nipype Documentation

Release 0.12.0

Neuroimaging in Python team

August 04, 2016, 00:17 PDT

Contents

Previous versions: 0.12.0 0.11.0

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CHAPTER 1

User Guide

Release 0.12.1
Date August 04, 2016, 00:17 PDT

1.1 Download and install

This page covers the necessary steps to install Nipype.

1.1.1 Nipype for users

Using conda

Installing nipype from the conda-forge channel can be achieved by adding conda-forge to your channels with:

```
conda config --add channels conda-forge
```

Once the conda-forge channel has been enabled, nipype can be installed with:

```
conda install nipype
```

It is possible to list all of the versions of nipype available on your platform with:

```
conda search nipype --channel conda-forge
```

For more information, please see https://github.com/conda-forge/nipype-feedstock

Using Pypi

The installation process is similar to other Python packages.
If you already have a Python environment set up, you can do:

```
easy_install nipype
```

or:

```
pip install nipype
```

Debian and Ubuntu

Add the NeuroDebian repository and install the `python-nipype` package using `apt-get` or your favorite package manager.

Mac OS X

The easiest way to get nipype running on Mac OS X is to install Anaconda or Canopy and then add nipype by executing:

```
easy_install nipype
```

From source

The current release is found here: https://github.com/nipy/nipype/releases/latest.
The development version: [zip tar.gz]
For previous versions: prior downloads
If you downloaded the source distribution named something like `nipype-x.y.tar.gz`, then unpack the tarball, change into the `nipype-x.y` directory and install nipype using:

```
pip install -r requirements.txt
python setup.py install
```

Note: Depending on permissions you may need to use `sudo`.

1.1.2 Nipype for developers

To check out the latest development version:

```
git clone git://github.com/nipy/nipype.git
```

or:

```
git clone https://github.com/nipy/nipype.git
```

After cloning:

```
pip install -r requirements.txt
python setup.py develop
```

Check out the list of nipype's current dependencies.

1.1.3 Testing the install

The best way to test the install is to run the test suite. If you have nose installed, then do the following:

```
python -c "import nipype; nipype.test()"
```

you can also test with nosetests:

```
nosetests --with-doctest <installation filepath>/nipype  --exclude=external --exclude=testing
```

or:

```
nosetests --with-doctest nipype
```

A successful test run should complete in a few minutes and end with something like:

```
Ran 13053 tests in 126.618s

OK (SKIP=66)
```

All tests should pass (unless you're missing a dependency). If SUBJECTS_DIR variable is not set some FreeSurfer related tests will fail. If any tests fail, please report them on our bug tracker.
On Debian systems, 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).

Avoiding any MATLAB calls from testing

On unix systems, set an empty environment variable:

```
export NIPYPE_NO_MATLAB=
```

This will skip any tests that require matlab.

1.1.4 Recommended Software

Strong Recommendations

IPython **0.10.2 - 1.0.0** Interactive python environment. This is necessary for some parallel components of the pipeline engine.
Matplotlib **1.0 - 1.2** Plotting library
RDFLib **4.1** RDFLibrary required for provenance export as RDF
Sphinx **1.1** Required for building the documentation
Graphviz Required for building the documentation. The python wrapper package (`graphviz`) and the program itself both need to be installed.

Interface Dependencies

You might not need some of the following packages, depending on what exactly you want to use nipype for. If you do need any of them, install nipype's wrapper package (`nipype.interfaces`), then install the programs separately onto your computer, just like you would install any other app.
FSL 4.1.0 or later
matlab 2008a or later
SPM SPM5 or later
FreeSurfer FreeSurfer v4.0.0 or later
AFNI 2009_12_31_1431 or later
Slicer 3.6 or later
Nipy 0.1.2+20110404 or later
Nitime (optional)
ANTS
MRtrix and MRtrix3
Camino
Camino2Trackvis
ConnectomeViewer

1.2 Running Nipype in a VM

Tip: Creating the Vagrant VM as described below requires an active internet connection.

Container technologies (Vagrant, Docker) allow creating and manipulating lightweight virtual environments. The Nipype source now contains a Vagrantfile to launch a Vagrant VM.
Requirements:

- Vagrant
- Virtualbox

After you have installed Vagrant and Virtualbox, you simply need to download the latest Nipype source and unzip/tar/compress it. Go into your terminal and switch to the nipype source directory. Make sure the Vagrantfile is in the directory. Now you can execute:

```
vagrant up
```

This will launch and provision the virtual machine.
The default virtual machine is built using Ubuntu Precise 64, linked to the NeuroDebian source repo and contains a 2 node Grid Engine for cluster execution.
The machine has a default IP address of *192.168.100.20* . From the vagrant startup directory you can log into the machine using:

```
vagrant ssh
```

Now you can install your favorite software using:

```
sudo apt-get install fsl afni
```

Also note that the directory in which you call *vagrant up* will be mounted under */vagrant* inside the virtual machine. You can also copy the Vagrantfile or modify it in order to mount a different directory/directories. Please read through Vagrant documentation on other features. The python environment is built using a miniconda distribution. Hence *conda* can be used to do your python package management inside the VM.

1.3 Tutorial : Interfaces

1.3.1 Specifying options

The nipype interface modules provide a Python interface to external packages like FSL and SPM. Within the module are a series of Python classes which wrap specific package functionality. For example, in the fsl module, the class `nipype.interfaces.fsl.Bet` wraps the `bet` command-line tool. Using the command-line tool, one would specify options using flags like `-o`, `-m`, `-f <f>`, etc... However, in nipype, options are assigned to Python attributes and can be specified in the following ways:
Options can be assigned when you first create an interface object:

```
import nipype.interfaces.fsl as fsl
mybet = fsl.BET(in_file='foo.nii', out_file='bar.nii')
result = mybet.run()
```

Options can be assigned through the `inputs` attribute:

```
import nipype.interfaces.fsl as fsl
mybet = fsl.BET()
mybet.inputs.in_file = 'foo.nii'
mybet.inputs.out_file = 'bar.nii'
result = mybet.run()
```

Options can be assigned when calling the `run` method:

```
import nipype.interfaces.fsl as fsl
mybet = fsl.BET()
result = mybet.run(in_file='foo.nii', out_file='bar.nii', frac=0.5)
```

1.3.2 Getting Help

In IPython you can view the docstrings which provide some basic documentation and examples.

```
In [2]: fsl.FAST?
Type:               type
Base Class: <type 'type'>
String Form:        <class 'nipype.interfaces.fsl.preprocess.FAST'>
Namespace:  Interactive
File:               /Users/satra/sp/nipype/interfaces/fsl/preprocess.py
Docstring:
    Use FSL FAST for segmenting and bias correction.

    For complete details, see the `FAST Documentation.
    <http://www.fmrib.ox.ac.uk/fsl/fast4/index.html>`_

    Examples
    --------
    >>> from nipype.interfaces import fsl
    >>> from nipype.testing import anatfile
```

```
    Assign options through the ``inputs`` attribute:

    >>> fastr = fsl.FAST()
    >>> fastr.inputs.in_files = anatfile
    >>> out = fastr.run() #doctest: +SKIP

Constructor information:
Definition: fsl.FAST(self, **inputs)
```

```
In [5]: spm.Realign?
Type:               type
Base Class:  <type 'type'>
String Form: <class 'nipype.interfaces.spm.preprocess.Realign'>
Namespace:   Interactive
File:               /Users/satra/sp/nipype/interfaces/spm/preprocess.py
Docstring:
    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 nipype.interfaces.spm as spm
    >>> realign = spm.Realign()
    >>> realign.inputs.in_files = 'functional.nii'
    >>> realign.inputs.register_to_mean = True
    >>> realign.run() # doctest: +SKIP

Constructor information:
Definition:  spm.Realign(self, **inputs)
```

All of the nipype.interfaces classes have an `help` method which provides information on each of the options one can assign.

```
In [6]: 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
     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 [7]: spm.Realign.help()
    Inputs
    ------

    Mandatory:
     in_files: list of filenames to realign

    Optional:
     fwhm: gaussian smoothing kernel width
     interp: degree of b-spline used for interpolation
     jobtype: one of: estimate, write, estwrite (default=estwrite)
     matlab_cmd: None
     mfile: Run m-code using m-file (default=True)
     paths: Paths to add to matlabpath
     quality: 0.1 = fast, 1.0 = precise
     register_to_mean: Indicate whether realignment is done to the mean image
     separation: sampling separation in mm
     weight_img: filename of weighting image
     wrap: Check if interpolation should wrap in [x,y,z]
     write_interp: degree of b-spline used for interpolation
     write_mask: True/False mask output image
     write_which: determines which images to reslice
     write_wrap: Check if interpolation should wrap in [x,y,z]

    Outputs
    -------
    mean_image: Mean image file from the realignment
    realigned_files: Realigned files
    realignment_parameters: Estimated translation and rotation parameters
```

Our interface-index documentation provides html versions of our docstrings and includes links to the specific package documentation. For instance, the `nipype.interfaces.fsl.Bet` docstring has a direct link to the online BET Documentation.

1.3.3 FSL interface example

Using FSL to realign a time_series:

```
    import nipype.interfaces.fsl as fsl
    realigner = fsl.McFlirt()
    realigner.inputs.in_file='timeseries4D.nii'
    result = realigner.run()
```

1.3.4 SPM interface example

Using SPM to realign a time-series:

```
import nipype.interfaces.spm as spm
from glob import glob
allepi = glob('epi*.nii') # this will return an unsorted list
allepi.sort()
realigner = spm.Realign()
realigner.inputs.in_files = allepi
result = realigner.run()
```

1.4 Interface caching

This section details the interface-caching mechanism, exposed in the `nipype.caching` module.

1.4.1 Interface caching: why and how

- *Pipelines* (also called *workflows*) specify processing by an execution graph. This is useful because it opens the door to dependency checking and enable *i)* to minimize recomputations, *ii)* to have the execution engine transparently deal with intermediate file manipulations.
  They however do not blend in well with arbitrary Python code, as they must rely on their own execution engine.
- *Interfaces* give fine control of the execution of each step with a thin wrapper on the underlying software. As a result that can easily be inserted in Python code.
  However, they force the user to specify explicit input and output file names and cannot do any caching.
  This is why nipype exposes an intermediate mechanism, *caching* that provides transparent output file management and caching within imperative Python code rather than a workflow.

1.4.2 A big picture view: using the `Memory` object

nipype caching relies on the *`Memory`* class: it creates an execution context that is bound to a disk cache:

```
>>> from nipype.caching import Memory
>>> mem = Memory(base_dir='.')
```

Note that the caching directory is a subdirectory called *nipype_mem* of the given *base_dir*. This is done to avoid polluting the base director.
In the corresponding execution context, nipype interfaces can be turned into callables that can be used as functions using the *`Memory.cache()`* method. For instance if we want to run the fslMerge command on a set of files:

```
>>> from nipype.interface import fsl
>>> fsl_merge = mem.cache(fsl.Merge)
```

Note that the *`Memory.cache()`* method takes interfaces **classes**, and not instances.
The resulting *fsl_merge* object can be applied as a function to parameters, that will form the inputs of the *merge* fsl commands. Those inputs are given as keyword arguments, bearing the same name as the name in the inputs specs of the interface. In IPython, you can also get the argument list by using the *fsl_merge?* synthax to inspect the docs:

```
In [10]: fsl_merge?
String Form:PipeFunc(nipype.interfaces.fsl.utils.Merge, base_dir=/home/varoquau/dev/nipype/nipyp
Namespace:  Interactive
File:       /home/varoquau/dev/nipype/nipype/caching/memory.py
Definition: fsl_merge(self, **kwargs)
Docstring:
Use fslmerge to concatenate images

Inputs
------
```

```
    Mandatory:
    dimension: dimension along which the file will be merged
    in_files: None

    Optional:
    args: Additional parameters to the command
    environ: Environment variables (default={})
    ignore_exception: Print an error message instead of throwing an exception in case the interface
    merged_file: None
    output_type: FSL output type

    Outputs
    -------
    merged_file: None
    Class Docstring:
    ...
```

Thus *fsl_merge* is applied to parameters as such:

```
>>> results = fsl_merge(dimension='t', in_files=['a.nii.gz', 'b.nii.gz'])
INFO:workflow:Executing node faa7888f5955c961e5c6aa70cbd5c807 in dir: /home/varoquau/dev/nipype/
INFO:workflow:Running: fslmerge -t /home/varoquau/dev/nipype/nipype/caching/nipype_mem/nipype-in
```

The results are standard nipype nodes results. In particular, they expose an *outputs* attribute that carries all the outputs of the process, as specified by the docs.

```
>>> results.outputs.merged_file
'/home/varoquau/dev/nipype/nipype/caching/nipype_mem/nipype-interfaces-fsl-utils-Merge/faa7888f5
```

Finally, and most important, if the node is applied to the same input parameters, it is not computed, and the results are reloaded from the disk:

```
>>> results = fsl_merge(dimension='t', in_files=['a.nii.gz', 'b.nii.gz'])
INFO:workflow:Executing node faa7888f5955c961e5c6aa70cbd5c807 in dir: /home/varoquau/dev/nipype/
INFO:workflow:Collecting precomputed outputs
```

Once the *Memory* is set up and you are applying it to data, an important thing to keep in mind is that you are using up disk cache. It might be useful to clean it using the methods that *Memory* provides for this: *Memory.clear_previous_runs()*, *Memory.clear_runs_since()*.

Example

A full-blown example showing how to stage multiple operations can be found in the `caching_example.py` file.

1.4.3 Usage patterns: working efficiently with caching

The goal of the *caching* module is to enable writing plain Python code rather than workflows. Use it: instead of data grabber nodes, use for instance the *glob* module. To vary parameters, use *for* loops. To make reusable code, write Python functions.

One good rule of thumb to respect is to avoid the usage of explicit filenames apart from the outermost inputs and outputs of your processing. The reason being that the caching mechanism of `nipy.caching` takes care of generating the unique hashes, ensuring that, when you vary parameters, files are not overridden by the output of different computations.

Debuging

If you need to inspect the running environment of the nodes, it may be useful to know where they were executed. With *nipype.caching*, you do not control this location as it is encoded by hashes.
To find out where an operation has been persisted, simply look in it's output variable:

```
out.runtime.cwd
```

Finally, the more you explore different parameters, the more you risk creating cached results that will never be reused. Keep in mind that it may be useful to flush the cache using *Memory.clear_previous_runs()* or *Memory.clear_runs_since()*.

1.4.4 API reference

The main class of the `nipype.caching` module is the *Memory* class:

class `nipype.caching.`**Memory**(*base_dir*)

Memory context to provide caching for interfaces

Parameters **base_dir: string** :

The directory name of the location for the caching

Methods

cache(interface)	Returns a callable that caches the output of an interface
clear_previous_runs([warn])	Remove all the cache that where not used in the latest run of the memory object: i.e.
clear_previous_runs([warn])	Remove all the cache that where not used in the latest run of the memory object: i.e.

cache(*interface*)

Returns a callable that caches the output of an interface

Parameters **interface: nipype interface** :

The nipype 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 nipype.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')
```

We can retrieve the resulting file from the outputs: >>> results.outputs.merged_file # doctest: +SKIP '...'

clear_previous_runs(*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(*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

Also used are the `PipeFunc`, callables that are returned by the *`Memory.cache()`* decorator:

class nipype.caching.memory.**PipeFunc**(*interface*, *base_dir*, *callback=None*)
Callable interface to nipype.interface objects
Use this to wrap nipype.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

__call__(**kwargs)
next()

__init__(*interface*, *base_dir*, *callback=None*)

Parameters **interface: a nipype 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.

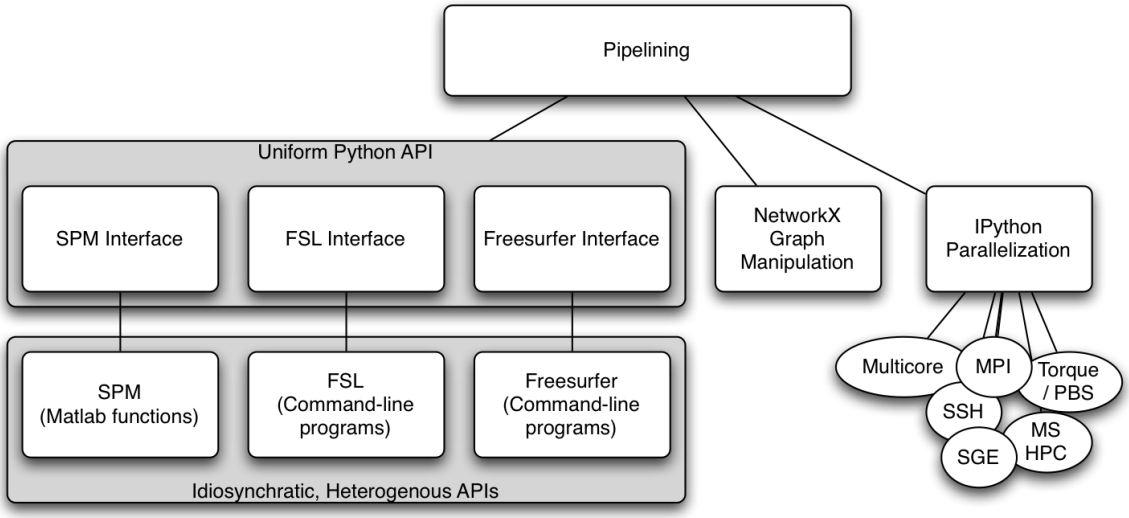
1.5 Tutorial : Workflows

This section presents several tutorials on how to setup and use pipelines. Make sure that you have the requirements satisfied and go through the steps required for the analysis tutorials.

1.5.1 Essential reading

Pipeline 101

A workflow or pipeline is built by connecting processes or nodes to each other. In the context of nipype, every interface can be treated as a pipeline node having defined inputs and outputs. Creating a workflow then is a matter of connecting appropriate outputs to inputs. Currently, workflows are limited to being directional and cannot have any loops, thereby creating an ordering to data flow. The following nipype component architecture might help understanding some of the tutorials presented here.



My first pipeline

Although the most trivial workflow consists of a single node, we will create a workflow with two nodes: a realign node that will send the realigned functional data to a smoothing node. It is important to note that setting up a workflow is separate from executing it.

1. Import appropriate modules

```
import nipype.interfaces.spm as spm          # the spm interfaces
import nipype.pipeline.engine as pe          # the workflow and node wrappers
```

2. Define nodes

Here we take instances of interfaces and make them pipeline compatible by wrapping them with pipeline specific elements. To determine the inputs and outputs of a given interface, please see *Tutorial : Interfaces*. Let's start with defining a realign node using the interface `nipype.interfaces.spm.Realign`

```
realigner = pe.Node(interface=spm.Realign(), name='realign')
realigner.inputs.in_files = 'somefuncrun.nii'
realigner.inputs.register_to_mean = True
```

This would be equivalent to:

```
realigner = pe.Node(interface=spm.Realign(infile='somefuncrun.nii',
                                          register_to_mean = True),
                    name='realign')
```

In Pythonic terms, this is saying that interface option in Node accepts an *instance* of an interface. The inputs to this interface can be set either later or while initializing the interface.

Note: In the above example, 'somefuncrun.nii' has to exist, otherwise the commands won't work. A node will check if appropriate inputs are being supplied.

Similar to the realigner node, we now set up a smoothing node.

