and a png file

Parameters

graph2use: 'orig', 'hierarchical' (default), 'flat', 'exec', 'colored' orig - creates a top level graph without expanding internal workflow nodes; flat - expands workflow nodes recursively; hierarchical - expands workflow nodes recursively with a notion on hierar-

chy; colored - expands workflow nodes recursively with a notion on hierarchy in color;
 exec - expands workflows to depict iterables

format: 'png', 'svg'

simple_form: boolean (default: True) Determines if the node name used in the graph should be of the form 'nodename (package)' when True or 'nodename.Class.package' when False.

write_hierarchical_dotfile (self, dotfilename=None, colored=False, simple_form=True)

93.8 sphinxext.plot_workflow

93.8.1 Module: sphinxext.plot_workflow

Inheritance diagram for `nipy.sphinxext.plot_workflow`:

plot_workflow.ImageFile

plot_workflow.GraphError

nipy.sphinxext.plot_workflow – Workflow plotting extension

A directive for including a nipy workflow graph in a Sphinx document.

This code is forked from the plot_figure sphinx extension of matplotlib.

By default, in HTML output, *workflow* will include a .png file with a link to a high-res .png. In LaTeX output, it will include a .pdf. The source code for the workflow may be included as **inline content** to the directive *workflow*:

```
.. workflow ::
    :graph2use: flat
    :simple_form: no

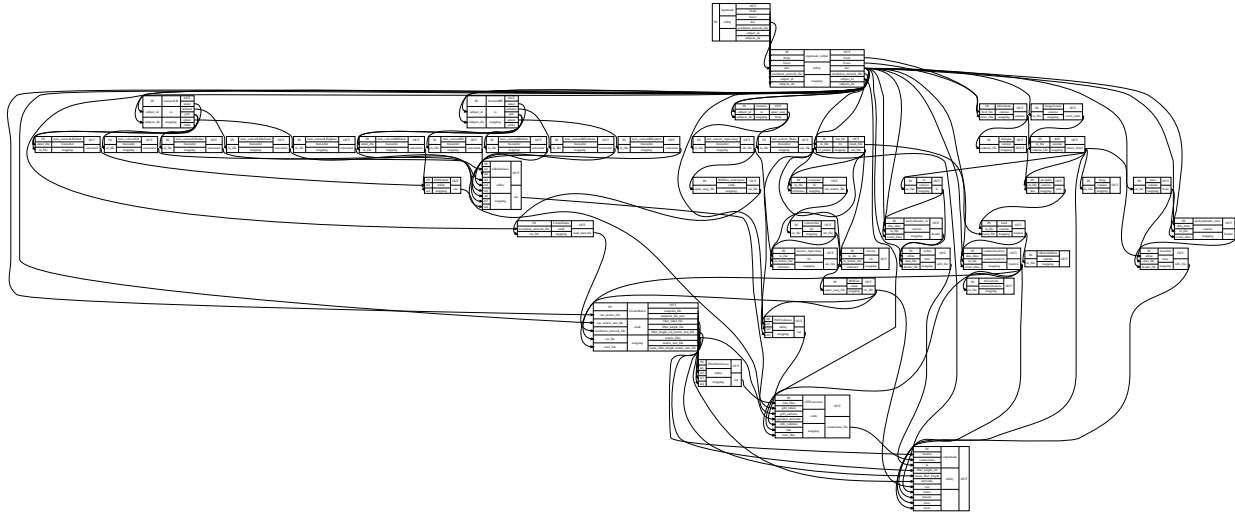
    from nipy.workflows.dmri.camino.connectivity_mapping import create_
    ↪connectivity_pipeline
```

(continues on next page)

(continued from previous page)

```
wf = create_connectivity_pipeline()
```

For example, the following graph has been generated inserting the previous code block in this documentation:



Options

The **workflow** directive supports the following options:

graph2use [{ 'hierarchical', 'colored', 'flat', 'orig', 'exec' }] Specify the type of graph to be generated.

simple_form: **bool** Whether the graph will be in detailed or simple form.

format [{ 'python', 'doctest' }] Specify the format of the input

include-source [bool] Whether to display the source code. The default can be changed using the *workflow_include_source* variable in *conf.py*

encoding [str] If this source file is in a non-UTF8 or non-ASCII encoding, the encoding must be specified using the *:encoding:* option. The encoding will not be inferred using the `-- coding --` metacomment.

Additionally, this directive supports all of the options of the *image* directive, except for *target* (since workflow will add its own target). These include *alt*, *height*, *width*, *scale*, *align* and *class*.

Configuration options

The workflow directive has the following configuration options:

graph2use Select a graph type to use

simple_form determines if the node name shown in the visualization is either of the form *nodename* (*package*) when set to True or *nodename.Class.package* when set to False.

wf_include_source Default value for the include-source option

wf_html_show_source_link Whether to show a link to the source in HTML.

wf_pre_code Code that should be executed before each workflow.

wf_basedir Base directory, to which *workflow::* file names are relative to. (If None or empty, file names are relative to the directory where the file containing the directive is.)

wf_formats

File formats to generate. List of tuples or strings:: [(suffix, dpi), suffix, ...]

that determine the file format and the DPI. For entries whose DPI was omitted, sensible defaults are chosen. When passing from the command line through *sphinx_build* the list should be passed as *suffix:dpi,suffix:dpi, ...*

wf_html_show_formats Whether to show links to the files in HTML.

wf_rcparams A dictionary containing any non-standard rcParams that should be applied before each workflow.

wf_apply_rcparams By default, rcParams are applied when *context* option is not used in a workflow directive. This configuration option overrides this behavior and applies rcParams before each workflow.

wf_working_directory By default, the working directory will be changed to the directory of the example, so the code can get at its data files, if any. Also its path will be added to *sys.path* so it can import any helper modules sitting beside it. This configuration option can be used to specify a central directory (also added to *sys.path*) where data files and helper modules for all code are located.

wf_template Provide a customized template for preparing restructured text.

93.8.2 Classes

GraphError

class `nipyne.sphinxext.plot_workflow.GraphError`

Bases: `RuntimeError`

Attributes

args

Methods

<code>with_traceback()</code>	Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.	–	set
-------------------------------	--	---	-----

__init__(*self*, /, *args, **kwargs)

Initialize self. See help(type(self)) for accurate signature.

args

with_traceback()

Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

ImageFile

class `nipyne.sphinxext.plot_workflow.ImageFile` (*basename*, *dirname*)

Bases: `object`

Methods

filename	
filenames	

__init__(*self*, *basename*, *dirname*)

Initialize self. See help(type(self)) for accurate signature.

filename(*self*, *fmt*)

filenames(*self*)

93.8.3 Functions

`nipyne.sphinxext.plot_workflow.contains_doctest` (*text*)

`nipyne.sphinxext.plot_workflow.get_wf_formats` (*config*)

`nipyne.sphinxext.plot_workflow.mark_wf_labels` (*app*, *document*)

To make graphs referenceable, we need to move the reference from the “htmlonly” (or “latexonly”) node to the actual figure node itself.

`nipyne.sphinxext.plot_workflow.out_of_date` (*original*, *derived*)

Returns True if derivative is out-of-date wrt original, both of which are full file paths.

```
nipy.sphinxext.plot_workflow.remove_coding(text)
```

Remove the coding comment, which exec doesn't like.

```
nipy.sphinxext.plot_workflow.render_figures(code, code_path, output_dir,
                                             output_base, context, func-
                                             tion_name, config, graph2use,
                                             simple_form, context_reset=False,
                                             close_figs=False)
```

Run a nipy workflow creation script and save the graph in *output_dir*. Save the images under *output_dir* with file names derived from *output_base*

```
nipy.sphinxext.plot_workflow.run(arguments, content, options, state_machine, state,
                                  lineno)
```

```
nipy.sphinxext.plot_workflow.run_code(code, code_path, ns=None, func-
                                       tion_name=None)
```

Import a Python module from a path, and run the function given by name, if function_name is not None.

```
nipy.sphinxext.plot_workflow.setup(app)
```

```
nipy.sphinxext.plot_workflow.unescape_doctest(text)
```

Extract code from a piece of text, which contains either Python code or doctests.

```
nipy.sphinxext.plot_workflow.wf_directive(name, arguments, options, content,
                                           lineno, content_offset, block_text, state,
                                           state_machine)
```

- Developer Guide

Release 1.2.2

Date September 09, 2019, 18:24 PDT

Since nipy is part of the [NIPY](#) project, we follow the same conventions documented in the [NIPY Developers Guide](#). For bleeding-edge version help see [Nightly documentation](#)

94.1 Interface Specifications

94.1.1 Before you start

Nipype is maintained by an enthusiastic group of developers, and we're excited to have you join us! In case of trouble, we encourage you to post on [NeuroStars](#) with the *nipype* tag. NeuroStars.org is a platform similar to StackOverflow but dedicated to neuroinformatics. You can also post on the nipype developers mailing list: <http://mail.python.org/mailman/listinfo/neuroimaging>. As we are sharing a mailing list with the nipy community, please add [nipype] to the message title. Alternatively, you're welcome to chat with us in the Nipype [Gitter](#) channel or in the BrainHack [Slack](#) channel. (Click [here](#) to join the Slack workspace.)