```
smoother = pe.Node(interface=spm.Smooth(fwhm=6), name='smooth')
```

Now we have two nodes with their inputs defined. Note that we have not defined an input file for the smoothing node. This will be done by connecting the realigner to the smoother in step 5.

3. Creating and configuring a workflow

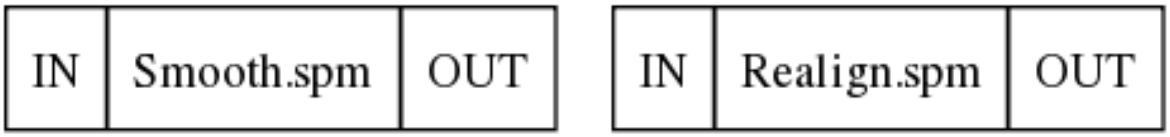
Here we create an instance of a workflow and indicate that it should operate in the current directory. The workflow's output will be placed in the `preproc` directory.

```
workflow = pe.Workflow(name='preproc')
workflow.base_dir = '.'
```

4. Adding nodes to workflows (optional)
If nodes are going to be connected (see step 5), this step is not necessary. However, if you would like to run a node by itself without connecting it to any other node, then you need to add it to the workflow. For adding nodes, order of nodes is not important.

```
workflow.add_nodes([smoother, realigner])
```

This results in a workflow containing two isolated nodes:



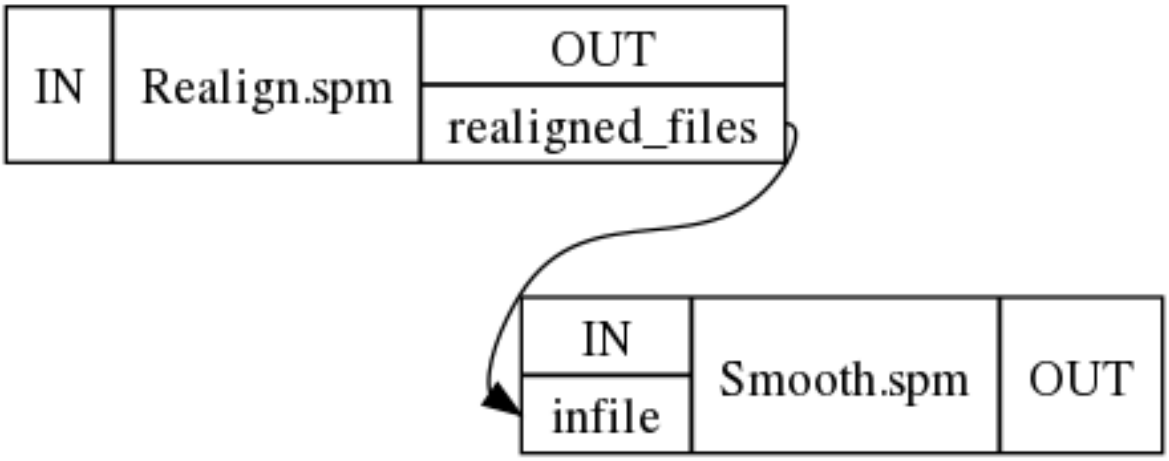
5. Connecting nodes to each other
We want to connect the output produced by the node realignment to the input of the node smoothing. This is done as follows.

```
workflow.connect(realigner, 'realigned_files', smoother, 'in_files')
```

Although not shown here, the following notation can be used to connect multiple outputs from one node to multiple inputs (see step 7 below).

```
workflow.connect([(realigner, smoother, [('realigned_files', 'in_files')])])
```

This results in a workflow containing two connected nodes:



6. Visualizing the workflow
The workflow is represented as a directed acyclic graph (DAG) and one can visualize this using the following command. In fact, the pictures above were generated using this.

```
workflow.write_graph()
```

This creates two files `graph.dot` and `graph_detailed.dot` inside `./preproc` and if graphviz is installed on your system it automatically converts it to png files. If graphviz is not installed you can take the dot files and load them in a graphviz visualizer elsewhere. You can specify how detailed the graph is going to be, by using the `graph2use` argument which takes the following options:

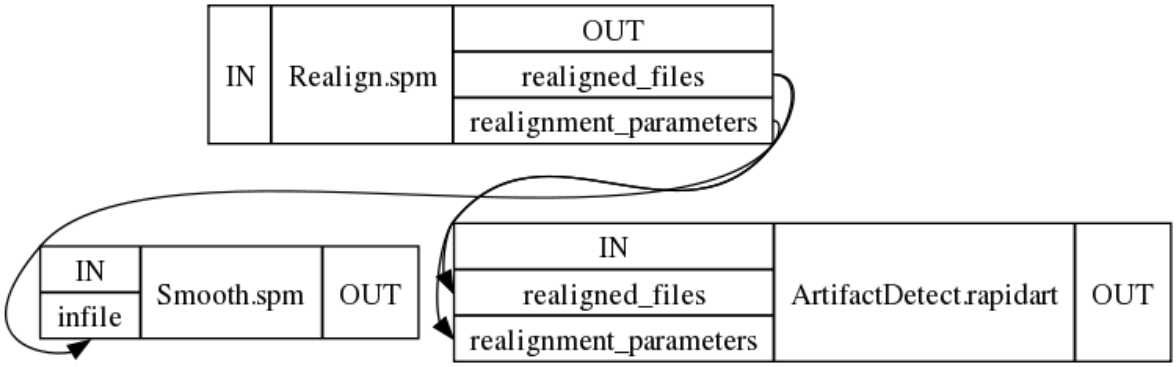
- hierarchical - creates a graph showing all embedded workflows (default)
- orig - creates a top level graph without expanding internal workflow nodes
- flat - expands workflow nodes recursively
- exec - expands workflows to depict iterables (be careful - can generate really large graphs)

7. Extend it
Now that you have seen a basic pipeline let's add another node to the above pipeline.

```
import nipype.algorithms.rapidart as ra
artdetect = pe.Node(interface=ra.ArtifactDetect(), name='artdetect')
artdetect.inputs.use_differences  = [True, False]
artdetect.inputs.use_norm = True
artdetect.inputs.norm_threshold = 0.5
artdetect.inputs.zintensity_threshold = 3
artdetect.inputs.parameter_source = "SPM"
artdetect.inputs.mask_type = "spm_global"
workflow.connect([(realigner, artdetect,
                   [('realigned_files', 'realigned_files'),
                    ('realignment_parameters','realignment_parameters')]
                  )])
```

Note: a) How an alternative form of connect was used to connect multiple output fields from the realign node to corresponding input fields of the artifact detection node.
b) The current visualization only shows connected input and output ports. It does not show all the parameters that you have set for a node.

This results in



8. Execute the workflow
Assuming that **somefuncrun.nii** is actually a file or you've replaced it with an appropriate one, you can run the pipeline with:

```
workflow.run()
```

This should create a folder called preproc in your current directory, inside which are three folders: realign, smooth and artdetect (the names of the nodes). The outputs of these routines are in these folders.
pipeline Connected series of processes (processes can be run parallel and or sequential)
workflow (kind of synonymous to pipeline) = hosting the nodes
node = switching-point within a pipeline, you can give it a name (in the above example e.g. realigner), a node usually requires an or several inputs and will produce an or several outputs
interface = specific software (e.g. FSL, SPM ...) are wrapped in interfaces, within a node instances of an interface can be run
modules for each interface the according modules have to be imported in the usual pythonic manner

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Now that you know how to construct a workflow and execute it, we will go into more advanced concepts. This tutorial focuses on `nipype.pipeline.engine.Workflow` `nipype.pipeline.engine.Node` and `nipype.pipeline.engine.MapNode`.
A workflow is a **directed acyclic graph (DAG)** consisting of nodes which can be of type *Workflow*, *Node* or *MapNode*. Workflows can be re-used and hierarchical workflows can be easily constructed.

'name' : the mandatory keyword arg

When instantiating a Workflow, Node or MapNode, a *name* has to be provided. For any given level of a workflow, no two nodes can have the same name. The engine will let you know if this is the case when you add nodes to a workflow either directly using *add_nodes* or using the *connect* function.
Names have many internal uses. They determine the name of the directory in which the workflow/node is run and the outputs are stored.

```
realigner = pe.Node(interface=spm.Realign(),
                    name='RealignSPM')
```

Now this output will be stored in a directory called *RealignSPM*. Proper naming of your nodes can be advantageous from the perspective that it provides a semantic descriptor aligned with your thought process. This name parameter is also used to refer to nodes in embedded workflows.

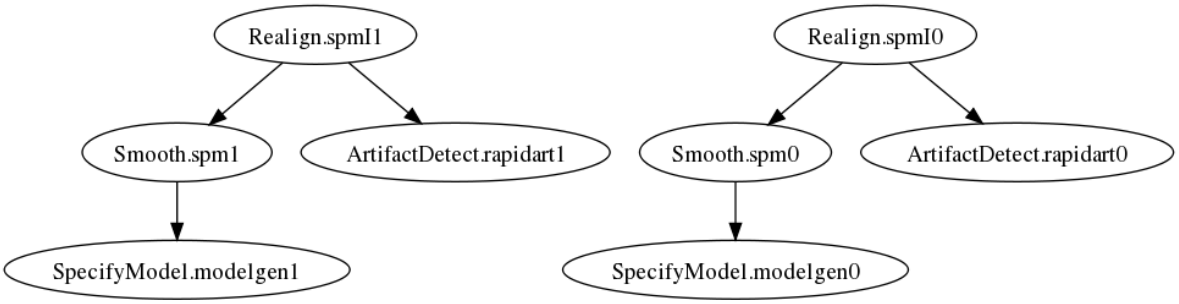
iterables This can only be set for Node and MapNode. This is syntactic sugar for running a subgraph with the Node/MapNode at its root in a `for` loop. For example, consider an fMRI preprocessing pipeline that you would like to run for all your subjects. You can define a workflow and then execute it for every single subject inside a `for` loop. Consider the simplistic example below, where startnode is a node belonging to workflow 'mywork.'

```
for s in subjects:
    startnode.inputs.subject_id = s
    mywork.run()
```

The pipeline engine provides a convenience function that simplifies this:

```
startnode.iterables = ('subject_id', subjects)
mywork.run()
```

This will achieve the same exact behavior as the for loop above. The workflow graph is:



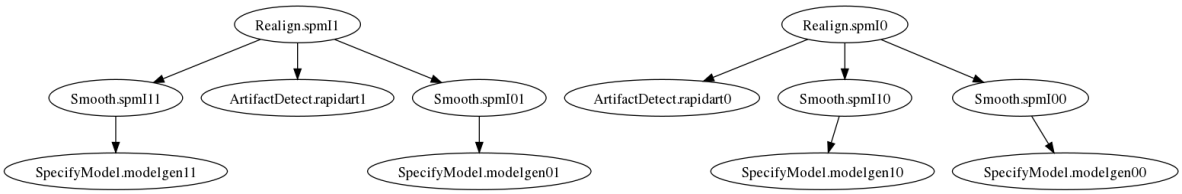
Now consider the situation in which you want the last node (typically smoothing) of your preprocessing pipeline to smooth using two different kernels (0 mm and 6 mm FWHM). Again the common approach would be:

```
for s in subjects:
    startnode.inputs.subject_id = s
    uptosmoothingworkflow.run()
    smoothnode.inputs.infile = lastnode.output.outfile
    for fwhm in [0, 6]:
        smoothnode.inputs.fwhm = fwhm
        remainingworkflow.run()
```

Instead of having multiple `for` loops at various stages, you can set up another set of iterables for the smoothnode.

```
startnode.iterables = ('subject_id', subjects)
smoothnode.iterables = ('fwhm', [0, 6])
mywork.run()
```

This will run the preprocessing workflow for two different smoothing kernels over all subjects.



Thus setting iterables has a multiplicative effect. In the above examples there is a separate, distinct specifymodel node that's executed for each combination of subject and smoothing.

iterfield This is a mandatory keyword arg for MapNode. This enables running the underlying interface over a set of inputs and is particularly useful when the interface can only operate on a single input. For example, the `nipype.interfaces.fsl.BET` will operate on only one (3d or 4d) NIfTI file. But wrapping BET in a MapNode can execute it over a list of files:

```
better = pe.MapNode(interface=fsl.Bet(), name='stripper',
                     iterfield=['in_file'])
better.inputs.in_file = ['file1.nii','file2.nii']
better.run()
```

This will create a directory called `stripper` and inside it two subdirectories called `in_file_0` and `in_file_1`. The output of running bet separately on each of those files will be stored in those two subdirectories.
This can be extended to run it on pairwise inputs. For example,

```
transform = pe.MapNode(interface=fs.ApplyVolTransform(),
                       name='warpvol',
                       iterfield=['source_file', 'reg_file'])
transform.inputs.source_file = ['file1.nii','file2.nii']
transform.inputs.reg_file = ['file1.reg','file2.reg']
transform.run()
```

The above will be equivalent to running transform by taking corresponding items from each of the two fields in iterfield. The subdirectories get always named with respect to the first iterfield.

overwrite The overwrite keyword arg forces a node to be rerun.

The *clone* function The *clone* function can be used to create a copy of a workflow. No references to the original workflow are retained. As such the clone function requires a name keyword arg that specifies a new name for the duplicate workflow.

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Modifying inputs to pipeline nodes

Two nodes can be connected as shown below.

```
workflow.connect(realigner, 'realigned_files', smoother, 'infile')
```

The connection mechanism allows for a function to be evaluated on the output field ('realigned files') of the source node (realigner) and have its result be sent to the input field ('infile') of the destination node (smoother).

```
def reverse_order(inlist):
    inlist.reverse()
    return inlist

workflow.connect(realigner, ('realigned_files', reverse_order),
                 smoother, 'infile')
```

This can be extended to provide additional arguments to the function. For example:

```
def reorder(inlist, order):
   return [inlist[item] for item in order]

workflow.connect(realigner, ('realigned_files', reorder, [2, 3, 0, 1]),
                 smoother, 'infile')
```

In this example, we assume the realigned_files produces a list of 4 files. We can reorder these files in a particular order using the modifier. Since such modifications are not tracked, they should be used with extreme care and only in cases where absolutely necessary. Often, one may find that it is better to insert a node rather than a function.

Distributed computation

The pipeline engine has built-in support for distributed computation on clusters. This can be achieved via plugin-modules for Python multiprocessing or the IPython distributed computing interface or SGE/PBS/Condor, provided the user sets up a workflow on a shared filesystem. These modules can take arguments that specify additional distribution engine parameters. For IPython the environment needs to be configured for distributed operation. Details are available at *Using Nipype Plugins*.
The default behavior is to run in series using the Linear plugin.

```
workflow.run()
```

In some cases it may be advantageous to run the workflow in series locally (e.g., debugging, small-short pipelines, large memory only interfaces, relocating working directory/updating hashes).

Debugging

When a crash happens while running a pipeline, a crashdump is stored in the pipeline's working directory unless the config option 'crashdumpdir' has been set (see :ref:config_options).
The crashdump is a compressed numpy file that stores a dictionary containing three fields:

1. node - the node that failed
2. execgraph - the graph that the node came from
3. traceback - from local or remote session for the failure.

We keep extending the information contained in the file and making it easier to troubleshoot the failures. However, in the meantime the following can help to recover information related to the failure.
in IPython do (`%pdb` in IPython is similar to `dbstop` if error in Matlab):

```
from nipype.utils.filemanip import loadflat
crashinfo = loadflat('crashdump....npz')
%pdb
crashinfo['node'].run()  # re-creates the crash
pdb> up  #typically, but not necessarily the crash is one stack frame up
pdb> inspect variables
pdb>quit
```

Relocation of workdir

In some circumstances, one might decide to move their entire working directory to a new location. It would be convenient to rerun only necessary components of the pipeline, instead of running all the nodes all over again. It is possible to do that with the `updatehash()` function.

```
workflow.run(updatehash=True)
```

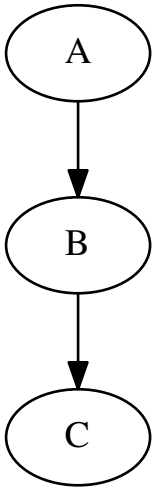
This will execute the workflow and update all the hash values that were stored without actually running any of the interfaces.

MapNode, iterfield, and iterables explained

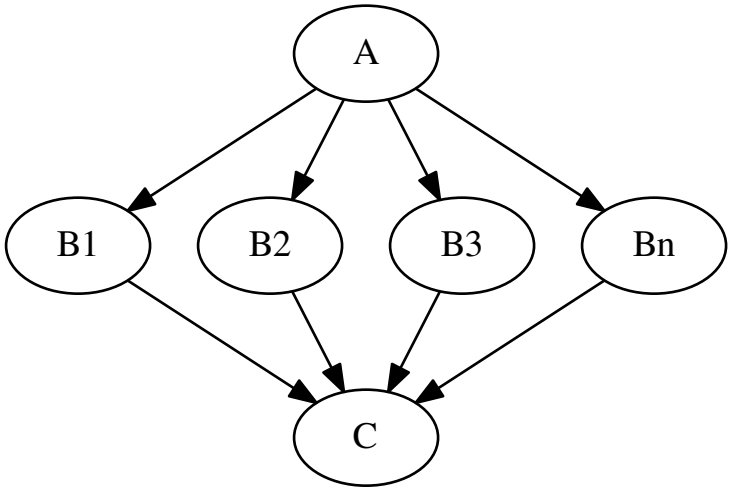
In this chapter we will try to explain the concepts behind MapNode, iterfield, and iterables.

MapNode and iterfield

Imagine that you have a list of items (lets say files) and you want to execute the same node on them (for example some smoothing or masking). Some nodes accept multiple files and do exactly the same thing on them, but some don't (they expect only one file). MapNode can solve this problem. Imagine you have the following workflow:



Node "A" outputs a list of files, but node "B" accepts only one file. Additionally "C" expects a list of files. What you would like is to run "B" for every file in the output of "A" and collect the results as a list and feed it to "C". Something like this:



The code to achieve this is quite simple

```
import nipype.pipeline.engine as pe
a = pe.Node(interface=A(), name="a")
b = pe.MapNode(interface=B(), name="b", iterfield=['in_file'])
c = pe.Node(interface=C(), name="c")

my_workflow = pe.Workflow(name="my_workflow")
my_workflow.connect([(a,b,[('out_files','in_file')]),
                     (b,c,[('out_file','in_files')])
                     ])
```

assuming that interfaces "A" and "C" have one input "in_files" and one output "out_files" (both lists of files). Interface "B" has single file input "in_file" and single file output "out_file".

You probably noticed that you connect nodes as if "B" could accept and output list of files. This is because it is wrapped using MapNode instead of Node. This special version of node will (under the bonnet) create an instance of "B" for every item in the list from the input. The compulsory argument "iterfield" defines which input should it iterate over (for example in single file smooth interface you would like to iterate over input files not the smoothing width). At the end outputs are collected into a list again. In other words this is map and reduce scenario.

You might have also noticed that the iterfield arguments expects a list of input names instead of just one name. This suggests that there can be more than one! Even though a bit confusing this is true. You can specify more than one input to iterate over but the lists that you provide (for all the inputs specified in iterfield) have to have the same length. MapNode will then pair the parameters up and run the first instance with first set of parameters and second with second set of parameters. For example, this code:

```
b = pe.MapNode(interface=B(), name="b", iterfield=['in_file', 'n'])
b.inputs.in_file = ['file', 'another_file', 'different_file']
b.inputs.n = [1,2,3]
b.run()
```

is almost the same as running

```
b1 = pe.Node(interface=B(), name="b1")
b1.inputs.in_file = 'file'
b1.inputs.n = 1
```

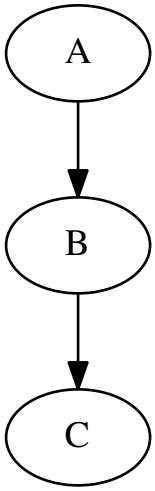
```
b2 = pe.Node(interface=B(), name="b2")
b2.inputs.in_file = 'another_file'
b2.inputs.n = 2

b3 = pe.Node(interface=B(), name="b3")
b3.inputs.in_file = 'different_file'
b3.inputs.n = 3
```

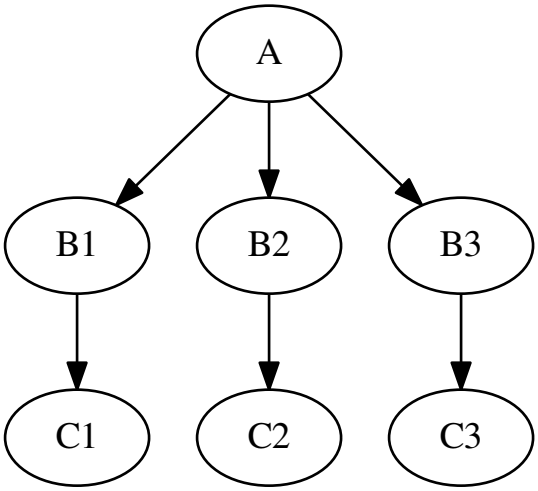
It is a rarely used feature, but you can sometimes find it useful.
In more advanced applications it is useful to be able to iterate over items of nested lists (for example [[1,2],[3,4]]). MapNode allows you to do this with the "nested=True" parameter. Outputs will preserve the same nested structure as the inputs.

Iterables

Now imagine a different scenario. You have your workflow as before



and there are three possible values of one of the inputs node "B" you would like to investigate (for example width of 2,4, and 6 pixels of a smoothing node). You would like to see how different parameters in node "B" would influence everything that depends on its outputs (node "C" in our example). Therefore the new graph should look like this:



Of course you can do it manually by creating copies of all the nodes for different parameter set, but this can be very time consuming, especially when there are more than one node taking inputs from "B". Luckily nipype supports this scenario! Its called iterables and and you use it this way:

```
import nipype.pipeline.engine as pe
a = pe.Node(interface=A(), name="a")
b = pe.Node(interface=B(), name="b")
b.iterables = ("n", [1, 2, 3])
c = pe.Node(interface=C(), name="c")

my_workflow = pe.Workflow(name="my_workflow")
my_workflow.connect([(a,b,[('out_file','in_file')]),
                     (b,c,[('out_file','in_file')])
                     ])
```

Assuming that you want to try out values 1, 2, and 3 of input "n" of the node "B". This will also create three different versions of node "C" - each with inputs from instances of node "C" with different values of "n".
Additionally, you can set multiple iterables for a node with a list of tuples in the above format.
Iterables are commonly used to execute the same workflow for many subjects. Usually one parametrises DataGrabber node with subject ID. This is achieved by connecting an IdentityInterface in front of DataGrabber. When you set iterables of the IdentityInterface to the list of subjects IDs, the same workflow will be executed for every subject. See fMRI: SPM, FSL to see this pattern in action.

DataGrabber and DataSink explained

In this chapter we will try to explain the concepts behind DataGrabber and *DataSink*.

Why do we need these interfaces?

A typical workflow takes data as input and produces data as the result of one or more operations. One can set the data required by a workflow directly as illustrated below.

```
from fsl_tutorial2 import preproc
preproc.base_dir = os.path.abspath('.')
preproc.inputs.inputspec.func = os.path.abspath('data/s1/f3.nii')
```

```
preproc.inputs.inputspec.struct = os.path.abspath('data/s1/struct.nii')
preproc.run()
```

Typical neuroimaging studies require running workflows on multiple subjects or different parameterizations of algorithms. One simple approach to that would be to simply iterate over subjects.

```
from fsl_tutorial2 import preproc
for name in subjects:
  preproc.base_dir = os.path.abspath('.')
  preproc.inputs.inputspec.func = os.path.abspath('data/%s/f3.nii'%name)
  preproc.inputs.inputspec.struct = os.path.abspath('data/%s/struct.nii'%name)
  preproc.run()
```

However, in the context of complex workflows and given that users typically arrange their imaging and other data in a semantically hierarchical data store, an alternative mechanism for reading and writing the data generated by a workflow is often necessary. As the names suggest DataGrabber is used to get at data stored in a shared file system while *DataSink* is used to store the data generated by a workflow into a hierarchical structure on disk.

DataGrabber

DataGrabber is an interface for collecting files from hard drive. It is very flexible and supports almost any file organization of your data you can imagine.
You can use it as a trivial use case of getting a fixed file. By default, DataGrabber stores its outputs in a field called outfiles.

```
import nipype.interfaces.io as nio
datasource1 = nio.DataGrabber()
datasource1.inputs.base_directory = os.getcwd()
datasource1.inputs.template = 'data/s1/f3.nii'
datasource1.inputs.sort_filelist = True
results = datasource1.run()
```

Or you can get at all uncompressed NIfTI files starting with the letter 'f' in all directories starting with the letter 's'.

```
datasource2.inputs.base_directory = '/mass'
datasource2.inputs.template = 'data/s*/f*.nii'
datasource1.inputs.sort_filelist = True
```

Two special inputs were used in these previous cases. The input *base_directory* indicates in which directory to search, while the input *template* indicates the string template to match. So in the previous case datagrabber is looking for path matches of the form */mass/data/s*/f**.

Note: When used with wildcards (e.g., s* and f* above) DataGrabber does not return data in sorted order. In order to force it to return data in sorted order, one needs to set the input *sorted* = *True*. However, when explicitly specifying an order as we will see below, *sorted* should be set to *False*.

More useful cases arise when the template can be filled by other inputs. In the example below, we define an input field for *datagrabber* called *run*. This is then used to set the template (see %d in the template).

```
datasource3 = nio.DataGrabber(infields=['run'])
datasource3.inputs.base_directory = os.getcwd()
datasource3.inputs.template = 'data/s1/f%d.nii'
datasource1.inputs.sort_filelist = True
datasource3.inputs.run = [3, 7]
```

This will return files *basedir/data/s1/f3.nii* and *basedir/data/s1/f7.nii*. We can take this a step further and pair subjects with runs.

```
datasource4 = nio.DataGrabber(infields=['subject_id', 'run'])
datasource4.inputs.template = 'data/%s/f%d.nii'
datasource1.inputs.sort_filelist = True
datasource4.inputs.run = [3, 7]
datasource4.inputs.subject_id = ['s1', 's3']
```

This will return files *basedir/data/s1/f3.nii* and *basedir/data/s3/f7.nii*.

A more realistic use-case In a typical study one often wants to grab different files for a given subject and store them in semantically meaningful outputs. In the following example, we wish to retrieve all the functional runs and the structural image for the subject 's1'.

```
datasource = nio.DataGrabber(infields=['subject_id'], outfields=['func', 'struct'])
datasource.inputs.base_directory = 'data'
datasource.inputs.template = '*'
datasource1.inputs.sort_filelist = True
datasource.inputs.field_template = dict(func='%s/f%d.nii',
                                        struct='%s/struct.nii')
datasource.inputs.template_args = dict(func=[['subject_id', [3,5,7,10]]],
                                       struct=[['subject_id']])
datasource.inputs.subject_id = 's1'
```

Two more fields are introduced: *field_template* and *template_args*. These fields are both dictionaries whose keys correspond to the *outfields* keyword. The *field_template* reflects the search path for each output field, while the *template_args* reflect the inputs that satisfy the template. The inputs can either be one of the named inputs specified by the *infields* keyword arg or it can be raw strings or integers corresponding to the template. For the *func* output, the **%s** in the *field_template* is satisfied by *subject_id* and the **%d** is field in by the list of numbers.

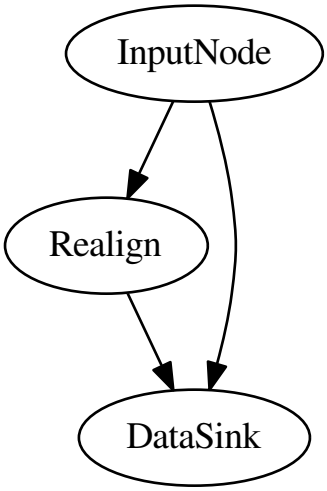
Note: We have not set *sorted* to *True* as we want the DataGrabber to return the functional files in the order it was specified rather than in an alphabetic sorted order.

DataSink

A workflow working directory is like a **cache**. It contains not only the outputs of various processing stages, it also contains various extraneous information such as execution reports, hashfiles determining the input state of processes. All of this is embedded in a hierarchical structure that reflects the iterables that have been used in the workflow. This makes navigating the working directory a not so pleasant experience. And typically the user is interested in preserving only a small percentage of these outputs. The *DataSink* interface can be used to extract components from this *cache* and store it at a different location. For XNAT-based storage, see *XNATSink* .

Note: Unlike other interfaces, a *DataSink*'s inputs are defined and created by using the workflow connect statement. Currently disconnecting an input from the *DataSink* does not remove that connection port.

Let's assume we have the following workflow.



The following code segment defines the *DataSink* node and sets the *base_directory* in which all outputs will be stored. The *container* input creates a subdirectory within the *base_directory*. If you are iterating a workflow over subjects, it may be useful to save it within a folder with the subject id.

```
datasink = pe.Node(nio.DataSink(), name='sinker')
datasink.inputs.base_directory = '/path/to/output'
workflow.connect(inputnode, 'subject_id', datasink, 'container')
```

If we wanted to save the realigned files and the realignment parameters to the same place the most intuitive option would be:

```
workflow.connect(realigner, 'realigned_files', datasink, 'motion')
workflow.connect(realigner, 'realignment_parameters', datasink, 'motion')
```

However, this will not work as only one connection is allowed per input port. So we need to create a second port. We can store the files in a separate folder.

```
workflow.connect(realigner, 'realigned_files', datasink, 'motion')
workflow.connect(realigner, 'realignment_parameters', datasink, 'motion.par')
```

The period (.) indicates that a subfolder called par should be created. But if we wanted to store it in the same folder as the realigned files, we would use the .@ syntax. The @ tells the *DataSink* interface to not create the subfolder. This will allow us to create different named input ports for *DataSink* and allow the user to store the files in the same folder.

```
workflow.connect(realigner, 'realigned_files', datasink, 'motion')
workflow.connect(realigner, 'realignment_parameters', datasink, 'motion.@par')
```

The syntax for the input port of *DataSink* takes the following form:

```
string[[.[@]]string[[.[@]]string] ...]
where parts between paired [] are optional.
```

MapNode In order to use *DataSink* inside a MapNode, it's inputs have to be defined inside the constructor using the *infields* keyword arg.

Parameterization As discussed in MapNode, iterfield, and iterables explained, one can run a workflow iterating over various inputs using the iterables attribute of nodes. This means that a given workflow can have multiple outputs depending on how many iterables are there. Iterables create working directory subfolders such as *_iterable_name_value*. The *parameterization* input parameter controls whether the data stored using *DataSink* is in a folder structure that contains this iterable information or not. It is generally recommended to set this to *True* when using multiple nested iterables.

Substitutions The *substitutions* and *substitutions_regexp* inputs allow users to modify the output destination path and name of a file. Substitutions are a list of 2-tuples and are carried out in the order in which they were entered. Assuming that the output path of a file is:

```
/root/container/_variable_1/file_subject_realigned.nii
```

we can use substitutions to clean up the output path.

```
datasink.inputs.substitutions = [('_variable', 'variable'),
                                 ('file_subject_', '')]
```

This will rewrite the file as:

```
/root/container/variable_1/realigned.nii
```

Note: In order to figure out which substitutions are needed it is often useful to run the workflow on a limited set of iterables and then determine the substitutions.

1.5.2 Beginner's guide

By Michael Notter. Available here

1.5.3 Example workflows

dMRI: Camino, DTI

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 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
import os                                    # system functions
```

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
```

```
        if isinstance(volume, list):
            volume = volume[0]
        nii = nb.load(volume)
        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
        if isinstance(volume, list):
            volume = volume[0]
        nii = nb.load(volume)
        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
        nii = nb.load(volume)
        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 `nipype.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipype.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(interface=util.IdentityInterface(fields=["dwi", "bvecs", "bvals"]), name="in
```

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 Probablistic 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 OOGL 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 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.

```
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')])])
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 experted 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

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 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.interfaces.freesurfer as fs    # freesurfer
import nipype.interfaces.cmtk as cmtk
import nipype.algorithms.misc as misc
import inspect

import os.path as op                         # system functions
import cmp                                     # connectome mapper
```

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 regions.