94.1.2 Overview

We're using the [Traits](#) (formerly known as Enthought Traits) package for all of our inputs and outputs. Traits allows us to validate user inputs and provides a mechanism to handle all the *special cases* in a simple and concise way through metadata. With the metadata, each input/output can have an optional set of metadata attributes (described in more detail below). The machinery for handling the metadata is located in the base classes, so all subclasses use the same code to handle these cases. This is in contrast to our previous code where every class defined it's own `_parse_inputs`, `run` and `aggregate_outputs` methods to handle these cases. Which of course leads to a dozen different ways to solve the same problem.

Traits is a big package with a lot to learn in order to take full advantage of. But don't be intimidated! To write a Nipype Trait Specification, you only need to learn a few of the basics of Traits. Here are a few starting points in the documentation:

- What are Traits? The [Introduction in the User Manual](#) gives a brief description of the functionality traits provides.
- Traits and metadata. The [second section of the User Manual](#) gives more details on traits and how to use them. Plus there a section describing metadata, including the metadata all traits have.
- If your interested in more of a *big picture* overview, [Gael wrote a good tutorial](#) that shows how to write a scientific application using traits for the benefit of the generated UI components. (For now, Nipype is not taking

advantage of the generated UI feature of traits.)

Traits version

We're using Traits version 4.x which can be installed from [pypi](#)

More documentation

Not everything is documented in the User Manual, in those cases the [API docs](#) is your next place to look.

94.1.3 Nipyre Interface Specifications

Each interface class defines two specifications: 1) an InputSpec and 2) an OutputSpec. Each of these are prefixed with the class name of the interfaces. For example, Bet has these specs:

- BETInputSpec
- BETOutputSpec

Each of these Specs are classes, derived from a base TraitedSpec class (more on these below). The InputSpec consists of attributes which correspond to different parameters for the tool they wrap/interface. In the case of a command-line tool like Bet, the InputSpec attributes correspond to the different command-line parameters that can be passed to Bet. When an interfaces class is instantiated, the InputSpec is bound to the `inputs` attribute of that object. Below is an example of how the `inputs` appear to a user for Bet:

```
>>> from nipyre.interfaces import fsl
>>> bet = fsl.BET()
>>> type(bet.inputs)
<class 'nipyre.interfaces.fsl.preprocess.BETInputSpec'>
>>> bet.inputs.<TAB>
bet.inputs.__class__          bet.inputs.center
bet.inputs.__delattr__       bet.inputs.environ
bet.inputs.__doc__           bet.inputs.frac
bet.inputs.__getattr__       bet.inputs.functional
bet.inputs.__hash__          bet.inputs.hashval
bet.inputs.__init__          bet.inputs.infile
bet.inputs.__new__           bet.inputs.items
bet.inputs.__reduce__        bet.inputs.mask
bet.inputs.__reduce_ex__     bet.inputs.mesh
bet.inputs.__repr__          bet.inputs.nooutput
bet.inputs.__setattr__       bet.inputs.outfile
bet.inputs.__str__           bet.inputs.outline
bet.inputs._generate_handlers bet.inputs.outputtype
bet.inputs._get_hashval      bet.inputs.radius
bet.inputs._hash_infile      bet.inputs.reduce_bias
bet.inputs._xor_inputs       bet.inputs.skull
bet.inputs._xor_warn         bet.inputs.threshold
bet.inputs.args              bet.inputs.vertical_gradient
```

Each Spec inherits from a parent Spec. The parent Specs provide attribute(s) that are common to all child classes. For example, FSL InputSpecs inherit from `interfaces.fsl.base.FSLTraitSpec`. `FSLTraitSpec` defines an `outputtype` attribute, which stores the file type (NIFTI, NIFTI_PAIR, etc...) for all generated output files.

InputSpec class hierarchy

Below is the current class hierarchy for InputSpec classes (from base class down to subclasses):

`TraitSpec`: Nipyre's primary base class for all Specs. Provides initialization, some nipyre-specific methods and any trait handlers we define. Inherits from `traits.HasTraits`.

`BaseInterfaceInputSpec`: Defines inputs common to all Interfaces (ignore_exception). If in doubt inherit from this.

CommandLineInputSpec: Defines inputs common to all command-line classes (args and environ)
 FSLTraitedSpec: Defines inputs common to all FSL classes (outputtype)
 SPMCommandInputSpec: Defines inputs common to all SPM classes (matlab_cmd, path, and mfile)
 FSTraitedSpec: Defines inputs common to all FreeSurfer classes (subjects_dir)
 MatlabInputSpec: Defines inputs common to all Matlab classes (script, nodesktop, nosplash, logfile, single_comp_thread, mfile, script_file, and paths)
 SlicerCommandLineInputSpec: Defines inputs common to all Slicer classes (module)

Most developers will only need to code at the the interface-level (i.e. implementing custom class inheriting from one of the above classes).

Output Specs

The OutputSpec defines the outputs that are generated, or possibly generated depending on inputs, by the tool. OutputSpecs inherit from `interfaces.base.TraitedSpec` directly.

94.1.4 Controlling outputs to terminal

It is very likely that the software wrapped within the interface writes to the standard output or the standard error of the terminal. Interfaces provide a means to access and retrieve these outputs, by using the `terminal_output` attribute:

```
import nipy.interfaces.fsl as fsl
mybet = fsl.BET(from_file='bet-settings.json')
mybet.terminal_output = 'file_split'
```

In the example, the `terminal_output = 'file_split'` will redirect the standard output and the standard error to split files (called `stdout.nipype` and `stderr.nipype` respectively). The possible values for `terminal_output` are:

- file** Redirects both standard output and standard error to the same file called `output.nipype`. Messages from both streams will be overlapped as they arrive to the file.
- file_split** Redirects the output streams separately, to `stdout.nipype` and `stderr.nipype` respectively, as described in the example.
- file_stdout** Only the standard output will be redirected to `stdout.nipype` and the standard error will be discarded.
- file_stderr** Only the standard error will be redirected to `stderr.nipype` and the standard output will be discarded.
- stream** Both output streams are redirected to the current logger printing their messages interleaved and immediately to the terminal.
- allatonce** Both output streams will be forwarded to a buffer and stored separately in the `runtime` object that the `run()` method returns. No files are written nor streams printed out to terminal.
- none** Both outputs are discarded

In all cases, except for the 'none' setting of `terminal_output`, the `run()` method will return a “runtime” object that will contain the streams in the corresponding properties (`runtime.stdout` for the standard output, `runtime.stderr` for the standard error, and `runtime.merged` for both when streams are mixed, eg. when using the `file` option).

```
import nipy.interfaces.fsl as fsl
mybet = fsl.BET(from_file='bet-settings.json')
mybet.terminal_output = 'file_split'
```

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```
...
result = mybet.run()
result.runtime.stdout
' ... captured standard output ...'
```

94.1.5 Traited Attributes

Each specification attribute is an instance of a Trait class. These classes encapsulate many standard Python types like Float and Int, but with additional behavior like type checking. (*See the documentation on traits for more information on these trait types.*) To handle unique behaviors of our attributes we use traits metadata. These are keyword arguments supplied in the initialization of the attributes. The base classes `BaseInterface` and `CommandLine` (defined in `nipy.interfaces.base`) check for the existence/or value of these metadata and handle the inputs/outputs accordingly. For example, all mandatory parameters will have the `mandatory = True` metadata:

```
class BetInputSpec(FSLTraitedSpec):
    infile = File(exists=True,
                  desc='input file to skull strip',
                  argstr='%s', position=0, mandatory=True)
```

Common

exists For files, use `nipy.interfaces.base.File` as the trait type. If the file must exist for the tool to execute, specify `exists = True` in the initialization of `File` (as shown in `BetInputSpec` above). This will trigger the underlying traits code to confirm the file assigned to that *input* actually exists. If it does not exist, the user will be presented with an error message:

```
>>> bet.inputs.infile = 'does_not_exist.nii'
-----
Traceback (most recent call last):
  File "<ipython console>", line 1, in <module>
  File "/Users/cburns/local/lib/python2.5/site-packages/nipy/interfaces/
↳base.py", line 76, in validate
    self.error( object, name, value )
  File "/Users/cburns/local/lib/python2.5/site-packages/enthought/traits/
↳trait_handlers.py", line 175, in error
    value )
TraitError: The 'infile' trait of a BetInputSpec instance must be a file
name, but a value of 'does_not_exist.nii' <type 'str'> was specified.
```

hash_files To be used with inputs that are defining output filenames. When this flag is set to false any Nipype will not try to hash any files described by this input. This is useful to avoid rerunning when the specified output file already exists and has changed.

desc All trait objects have a set of default metadata attributes. `desc` is one of those and is used as a simple, one-line docstring. The `desc` is printed when users use the `help()` methods.

Required: This metadata is required by all nipype interface classes.

usedefault Set this metadata to True when the *default value* for the trait type of this attribute is an acceptable value. All trait objects have a default value, `traits.Int` has a default of 0, `traits.Float` has a default of 0.0, etc... You can also define a default value when you define the class. For example, in the code below all objects of `Foo` will have a default value of 12 for `x`:

```
>>> import enthought.traits.api as traits
>>> class Foo(traits.HasTraits):
...     x = traits.Int(12)
```

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```

...     y = traits.Int
...
>>> foo = Foo()
>>> foo.x
12
>>> foo.y
0