```
def get_vox_dims(volume):
    import nibabel as nb
    if isinstance(volume, list):
        volume = volume[0]
    nii = nb.load(volume)
    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
    if isinstance(volume, list):
        volume = volume[0]
    nii = nb.load(volume)
    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
    nii = nb.load(volume)
    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.FSCommand.set_default_subjects_dir(subjects_dir)
subject_list = ['subj1']
```

An infosource 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_i
```

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 probabilitiy 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=cam2trk.Camino2Trackvis(), name="camino2trk")
camino2trackvis.inputs.min_length = 30
camino2trackvis.inputs.voxel_order = 'LAS'
trk2camino = pe.Node(interface=cam2trk.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')
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_in
```

Here 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.

```
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), 'an
mapping.connect([(FreeSurferSourceRH, mris_convertRHlabels, [(('annot', select_aparc_annot), 'an
```

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 nipype/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_f

    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')])]
    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")])])
    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

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!

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          # pypeline engine
import nipype.interfaces.fsl as fsl
import nipype.interfaces.freesurfer as fs    # freesurfer
import nipype.interfaces.mrtrix as mrtrix
import nipype.algorithms.misc as misc
import nipype.interfaces.cmtk as cmtk
import nipype.interfaces.dipy as dipy
import inspect
import os
import os.path as op                         # system functions
from nipype.workflows.dmri.fsl.dti import create_eddy_correct_pipeline
from nipype.workflows.dmri.camino.connectivity_mapping import select_aparc_annot
from nipype.utils.misc import package_check
import warnings
from nipype.workflows.dmri.connectivity.nx import create_networkx_pipeline, create_cmats_to_csv_
from nipype.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.FSCommand.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')

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", "bval
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'
```

Creating the workflow's nodes

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.MRIConvert(), 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')
```

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.

```
estimateresponse = pe.Node(interface=mrtrix.EstimateResponseForSH(), name='estimateresponse')
estimateresponse.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.ProbabilisticSphericallyDeconvolutedStreamlineTrac
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.MRTrix2TrackVis(), name='tck2trk')
trk2tdi = pe.Node(interface=dipy.TrackDensityMap(), name='trk2tdi')
```

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

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.inputspec.lookup_file = lookup_file
```

Connecting the workflow

Here we connect our processing pipeline.

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")])])

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), 'an
mapping.connect([(FreeSurferSourceRH, mris_convertRHlabels, [(('annot', select_aparc_annot), 'an
```

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")])])

    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, mulitplies 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, estimateresponse, [("outputnode.eddy_corrected", "in_file")])])
    mapping.connect([(fsl2mrtrix, estimateresponse, [("encoding_file", "encoding_file")])])
    mapping.connect([(threshold_FA, estimateresponse, [("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([(estimateresponse, 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")])])
    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")])])
```

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")])])

    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_network
    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_
```

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')
    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 fslinfo 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          # pypeline 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('networkx', '1.0', 'tutorial1')
    package_check('IPython', '0.10', 'tutorial1')
```

Setting up workflows

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

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']])

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 `nipype.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipype.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
```

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')])
])
```

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('dtiresults')


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

Setup the pipeline that combines the two workflows: tractography and 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'),
                                 ('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 fslinfo 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          # pypeline 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('networkx', '1.0', 'tutorial1')
    package_check('IPython', '0.10', 'tutorial1')
```

Setting up workflows

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

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 `nipype.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipype.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
```

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')])
])
```

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')])
])
```

Setup the pipeline that combines the two 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
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.

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          # pypeline 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('networkx', '1.0', 'tutorial1')
package_check('IPython', '0.10', 'tutorial1')
```

Setting up workflows

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

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 `nipype.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipype.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
```

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')])
    ])
```

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('dtiresults')


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

Setup the pipeline that combines the two workflows: tractography and 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
                                        ('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

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/
- CTMK: 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.

Import the workflows First, we import the necessary modules from nipype.

```
import nipype.interfaces.fsl as fsl
import nipype.interfaces.freesurfer as fs     # freesurfer
import os.path as op                          # system functions
import cmp
from nipype.workflows.dmri.camino.group_connectivity import create_group_connectivity_pipeline
from nipype.workflows.dmri.connectivity.group_connectivity import (create_merge_networks_by_grou
                                                                   create_merge_group_networks_w
```

Set the proper directories First, we import the necessary modules from nipype.

```
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')
```

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')
```

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 arbitary 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:

- nipype/workflows/dmri/mrtrix/group_connectivity.py
- nipype/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

        # 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_

        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, subject
        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
    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, outpu
    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

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/
- CTMK: 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.

Import the workflows First, we import the necessary modules from nipype.

```
import nipype.interfaces.fsl as fsl
import nipype.interfaces.freesurfer as fs     # freesurfer
import os.path as op                          # system functions
import cmp
from nipype.workflows.dmri.mrtrix.group_connectivity import create_group_connectivity_pipeline
from nipype.workflows.dmri.connectivity.group_connectivity import (create_merge_network_results_
```

Set the proper directories First, we import the necessary modules from nipype.

```
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')
```

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')
```

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 arbitary 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:

- nipype/workflows/dmri/mrtrix/group_connectivity.py
- nipype/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 are 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

        # Here with invert the b-vectors in the Y direction and set the maximum harmonic order of th
        # 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
        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,
        l2pipeline.inputs.l2inputnode.network_file = cmp_config._get_lausanne_parcellation('Lausanne
        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, out
    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, outpu
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: DTI - MRtrix, FSL

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']],
            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="in
```

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.

```
estimateresponse = pe.Node(interface=mrtrix.EstimateResponseForSH(), name='estimateresponse')
estimateresponse.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.ProbabilisticSphericallyDeconvolutedStreamlineTrac
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.MRTrix2TrackVis(), name='tck2trk')
```

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")])])

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, mulitplies 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, estimateresponse, [("out_file", "in_file")])])
tractography.connect([(fsl2mrtrix, estimateresponse, [("encoding_file", "encoding_file")])])
tractography.connect([(threshold_FA, estimateresponse, [("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([(estimateresponse, 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")])])
    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.

dMRI: Preprocessing

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,
# 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 contained in subject_list.

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

Now we create a `nipype.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 actual processing functions

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

Setup for dMRI preprocessing

In this section we initialize the appropriate workflow for preprocessing of diffusion images.

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)
```

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()
```

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), 'l1')

    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'
    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),
                                                  'l1_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), 'l2')
    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

    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 nipype to analyze a data set:

```
    python fmri_ants_openfmri.py --datasetdir ds107
```

```
    from __future__ import division
    from builtins import range

    from nipype import config
    config.enable_provenance()


    from glob import glob
    import os

    import nipype.pipeline.engine as pe
    import nipype.algorithms.modelgen as model
    import nipype.algorithms.rapidart as ra
    from nipype.algorithms.misc import TSNR
    from nipype.external.six import string_types
    from nipype.interfaces.c3 import C3dAffineTool
    import nipype.interfaces.io as nio
    import nipype.interfaces.utility as niu
    from nipype.workflows.fmri.fsl import (create_featreg_preproc,
                                           create_modelfit_workflow,
                                           create_fixed_effects_flow)
```

```
    from nipype import LooseVersion
    from nipype import Workflow, Node, MapNode
    from nipype.interfaces import (fsl, Function, ants, freesurfer)

    from nipype.interfaces.utility import Merge, IdentityInterface
    from nipype.utils.filemanip import filename_to_list
    from nipype.interfaces.io import FreeSurferSource
    import nipype.interfaces.freesurfer as fs

    version = 0
    if fsl.Info.version() 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 nipype.utils.filemanip import filename_to_list, list_to_filename, split_filenam
               'from scipy.special import legendre'
               ]


    def median(in_files):
        """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)
            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 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
    """

    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')
```

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')
```

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 = 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

```
    pickfirst = lambda x: x[0]

    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.inputs.terminal_output = 'file'

    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.inputs.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

    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
    """

    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

```
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 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]]
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': '-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

```
pickfirst = lambda x: x[0]

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.inputs.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.inputs.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')
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)
        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

        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:
        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')]),
            ])

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'),
                 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, string_types):
        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')])
            ])

# Comute 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(Function(input_names=['in_files'],
                                output_names=['median_file'],
                                function=median,
                                imports=imports),
                       name='median')
    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.inputspec.subjects_dir = subjects_dir
        registration.inputs.inputspec.target_image = fsl.Info.standard_image('MNI152_T1_2mm_brain.ni
        if target:
            registration.inputs.inputspec.target_image = target
    else:
        wf.connect(datasource, 'anat', registration, 'inputspec.anatomical_image')
        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_br
        registration.inputs.inputspec.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, 'inputspec.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, 'outputspec.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, 'outputspec.aparc', get_roi_mean, 'segmentation_file')

        get_roi_tsnr = pe.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')
```

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'],
                                   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

```
    preproc.inputs.inputspec.fwhm = fwhm
    gethighpass.inputs.hpcutoff = hpcutoff
    modelspec.inputs.high_pass_filter_cutoff = hpcutoff
    modelfit.inputs.inputspec.bases = {'dgamma': {'derivs': use_derivatives}}
    modelfit.inputs.inputspec.model_serial_correlations = True
    modelfit.inputs.inputspec.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',
                            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.

Preparing environment

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.

Step 1 Link the *fsaverage* directory for your freesurfer distribution. To do this type:

```
cd nipype-tutorial/fsdata
ln -s $FREESURFER_HOME/subjects/fsaverage
cd ..
```

Defining the workflow

```
from __future__ import print_function
from builtins import range

import os                                    # system functions

import nipype.algorithms.modelgen as model   # model generation
import nipype.algorithms.rapidart as ra      # artifact detection
import nipype.interfaces.freesurfer as fs    # freesurfer
import nipype.interfaces.io as nio           # i/o routines
import nipype.interfaces.matlab as mlab      # how to run matlab
import nipype.interfaces.spm as spm          # spm
import nipype.interfaces.utility as util     # utility
import nipype.pipeline.engine as pe          # pypeline engine
```

Preliminaries 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 node.

```
# 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')
```

Setup preprocessing workflow

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

Use `nipype.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 `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(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 `nipype.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 `nipype.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 `nipype.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 `nipype.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 `nipype.interfaces.spm.Smooth`. In addition, we use a smoothing routine from freesurfer (`nipype.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')]),
                    ])
```

Set up volume analysis workflow

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

Generate SPM-specific design information using `nipype.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 `nipype.interfaces.spm.Level1Design`.

```
level1design = pe.Node(interface=spm.Level1Design(), name="level1design")
level1design.inputs.bases = {'hrf': {'derivs': [0, 0]}}
```

Use `nipype.interfaces.spm.EstimateModel` to determine the parameters of the model.

```
level1estimate = pe.Node(interface=spm.EstimateModel(), name="level1estimate")
level1estimate.inputs.estimation_method = {'Classical': 1}
```

Use `nipype.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, 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')]),
                     ])
```

Set up surface analysis workflow We simply clone the volume analysis workflow.

```
surfanalysis = volanalysis.clone(name='surfanalysis')
```

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 `nipype.interfaces.freesurfer.MRIConvert` 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.MRIConvert(out_type='nii'), name='convert2nii')
convert2 = pe.MapNode(interface=fs.MRIConvert(out_type='nii'),
                      iterfield=['in_file'],
                      name='convertimg2nii')
```

Use `nipype.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 `nipype.interfaces.freesurfer.ApplyVolTransform` to convert contrast images into freesurfer space.

```
normwreg = pe.MapNode(interface=fs.ApplyVolTransform(),
                      iterfield=['source_file'],
                      name='applyreg2con')
```

Use `nipype.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')]),
                 ])
```

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', 'realign.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, [('realign.realignment_parameters',
                                             'modelspec.realignment_parameters'),
                                            ('volsmooth.smoothed_files',
                                             'modelspec.functional_runs'),
                                            ('art.outlier_files',
                                             'modelspec.outlier_files'),
                                            ('threshold.binary_file',
                                             'level1design.mask_image')]),
                    (preproc, surfanalysis, [('realign.realignment_parameters',
                                              'modelspec.realignment_parameters'),
                                             ('surfsmooth.smoothed_file',
                                              'modelspec.functional_runs'),
```

```
                                                ('art.outlier_files',
                                                 'modelspec.outlier_files'),
                                                ('threshold.binary_file',
                                                 'level1design.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',
                                                 'convertimg2nii.in_file'),
                                                ])
                        ])
```

Data specific components The nipype 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 `nipype.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipype.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
```

Set preprocessing parameters

```
    l1pipeline.inputs.preproc.fssource.subjects_dir = subjects_dir
    l1pipeline.inputs.preproc.volsmooth.fwhm = 4
    l1pipeline.inputs.preproc.surfsmooth.surface_fwhm = 5
```

```
l1pipeline.inputs.preproc.surfsmooth.vol_fwhm = 4
```

Experimental paradigm specific components Here we create a function that returns subject-specific information about the experimental paradigm. This is used by the `nipype.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 nipype.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]
```

Set up node specific inputs We replicate the modelspec parameters separately for the surface- and volume-based analysis.

```
modelspecref = l1pipeline.inputs.volanalysis.modelspec
modelspecref.input_units = 'secs'
modelspecref.time_repetition = 3.
modelspecref.high_pass_filter_cutoff = 120

modelspecref = l1pipeline.inputs.surfanalysis.modelspec
modelspecref.input_units = 'secs'
modelspecref.time_repetition = 3.
modelspecref.high_pass_filter_cutoff = 120

l1designref = l1pipeline.inputs.volanalysis.level1design
l1designref.timing_units = modelspecref.output_units
l1designref.interscan_interval = modelspecref.time_repetition

l1designref = l1pipeline.inputs.surfanalysis.level1design
l1designref.timing_units = modelspecref.output_units
l1designref.interscan_interval = modelspecref.time_repetition

l1pipeline.inputs.inputnode.contrasts = contrasts
```

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 `nipype.pipeline.engine.Workfow` 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')]),
                ])
```

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) that visually represents the workflow.

```
if __name__ == '__main__':
    level1.run()
    level1.write_graph(graph2use='flat')
```

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/l1out')
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.

fMRI: FSL

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 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
```

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')
```

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.

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
    funcfile = func
    if isinstance(func, list):
        funcfile = func[0]
    _, _, _, timepoints = load(funcfile).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'])
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 getthreshop(thresh):
    return '-thr %.10f -Tmin -bin' % (0.1 * thresh[0][1])
preproc.connect(getthresh, ('out_stat', getthreshop), 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")
```

```
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')]),
                 (dilatemask, art, [('out_file', 'mask_file')]),
                 ])
```

Set up model fitting workflow

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

Use `nipype.algorithms.modelgen.SpecifyModel` to generate design information.

```
modelspec = pe.Node(interface=model.SpecifyModel(), name="modelspec")
```

Use `nipype.interfaces.fsl.Level1Design` to generate a run specific fsf file for analysis

```
level1design = pe.Node(interface=fsl.Level1Design(), name="level1design")
```

Use `nipype.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 `nipype.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 `nipype.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, level1design, [('session_info', 'session_info')]),
    (level1design, 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')]),
])
```

Set up fixed-effects workflow

```
fixed_fx = pe.Workflow(name='fixedfx')
```

Use `nipype.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 `nipype.interfaces.fsl.L2Model` to generate subject and condition specific level 2 model design files

```
level2model = pe.Node(interface=fsl.L2Model(),
                      name='l2model')
```

Use `nipype.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')]),
                  ])
```

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'),
                                         ('highpass.out_file', 'modelestimate.in_file')]),
                    (preproc, fixed_fx, [('coregister.out_file', 'flameo.mask_file')]),
                    (modelfit, fixed_fx, [(('conestimate.copes', sort_copes), 'copemerge.in_file
                                           (('conestimate.varcopes', sort_copes), 'varcopemerge.i
                                           (('conestimate.copes', num_copes), 'l2model.num_copes'
                                           ])
                    ])
```

Experiment specific components

The nipype 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 `nipype.interfaces.io.DataSource` object and fill in the information from above about the layout of our data. The `nipype.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')
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 `nipype.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 nipype.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
```

Set up complete workflow

```
l1pipeline = pe.Workflow(name="level1")
l1pipeline.base_dir = os.path.abspath('./fsl/workingdir')
l1pipeline.config = {"execution": {"crashdump_dir": os.path.abspath('./fsl/crashdumps')}}

l1pipeline.connect([(infosource, datasource, [('subject_id', 'subject_id')]),
                    (infosource, firstlevel, [(('subject_id', subjectinfo), 'modelfit.modelspec.
                    (datasource, firstlevel, [('struct', 'preproc.inputspec.struct'),
                                              ('func', 'preproc.inputspec.func'),
                                              ]),
                    ])
```

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 `nipype.pipeline.engine.Pipeline.Run` function needs to be called.