```

Nipyne only passes inputs on to the underlying package if they have been defined (more on this later). So if you specify `usedefault = True`, you are telling the parser to pass the default value on to the underlying package. Let's look at the `InputSpec` for SPM Realign:

```

class RealignInputSpec(BaseInterfaceInputSpec):
    jobtype = traits.Enum('estwrite', 'estimate', 'write',
                          desc='one of: estimate, write, estwrite',
                          usedefault=True)

```

Here we've defined `jobtype` to be an enumerated trait type, `Enum`, which can be set to one of the following: `estwrite`, `estimate`, or `write`. In a container, the default is always the first element. So in this case, the default will be `estwrite`:

```

>>> from nipyne.interfaces import spm
>>> rlgn = spm.Realign()
>>> rlgn.inputs.infile
<undefined>
>>> rlgn.inputs.jobtype
'estwrite'

```

xor and requires Both of these accept a list of trait names. The `xor` metadata reflects mutually exclusive traits, while the `requires` metadata reflects traits that have to be set together. When a `xor`-ed trait is set, all other traits belonging to the list are set to `Undefined`. The function `check_mandatory_inputs` ensures that all requirements (both mandatory and via the `requires` metadata are satisfied). These are also reflected in the help function.

copyfile This is metadata for a `File` or `Directory` trait that is relevant only in the context of wrapping an interface in a `Node` and `MapNode`. `copyfile` can be set to either `True` or `False`. `False` indicates that contents should be symlinked, while `True` indicates that the contents should be copied over.

min_ver and max_ver These metadata determine if a particular trait will be available when a given version of the underlying interface runs. Note that this check is performed at runtime.:

```

class RealignInputSpec(BaseInterfaceInputSpec):
    jobtype = traits.Enum('estwrite', 'estimate', 'write', min_ver='5',
                          usedefault=True)

```

deprecated and new_name This is metadata for removing or renaming an input field from a spec.:

```

class RealignInputSpec(BaseInterfaceInputSpec):
    jobtype = traits.Enum('estwrite', 'estimate', 'write',
                          deprecated='0.8',
                          desc='one of: estimate, write, estwrite',
                          usedefault=True)

```

In the above example this means that the `jobtype` input is deprecated and will be removed in version 0.8. Deprecation should be set to two versions from current release. Raises `TraitError` after package version crosses the deprecation version.

For inputs that are being renamed, one can specify the new name of the field.:

```

class RealignInputSpec(BaseInterfaceInputSpec):
    jobtype = traits.Enum('estwrite', 'estimate', 'write',

```

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```

        deprecated='0.8', new_name='job_type',
        desc='one of: estimate, write, estwrite',
        usedefault=True)
    job_type = traits.Enum('estwrite', 'estimate', 'write',
        desc='one of: estimate, write, estwrite',
        usedefault=True)

```

In the above example, the *jobtype* field is being renamed to *job_type*. When *new_name* is provided it must exist as a trait, otherwise an exception will be raised.

Note: The version information for *min_ver*, *max_ver* and *deprecated* has to be provided as a string. For example, *min_ver*='0.1'.

CommandLine

argstr The metadata keyword for specifying the format strings for the parameters. This was the *value* string in the *opt_map* dictionaries of Nipy 0.2 code. If we look at the *FlirtInputSpec*, the *argstr* for the reference file corresponds to the argument string I would need to provide with the command-line version of *flirt*:

```

class FlirtInputSpec(FSLTraitedSpec):
    reference = File(exists = True, argstr = '-ref %s', mandatory = True,
        position = 1, desc = 'reference file')

```

Required: This metadata is required by all command-line interface classes.

position This metadata is used to specify the position of arguments. Both positive and negative values are accepted. *position* = 0 will position this argument as the first parameter after the command name. *position* = -1 will position this argument as the last parameter, after all other parameters.

genfile If True, the *genfile* metadata specifies that a filename should be generated for this parameter *if-and-only-if* the user did not provide one. The nipy convention is to automatically generate output filenames when not specified by the user both as a convenience for the user and so the pipeline can easily gather the outputs. Requires *_gen_filename()* method to be implemented. This way should be used if the desired file name is dependent on some runtime variables (such as file name of one of the inputs, or current working directory). In case when it should be fixed it's recommended to just use *usedefault*.

sep For List traits the string with which elements of the list will be joined.

name_source Indicates the list of input fields from which the value of the current File output variable will be drawn. This input field must be the name of a File. Chaining is allowed, meaning that an input field can point to another as *name_source*, which also points as *name_source* to a third field. In this situation, the templates for substitutions are also accumulated.

name_template By default a *%s_generated* template is used to create the output filename. This metadata keyword allows overriding the generated name.

keep_extension Use this and set it True if you want the extension from the input to be kept.

SPM

field name of the structure referred by the SPM job manager

Required: This metadata is required by all SPM-mediated interface classes.

94.1.6 Defining an interface class

Common

When you define an interface class, you will define these attributes and methods:

- *input_spec*: the *InputSpec*
- *output_spec*: the *OutputSpec*

- `_list_outputs()`: Returns a dictionary containing names of generated files that are expected after package completes execution. This is used by `BaseInterface.aggregate_outputs` to gather all output files for the pipeline.

CommandLine

For command-line interfaces:

- `_cmd`: the command-line command
- If you used genfile:
 - `_gen_filename(name)`: Generate filename, used for filenames that nipype generates as a convenience for users. This is for parameters that are required by the wrapped package, but we're generating from some other parameter. For example, `BET.inputs.outfile` is required by BET but we can generate the name from `BET.inputs.infile`. Override this method in subclass to handle.
- And optionally:
 - `_redirect_x`: If set to True it will make Nipype start Xvfb before running the interface and redirect X output to it. This is useful for
- `_format_arg(name, spec, value)`: For extra formatting of the input values before passing them to `generic_parse_inputs()` method.

For example this is the class definition for Flirt, minus the docstring:

```
class FLIRTInputSpec(FSLCommandInputSpec):
    in_file = File(exists=True, argstr='-in %s', mandatory=True,
                   position=0, desc='input file')
    reference = File(exists=True, argstr='-ref %s', mandatory=True,
                    position=1, desc='reference file')
    out_file = File(argstr='-out %s', desc='registered output file',
                   name_source=['in_file'], name_template='%s_flirt',
                   position=2, hash_files=False)
    out_matrix_file = File(argstr='-omat %s',
                          name_source=['in_file'], keep_extension=True,
                          name_template='%s_flirt.mat',
                          desc='output affine matrix in 4x4 asciii format',
                          position=3, hash_files=False)
    out_log = File(name_source=['in_file'], keep_extension=True,
                  requires=['save_log'],
                  name_template='%s_flirt.log', desc='output log')
    ...

class FLIRTOutputSpec(TraitSpec):
    out_file = File(exists=True,
                   desc='path/name of registered file (if generated)')
    out_matrix_file = File(exists=True,
                          desc='path/name of calculated affine transform '
                              '(if generated)')
    out_log = File(desc='path/name of output log (if generated)')

class Flirt(FSLCommand):
    _cmd = 'flirt'
    input_spec = FlirtInputSpec
    output_spec = FlirtOutputSpec
```

There are two possible output files `out_file` and `outmatrix`, both of which can be generated if not specified by the user.

Also notice the use of `self._gen_fname()` - a FSLCommand helper method for generating filenames (with extensions conforming with FSLOUTPUTTYPE).

See also [How to wrap a command line tool](#).

SPM

For SPM-mediated interfaces:

- `_jobtype` and `_jobname`: special names used by the SPM job manager. You can find them by saving your batch job as an `.m` file and looking up the code.

And optionally:

- `_format_arg(name, spec, value)`: For extra formatting of the input values before passing them to `generic_parse_inputs()` method.

Matlab

See *How to wrap a MATLAB script*.

Python

See *How to wrap a Python script*.

94.1.7 Undefined inputs

All the inputs and outputs that were not explicitly set (And do not have a `usedefault` flag - see above) will have Undefined value. To check if something is defined you have to explicitly call `isdefined` function (comparing to `None` will not work).

94.1.8 Example of inputs

Below we have an example of using `Bet`. We can see from the help which inputs are mandatory and which are optional, along with the one-line description provided by the `desc` metadata:

```
>>> from nipy.interfaces import fsl
>>> fsl.BET.help()
Inputs
-----

Mandatory:
  infile: input file to skull strip

Optional:
  args: Additional parameters to the command
  center: center of gravity in voxels
  environ: Environment variables (default={})
  frac: fractional intensity threshold
  functional: apply to 4D fMRI data
  mask: create binary mask image
  mesh: generate a vtk mesh brain surface
  nooutput: Don't generate segmented output
  outfile: name of output skull stripped image
  outline: create surface outline image
  outputtype: None
  radius: head radius
  reduce_bias: bias field and neck cleanup
  skull: create skull image
  threshold: apply thresholding to segmented brain image and mask
  vertical_gradient: vertical gradient in fractional intensity threshold (-1, 1)

Outputs
-----
maskfile: path/name of binary brain mask (if generated)
```

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```

meshfile: path/name of vtk mesh file (if generated)
outfile: path/name of skullstripped file
outlinefile: path/name of outline file (if generated)

```

Here we create a bet object and specify the required input. We then check our inputs to see which are defined and which are not:

```

>>> bet = fsl.BET(infile = 'f3.nii')
>>> bet.inputs
args = <undefined>
center = <undefined>
environ = {'FSLOUTPUTTYPE': 'NIFTI_GZ'}
frac = <undefined>
functional = <undefined>
infile = f3.nii
mask = <undefined>
mesh = <undefined>
nooutput = <undefined>
outfile = <undefined>
outline = <undefined>
outputtype = NIFTI_GZ
radius = <undefined>
reduce_bias = <undefined>
skull = <undefined>
threshold = <undefined>
vertical_gradient = <undefined>
>>> bet.cmdline
'bet f3.nii /Users/cburns/data/nipyne/s1/f3_brain.nii.gz'

```

We also checked the command-line that will be generated when we run the command and can see the generated output filename `f3_brain.nii.gz`.

94.2 How to wrap a command line tool

The aim of this section is to describe how external programs and scripts can be wrapped for use in Nipype either as interactive interfaces or within the workflow/pipeline environment. Currently, there is support for command line executables/scripts and matlab scripts. One can also create pure Python interfaces. The key to defining interfaces is to provide a formal specification of inputs and outputs and determining what outputs are generated given a set of inputs.

94.2.1 Defining inputs and outputs

In Nipype we use Enthought Traits to define inputs and outputs of the interfaces. This allows to introduce easy type checking. Inputs and outputs are grouped into separate classes (usually suffixed with `InputSpec` and `OutputSpec`). For example:

```

class ExampleInputSpec(TraitSpec):
    input_volume = File(desc = "Input volume", exists = True,
                        mandatory = True)
    parameter = traits.Int(desc = "some parameter")

class ExampleOutputSpec(TraitSpec):
    output_volume = File(desc = "Output volume", exists = True)

```

For the Traits (and Nipype) to work correctly output and input spec has to be inherited from `TraitSpec` (however, this does not have to be direct inheritance).

Traits (File, Int etc.) have different parameters (called metadata). In the above example we have used the `desc` metadata which holds human readable description of the input. The `mandatory` flag forces Nipype to throw an exception if the input was not set. `exists` is a special flag that works only for File traits and checks if the provided file exists. More details can be found at [Interface Specifications](#).

The input and output specifications have to be connected to the our example interface class:

```
class Example(Interface):
    input_spec = ExampleInputSpec
    output_spec = ExampleOutputSpec
```

Where the names of the classes grouping inputs and outputs were arbitrary the names of the fields within the interface they are assigned are not (it always has to be `input_spec` and `output_spec`). Of course this interface does not do much because we have not specified how to process the inputs and create the outputs. This can be done in many ways.

94.2.2 Command line executable

As with all interfaces command line wrappers need to have inputs defined. Command line input spec has to inherit from `CommandLineInputSpec` which adds two extra inputs: `environ` (a dictionary of environmental variables), and `args` (a string defining extra flags). In addition input spec can define the relation between the inputs and the generated command line. To achieve this we have added two metadata: `argstr` (string defining how the argument should be formatted) and `position` (number defining the order of the arguments). For example

```
class ExampleInputSpec(CommandLineSpec):
    input_volume = File(desc = "Input volume", exists = True,
                        mandatory = True, position = 0, argstr="%s")
    parameter = traits.Int(desc = "some parameter", argstr = "--param %d")
```

As you probably noticed the `argstr` is a printf type string with formatting symbols. For an input defined in `InputSpec` to be included into the executed commandline `argstr` has to be included. Additionally inside the main interface class you need to specify the name of the executable by assigning it to the `_cmd` field. Also the main interface class needs to inherit from `CommandLine`:

```
class Example(CommandLine):
    _cmd = 'my_command'
    input_spec = ExampleInputSpec
    output_spec = ExampleOutputSpec
```

There is one more thing we need to take care of. When the executable finishes processing it will presumably create some output files. We need to know which files to look for, check if they exist and expose them to whatever node would like to use them. This is done by implementing `_list_outputs` method in the main interface class. Basically what it does is assigning the expected output files to the fields of our output spec:

```
def _list_outputs(self):
    outputs = self.output_spec().get()
    outputs['output_volume'] = os.path.abspath('name_of_the_file_this_cmd_
↳made.nii')
    return outputs
```

Sometimes the inputs need extra parsing before turning into command line parameters. For example imagine a parameter selecting between three methods: “old”, “standard” and “new”. Imagine also that the command line accept this as a parameter “--method=” accepting 0, 1 or 2. Since we are aiming to make nipype scripts as informative as possible it’s better to define the inputs as following:

```
class ExampleInputSpec(CommandLineSpec):
    method = traits.Enum("old", "standard", "new", desc = "method",
                        argstr="--method=%d")
```


Here we've used the Enum trait which restricts input a few fixed options. If we would leave it as it is it would not work since the `argstr` is expecting numbers. We need to do additional parsing by overloading the following method in the main interface class:

```
def _format_arg(self, name, spec, value):
    if name == 'method':
        return spec.argstr%{"old":0, "standard":1, "new":2}[value]
    return super(Example, self)._format_arg(name, spec, value)
```

Here is a minimalistic interface for the `gzip` command:

```
from nipy.interfaces.base import (
    TraitedSpec,
    CommandLineInputSpec,
    CommandLine,
    File
)
import os

class GZipInputSpec(CommandLineInputSpec):
    input_file = File(desc="File", exists=True, mandatory=True, argstr="%s")

class GZipOutputSpec(TraitedSpec):
    output_file = File(desc = "Zip file", exists = True)

class GZipTask(CommandLine):
    input_spec = GZipInputSpec
    output_spec = GZipOutputSpec
    cmd = 'gzip'

    def _list_outputs(self):
        outputs = self.output_spec().get()
        outputs['output_file'] = os.path.abspath(self.inputs.input_file + ".gz")
        return outputs

if __name__ == '__main__':
    zipper = GZipTask(input_file='an_existing_file')
    print zipper.cmdline
    zipper.run()
```

94.2.3 Creating outputs on the fly

In many cases, command line executables will require specifying output file names as arguments on the command line. We have simplified this procedure with three additional metadata terms: `name_source`, `name_template`, `keep_extension`.

For example in the `InvWarp` class, the `inverse_warp` parameter is the name of the output file that is created by the routine.

```
class InvWarpInputSpec(FSLCommandInputSpec):
    ...
    inverse_warp = File(argstr='--out=%s', name_source=['warp'],
                        hash_files=False, name_template='%s_inverse',
    ...
```

we add several metadata to `inputspec`.

name_source indicates which field to draw from, this field must be the name of a File.

hash_files indicates that the input for this field if provided should not be used in computing the input hash for this interface.

name_template (optional) overrides the default `_generated` suffix

output_name (optional) name of the output (if this is not set same name as the input will be assumed)

keep_extension (optional) if you want the extension from the input or `name_template` to be kept. The `name_template` extension always overrides the input extension.

In addition one can add functionality to your class or base class, to allow changing extensions specific to package or interface. This overload function is triggered only if `keep_extension` is not defined.

```
def self._overload_extension(self, value):
    return value #do whatever you want here with the name
```

Finally, in the outputspec make sure the name matches that of the inputspec.

```
class InvWarpOutputSpec(TraitedSpec):
    inverse_warp = File(exists=True,
                        desc=('Name of output file, containing warps that '
                              'are the "reverse" of those in --warp.'))
```

94.3 How to wrap a MATLAB script

94.3.1 Example 1

This is a minimal script for wrapping MATLAB code. You should replace the MATLAB code template, and define appropriate inputs and outputs.

```
from nipyne.interfaces.matlab import MatlabCommand
from nipyne.interfaces.base import TraitedSpec, \
    BaseInterface, BaseInterfaceInputSpec, File
import os
from string import Template

class ConmapTxt2MatInputSpec(BaseInterfaceInputSpec):
    in_file = File(exists=True, mandatory=True)
    out_file = File('cmatrix.mat', usedefault=True)

class ConmapTxt2MatOutputSpec(TraitedSpec):
    out_file = File(exists=True)

class ConmapTxt2Mat(BaseInterface):
    input_spec = ConmapTxt2MatInputSpec
    output_spec = ConmapTxt2MatOutputSpec

    def _run_interface(self, runtime):
        d = dict(in_file=self.inputs.in_file,
                 out_file=self.inputs.out_file)
        # This is your MATLAB code template
        script = Template("""in_file = '$in_file';
                             out_file = '$out_file';
                             ConmapTxt2Mat(in_file, out_file);
                             exit;
                             """).substitute(d)
```

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```

# mfile = True will create an .m file with your script and executed.
# Alternatively
# mfile can be set to False which will cause the matlab code to be
# passed
# as a commandline argument to the matlab executable
# (without creating any files).
# This, however, is less reliable and harder to debug
# (code will be reduced to
# a single line and stripped of any comments).
mlab = MatlabCommand(script=script, mfile=True)
result = mlab.run()
return result.runtime

def _list_outputs(self):
    outputs = self._outputs().get()
    outputs['out_file'] = os.path.abspath(self.inputs.out_file)
    return outputs

```

Example source code

You can download the source code of this example.

94.3.2 Example 2

By subclassing `nipyne.interfaces.matlab.MatlabCommand` for your main class, and `nipyne.interfaces.matlab.MatlabInputSpec` for your input and output spec, you gain access to some useful MATLAB hooks