```
if __name__ == '__main__':
    l1pipeline.write_graph()
    outgraph = l1pipeline.run()
    # l1pipeline.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: 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 nipype.interfaces import io as nio         # Data i/o
from nipype.interfaces import utility as niu    # Utilities
from nipype.interfaces import fsl               # fsl
from nipype.pipeline import engine as pe        # pypeline engine
from nipype.algorithms import modelgen as model   # model generation
from nipype.workflows.fmri.fsl import (create_featreg_preproc,
                                       create_modelfit_workflow,
                                       create_reg_workflow)
from nipype.interfaces.base import Bunch
```

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')
```

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


inputnode = pe.Node(niu.IdentityInterface(fields=['in_data']), name='inputnode')
# Specify the subject directories
# Map field names to individual subject runs.
info = dict(func=[['fmri']],
            struct=[['structural']])
```

Now we create a `nipype.interfaces.io.DataSource` object and fill in the information from above about the layout of our data. The `nipype.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(18
                                       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.
    registration.inputs.inputspec.config_file = 'T1_2_MNI152_2mm'
```

Set up complete workflow

```
    l1pipeline = pe.Workflow(name="level1")
    l1pipeline.base_dir = os.path.abspath('./fsl_feeds/workingdir')
    l1pipeline.config = {"execution": {"crashdump_dir": os.path.abspath('./fsl_feeds/crashdumps')}}

    l1pipeline.connect(inputnode, 'in_data', datasource, 'base_directory')
    l1pipeline.connect(datasource, 'func', preproc, 'inputspec.func')
    l1pipeline.connect(preproc, 'outputspec.highpassed_files', modelspec, 'functional_runs')
    l1pipeline.connect(preproc, 'outputspec.motion_parameters', modelspec, 'realignment_parameters')
    l1pipeline.connect(modelspec, 'session_info', modelfit, 'inputspec.session_info')
    l1pipeline.connect(preproc, 'outputspec.highpassed_files', modelfit, 'inputspec.functional_data'
    l1pipeline.connect(preproc, 'outputspec.mean', registration, 'inputspec.mean_image')
    l1pipeline.connect(datasource, 'struct', registration, 'inputspec.anatomical_image')
    l1pipeline.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/l1out')
    datasink.inputs.substitutions = [('fmri_dtype_mcf_mask_smooth_mask_gms_mean_warp', 'meanfunc')]
    # store relevant outputs from various stages of the 1st level analysis
    l1pipeline.connect(registration, 'outputspec.transformed_files', datasink, 'level1.@Z')
    l1pipeline.connect(registration, 'outputspec.transformed_mean', datasink, 'meanfunc')
```

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 `nipype.pipeline.engine.Pipeline.Run` function needs to be called.

```
    if __name__ == '__main__':
        l1pipeline.inputs.inputnode.in_data = os.path.abspath('feeds/data')
        l1pipeline.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: 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 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)
```

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()

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.functic
                            ])
```

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'),
                                                  (('outputspec.varcopes',
                                                    sort_copes),
                                                   'inputspec.varcopes'),
                                                  (('outputspec.copes', num_copes),
                                                   'l2model.num_copes'),
                                                  ])
                            ])
```

Experiment specific components

The nipype 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 `nipype.interfaces.io.DataSource` object and fill in the information from above about the layout of our data. The `nipype.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 = 'nipype-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.

```
featinput = level1_workflow.get_node('featpreproc.inputspec')
featinput.iterables = ('fwhm', [5., 10.])

hpcutoff = 120.
TR = 3.
featinput.inputs.highpass = hpcutoff / (2. * TR)
```

Setup a function that returns subject-specific information about the experimental paradigm. This is used by the `nipype.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 nipype.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.inputspec.interscan_interval = TR
modelfit.inputs.inputspec.bases = {'dgamma': {'derivs': False}}
modelfit.inputs.inputspec.contrasts = contrasts
modelfit.inputs.inputspec.model_serial_correlations = True
modelfit.inputs.inputspec.film_threshold = 1000

level1_workflow.base_dir = os.path.abspath('./fsl/workingdir')
level1_workflow.config['execution'] = dict(crashdump_dir=os.path.abspath('./fsl/crashdumps'))

level1_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')]),
                         ])
```

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 `nipype.pipeline.engine.Pipeline.Run` function needs to be called.

```
if __name__ == '__main__':
    # level1_workflow.write_graph()
    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 nipype tutorial directory:

```
python fmri_nipy_glm.py
```

```
from __future__ import print_function
from builtins import range

from nipype.interfaces.nipy.model import FitGLM, EstimateContrast
from nipype.interfaces.nipy.preprocess import ComputeMask
```

Import necessary modules from nipype.

```
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.rapidart as ra      # artifact detection
import nipype.algorithms.modelgen as model   # model specification
import os                                    # system functions
```

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 nipype 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']
# 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)
```

Preprocessing pipeline nodes

Now we create a `nipype.interfaces.io.DataSource` object and fill in the information from above about the layout of our data. The `nipype.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 `nipype.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 `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(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 `nipype.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 `nipype.interfaces.spm.Smooth`.

```
smooth = pe.Node(interface=spm.Smooth(), name="smooth")
smooth.inputs.fwhm = 4
```

Set up analysis components

Here we create a function that returns subject-specific information about the experimental paradigm. This is used by the `nipype.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 nipype.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 `nipype.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]
```

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 `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 sub-directories.
The `nipype.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")])
                    ])

if __name__ == '__main__':
    l1pipeline.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

A growing number of datasets are available on OpenfMRI. This script demonstrates how to use nipype to analyze a data set:

```
python fmri_openfmri.py --datasetdir ds107
```

```
from __future__ import division
from builtins import range

from glob import glob
import os

import nipype.pipeline.engine as pe
import nipype.algorithms.modelgen as model
import nipype.algorithms.rapidart as ra
import nipype.interfaces.fsl as fsl
import nipype.interfaces.io as nio
import nipype.interfaces.utility as niu
from nipype.external.six import string_types
from nipype.workflows.fmri.fsl import (create_featreg_preproc,
                                       create_modelfit_workflow,
                                       create_fixed_effects_flow,
                                       create_reg_workflow)

fsl.FSLCommand.set_default_output_type('NIFTI_GZ')


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)
    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]])
        files = glob(os.path.join(base_dir,
                                  subject_id,
                                  'BOLD',
                                  'task%03d_run*' % (idx + 1)))
        run_ids.insert(idx, list(range(1, len(files) + 1)))
    TR = np.genfromtxt(os.path.join(base_dir, 'scan_key.txt'))[1]
    return run_ids[task_id - 1], conds[task_id - 1], TR


def analyze_openfmri_dataset(data_dir, subject=None, model_id=None,
                             task_id=None, output_dir=None, subj_prefix='*'):
    """Analyzes an open fmri dataset

    Parameters
    ----------

    data_dir : str
        Path to the base data directory

    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()
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

```
    datasource = pe.Node(nio.DataGrabber(infields=['subject_id', 'run_id',
                                                   'task_id', 'model_id'],
                                         outfields=['anat', 'bold', 'behav',
                                                    'contrasts']),
                         name='datasource')
    datasource.inputs.base_directory = data_dir
    datasource.inputs.template = '*'
    datasource.inputs.field_template = {'anat': '%s/anatomy/highres001.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']]}
    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')]),
                ])

    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
        contrast_def = np.genfromtxt(contrast_file, dtype=object)
        if len(contrast_def.shape) == 1:
            contrast_def = contrast_def[None, :]
        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'),
                     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):
        out_behav = []
        if isinstance(behav, string_types):
            behav = [behav]
        for val in behav:
            if not isinstance(val, list):
                out_behav.append([val])
```

```
            else:
                out_behav.append(val)
        return out_behav

    wf.connect(subjinfo, 'TR', modelspec, 'time_repetition')
    wf.connect(datasource, ('behav', check_behav_list), modelspec, 'event_files')
    wf.connect(subjinfo, 'TR', modelfit, 'inputspec.interscan_interval')
    wf.connect(subjinfo, 'conds', contrastgen, 'conds')
    wf.connect(datasource, 'contrasts', contrastgen, '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')])
                ])
```

Reorder the copes so that now it combines across runs

```
    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]

    wf.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'),
                                      (('outputspec.varcopes',
                                        sort_copes),
                                       'inputspec.varcopes'),
                                      (('outputspec.copes', num_copes),
                                       'l2model.num_copes'),
                                      ])
                ])

    wf.connect(preproc, 'outputspec.mean', registration, 'inputspec.mean_image')
```

```
wf.connect(datasource, 'anat', registration, 'inputspec.anatomical_image')
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.
registration.inputs.inputspec.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, 'inputspec.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, 'outputspec.transformed_files',
           splitfunc, 'in_files')
```

Connect to a datasink

```
def get_subs(subject_id, conds, 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)))
        return subs

    subsgen = pe.Node(niu.Function(input_names=['subject_id', 'conds',
                                                'model_id', 'task_id'],
                                   output_names=['substitutions'],
                                   function=get_subs),
                      name='subsgen')

    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([(splitfunc, datasink,
                 [('copes', 'copes.mni'),
                  ('varcopes', 'varcopes.mni'),
                  ('zstats', 'zstats.mni'),
                  ])])
    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

```
    hpcutoff = 120.
    preproc.inputs.inputspec.fwhm = 6.0
    gethighpass.inputs.hpcutoff = hpcutoff
    modelspec.inputs.high_pass_filter_cutoff = hpcutoff
    modelfit.inputs.inputspec.bases = {'dgamma': {'derivs': True}}
    modelfit.inputs.inputspec.model_serial_correlations = True
    modelfit.inputs.inputspec.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("-o", "--output_dir", dest="outdir",
                            help="Output directory base")
        parser.add_argument("-w", "--work_dir", dest="work_dir",
                            help="Working 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()
        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))
        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)
        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: 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 RuntimeWarning, 'Slicer not fully implmented'
from nipype.interfaces.slicer import BRAINSFit, BRAINSResample
```

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 os                                    # system functions
```

Preliminaries

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('networkx', '1.0', 'tutorial1')
package_check('IPython', '0.10', 'tutorial1')
```

The nipype 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']],
            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)
```

Preprocessing pipeline nodes

Now we create a `nipype.interfaces.io.DataSource` object and fill in the information from above about the layout of our data. The `nipype.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 Nipype source distribution under the `examples` directory.

fMRI: SPM, FSL

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 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          # pypeline engine
import nipype.algorithms.rapidart as ra      # artifact detection
import nipype.algorithms.modelgen as model   # model specification
import nipype.interfaces.matlab as mlab
```

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 nipype.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 nipype 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)
```

Preprocessing pipeline nodes

Now we create a `nipype.interfaces.io.DataSource` object and fill in the information from above about the layout of our data. The `nipype.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 `nipype.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 `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(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 `nipype.interfaces.fsl.BET`.

```
skullstrip = pe.Node(interface=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(interface=spm.Coregister(), name="coregister")
coregister.inputs.jobtype = 'estimate'
```

Warp functional and structural data to SPM's T1 template using `nipype.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 `nipype.interfaces.spm.Smooth`.

```
smooth = pe.Node(interface=spm.Smooth(), name="smooth")
fwhmlist = [4]
smooth.iterables = ('fwhm', fwhmlist)
```

Set up analysis components

Here we create a function that returns subject-specific information about the experimental paradigm. This is used by the `nipype.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 nipype.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 `nipype.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 `nipype.interfaces.spm.Level1Design`.

```
level1design = pe.Node(interface=spm.Level1Design(), name="level1design")
level1design.inputs.timing_units = modelspec.inputs.output_units
level1design.inputs.interscan_interval = modelspec.inputs.time_repetition
level1design.inputs.bases = {'hrf': {'derivs': [0, 0]}}
```

Use `nipype.interfaces.spm.EstimateModel` to determine the parameters of the model.

```
level1estimate = pe.Node(interface=spm.EstimateModel(), name="level1estimate")
level1estimate.inputs.estimation_method = {'Classical': 1}
```

Use `nipype.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}}
```

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 `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 sub-directories.

The `nipype.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')]),
                    (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, level1design, [('session_info', 'session_info')]),
                        (skullstrip, level1design, [('mask_file', 'mask_image')]),
                        (level1design, level1estimate, [('spm_mat_file', 'spm_mat_file')]),
                        (level1estimate, contrastestimate, [('spm_mat_file', 'spm_mat_file'),
                                                            ('beta_images', 'beta_images'),
                                                            ('residual_image', 'residual_image')]),
                        ])
```

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(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_i

    # 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')]),
                        (level1design, datasink, [('spm_mat_file', 'model.pre-estimate')]),
                        (level1estimate, 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')]),
                        ])
```

Setup level 2 pipeline

Use `nipype.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_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 `nipype.interfaces.spm.OneSampleTTestDesign` to perform a simple statistical analysis of the contrasts from the group of subjects (n=2 in this example).

```
# setup a 1-sample t-test node
onesamplettestdes = pe.Node(interface=spm.OneSampleTTestDesign(), name="onesampttestdes")
l2estimate = pe.Node(interface=spm.EstimateModel(), name="level2estimate")
l2estimate.inputs.estimation_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 -> onesamplettest).

```
l2pipeline = pe.Workflow(name="level2")
l2pipeline.base_dir = os.path.abspath('spm_tutorial/l2output')
l2pipeline.connect([(l2source, onesamplettestdes, [('outfiles', 'in_files')]),
                    (onesamplettestdes, l2estimate, [('spm_mat_file', 'spm_mat_file')]),
                    (l2estimate, l2conestimate, [('spm_mat_file', 'spm_mat_file'),
                                                 ('beta_images', 'beta_images'),
                                                 ('residual_image', 'residual_image')]),
                    ])
```

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 `nipype.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 Nipype source distribution under the `examples` directory.

fMRI: SPM Auditory dataset

Introduction

The fmri_spm_auditory.py recreates the classical workflow described in the SPM8 manual 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.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 specification
import os                                    # system functions
```

Preliminaries

```
# Set the way matlab should be called
mlab.MatlabCommand.set_default_matlab_cmd("matlab -nodesktop -nosplash")
```

Setting up workflows 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.

Setup preprocessing 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 insteead 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 (explauned later on). Use `nipype.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 `nipype.interfaces.spm.Realign` for motion correction and register all images to the mean image.

```
realign = pe.Node(interface=spm.Realign(), name="realign")
```

Use `nipype.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 `nipype.interfaces.spm.Normalize`. The tutorial data set includes the template 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 `nipype.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 van infer it from data using the following function:

```
def get_vox_dims(volume):
    import nibabel as nb
    if isinstance(volume, list):
        volume = volume[0]
    nii = nb.load(volume)
    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')]),
                 (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_vo
                 (realign, normalize_func, [('realigned_files', 'apply_to_files'),
                                            (('realigned_files', get_vox_dims), 'write_voxel_siz
                 (normalize_func, smooth, [('normalized_files', 'in_files')]),
                 ])
```

Set up analysis workflow

```
l1analysis = pe.Workflow(name='analysis')
```

Generate SPM-specific design information using `nipype.interfaces.spm.SpecifyModel`.

```
modelspec = pe.Node(interface=model.SpecifySPMModel(), name="modelspec")
```

Generate a first level SPM.mat file for analysis `nipype.interfaces.spm.Level1Design`.

```
level1design = pe.Node(interface=spm.Level1Design(), name="level1design")
level1design.inputs.bases = {'hrf': {'derivs': [0, 0]}}
```

Use `nipype.interfaces.spm.EstimateModel` to determine the parameters of the model.

```
level1estimate = pe.Node(interface=spm.EstimateModel(), name="level1estimate")
level1estimate.inputs.estimation_method = {'Classical': 1}

threshold = pe.Node(interface=spm.Threshold(), name="threshold")
```

Use `nipype.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, 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', 'stat_image')]),
                        ])
```

Preproc + Analysis pipeline

```
l1pipeline = pe.Workflow(name='firstlevel')
l1pipeline.connect([(preproc, l1analysis, [('realign.realignment_parameters',
                                            'modelspec.realignment_parameters')])])
```

Pluging 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:
    l1pipeline.connect([(preproc, l1analysis, [('smooth.smoothed_files',
                                                'modelspec.functional_runs')])])
else:
    def makelist(item):
        return [item]
    l1pipeline.connect([(preproc, l1analysis, [(('smooth.smoothed_files', makelist),
                                                'modelspec.functional_runs')])])
```

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/auditor
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 `nipype.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipype.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
```

Experimental paradigm specific components Here we create a structure that provides information about the experimental paradigm. This is used by the `nipype.interfaces.spm.SpecifyModel` to create the information necessary to generate an SPM design matrix.

```
from nipype.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 = l1pipeline.inputs.analysis.modelspec
modelspecref.input_units = 'scans'
modelspecref.output_units = 'scans'
modelspecref.time_repetition = 7
modelspecref.high_pass_filter_cutoff = 120

l1designref = l1pipeline.inputs.analysis.level1design
l1designref.timing_units = modelspecref.output_units
l1designref.interscan_interval = modelspecref.time_repetition

l1pipeline.inputs.preproc.smooth.fwhm = [6, 6, 6]
l1pipeline.inputs.analysis.modelspec.subject_info = subjectinfo
l1pipeline.inputs.analysis.contrastestimate.contrasts = contrasts
l1pipeline.inputs.analysis.threshold.contrast_index = 1
```

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 `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 sub-directories.
The `nipype.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, l1pipeline, [('struct', 'preproc.coregister.source')])
                ])
if merge_to_4d:
    level1.connect([(datasource, l1pipeline, [('func', 'preproc.merge.in_files')])])
else:
    level1.connect([(datasource, l1pipeline, [('func', 'preproc.realign.in_files')])])
```

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(interface=nio.DataSink(), name="datasink")
datasink.inputs.base_directory = os.path.abspath('spm_auditory_tutorial/l1output')


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

# 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'
                ])
```

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 `nipype.pipeline.engine.Pipeline.Run` function needs to be called.