```

from nipyne.interfaces.base import traits
from nipyne.interfaces.base import TraitedSpec
from nipyne.interfaces.matlab import MatlabCommand, MatlabInputSpec

class HelloWorldInputSpec(MatlabInputSpec):
    name = traits.Str(mandatory=True,
                      desc='Name of person to say hello to')

class HelloWorldOutputSpec(TraitedSpec):
    matlab_output = traits.Str()

class HelloWorld(MatlabCommand):
    """Basic Hello World that displays Hello <name> in MATLAB

    Returns
    -----

    matlab_output : capture of matlab output which may be
                    parsed by user to get computation results

    Examples
    -----

    >>> hello = HelloWorld()

```

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```

>>> hello.inputs.name = 'hello_world'
>>> out = hello.run()
>>> print out.outputs.matlab_output
"""

input_spec = HelloWorldInputSpec
output_spec = HelloWorldOutputSpec

def _my_script(self):
    """This is where you implement your script"""
    script = """
    disp('Hello %s Python')
    two = 1 + 1
    """ % (self.inputs.name)
    return script

def run(self, **inputs):
    # Inject your script
    self.inputs.script = self._my_script()
    results = super(MatlabCommand, self).run(**inputs)
    stdout = results.runtime.stdout
    # Attach stdout to outputs to access matlab results
    results.outputs.matlab_output = stdout
    return results

def _list_outputs(self):
    outputs = self._outputs().get()
    return outputs

```

Example source code

You can download the source code of this example.

94.4 How to wrap a Python script

This is a minimal pure python interface. As you can see all you need to do is to define inputs, outputs, `_run_interface()` (not `run()`), and `_list_outputs`.

```

from nipy.interfaces.base import BaseInterface, \
    BaseInterfaceInputSpec, traits, File, TraitSpec
from nipy.utils.filemanip import split_filename

import nibabel as nb
import numpy as np
import os

class SimpleThresholdInputSpec(BaseInterfaceInputSpec):
    volume = File(exists=True, desc='volume to be thresholded', mandatory=True)
    threshold = traits.Float(desc='everything below this value will be set to zero
→ ',
                            mandatory=True)

class SimpleThresholdOutputSpec(TraitSpec):
    thresholded_volume = File(exists=True, desc="thresholded volume")

```

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```

class SimpleThreshold(BaseInterface):
    input_spec = SimpleThresholdInputSpec
    output_spec = SimpleThresholdOutputSpec

    def _run_interface(self, runtime):
        fname = self.inputs.volume
        img = nb.load(fname)
        data = np.array(img.get_data())

        active_map = data > self.inputs.threshold

        thresholded_map = np.zeros(data.shape)
        thresholded_map[active_map] = data[active_map]

        new_img = nb.Nifti1Image(thresholded_map, img.affine, img.header)
        _, base, _ = split_filename(fname)
        nb.save(new_img, base + '_thresholded.nii')

        return runtime

    def _list_outputs(self):
        outputs = self._outputs().get()
        fname = self.inputs.volume
        _, base, _ = split_filename(fname)
        outputs["thresholded_volume"] = os.path.abspath(base + '_thresholded.nii')
        return outputs

```

94.5 Working with *nipy* source code

Contents:

94.5.1 Introduction

These pages describe a [git](#) and [github](#) workflow for the [nipy](#) project.

There are several different workflows here, for different ways of working with *nipy*.

This is not a comprehensive [git](#) reference, it's just a workflow for our own project. It's tailored to the [github](#) hosting service. You may well find better or quicker ways of getting stuff done with [git](#), but these should get you started.

For general resources for learning [git](#) see [git resources](#).

94.5.2 Install git

Overview

Debian / Ubuntu	<code>sudo apt-get install git-core</code>
Fedora	<code>sudo yum install git-core</code>
Windows	Download and install msysGit
OS X	Use the git-osx-installer

In detail

See the [git](#) page for the most recent information.

Have a look at the [github](#) install help pages available from [github help](#)

There are good instructions here: http://book.git-scm.com/2_installing_git.html

94.5.3 Following the latest source

These are the instructions if you just want to follow the latest *nipyre* source, but you don't need to do any development for now.

The steps are:

- *Install git*
- get local copy of the git repository from [github](#)
- update local copy from time to time

Get the local copy of the code

From the command line:

```
git clone git://github.com/nipy/nipyre.git
```

You now have a copy of the code tree in the new *nipyre* directory.

Updating the code

From time to time you may want to pull down the latest code. Do this with:

```
cd nipyre
git pull
```

The tree in *nipyre* will now have the latest changes from the initial repository.

94.5.4 Making a patch

You've discovered a bug or something else you want to change in *nipyre* .. — excellent!

You've worked out a way to fix it — even better!

You want to tell us about it — best of all!

The easiest way is to make a *patch* or set of patches. Here we explain how. Making a patch is the simplest and quickest, but if you're going to be doing anything more than simple quick things, please consider following the *Git for development* model instead.

Making patches

Overview

```
# tell git who you are
git config --global user.email you@yourdomain.example.com
git config --global user.name "Your Name Comes Here"
# get the repository if you don't have it
git clone git://github.com/nipy/nipyre.git
# make a branch for your patching
cd nipyre
git branch the-fix-im-thinking-of
git checkout the-fix-im-thinking-of
# hack, hack, hack
# Tell git about any new files you've made
git add somewhere/tests/test_my_bug.py
# commit work in progress as you go
git commit -am 'BF - added tests for Funny bug'
# hack hack, hack
git commit -am 'BF - added fix for Funny bug'
```

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```
# make the patch files
git format-patch -M -C master
```

Then, send the generated patch files to the [nipyne mailing list](#) — where we will thank you warmly.

In detail

1. Tell `git` who you are so it can label the commits you've made:

```
git config --global user.email you@yourdomain.example.com
git config --global user.name "Your Name Comes Here"
```

2. If you don't already have one, clone a copy of the [nipyne](#) repository:

```
git clone git://github.com/nipy/nipyne.git
cd nipyne
```

3. Make a 'feature branch'. This will be where you work on your bug fix. It's nice and safe and leaves you with access to an unmodified copy of the code in the main branch:

```
git branch the-fix-im-thinking-of
git checkout the-fix-im-thinking-of
```

4. Do some edits, and commit them as you go:

```
# hack, hack, hack
# Tell git about any new files you've made
git add somewhere/tests/test_my_bug.py
# commit work in progress as you go
git commit -am 'BF - added tests for Funny bug'
# hack hack, hack
git commit -am 'BF - added fix for Funny bug'
```

Note the `-am` options to `commit`. The `m` flag just signals that you're going to type a message on the command line. The `a` flag — you can just take on faith — or see [why the -a flag?](#).

5. When you have finished, check you have committed all your changes:

```
git status
```

6. Finally, make your commits into patches. You want all the commits since you branched from the `master` branch:

```
git format-patch -M -C master
```

You will now have several files named for the commits:

```
0001-BF-added-tests-for-Funny-bug.patch
0002-BF-added-fix-for-Funny-bug.patch
```

Send these files to the [nipyne mailing list](#).

When you are done, to switch back to the main copy of the code, just return to the `master` branch:

```
git checkout master
```

Moving from patching to development

If you find you have done some patches, and you have one or more feature branches, you will probably want to switch to development mode. You can do this with the repository you have.

Fork the [nipyne](#) repository on [github](#) — [Making your own copy \(fork\) of nipyne](#). Then:

```
# checkout and refresh master branch from main repo
git checkout master
git pull origin master
# rename pointer to main repository to 'upstream'
git remote rename origin upstream
# point your repo to default read / write to your fork on github
git remote add origin git@github.com:your-user-name/nipytype.git
# push up any branches you've made and want to keep
git push origin the-fix-im-thinking-of
```

Then you can, if you want, follow the *Development workflow*.

94.5.5 Git for development

Contents:

Making your own copy (fork) of nipytype

You need to do this only once. The instructions here are very similar to the instructions at <http://help.github.com/forking/> — please see that page for more detail. We’re repeating some of it here just to give the specifics for the *nipytype* project, and to suggest some default names.

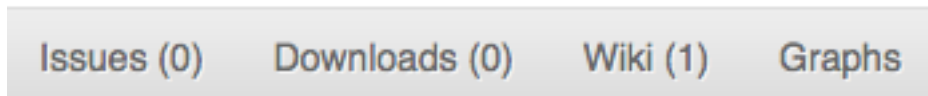
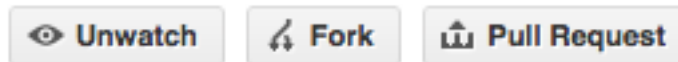
Set up and configure a github account

If you don’t have a *github* account, go to the *github* page, and make one.

You then need to configure your account to allow write access — see the *Generating SSH keys help* on *github help*.

Create your own forked copy of nipytype

1. Log into your *github* account.
2. Go to the *nipytype* github home at *nipytype github*.
3. Click on the *fork* button:



Now, after a short pause and some ‘Hardcore forking action’, you should find yourself at the home page for your own forked copy of *nipytype*.