```
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: 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 nipype tutorial directory:

```
python fmri_spm_dartel.py
```

Import necessary modules from nipype.

```
from __future__ import print_function
from builtins import range

import nipype.interfaces.io as nio           # Data i/o
import nipype.interfaces.spm as spm          # spm
import nipype.workflows.fmri.spm as spm_wf          # spm
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.rapidart as ra      # artifact detection
import nipype.algorithms.modelgen as model   # model specification
import os                                    # system functions
```

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')
```

Setting up workflows

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.

Setup preprocessing 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.DARTELNorm2MNI(modulate=True), name='normalize_and_smoot
fwhmlist = [4]
normalize_and_smooth_func.iterables = ('fwhm', fwhmlist)
```

Normalize structural data using DARTEL template

```
normalize_struct = pe.Node(spm.DARTELNorm2MNI(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')]),
                      ])
```

Set up analysis workflow

```
l1analysis = pe.Workflow(name='analysis')
```

Generate SPM-specific design information using `nipype.interfaces.spm.SpecifyModel`.

```
modelspec = pe.Node(model.SpecifySPMModel(), name="modelspec")
modelspec.inputs.concatenate_runs = True
```

Generate a first level SPM.mat file for analysis `nipype.interfaces.spm.Level1Design`.

```
level1design = pe.Node(spm.Level1Design(), name="level1design")
level1design.inputs.bases = {'hrf': {'derivs': [0, 0]}}
```

Use `nipype.interfaces.spm.EstimateModel` to determine the parameters of the model.

```
level1estimate = pe.Node(spm.EstimateModel(), name="level1estimate")
level1estimate.inputs.estimation_method = {'Classical': 1}
```

Use `nipype.interfaces.spm.EstimateContrast` to estimate the first level contrasts specified in a few steps above.

```
contrastestimate = pe.Node(spm.EstimateContrast(), name="contrastestimate")
```

Use :class: *nipype.interfaces.utility.Select* to select each contrast for reporting.

```
selectcontrast = pe.Node(niu.Select(), name="selectcontrast")
```

Use `nipype.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 `nipype.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, level1estimate, [('spm_mat_file', 'spm_mat_file')]),
                    (level1estimate, 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')])
                    ])
```

Preproc + Analysis pipeline

```
l1pipeline = pe.Workflow(name='firstlevel')
l1pipeline.connect([(preproc, l1analysis, [('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')]),
                           ])
```

Data specific components

The nipype 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 `nipype.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipype.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 = 'nipype-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 = 'nipype-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 nipype.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")
```

Experimental paradigm specific components

Here we create a function that returns subject-specific information about the experimental paradigm. This is used by the `nipype.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 nipype.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 = l1pipeline.inputs.analysis.modelspec
modelspecref.input_units = 'secs'
modelspecref.output_units = 'secs'
modelspecref.time_repetition = 3.
modelspecref.high_pass_filter_cutoff = 120

l1designref = l1pipeline.inputs.analysis.level1design
l1designref.timing_units = modelspecref.output_units
l1designref.interscan_interval = modelspecref.time_repetition


l1pipeline.inputs.analysis.contrastestimate.contrasts = contrasts


# Iterate over each contrast and create report images.
selectcontrast.iterables = ('index', [[i] for i in range(len(contrasts))])
```

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 `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 sub-directories.
The `nipype.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_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')]),
                (datasource, l1pipeline, [('func', 'preproc.realign.in_files'),
                                          ('struct', 'preproc.coregister.target'),
                                          ('struct', 'preproc.normalize_struct.apply_to_files')]
                (dartel_workflow, l1pipeline, [('outputspec.template_file', 'preproc.normalize_s
                                               ('outputspec.template_file', 'preproc.normalize_a
                (infosource, pick_flow, [('subject_id', 'subject_id')]),
                (dartel_workflow, pick_flow, [('outputspec.flow_fields', 'dartel_flow_fields')])
                (pick_flow, l1pipeline, [('dartel_flow_field', 'preproc.normalize_struct.flowfie
                                         ('dartel_flow_field', 'preproc.normalize_and_smooth_fun
                (infosource, l1pipeline, [(('subject_id', subjectinfo),
                                           'analysis.modelspec.subject_info')]),
                ])
```

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 = 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' % su

# 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'
                (infosource, report, [('subject_id', 'container'),
                                      (('subject_id', getstripdir), 'strip_dir')]),
                (l1pipeline, report, [('analysis.slicestats.out_file', '@report')]),
                ])
```

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 `nipype.pipeline.engine.Pipeline.Run` function needs to be called.

```
if __name__ == '__main__':
    level1.run(plugin_args={'n_procs': 4})
    level1.write_graph()
```

Setup level 2 pipeline

Use `nipype.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_%
# iterate over all contrast images
l2source.iterables = [('fwhm', fwhmlist),
                      ('con', contrast_ids)]
l2source.inputs.sort_filelist = True
```

Use `nipype.interfaces.spm.OneSampleTTestDesign` to perform a simple statistical analysis of the contrasts from the group of subjects (n=2 in this example).

```
# setup a 1-sample t-test node
onesamplettestdes = 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 -> onesamplettest).

```
l2pipeline = pe.Workflow(name="level2")
l2pipeline.base_dir = os.path.abspath('spm_dartel_tutorial/l2output')
l2pipeline.connect([(l2source, onesamplettestdes, [('outfiles', 'in_files')]),
                    (onesamplettestdes, l2estimate, [('spm_mat_file', 'spm_mat_file')]),
                    (l2estimate, l2conestimate, [('spm_mat_file', 'spm_mat_file'),
                                                 ('beta_images', 'beta_images'),
                                                 ('residual_image', 'residual_image')]),
                    ])
```

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 Nipype source distribution under the `examples` directory.

fMRI: Famous vs non-famous faces, SPM

Introduction

The fmri_spm_face.py recreates the classical workflow described in the SPM8 manual 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 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
import os                                    # system functions
```

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")
# If SPM is not in your MATLAB path you should add it here
# mlab.MatlabCommand.set_default_paths('/path/to/your/spm8')
```

Setting up workflows 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.

Setup preprocessing 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(interface=spm.Realign(), name="realign")

slice_timing = pe.Node(interface=spm.SliceTiming(), name="slice_timing")
```

Use `nipype.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 `nipype.interfaces.spm.Normalize`. The tutorial data set includes the template 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 `nipype.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 van infer it from data using the following function:

```
def get_vox_dims(volume):
    import nibabel as nb
    if isinstance(volume, list):
        volume = volume[0]
    nii = nb.load(volume)
    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_vox
                      (realign, slice_timing, [('realigned_files', 'in_files')]),
                      (slice_timing, normalize_func, [('timecorrected_files', 'apply_to_files'),
                                                      (('timecorrected_files', get_vox_dims), 'write_
                      (normalize_func, smooth, [('normalized_files', 'in_files')]),
                      ])
```

Set up analysis workflow

```
l1analysis = pe.Workflow(name='analysis')
```

Generate SPM-specific design information using `nipype.interfaces.spm.SpecifyModel`.

```
modelspec = pe.Node(interface=model.SpecifySPMModel(), name="modelspec")
```

Generate a first level SPM.mat file for analysis `nipype.interfaces.spm.Level1Design`.

```
level1design = pe.Node(interface=spm.Level1Design(), name="level1design")
```

Use `nipype.interfaces.spm.EstimateModel` to determine the parameters of the model.

```
level1estimate = pe.Node(interface=spm.EstimateModel(), name="level1estimate")
level1estimate.inputs.estimation_method = {'Classical': 1}

threshold = pe.Node(interface=spm.Threshold(), name="threshold")
```

Use `nipype.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')]),
                    ])
```

Preproc + Analysis pipeline

```
l1pipeline = pe.Workflow(name='firstlevel')
l1pipeline.connect([(preproc, l1analysis, [('realign.realignment_parameters',
                                            'modelspec.realignment_parameters')])])
```

Pluging 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')])])
```

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_re
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 `nipype.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipype.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
```

Experimental paradigm specific components Here we create a structure that provides information about the experimental paradigm. This is used by the `nipype.interfaces.spm.SpecifyModel` to create the information necessary to generate an SPM design matrix.

```
from nipype.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)'],
    cond2 = ('positive effect of condition_dtemo', 'T', ['N1*bf(2)', 'N2*bf(2)', 'F1*bf(2)', 'F2*bf(
    cond3 = ('positive effect of condition_ddisp', 'T', ['N1*bf(3)', 'N2*bf(3)', 'F1*bf(3)', 'F2*bf(
    # non-famous > famous
    fam1 = ('positive effect of Fame', 'T', ['N1*bf(1)', 'N2*bf(1)', 'F1*bf(1)', 'F2*bf(1)'], [1, 1,
    fam2 = ('positive effect of Fame_dtemp', 'T', ['N1*bf(2)', 'N2*bf(2)', 'F1*bf(2)', 'F2*bf(2)'],
    fam3 = ('positive effect of Fame_ddisp', 'T', ['N1*bf(3)', 'N2*bf(3)', 'F1*bf(3)', 'F2*bf(3)'],
    # rep1 > rep2
    rep1 = ('positive effect of Rep', 'T', ['N1*bf(1)', 'N2*bf(1)', 'F1*bf(1)', 'F2*bf(1)'], [1, -1,
    rep2 = ('positive effect of Rep_dtemp', 'T', ['N1*bf(2)', 'N2*bf(2)', 'F1*bf(2)', 'F2*bf(2)'], [
    rep3 = ('positive effect of Rep_ddisp', 'T', ['N1*bf(3)', 'N2*bf(3)', 'F1*bf(3)', 'F2*bf(3)'], [
    int1 = ('positive interaction of Fame x Rep', 'T', ['N1*bf(1)', 'N2*bf(1)', 'F1*bf(1)', 'F2*bf(1
    int2 = ('positive interaction of Fame x Rep_dtemp', 'T', ['N1*bf(2)', 'N2*bf(2)', 'F1*bf(2)', 'F
    int3 = ('positive interaction of Fame x Rep_ddisp', 'T', ['N1*bf(3)', 'N2*bf(3)', 'F1*bf(3)', 'F

    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,
```

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 contrats 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])
fcont1 = ('Famous Lag', 'F', [cont1, cont2])
paramcontrasts = [cont1, cont2, fcont1]

paramanalysis = l1analysis.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

l1pipeline.connect([(preproc, paramanalysis, [('realign.realignment_parameters',
                                               'modelspec.realignment_parameters'),
                                              (('smooth.smoothed_files', makelist),
                                               'modelspec.functional_runs')])])
```

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 `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 sub-directories.

The `nipype.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, l1pipeline, [('struct', 'preproc.coregister.source'),
                                          ('func', 'preproc.realign.in_files')])
                ])
```

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(interface=nio.DataSink(), name="datasink")
datasink.inputs.base_directory = os.path.abspath('spm_auditory_tutorial/l1output')


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

# 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', 'paramcont
                                        ('paramanalysis.contrastestimate.spmT_images', 'paramcon
                ])
```

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 `nipype.pipeline.engine.Pipeline.Run` function needs to be called.

```
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 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
```

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')
```

Setting up workflows

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, 'nipype-tutorial/data/T1.nii'))

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 `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'
```

Warp functional and structural data to SPM's T1 template using `nipype.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 `nipype.interfaces.spm.Smooth`.

```
smooth = pe.Node(spm.Smooth(), name="smooth")
fwhmlist = [4]
smooth.iterables = ('fwhm', fwhmlist)

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')]),
                 ])
```

Set up analysis workflow

```
l1analysis = pe.Workflow(name='analysis')
```

Generate SPM-specific design information using `nipype.interfaces.spm.SpecifyModel`.

```
modelspec = pe.Node(model.SpecifySPMModel(), name="modelspec")
modelspec.inputs.concatenate_runs = True
```

Generate a first level SPM.mat file for analysis `nipype.interfaces.spm.Level1Design`.

```
level1design = pe.Node(spm.Level1Design(), name="level1design")
level1design.inputs.bases = {'hrf': {'derivs': [0, 0]}}
```

Use `nipype.interfaces.spm.EstimateModel` to determine the parameters of the model.

```
level1estimate = pe.Node(spm.EstimateModel(), name="level1estimate")
level1estimate.inputs.estimation_method = {'Classical': 1}
```

Use `nipype.interfaces.spm.EstimateContrast` to estimate the first level contrasts specified in a few steps above.

```
contrastestimate = pe.Node(spm.EstimateContrast(), name="contrastestimate")
```

Use :class: *nipype.interfaces.utility.Select* to select each contrast for reporting.

```
selectcontrast = pe.Node(niu.Select(), name="selectcontrast")
```

Use `nipype.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 `nipype.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, level1estimate, [('spm_mat_file', 'spm_mat_file')]),
                    (level1estimate, 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')])
                    ])
```

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',
                                            'level1design.mask_image'),
                                           ('normalize.normalized_source',
                                            'overlaystats.background_image')]),
                    ])
```

Data specific components

The nipype 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 `nipype.interfaces.io.DataGrabber` object and fill in the information from above about the layout of our data. The `nipype.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 = 'nipype-tutorial/data/%s/%s.nii'
datasource.inputs.template_args = info
datasource.inputs.sort_filelist = True
```

Experimental paradigm specific components

Here we create a function that returns subject-specific information about the experimental paradigm. This is used by the `nipype.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 nipype.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 = l1pipeline.inputs.analysis.modelspec
modelspecref.input_units = 'secs'
modelspecref.output_units = 'secs'
modelspecref.time_repetition = 3.
modelspecref.high_pass_filter_cutoff = 120

l1designref = l1pipeline.inputs.analysis.level1design
l1designref.timing_units = modelspecref.output_units
l1designref.interscan_interval = modelspecref.time_repetition


l1pipeline.inputs.analysis.contrastestimate.contrasts = contrasts


# Iterate over each contrast and create report images.
selectcontrast.iterables = ('index', [[i] for i in range(len(contrasts))])
```

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 `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 sub-directories.
The `nipype.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 = op.abspath('spm_tutorial2/workingdir')

level1.connect([(inputnode, datasource,  [('in_data', 'base_directory')]),
                (infosource, datasource, [('subject_id', 'subject_id')]),
                (datasource, l1pipeline, [('func', 'preproc.realign.in_files'),
                                          ('struct', 'preproc.coregister.target'),
                                          ('struct', 'preproc.normalize.source')]),
                (infosource, l1pipeline, [(('subject_id', subjectinfo),
                                           'analysis.modelspec.subject_info')]),
                ])
```

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')]),
                (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')]),
                ])
```

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 `nipype.pipeline.engine.Pipeline.Run` function needs to be called.

```
if __name__ == '__main__':
    level1.run('MultiProc')
    level1.write_graph()
```

Setup level 2 pipeline

Use `nipype.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 `nipype.interfaces.spm.OneSampleTTestDesign` to perform a simple statistical analysis of the contrasts from the group of subjects (n=2 in this example).

```
# setup a 1-sample t-test node
onesamplettestdes = 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 -> onesamplettest).