Set up your fork

First you follow the instructions for *Making your own copy (fork) of nipytype*.

Overview

```
git clone git@github.com:your-user-name/nipytype.git
cd nipytype
git remote add upstream git://github.com/nipy/nipytype.git
```


In detail

Clone your fork

1. Clone your fork to the local computer with `git clone git@github.com:your-user-name/nipyre.git`
2. Investigate. Change directory to your new repo: `cd nipyre`. Then `git branch -a` to show you all branches. You'll get something like:

```
* master
remotes/origin/master
```

This tells you that you are currently on the `master` branch, and that you also have a remote connection to `origin/master`. What remote repository is `remote/origin`? Try `git remote -v` to see the URLs for the remote. They will point to your [github](#) fork.

Now you want to connect to the upstream [nipyre github](#) repository, so you can merge in changes from trunk.

Linking your repository to the upstream repo

```
cd nipyre
git remote add upstream git://github.com/nipy/nipyre.git
```

`upstream` here is just the arbitrary name we're using to refer to the main [nipyre](#) repository at [nipyre github](#). Note that we've used `git://` for the URL rather than `git@`. The `git://` URL is read only. This means we that we can't accidentally (or deliberately) write to the upstream repo, and we are only going to use it to merge into our own code.

Just for your own satisfaction, show yourself that you now have a new 'remote', with `git remote -v` show, giving you something like:

```
upstream      git://github.com/nipy/nipyre.git (fetch)
upstream      git://github.com/nipy/nipyre.git (push)
origin        git@github.com:your-user-name/nipyre.git (fetch)
origin        git@github.com:your-user-name/nipyre.git (push)
```

Configure git

Overview

Your personal `git` configurations are saved in the `.gitconfig` file in your home directory. Here is an example `.gitconfig` file:

```
[user]
  name = Your Name
  email = you@yourdomain.example.com

[alias]
  ci = commit -a
  co = checkout
  st = status -a
  stat = status -a
  br = branch
  wdiff = diff --color-words

[core]
  editor = vim
```

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```
[merge]
    summary = true
```

You can edit this file directly or you can use the `git config --global` command:

```
git config --global user.name "Your Name"
git config --global user.email you@yourdomain.example.com
git config --global alias.ci "commit -a"
git config --global alias.co checkout
git config --global alias.st "status -a"
git config --global alias.stat "status -a"
git config --global alias.br branch
git config --global alias.wdiff "diff --color-words"
git config --global core.editor vim
git config --global merge.summary true
```

To set up on another computer, you can copy your `~/ .gitconfig` file, or run the commands above.

In detail

user.name and user.email

It is good practice to tell `git` who you are, for labeling any changes you make to the code. The simplest way to do this is from the command line:

```
git config --global user.name "Your Name"
git config --global user.email you@yourdomain.example.com
```

This will write the settings into your `git` configuration file, which should now contain a user section with your name and email:

```
[user]
    name = Your Name
    email = you@yourdomain.example.com
```

Of course you'll need to replace `Your Name` and `you@yourdomain.example.com` with your actual name and email address.

Aliases

You might well benefit from some aliases to common commands.

For example, you might well want to be able to shorten `git checkout` to `git co`. Or you may want to alias `git diff --color-words` (which gives a nicely formatted output of the diff) to `git wdiff`.

The following `git config --global` commands:

```
git config --global alias.ci "commit -a"
git config --global alias.co checkout
git config --global alias.st "status -a"
git config --global alias.stat "status -a"
git config --global alias.br branch
git config --global alias.wdiff "diff --color-words"
```

will create an alias section in your `.gitconfig` file with contents like this:

```
[alias]
    ci = commit -a
    co = checkout
```

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```
st = status -a
stat = status -a
br = branch
wdiff = diff --color-words
```

Editor

You may also want to make sure that your editor of choice is used

```
git config --global core.editor vim
```

Merging

To enforce summaries when doing merges (~/.gitconfig file again):

```
[merge]
  log = true
```

Or from the command line:

```
git config --global merge.log true
```

Development workflow

You already have your own forked copy of the [nipyre](#) repository, by following *Making your own copy (fork) of nipyre*, *Set up your fork*, and you have configured [git](#) by following *Configure git*.

Workflow summary

- Keep your `master` branch clean of edits that have not been merged to the main [nipyre](#) development repo. Your `master` then will follow the main [nipyre](#) repository.
- Start a new *feature branch* for each set of edits that you do.
- If you can avoid it, try not to merge other branches into your feature branch while you are working.
- Ask for review!

This way of working really helps to keep work well organized, and in keeping history as clear as possible. See — for example — [linux git workflow](#).

Making a new feature branch

```
git branch my-new-feature
git checkout my-new-feature
```

Generally, you will want to keep this also on your public [github](#) fork of [nipyre](#). To do this, you [git push](#) this new branch up to your [github](#) repo. Generally (if you followed the instructions in these pages, and by default), [git](#) will have a link to your [github](#) repo, called `origin`. You push up to your own repo on [github](#) with:

```
git push origin my-new-feature
```

In [git >1.7](#) you can ensure that the link is correctly set by using the `--set-upstream` option:

```
git push --set-upstream origin my-new-feature
```

From now on [git](#) will know that `my-new-feature` is related to the `my-new-feature` branch in the [github](#) repo.

The editing workflow

Overview

```
# hack hack
git add my_new_file
git commit -am 'NF - some message'
git push
```

In more detail

1. Make some changes
2. See which files have changed with `git status` (see [git status](#)). You'll see a listing like this one:

```
# On branch ny-new-feature
# Changed but not updated:
#   (use "git add <file>..." to update what will be committed)
#   (use "git checkout -- <file>..." to discard changes in working directory)
#
#   modified:   README
#
# Untracked files:
#   (use "git add <file>..." to include in what will be committed)
#
#   INSTALL
no changes added to commit (use "git add" and/or "git commit -a")
```

3. Check what the actual changes are with `git diff` ([git diff](#)).
4. Add any new files to version control `git add new_file_name` (see [git add](#)).
5. To commit all modified files into the local copy of your repo., do `git commit -am 'A commit message'`. Note the `-am` options to commit. The `m` flag just signals that you're going to type a message on the command line. The `a` flag — you can just take on faith — or see [why the -a flag?](#) — and the helpful use-case description in the [tangled working copy problem](#). The `git commit` manual page might also be useful.
6. To push the changes up to your forked repo on [github](#), do a `git push` (see [git push](#)).

Asking for code review

1. Go to your repo URL — e.g. <http://github.com/your-user-name/nipyre>.
2. Click on the *Branch list* button:



3. Click on the *Compare* button for your feature branch — here `my-new-feature`:

NAME	STATE
my-new-feature Last updated 18 minutes ago	0 ahead 0 behind
	
	 Compare

4. If asked, select the *base* and *comparison* branch names you want to compare. Usually these will be `master` and `my-new-feature` (where that is your feature branch name).

- At this point you should get a nice summary of the changes. Copy the URL for this, and post it to the [nipyre mailing list](#), asking for review. The URL will look something like: `http://github.com/your-user-name/nipyre/compare/master...my-new-feature`. There's an example at <http://github.com/matthew-brett/nipy/compare/master...find-install-data>. See: <http://github.com/blog/612-introducing-github-compare-view> for more detail.

The generated comparison, is between your feature branch `my-new-feature`, and the place in `master` from which you branched `my-new-feature`. In other words, you can keep updating `master` without interfering with the output from the comparison. More detail? Note the three dots in the URL above (`master...my-new-feature`).

Two vs three dots

Imagine a series of commits A, B, C, D... Imagine that there are two branches, *topic* and *master*. You branched *topic* off *master* when *master* was at commit 'E'. The graph of the commits looks like this:

```

      A---B---C topic
      /
D---E---F---G master

```

Then:

```
git diff master..topic
```

will output the difference from G to C (i.e. with effects of F and G), while:

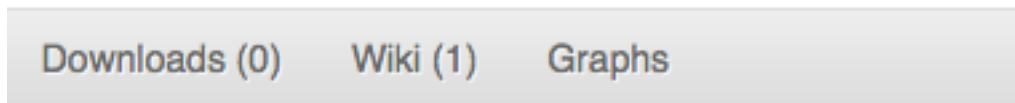
```
git diff master...topic
```

would output just differences in the topic branch (i.e. only A, B, and C).¹

Asking for your changes to be merged with the main repo

When you are ready to ask for the merge of your code:

- Go to the URL of your forked repo, say `http://github.com/your-user-name/nipyre.git`.
- Click on the 'Pull request' button:



Enter a message; we suggest you select only `nipyre` as the recipient. The message will go to the [nipyre mailing list](#). Please feel free to add others from the list as you like.

Merging from trunk

This updates your code from the upstream [nipyre github](#) repo.

Overview

```
# go to your master branch
git checkout master
# pull changes from github
```

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¹ Thanks to Yarik Halchenko for this explanation.