```
l2pipeline = pe.Workflow(name="level2")
l2pipeline.base_dir = op.abspath('spm_tutorial2/l2output')
l2pipeline.connect([(l2source, onesamplettestdes, [('outfiles', 'in_files')]),
                    (onesamplettestdes, l2estimate, [('spm_mat_file', 'spm_mat_file')]),
                    (l2estimate, l2conestimate, [('spm_mat_file', 'spm_mat_file'),
                                                 ('beta_images', 'beta_images'),
                                                 ('residual_image', 'residual_image')]),
                    ])
```

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 nipype 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 nipype.interfaces import fsl
fsl.FSLCommand.set_default_output_type('NIFTI')

from nipype.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
# 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
from builtins import range

import os

from nipype.interfaces.base import CommandLine
CommandLine.set_default_terminal_output('allatonce')


from dicom import read_file

from nipype.interfaces import (spm, fsl, Function, ants, freesurfer)
from nipype.interfaces.c3 import C3dAffineTool

fsl.FSLCommand.set_default_output_type('NIFTI')

from nipype import Workflow, Node, MapNode
from nipype.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 nipype.algorithms.rapidart import ArtifactDetect
from nipype.algorithms.misc import TSNR
from nipype.interfaces.utility import Rename, Merge, IdentityInterface
from nipype.utils.filemanip import filename_to_list
from nipype.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 nipype.utils.filemanip import filename_to_list, list_to_filename, split_filenam
           '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
        ----------

        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
        average = None
        for idx, filename in enumerate(filename_to_list(in_files)):
            img = nb.load(filename)
            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 nipype.utils.filemanip import split_filename, list_to_filename
```

```
        import numpy as np
        import nibabel as nb
        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)
            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
            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="%.10f")
            out_files.append(filename)
        return out_files


    def build_filter1(motion_params, comp_norm, outliers, detrend_poly=None):
        """Builds a regressor set comprisong 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])
            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="%.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
        import os
        imgseries = nb.load(realigned_file)
        components = None
        for filename in filename_to_list(mask_file):
            mask = nb.load(filename).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.
            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="%.10f")
        return components_file


    def rename(in_files, suffix=None):
        from nipype.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 nipype.utils.filemanip import split_filename
        import nibabel as nb
        import os
        img = nb.load(timeseries_file)
        data = img.get_data()
        roiimg = nb.load(label_file)
        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
        lh_data = nb.load(left).get_data()
        rh_data = nb.load(right).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
            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')
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 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]]
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.inputs.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)

    # Comute 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(Function(input_names=['in_files'],
                                output_names=['median_file'],
                                function=median,
                                imports=imports),
                       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 `nipype.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 = '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 nipype.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=['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),
                    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 `nipype.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.inputs.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, '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),
                          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 nipype.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

    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')

    # 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(samplerrh, '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')
    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_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.fsdir),
                      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="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", 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))
    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

```
from __future__ import division
from builtins import range

import os

from nipype.interfaces.base import CommandLine
CommandLine.set_default_terminal_output('allatonce')
```

```
    from dcmstack.extract import default_extractor
    from dicom import read_file

    from nipype.interfaces import (fsl, Function, ants, freesurfer, nipy)
    from nipype.interfaces.c3 import C3dAffineTool

    fsl.FSLCommand.set_default_output_type('NIFTI_GZ')

    from nipype import Workflow, Node, MapNode

    from nipype.algorithms.rapidart import ArtifactDetect
    from nipype.algorithms.misc import TSNR
    from nipype.interfaces.utility import Rename, Merge, IdentityInterface
    from nipype.utils.filemanip import filename_to_list
    from nipype.interfaces.io import DataSink, FreeSurferSource
    import nipype.interfaces.freesurfer as fs

    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 nipype.utils.filemanip import filename_to_list, list_to_filename, split_filenam
               'from scipy.special import legendre'
               ]


    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):
        """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)
            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)
            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))
            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="%.10f")
            out_files.append(filename)
        return out_files


    def build_filter1(motion_params, comp_norm, outliers, detrend_poly=None):
        """Builds a regressor set comprisong 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):
                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="%.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
        """
        imgseries = nb.load(realigned_file)
        components = None
        for filename in filename_to_list(mask_file):
            mask = nb.load(filename).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.
            stdX[np.isnan(stdX)] = 1.
            stdX[np.isinf(stdX)] = 1.
            X = (X - np.mean(X, axis=0)) / stdX
            u, _, _ = sp.linalg.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="%.10f")
        return components_file


    def rename(in_files, suffix=None):
        from nipype.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)
    data = img.get_data()
    roiimg = nb.load(label_file)
    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
    """
    lh_data = nb.load(left).get_data()
    rh_data = nb.load(right).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
            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',
                                                              '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(binarize, "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')
```

Binarize the segmentation

```
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 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]]
    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', 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.inputs.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')
    register.connect(bbregister, '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}

        # Comute TSNR on realigned data regressing polynomials upto 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(Function(input_names=['in_files'],
                                    output_names=['median_file'],
                                    function=median,
                                    imports=imports),
                           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 `nipype.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 nipype.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')

# 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(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.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, '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),
                    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 `nipype.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.inputs.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),
                          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 nipype.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')

    # 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(samplerrh, '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 += [("_makecompcorfilter%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 = [('_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, datasink, [('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, '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_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.fsdir),
                      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 - "
                                  "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)
        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")
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]

    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

    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.estimation_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', 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')

    main_workflow = pe.Workflow(name="main_workflow")
    main_workflow.base_dir = "smoothing_comparison_workflow"
    main_workflow.connect(preprocessing, "realign.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, "level1design.mask_image")

    datasource = pe.Node(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, 'realign.in_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
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', '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', 'passiveImagesDiction
                     run_without_submitting=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_imag
tbuilder.connect(datasource, 'imageList', buildTemplateIteration1, 'inputspec.images')
tbuilder.connect(datasource, 'passiveImagesDictionariesList', buildTemplateIteration1, 'inputspe
```

7. Define the second iteration of template building

```
buildTemplateIteration2 = ANTSTemplateBuildSingleIterationWF('iteration02')
tbuilder.connect(buildTemplateIteration1, 'outputspec.template', buildTemplateIteration2, 'input
tbuilder.connect(datasource, 'imageList', buildTemplateIteration2, 'inputspec.images')
tbuilder.connect(datasource, 'passiveImagesDictionariesList', buildTemplateIteration2, 'inputspe
```

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, 'Pa
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 Nipype 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
from future import standard_library
standard_library.install_aliases()

import os
import urllib.request
import urllib.error
import urllib.parse
from nipype.interfaces.ants import Registration
```

2. Download T1 volumes into home directory

```
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'),
]
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'),
]
```

3. Define the parameters of the registration

```
reg = Registration()
reg.inputs.fixed_image = input_images[0]
reg.inputs.moving_image = input_images[1]
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 Nipype source distribution under the `examples` directory.

sMRI: 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', '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))
```

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_T
        {'T1': os.path.join(mydatadir, '02_T1_half.nii.gz'), 'INV_T1': os.path.join(mydatadir, '02_T
        {'T1': os.path.join(mydatadir, '03_T1_half.nii.gz'), 'INV_T1': os.path.join(mydatadir, '03_T
    ]
    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': '
```

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', 'ListOfIm
                                                                  'registrationImageTypes', 'interpo
                         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 smp1 8-12 -l mem_free=6000M -o /dev/null

tbuilder.connect(initAvg, 'output_average_image', buildTemplateIteration1, 'inputspec.fixed_imag
tbuilder.connect(datasource, 'ListOfImagesDictionaries', buildTemplateIteration1, 'inputspec.Lis
tbuilder.connect(datasource, 'registrationImageTypes', buildTemplateIteration1, 'inputspec.regis
tbuilder.connect(datasource, 'interpolationMapping', buildTemplateIteration1, 'inputspec.interpo
```

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 smp1 8-12 -l mem_free=6000M -o /dev/null
tbuilder.connect(buildTemplateIteration1, 'outputspec.template', buildTemplateIteration2, 'input
tbuilder.connect(datasource, 'ListOfImagesDictionaries', buildTemplateIteration2, 'inputspec.Lis
tbuilder.connect(datasource, 'registrationImageTypes', buildTemplateIteration2, 'inputspec.regis
tbuilder.connect(datasource, 'interpolationMapping', buildTemplateIteration2, 'inputspec.interpo
```

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, 'Pa
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 Nipype 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, MedicAlgorithmSPECTRE

wf = pe.Workflow("skullstripping")

mask = pe.Node(JistIntensityMp2rageMasking(), name="masking")
mask.inputs.inSecond = "/Users/filo/7t_trt/niftis/sub001/session_1/MP2RAGE_INV2.nii.gz"
mask.inputs.inQuantitative = "/Users/filo/7t_trt/niftis/sub001/session_1/MP2RAGE_UNI.nii.gz"
mask.inputs.inT1weighted = "/Users/filo/7t_trt/niftis/sub001/session_1/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="l1workflow")
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'])
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="l1workflow")
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

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.

Packages and Data Setup

Import the necessary modules and workflow from nipype.

```
import nipype.pipeline.engine as pe          # pypeline 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
```

Directories

Set the default directory and lookup table (LUT) paths

```
fs_dir = os.environ['FREESURFER_HOME']
lookup_file = op.join(fs_dir, 'FreeSurferColorLUT.txt')
subjects_dir = op.join(fs_dir, 'subjects/')
output_dir = './tessellate_tutorial'
```

Inputs

Create the tessellation workflow and set inputs Here we will choose Gifti (gii) as the output format, because we want to able to view the surface in ConnectomeViewer.
In you intend to view the meshes in gmsh or Blender, you should change the workflow creation to use stereolithographic (stl) format.

```
tessflow = create_tessellation_flow(name='tessflow', out_format='gii')
tessflow.inputs.inputspec.subject_id = 'fsaverage'
tessflow.inputs.inputspec.subjects_dir = subjects_dir
tessflow.inputs.inputspec.lookup_file = lookup_file
```

We also create a conditional node to package the surfaces for ConnectomeViewer. Simply set cff to "False" to ignore this step.

```
cff = True
if cff:
    cff = pe.Node(interface=cmtk.CFFConverter(), name='cff')
    cff.inputs.out_file = 'Meshes.cff'
```

Outputs

Create a datasink to organize the smoothed meshes Using regular-expression substitutions we can remove the extraneous folders generated by the mapnode.

```
datasink = pe.Node(interface=nio.DataSink(), name="datasink")
datasink.inputs.base_directory = 'meshes'
datasink.inputs.regexp_substitutions = [('_smoother[\d]*/', '')]
```

Execution

Finally, create and run another pipeline that connects the workflow and datasink

```
tesspipe = pe.Workflow(name='tessellate_tutorial')
tesspipe.base_dir = output_dir
tesspipe.connect([(tessflow, datasink, [('outputspec.meshes', '@meshes.all')])])
```

If the surfaces are to be packaged, this will connect the CFFConverter node to the tessellation and smoothing workflow, as well as to the datasink.

```
if cff:
    tesspipe.connect([(tessflow, cff, [('outputspec.meshes', 'gifti_surfaces')])])
```

```
        tesspipe.connect([(cff, datasink, [('connectome_file', '@cff')])])

    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          # pypeline 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 definition which allows using the same definition for many model estimation implemantations (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 Work-

flow 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.estimation_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, "realign.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, 'realign.in_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 Nipype 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 nipype specific configuration). Note that nipype does not need to be run through ipython - it is just much nicer to do interactive work in it.

```
cd $TDPATH
ipython -p nipype
```

For every neuroimaging procedure supported by nipype there exists a wrapper - a small piece of code managing the underlying software (FSL, SPM, AFNI etc.). We call those interfaces. They are standarised so we can hook them up together. Lets have a look at some of them.

```
In [1]: import nipype.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
     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 nipype.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 nipype at our online documentation at http://nipy.sourceforge.net/nipype/documentation.html#documentation . Check it out now.

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

import nipype.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()
```

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 nipype 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 nipype.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 folde
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()
```

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()
```

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.inputspec.func = os.path.abspath('data/s1/f3.nii')
preproc.inputs.inputspec.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()
```

Visualizing workflows 1

So what did we run in this precanned workflow

```
preproc.write_graph()
```

Datasink

Datasink is a special interface for copying and arranging results.

```
import nipype.interfaces.io as nio

preproc.inputs.inputspec.func = os.path.abspath('data/s1/f3.nii')
preproc.inputs.inputspec.struct = os.path.abspath('data/s1/struct.nii')
datasink = pe.Node(interface=nio.DataSink(), name='sinker')
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()
```

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()
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)
```

Iterables

Iterables is a special field of the Node class that enables to iterate all workfloes/nodes connected to it over some parameters. Here we'll use it to iterate over two subjects.

```
import nipype.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']), nam
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', 'stru
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()
```

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 Nipype source distribution under the `examples` directory.

1.5.4 Requirements

All tutorials
Release 0.4 of nipype and it's dependencies have been installed
Analysis tutorials
FSL, FreeSurfer, Camino, ConnectomeViewer and MATLAB are available and callable from the command line

SPM 5/8/12 is installed and callable in matlab
Space: 3-10 GB

1.5.5 Checklist for analysis tutorials

For the analysis tutorials, we will be using a slightly modified version of the FBIRN Phase I travelling data set.
1. Download and extract the Pipeline tutorial data (429MB). (md5: d175083784c5167de4ea11b43b37c166)
2. Ensure that all programs are available by calling `bet`, `matlab` and then `which spm` within matlab to ensure you have spm5/8/12 in your matlab path.

1.6 Using Nipype Plugins

The workflow engine supports a plugin architecture for workflow execution. The available plugins allow local and distributed execution of workflows and debugging. Each available plugin is described below.
Current plugins are available for Linear, Multiprocessing, IPython distributed processing platforms and for direct processing on SGE, PBS, HTCondor, LSF, *OAR*, and SLURM. We anticipate future plugins for the Soma workflow.

Note: The current distributed processing plugins rely on the availability of a shared filesystem across computational nodes.
A variety of config options can control how execution behaves in this distributed context. These are listed later on in this page.

All plugins can be executed with:

```
workflow.run(plugin=PLUGIN_NAME, plugin_args=ARGS_DICT)
```

Optional arguments:

```
status_callback : a function handle
max_jobs : maximum number of concurrent jobs
max_tries : number of times to try submitting a job
retry_timeout : amount of time to wait between tries
```

Note: Except for the status_callback, the remaining arguments only apply to the distributed plugins: MultiProc/IPython(X)/SGE/PBS/HTCondor/HTCondorDAGMan/LSF

For example:

1.6.1 Plugins

Debug

This plugin provides a simple mechanism to debug certain components of a workflow without executing any node.
Mandatory arguments:

```
callable :  A function handle that receives as arguments a node and a graph
```

The function callable will called for every node from a topological sort of the execution graph.

Linear

This plugin runs the workflow one node at a time in a single process locally. The order of the nodes is determined by a topological sort of the workflow:

```
workflow.run(plugin='Linear')
```

MultiProc

Uses the Python multiprocessing library to distribute jobs as new processes on a local system.
Optional arguments:

```
n_procs :  Number of processes to launch in parallel, if not set number of
processors/threads will be automatically detected
```

To distribute processing on a multicore machine, simply call:

```
workflow.run(plugin='MultiProc')
```

This will use all available CPUs. If on the other hand you would like to restrict the number of used resources (to say 2 CPUs), you can call:

```
workflow.run(plugin='MultiProc', plugin_args={'n_procs' : 2}
```

IPython

This plugin provide access to distributed computing using IPython parallel machinery.

Note: We provide backward compatibility with IPython versions earlier than 0.10.1 using the IPythonX plugin. This plugin will be deprecated as of version 0.13 of Nipype.
Please read the IPython documentation to determine how to setup your cluster for distributed processing. This typically involves calling ipcluster.

Once the clients have been started, any pipeline executed with:

```
workflow.run(plugin='IPython')
```

SGE/PBS

In order to use nipype with SGE or PBS you simply need to call:

```
workflow.run(plugin='SGE')
workflow.run(plugin='PBS')
```

Optional arguments:

```
template: custom template file to use
qsub_args: any other command line args to be passed to qsub.
max_jobname_len: (PBS only) maximum length of the job name.  Default 15.
```

For example, the following snippet executes the workflow on myqueue with a custom template:

```
workflow.run(plugin='SGE',
   plugin_args=dict(template='mytemplate.sh', qsub_args='-q myqueue')
```

In addition to overall workflow configuration, you can use node level configuration for PBS/SGE:

```
node.plugin_args = {'qsub_args': '-l nodes=1:ppn=3'}
```

this would apply only to the node and is useful in situations, where a particular node might use more resources than other nodes in a workflow.

Note: Setting the keyword *overwrite* would overwrite any global configuration with this local configuration:

```
node.plugin_args = {'qsub_args': '-l nodes=1:ppn=3', 'overwrite': True}
```

SGEGraph

SGEGraph is an execution plugin working with Sun Grid Engine that allows for submitting entire graph of dependent jobs at once. This way Nipype does not need to run a monitoring process - SGE takes care of this. The use of *SGEGraph* is preferred over SGE since the latter adds unnecessary load on the submit machine.

Note: When rerunning unfinished workflows using SGEGraph you may decide not to submit jobs for Nodes that previously finished running. This can speed up execution, but new or modified inputs that would previously trigger a Node to rerun will be ignored. The following option turns on this functionality:

```
workflow.run(plugin='SGEGraph', plugin_args = {'dont_resubmit_completed_jobs': True})
```

LSF

Submitting via LSF is almost identical to SGE above above except for the optional arguments field:

```
workflow.run(plugin='LSF')
```

Optional arguments:

```
template: custom template file to use
bsub_args: any other command line args to be passed to bsub.
```

SLURM

Submitting via SLURM is almost identical to SGE above except for the optional arguments field:
workflow.run(plugin='SLURM')
Optional arguments:

```
template: custom template file to use
sbatch_args: any other command line args to be passed to bsub.
```

SLURMGraph

SLURMGraph is an execution plugin working with SLURM that allows for submitting entire graph of dependent jobs at once. This way Nipype does not need to run a monitoring process - SLURM takes care of this. The use of *SLURMGraph* plugin is preferred over the vanilla SLURM plugin since the latter adds unnecessary load on the submit machine.

Note: When rerunning unfinished workflows using SLURMGraph you may decide not to submit jobs for Nodes that previously finished running. This can speed up execution, but new or modified inputs that would previously trigger a Node to rerun will be ignored. The following option turns on this functionality:

```
workflow.run(plugin='SLURMGraph', plugin_args = {'dont_resubmit_completed_jobs': True})
```

HTCondor

DAGMan

With its DAGMan component HTCondor (previously Condor) allows for submitting entire graphs of dependent jobs at once (similar to *SGEGraph* and *SLURMGraph*). With the `CondorDAGMan` plug-in Nipype can utilize this functionality to submit complete workflows directly and in a single step. Consequently, and in contrast to other plug-ins, workflow execution returns almost instantaneously – Nipype is only used to generate the workflow graph, while job scheduling and dependency resolution are entirely managed by HTCondor.