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```
git fetch upstream
# merge from upstream
git merge upstream/master
```

In detail

We suggest that you do this only for your `master` branch, and leave your ‘feature’ branches unmerged, to keep their history as clean as possible. This makes code review easier:

```
git checkout master
```

Make sure you have done *Linking your repository to the upstream repo*.

Merge the upstream code into your current development by first pulling the upstream repo to a copy on your local machine:

```
git fetch upstream
```

then merging into your current branch:

```
git merge upstream/master
```

Deleting a branch on github

```
git checkout master
# delete branch locally
git branch -D my-unwanted-branch
# delete branch on github
git push origin :my-unwanted-branch
```

(Note the colon `:` before `test-branch`. See also: <http://github.com/guides/remove-a-remote-branch>)

Several people sharing a single repository

If you want to work on some stuff with other people, where you are all committing into the same repository, or even the same branch, then just share it via [github](#).

First fork nipytype into your account, as from *Making your own copy (fork) of nipytype*.

Then, go to your forked repository github page, say `http://github.com/your-user-name/nipytype`. Click on the ‘Admin’ button, and add anyone else to the repo as a collaborator:



Now all those people can do:

```
git clone git@github.com:your-user-name/nipytype.git
```

Remember that links starting with `git@` use the ssh protocol and are read-write; links starting with `git://` are read-only.

Your collaborators can then commit directly into that repo with the usual:

```
git commit -am 'ENH - much better code'
git push origin master # pushes directly into your repo
```

Exploring your repository

To see a graphical representation of the repository branches and commits:

```
gitk --all
```

To see a linear list of commits for this branch:

```
git log
```

You can also look at the [network graph visualizer](#) for your [github](#) repo.

94.5.6 git resources

Tutorials and summaries

- [github help](#) has an excellent series of how-to guides.
- [learn.github](#) has an excellent series of tutorials
- The [pro git book](#) is a good in-depth book on git.
- A [git cheat sheet](#) is a page giving summaries of common commands.
- The [git user manual](#)
- The [git tutorial](#)
- The [git community book](#)
- [git ready](#) — a nice series of tutorials
- [git casts](#) — video snippets giving git how-tos.
- [git magic](#) — extended introduction with intermediate detail
- The [git parable](#) is an easy read explaining the concepts behind git.
- Our own [git foundation](#) expands on the [git parable](#).
- Fernando Perez' git page — [Fernando's git page](#) — many links and tips
- A good but technical page on [git concepts](#)
- [git svn crash course](#): [git](#) for those of us used to [subversion](#)

Advanced git workflow

There are many ways of working with [git](#); here are some posts on the rules of thumb that other projects have come up with:

- Linus Torvalds on [git management](#)
- Linus Torvalds on [linux git workflow](#) . Summary; use the git tools to make the history of your edits as clean as possible; merge from upstream edits as little as possible in branches where you are doing active development.

Manual pages online

You can get these on your own machine with (e.g) `git help push` or (same thing) `git push --help`, but, for convenience, here are the online manual pages for some common commands:

- [git add](#)
- [git branch](#)
- [git checkout](#)
- [git clone](#)
- [git commit](#)
- [git config](#)
- [git diff](#)
- [git log](#)
- [git pull](#)

- `git push`
- `git remote`
- `git status`

94.6 Architecture (discussions from 2009)

This section reflects notes and discussion between developers during the start of the nipyre project in 2009.

94.6.1 Design Guidelines

These are guidelines that the core nipyre developers have agreed on:

Interfaces should keep all parameters affecting construction of the appropriate command in the “input” bunch. The `.run()` method of an Interface should include all required inputs as explicitly named parameters, and they should take a default value of `None`.

Any Interface should at a minimum support `cwd` as a command-line argument to `.run()`. This may be accomplished by allowing `cwd` as an element of the input Bunch, or handled as a separate case.

Relatedly, any Interface should output all files to `cwd` if it is set, and otherwise to `os.getcwd()` (or equivalent).

We need to decide on a consistent policy towards the maintenance of paths to files. It seems like the best strategy might be to do absolute (`os.realpath()`) filenames by default, allowing for relative paths by explicitly including something that doesn’t start with a `’/’`. This could include `’.’` in some sort of path-spec.

Class attributes should never be modified by an instance of that class. And probably not ever.

94.6.2 Providing for Provenance

The following is a specific discussion that should be thought out and more generally applied to the way we handle auto-generation / or “sourcing” of settings in an interface.

There are two possible sources (at a minimum) from which the interface instance could obtain “outputtype” - itself, or `FSLInfo`. Currently, the outputtype gets read from `FSLInfo` if `self.outputtype` (er, `_outputtype`?) is `None`.

In the case of other `opt_map` specifications, there are defaults that get specified if the value is `None`. For example output filenames are often auto-generated. If you look at the code for `fsl.Bet` for example, there is no way for the outfile to get picked up at the pipeline level, because it is a transient variable. This is OK, as the generation of the outfile name is contingent ONLY on inputs which ARE available to the pipeline machinery (i.e., via inspection of the `Bet` instance’s attributes).

However, with `outputtype`, we are in a situation in which “autogeneration” incorporates potentially transient information external to the instance itself. Thus, some care needs to be taken in always ensuring this information is hashable.

94.6.3 Design Principles

These are (currently) Dav Clark’s best guess at what the group might agree on:

It should be very easy to figure out what was done by the pipeline.

Code should support relocatability - this could be via URIs, relative paths or potentially other mechanisms.

Unless otherwise called for, code should be thread safe, just in case.

The pipeline should make it easy to change aspects of an analysis with minimal recomputation, downloading, etc. (This is not the case currently - any change will overwrite the old node). Also, the fact that multiple files get rolled into a single node is problematic for similar reasons. E.g. - `node([file1 ... file100])` will get recomputed if we add only one file!.

However, it should also be easy to identify and delete things you don’t need anymore.

Pipelines and bits of pipelines should be easy to share.

Things that are the same should be called the same thing in most places. For interfaces that have an obvious meaning for the terms, “infiles” and “outfile(s)”. If a file is in both the inputs and outputs, it should be called the same thing in both places. If it is produced by one interface and consumed by another, same thing should be used.

94.6.4 Discussions

Auto-generated filenames

In refactoring the inputs in the traitlets branch I'm working through the different ways that filenames are generated and want to make sure the interface is consistent. The notes below are all using `fsl.Bet` as that's the first class we're Traiting. Other interface classes may handle this differently, but should agree on a convention and apply it across all Interfaces (if possible).

Current Rules

These rules are for `fsl.Bet`, but it appears they are the same for all `fsl` and `spm` Interfaces.

`Bet` has two mandatory parameters, `infile` and `outfile`. These are the rules for how they are handled in different use cases.

1. If `infile` or `outfile` are absolute paths, they are used as-is and never changed. This allows users to override any filename/path generation.
2. If `outfile` is not specified, a filename is generated.
3. Generated filenames (at least for `outfile`) are based on:
 - `infile`, the filename minus the extensions.
 - A suffix specified by the Interface. For example `Bet` uses `_brain` suffix.
 - The current working directory, `os.getcwd()`. Example:
If `infile == 'foo.nii'` and the cwd is `/home/cburns` then generated `outfile` for `Bet` will be `/home/cburns/foo_brain.nii.gz`
4. If `outfile` is not an absolute path, for instance just a filename, the absolute path is generated using `os.path.realpath`. This absolute path is needed to make sure the packages (`Bet` in this case) write the output file to a location of our choosing. The generated absolute path is only used in the `cmdline` at runtime and does not overwrite the class attr `self.inputs.outfile`. It is generated only when the `cmdline` is invoked.

Walking through some examples

In this example we assign `infile` directly but `outfile` is generated in `Bet._parse_inputs` based on `infile`. The generated `outfile` is only used in the `cmdline` at runtime and not stored in `self.inputs.outfile`. This seems correct.

```
In [15]: from nipy.interfaces import fsl

In [16]: mybet = fsl.Bet()

In [17]: mybet.inputs.infile = 'foo.nii'

In [18]: res = mybet.run()

In [19]: res.runtime.cmdline
Out[19]: 'bet foo.nii /Users/cburns/src/nipy-sf/nipytype/trunk/nipytype/interfaces/
↳tests/foo_brain.nii.gz'

In [21]: mybet.inputs
Out[21]: Bunch(center=None, flags=None, frac=None, functional=None,
infile='foo.nii', mask=None, mesh=None, nooutput=None, outfile=None,
outline=None, radius=None, reduce_bias=None, skull=None, threshold=None,
verbose=None, vertical_gradient=None)

In [24]: mybet.cmdline
Out[24]: 'bet foo.nii /Users/cburns/src/nipy-sf/nipytype/trunk/nipytype/interfaces/
↳tests/foo_brain.nii.gz'
```

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```
In [25]: mybet.inputs.outfile

In [26]: mybet.inputs.infile
Out[26]: 'foo.nii'
```

We get the same behavior here when we assign infile at initialization:

```
In [28]: mybet = fsl.Bet(infile='foo.nii')

In [29]: mybet.cmdline
Out[29]: 'bet foo.nii /Users/cburns/src/nipy-sf/nipype/trunk/nipype/interfaces/
↳tests/foo_brain.nii.gz'

In [30]: mybet.inputs
Out[30]: Bunch(center=None, flags=None, frac=None, functional=None,
infile='foo.nii', mask=None, mesh=None, nooutput=None, outfile=None,
outline=None, radius=None, reduce_bias=None, skull=None, threshold=None,
verbose=None, vertical_gradient=None)

In [31]: res = mybet.run()

In [32]: res.runtime.cmdline
Out[32]: 'bet foo.nii /Users/cburns/src/nipy-sf/nipype/trunk/nipype/interfaces/
↳tests/foo_brain.nii.gz'
```

Here we specify absolute paths for both infile and outfile. The command line's look as expected:

```
In [53]: import os

In [54]: mybet = fsl.Bet()

In [55]: mybet.inputs.infile = os.path.join('/Users/cburns/tmp/junk', 'foo.nii')
In [56]: mybet.inputs.outfile = os.path.join('/Users/cburns/tmp/junk', 'bar.nii')

In [57]: mybet.cmdline
Out[57]: 'bet /Users/cburns/tmp/junk/foo.nii /Users/cburns/tmp/junk/bar.nii'

In [58]: res = mybet.run()

In [59]: res.runtime.cmdline
Out[59]: 'bet /Users/cburns/tmp/junk/foo.nii /Users/cburns/tmp/junk/bar.nii'
```

Here passing in a new outfile in the run method will update mybet.inputs.outfile to the passed in value. Should this be the case?

```
In [110]: mybet = fsl.Bet(infile='foo.nii', outfile='bar.nii')

In [111]: mybet.inputs.outfile
Out[111]: 'bar.nii'

In [112]: mybet.cmdline
Out[112]: 'bet foo.nii /Users/cburns/src/nipy-sf/nipype/trunk/nipype/interfaces/
↳tests/bar.nii'

In [113]: res = mybet.run(outfile = os.path.join('/Users/cburns/tmp/junk', 'not_
↳bar.nii'))
```

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```
In [114]: mybet.inputs.outfile
Out[114]: '/Users/cburns/tmp/junk/not_bar.nii'

In [115]: mybet.cmdline
Out[115]: 'bet foo.nii /Users/cburns/tmp/junk/not_bar.nii'
```

In this case we provide `outfile` but not as an absolute path, so the absolute path is generated and used for the `cmdline` when run, but `mybet.inputs.outfile` is not updated with the absolute path.

```
In [74]: mybet = fsl.Bet(infile='foo.nii', outfile='bar.nii')

In [75]: mybet.inputs.outfile
Out[75]: 'bar.nii'

In [76]: mybet.cmdline
Out[76]: 'bet foo.nii /Users/cburns/src/nipy-sf/nipyne/trunk/nipyne/interfaces/
↳tests/bar.nii'

In [77]: res = mybet.run()

In [78]: res.runtime.cmdline
Out[78]: 'bet foo.nii /Users/cburns/src/nipy-sf/nipyne/trunk/nipyne/interfaces/
↳tests/bar.nii'

In [80]: res.interface.inputs.outfile
Out[80]: 'bar.nii'
```

94.7 W3C PROV support

94.7.1 Overview

We're using the the [W3C PROV data model](#) to capture and represent provenance in Nipyne.

For an overview see:

[PROV-DM overview](#)

Each interface writes out a `provenance.json` (currently `prov-json`) or `provenance.rdf` (if `rdflib` is available) file. The workflow engine can also write out a provenance of the workflow if instructed.

This is very much an experimental feature as we continue to refine how exactly the provenance should be stored and how such information can be used for reporting or reconstituting workflows. By default provenance writing is disabled for the 0.9 release, to enable insert the following code at the top of your script:

```
>>> from nipyne import config
>>> config.enable_provenance()
```

94.8 Software using Nipyne

94.8.1 Configurable Pipeline for the Analysis of Connectomes (C-PAC)

C-PAC is an open-source software pipeline for automated preprocessing and analysis of resting-state fMRI data. C-PAC builds upon a robust set of existing software packages including AFNI, FSL, and ANTS, and makes it easy for both novice users and experts to explore their data using a wide array of analytic tools. Users define analysis pipelines by specifying a combination of preprocessing options and analyses to be run on an arbitrary number of subjects. Results can then be compared across groups using the integrated group statistics feature. C-PAC makes extensive use of Nipyne Workflows and Interfaces.

94.8.2 BRAINSTools

BRAINSTools is a suite of tools for medical image processing focused on brain analysis.

94.8.3 Brain Imaging Pipelines (BIPs)

BIPs is a set of predefined Nipyne workflows coupled with a graphical interface and ability to save and share workflow configurations. It provides both Nipyne Workflows and Interfaces.

94.8.4 BROCCOLI

BROCCOLI is a piece of software for fast fMRI analysis on many core CPUs and GPUs. It provides Nipyne Interfaces.

94.8.5 Forward

Forward is set of tools simplifying the preparation of accurate electromagnetic head models for EEG forward modeling. It uses Nipyne Workflows and Interfaces.

94.8.6 Limbo

Limbo is a toolbox for finding brain regions that are neither significantly active nor inactive, but rather “in limbo”. It was build using custom Nipyne Interfaces and Workflows.

94.8.7 Lyman

Lyman is a high-level ecosystem for analyzing task based fMRI neuroimaging data using open-source software. It aims to support an analysis workflow that is powerful, flexible, and reproducible, while automating as much of the processing as possible. It is build upon Nipyne Workflows and Interfaces.

94.8.8 Medimsight

Medimsight is a commercial service medical imaging cloud platform. It uses Nipyne to interface with various neuroimaging software.

94.8.9 MIA

MIA MIA is a a toolkit for gray scale medical image analysis. It provides Nipyne interfaces for easy integration with other software.

94.8.10 Mindboggle

Mindboggle software package automates shape analysis of anatomical labels and features extracted from human brain MR image data. Mindboggle can be run as a single command, and can be easily installed as a cross-platform virtual machine for convenience and reproducibility of results. Behind the scenes, open source Python and C++ code run within a Nipyne pipeline framework.

94.8.11 OpenfMRI

OpenfMRI is a repository for task based fMRI datasets. It uses Nipyne for automated analysis of the deposited data.

94.8.12 serial functional Diffusion Mapping (sfDM)

‘sfDM <<http://github.com/PIRCImagingTools/sfDM>>’ is a software package for looking at changes in diffusion profiles of different tissue types across time. It uses Nipyne to process the data.

94.8.13 The Stanford CNI MRS Library (SMAL)

SMAL is a library providing algorithms and methods to read and analyze data from Magnetic Resonance Spectroscopy (MRS) experiments. It provides an API for fitting models of the spectral line-widths of several different molecular species, and quantify their relative abundance in human brain tissue. SMAL uses Nipype Workflows and Interfaces.

94.8.14 tract_querier

tract_querier is a White Matter Query Language tool. It provides Nipype interfaces.

94.9 Testing nipype

In order to ensure the stability of each release of Nipype, the project uses two continuous integration services: **CircleCI** and **Travis CI**. If both batteries of tests are passing, the following badges should be shown in green color:



94.9.1 Installation for developers

To check out the latest development version:

```
git clone https://github.com/nipy/nipype.git
```

After cloning:

```
cd nipype
pip install -r requirements.txt
pip install -e .[dev]
```

94.9.2 Test implementation

Nipype testing framework is built upon **pytest**.

After installation in developer mode, the tests can be run with the following command at the root folder of the project

```
pytest -v --doctest-modules nipype
```

A successful test run should complete in 10-30 minutes and end with something like:

```
-----
2445 passed, 41 skipped, 7 xfailed in 1277.66 seconds
```

No test should fail (unless you're missing a dependency). If the `SUBJECTS_DIR`` environment variable is not set, some FreeSurfer related tests will fail. If any of the tests failed, please report them on our [bug tracker](#).

On Debian systems with a local copy of MATLAB installed, set the following environment variable before running tests:

```
export MATLABCMD=$pathtomatlabdir/bin/$platform/MATLAB
```

where `$pathtomatlabdir` is the path to your matlab installation and `$platform` is the directory referring to x86 or x64 installations (typically `glnxa64` on 64-bit installations).

Skipped tests

Nipype will skip some tests depending on the currently available software and data dependencies. Installing software dependencies and downloading the necessary data will reduce the number of skipped tests.

A few tests in Nipype make use of some images distributed within the [FSL course data](#). This reduced version of the package can be downloaded [here](#). To enable the tests depending on these data, just unpack the targz file and set the `FSL_COURSE_DATA` environment variable to point to that folder. Note, that the test execution time can increase significantly with these additional tests.

Xfailed tests

Some tests are expect to fail until the code will be changed or for other reasons.

94.9.3 Testing Nipype using Docker

Nipype is tested inside Docker containers and users can use nipype images to test local versions. First, install the [Docker Engine](#). Nipype has one base docker image called `nipype/nipype:base`, that contains several useful tools

(FreeSurfer, AFNI, FSL, ANTs, etc.), and additional test images for specific Python versions: `py27` for Python 2.7 and `py36` for Python 3.6. Users can pull the nipype image for Python 3.6 as follows:

```
docker pull nipype/nipype:py36
```

In order to test a local version of nipype you can run test within container as follows:

```
docker run -it -v $PWD:/src/nipype --rm nipype/nipype:py36 py.test -v --doctest-  
↳modules /src/nipype/nipype
```

94.9.4 Additional comments

If the project is tested both on your local OS and within a Docker container, you might have to remove all `__pycache__` directories before switching between your OS and a container.

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