Please note that although DAGMan supports specification of data dependencies as well as data provisioning on compute nodes this functionality is currently not supported by this plug-in. As with all other batch systems supported by Nipype, only HTCondor pools with a shared file system can be used to process Nipype workflows. Workflow execution with HTCondor DAGMan is done by calling:

```
workflow.run(plugin='CondorDAGMan')
```

Job execution behavior can be tweaked with the following optional plug-in arguments. The value of most arguments can be a literal string or a filename, where in the latter case the content of the file will be used as the argument value:

```
submit_template : submit spec template for individual jobs in a DAG (see
            CondorDAGManPlugin.default_submit_template for the default.
initial_specs : additional submit specs that are prepended to any job's
            submit file
override_specs : additional submit specs that are appended to any job's
            submit file
wrapper_cmd : path to an exectuable that will be started instead of a node
            script. This is useful for wrapper script that execute certain
            functionality prior or after a node runs. If this option is
            given the wrapper command is called with the respective Python
            exectuable and the path to the node script as final arguments
wrapper_args : optional additional arguments to a wrapper command
dagman_args : arguments to be prepended to the job execution script in the
             dagman call
block : if True the plugin call will block until Condor has finished
        prcoessing the entire workflow (default: False)
```

Please see the HTCondor documentation for details on possible configuration options and command line arguments.

Using the `wrapper_cmd` argument it is possible to combine Nipype workflow execution with checkpoint/migration functionality offered by, for example, DMTCP. This is especially useful in the case of workflows with long running nodes, such as Freesurfer's recon-all pipeline, where Condor's job prioritization algorithm could lead to jobs being evicted from compute nodes in order to maximize overall troughput. With checkpoint/migration enabled such a job would be checkpointed prior eviction and resume work from the checkpointed state after being rescheduled – instead of restarting from scratch.

On a Debian system, executing a workflow with support for checkpoint/migration for all nodes could look like this:

```
# define common parameters
dmtcp_hdr = """
should_transfer_files = YES
when_to_transfer_output = ON_EXIT_OR_EVICT
kill_sig = 2
environment = DMTCP_TMPDIR=./;JALIB_STDERR_PATH=/dev/null;DMTCP_PREFIX_ID=$(CLUSTER)_$(PROCESS)
"""
shim_args = "--log %(basename)s.shimlog --stdout %(basename)s.shimout --stderr %(basename)s.shim
# run workflow
workflow.run(
      plugin='CondorDAGMan',
      plugin_args=dict(initial_specs=dmtcp_hdr,
                       wrapper_cmd='/usr/lib/condor/shim_dmtcp',
                       wrapper_args=shim_args)
      )
```

OAR

In order to use nipype with *OAR* you simply need to call:

```
workflow.run(plugin='OAR')
```

Optional arguments:

```
template: custom template file to use
oar_args: any other command line args to be passed to qsub.
max_jobname_len: (PBS only) maximum length of the job name.  Default 15.
```

For example, the following snippet executes the workflow on myqueue with a custom template:

```
workflow.run(plugin='oar',
   plugin_args=dict(template='mytemplate.sh', oarsub_args='-q myqueue')
```

In addition to overall workflow configuration, you can use node level configuration for OAR:

```
node.plugin_args = {'overwrite': True, 'oarsub_args': '-l "nodes=1/cores=3"'}
```

this would apply only to the node and is useful in situations, where a particular node might use more resources than other nodes in a workflow. You need to set the 'overwrite' flag to bypass the general settings-template you defined for the other nodes.

`qsub` emulation

Note: This plug-in is deprecated and users should migrate to the more robust and more versatile `CondorDAGMan` plug-in.

Despite the differences between HTCondor and SGE-like batch systems the plugin usage (incl. supported arguments) is almost identical. The HTCondor plugin relies on a `qsub` emulation script for HTCondor, called `condor_qsub` that can be obtained from a Git repository on git.debian.org. This script is currently not shipped with a standard HTCondor distribution, but is included in the HTCondor package from http://neuro.debian.net. It is sufficient to download this script and install it in any location on a system that is included in the `PATH` configuration.
Running a workflow in a HTCondor pool is done by calling:

```
workflow.run(plugin='Condor')
```

The plugin supports a limited set of qsub arguments (`qsub_args`) that cover the most common use cases. The `condor_qsub` emulation script translates qsub arguments into the corresponding HTCondor terminology and handles the actual job submission. For details on supported options see the manpage of `condor_qsub`.
Optional arguments:

```
qsub_args: any other command line args to be passed to condor_qsub.
```

1.7 Configuration File

Some of the system wide options of Nipype can be configured using a configuration file. Nipype looks for the file in the local folder under the name `nipype.cfg` and in `~/.nipype/nipype.cfg` (in this order). If an option will not be specified a default value will be assumed. The file is divided into following sections:

1.7.1 Logging

workflow_level How detailed the logs regarding workflow should be (possible values: `INFO` and `DEBUG`; default value: `INFO`)

filemanip_level How detailed the logs regarding file operations (for example overwriting warning) should be (possible values: `INFO` and `DEBUG`; default value: `INFO`)

interface_level How detailed the logs regarding interface execution should be (possible values: `INFO` and `DEBUG`; default value: `INFO`)

log_to_file Indicates whether logging should also send the output to a file (possible values: `true` and `false`; default value: `false`)

log_directory Where to store logs. (string, default value: home directory)

log_size Size of a single log file. (integer, default value: 254000)

log_rotate How many rotation should the log file make. (integer, default value: 4)

1.7.2 Execution

plugin This defines which execution plugin to use. (possible values: `Linear`, `MultiProc`, `SGE`, `IPython`; default value: `Linear`)

stop_on_first_crash Should the workflow stop upon first node crashing or try to execute as many nodes as possible? (possible values: `true` and `false`; default value: `false`)

stop_on_first_rerun Should the workflow stop upon first node trying to recompute (by that we mean rerunning a node that has been run before - this can happen due changed inputs and/or hash_method since the last run). (possible values: `true` and `false`; default value: `false`)

hash_method Should the input files be checked for changes using their content (slow, but 100% accurate) or just their size and modification date (fast, but potentially prone to errors)? (possible values: `content` and `timestamp`; default value: `content`)

keep_inputs Ensures that all inputs that are created in the nodes working directory are kept after node execution (possible values: `true` and `false`; default value: `false`)

single_thread_matlab Should all of the Matlab interfaces (including SPM) use only one thread? This is useful if you are parallelizing your workflow using MultiProc or IPython on a single multicore machine. (possible values: `true` and `false`; default value: `true`)

display_variable What `DISPLAY` variable should all command line interfaces be run with. This is useful if you are using xnest or Xvfb and you would like to redirect all spawned windows to it. (possible values: any X server address; default value: not set)

remove_unnecessary_outputs This will remove any interface outputs not needed by the workflow. If the required outputs from a node changes, rerunning the workflow will rerun the node. Outputs of leaf nodes (nodes whose outputs are not connected to any other nodes) will never be deleted independent of this parameter. (possible values: `true` and `false`; default value: `true`)

try_hard_link_datasink When the DataSink is used to produce an orginized output file outside of nipypes internal cache structure, a file system hard link will be attempted first. A hard link allow multiple file paths to point to the same physical storage location on disk if the conditions allow. By refering to the same physical file on disk (instead of copying files byte-by-byte) we can avoid unnecessary data duplication. If hard links are not supported for the source or destination paths specified, then a standard byte-by-byte copy is used. (possible values: `true` and `false`; default value: `true`)

use_relative_paths Should the paths stored in results (and used to look for inputs) be relative or absolute. Relative paths allow moving the whole working directory around but may cause problems with symlinks. (possible values: `true` and `false`; default value: `false`)

local_hash_check Perform the hash check on the job submission machine. This option minimizes the number of jobs submitted to a cluster engine or a multiprocessing pool to only those that need to be rerun. (possible values: `true` and `false`; default value: `true`)

job_finished_timeout When batch jobs are submitted through, SGE/PBS/Condor they could be killed externally. Nipype checks to see if a results file exists to determine if the node has completed. This timeout determines for how long this check is done after a job finish is detected. (float in seconds; default value: 5)

remove_node_directories (EXPERIMENTAL) Removes directories whose outputs have already been used up. Doesn't work with IdentiInterface or any node that patches data through (without copying) (possible values: `true` and `false`; default value: `false`)

stop_on_unknown_version If this is set to True, an underlying interface will raise an error, when no version information is available. Please notify developers or submit a patch.

parameterize_dirs If this is set to True, the node's output directory will contain full parameterization of any iterable, otherwise parameterizations over 32 characters will be replaced by their hash. (possible values: `true` and `false`; default value: `true`)

poll_sleep_duration This controls how long the job submission loop will sleep between submitting all pending jobs and checking for job completion. To be nice to cluster schedulers the default is set to 60 seconds.

xvfb_max_wait Maximum time (in seconds) to wait for Xvfb to start, if the _redirect_x parameter of an Interface is True.

1.7.3 Example

```
[logging]
workflow_level = DEBUG

[execution]
stop_on_first_crash = true
hash_method = timestamp
display_variable = :1
```

Workflow.config property has a form of a nested dictionary reflecting the structure of the .cfg file.

```
myworkflow = pe.Workflow()
myworkflow.config['execution'] = {'stop_on_first_rerun': 'True',
                                  'hash_method': 'timestamp'}
```

You can also directly set global config options in your workflow script. An example is shown below. This needs to be called before you import the pipeline or the logger. Otherwise logging level will not be reset.

```
from nipype import config
cfg = dict(logging=dict(workflow_level = 'DEBUG'),
           execution={'stop_on_first_crash': False,
                      'hash_method': 'content'})
config.update_config(cfg)
```

1.7.4 Enabling logging to file

By default, logging to file is disabled. One can enable and write the file to a location of choice as in the example below.

```
import os
from nipype import config, logging
config.update_config({'logging': {'log_directory': os.getcwd(),
                                  'log_to_file': True}})
logging.update_logging(config)
```

The logging update line is necessary to change the behavior of logging such as output directory, logging level, etc.,.

1.7.5 Debug configuration

To enable debug mode, one can insert the following lines:

```
from nipype import config, logging
config.enable_debug_mode()
logging.update_logging(config)
```

In this mode the following variables are set:

```
config.set('execution', 'stop_on_first_crash', 'true')
config.set('execution', 'remove_unnecessary_outputs', 'false')
config.set('logging', 'workflow_level', 'DEBUG')
config.set('logging', 'interface_level', 'DEBUG')
```

1.8 Debugging Nipype Workflows

Throughout Nipype we try to provide meaningful error messages. If you run into an error that does not have a meaningful error message please let us know so that we can improve error reporting.
Here are some notes that may help debugging workflows or understanding performance issues.

1. Always run your workflow first on a single iterable (e.g. subject) and gradually increase the execution distribution complexity (Linear->MultiProc-> SGE).
2. Use the debug config mode. This can be done by setting:

```
from nipype import config
config.enable_debug_mode()
```

   as the first import of your nipype script.

   Note: Turning on debug will rerun your workflows and will rerun them after debugging is turned off.

3. There are several configuration options that can help with debugging. See *Configuration File* for more details:

```
keep_inputs
remove_unnecessary_outputs
stop_on_first_crash
stop_on_first_rerun
```

4. When running in distributed mode on cluster engines, it is possible for a node to fail without generating a crash file in the crashdump directory. In such cases, it will store a crash file in the *batch* directory.
5. All Nipype crashfiles can be inspected with the *nipype_display_crash* utility.
6. The *nipype_crash_search* command allows you to search for regular expressions in the tracebacks of the Nipype crashfiles within a log folder.
7. Nipype determines the hash of the input state of a node. If any input contains strings that represent files on the system path, the hash evaluation mechanism will determine the timestamp or content hash of each of those files. Thus any node with an input containing huge dictionaries (or lists) of file names can cause serious performance penalties.
8. For HUGE data processing, 'stop_on_first_crash':'False', is needed to get the bulk of processing done, and then 'stop_on_first_crash':'True', is needed for debugging and finding failing cases. Setting 'stop_on_first_crash': 'False' is a reasonable option when you would expect 90% of the data to execute properly.
9. Sometimes nipype will hang as if nothing is going on and if you hit Ctrl+C you will get a *ConcurrentLogHandler* error. Simply remove the pypeline.lock file in your home directory and continue.
10. One many clusters with shared NFS mounts synchronization of files across clusters may not happen before the typical NFS cache timeouts. When using PBS/LSF/SGE/Condor plugins in such cases the workflow may crash because it cannot retrieve the node result. Setting the *job_finished_timeout* can help: workflow.config['execution']['job_finished_timeout'] = 65

1.9 The SelectFiles Interfaces

Nipype 0.9 introduces a new interface for intelligently finding files on the disk and feeding them into your workflows: *SelectFiles*. SelectFiles is intended as a simpler alternative to the DataGrabber interface that was discussed previously in DataGrabber and DataSink explained.
SelectFiles is built on Python format strings, which are similar to the Python string interpolation feature you are likely already familiar with, but advantageous in several respects. Format strings allow you to replace named sections of template strings set off by curly braces (*{}*), possibly filtered through a set of functions that control how the values are rendered into the string. As a very basic example, we could write

```
msg = "This workflow uses {package}"
```

and then format it with keyword arguments:

```
print msg.format(package="FSL")
```

SelectFiles only requires that you provide templates that can be used to find your data; the actual formatting happens behind the scenes.
Consider a basic example in which you want to select a T1 image and multple functional images for a number of subjects. Invoking SelectFiles in this case is quite straightforward:

```
from nipype import SelectFiles
templates = dict(T1="data/{subject_id}/struct/T1.nii",
                 epi="data/{subject_id}/func/epi_run*.nii")
sf = SelectFiles(templates)
```

SelectFiles will take the *templates* dictionary and parse it to determine its own inputs and oututs. Specifically, each name used in the format spec (here just *subject_id*) will become an interface input, and each key in the dictionary (here *T1* and *epi*) will become interface outputs. The *templates* dictionary thus succinctly links the node inputs to the appropriate outputs. You'll also note that, as was the case with DataGrabber, you can use basic glob syntax to match multiple files for a given output field. Additionally, any of the conversions outlined in the Python documentation for format strings can be used in the templates.
There are a few other options that help make SelectFiles flexible enough to deal with any situation where you need to collect data. Like DataGrabber, SelectFiles has a *base_directory* parameter that allows you to specify a path that is common to all of the values in the *templates* dictionary. Additionally, as *glob* does not return a sorted list, there is also a *sort_filelist* option, taking a boolean, to control whether sorting should be applied (it is True by default).
The final input is *force_lists*, which controls how SelectFiles behaves in cases where only a single file matches the template. The default behavior is that when a template matches multiple files they are returned as a list, while a single file is returned as a string. There may be situations where you want to force the outputs to always be returned as a list (for example, you are writing a workflow that expects to operate on several runs of data, but some of your subjects only have a single run). In this case, *force_lists* can be used to tune the outputs of the interface. You can either use a boolean value, which will be applied to every output the interface has, or you can provide a list of the output fields that should be coerced to a list. Returning to our basic example, you may want to ensure that the *epi* files are returned as a list, but you only ever will have a single *T1* file. In this case, you would do

```
sf = SelectFiles(templates, force_lists=["epi"])
```

1.10 The Function Interface

Most Nipype interfaces provide access to external programs, such as FSL binaries or SPM routines. However, a special interface, `nipype.interfaces.utility.Function`, allows you to wrap arbitrary Python code in the Interface framework and seamlessly integrate it into your workflows.

1.10.1 A Simple Function Interface

The most important component of a working Function interface is a Python function. There are several ways to associate a function with a Function interface, but the most common way will involve functions you code yourself as part of your Nipype scripts. Consider the following function:

```
def add_two(val):
    return val + 2
```

This simple function takes a value, adds 2 to it, and returns that new value.
Just as Nipype interfaces have inputs and outputs, Python functions have inputs, in the form of parameters or arguments, and outputs, in the form of their return values. When you define a Function interface object with an existing function, as in the case of `add_two()` above, you must pass the constructor information about the function's inputs, its outputs, and the function itself. For example,

```
from nipype.interfaces.utility import Function
add_two_interface = Function(input_names=["val"],
                             output_names=["out_val"],
                             function=add_two)
```

Then you can set the inputs and run just as you would with any other interface:

```
add_two_interface.inputs.val = 2
res = add_two_interface.run()
print res.outputs.out_val
```

Which would print `4`.
Note that, if you are working interactively, the Function interface is unable to use functions that are defined within your interpreter session. (Specifically, it can't use functions that live in the `__main__` namespace).

1.10.2 Using External Packages

Chances are, you will want to write functions that do more complicated processing, particularly using the growing stack of Python packages geared towards neuroimaging, such as Nibabel, Nipy, or PyMVPA.
While this is completely possible (and, indeed, an intended use of the Function interface), it does come with one important constraint. The function code you write is executed in a standalone environment, which means that any external functions or classes you use have to be imported within the function itself:

```
def get_n_trs(in_file):
    import nibabel
    f = nibabel.load(in_file)
    return f.shape[-1]
```

Without explicitly importing Nibabel in the body of the function, this would fail.
Alternatively, it is possible to provide a list of strings corresponding to the imports needed to execute a function as a parameter of the *Function* constructor. This allows for the use of external functions that do not import all external definitions inside the function body.

1.10.3 Hello World - Function interface in a workflow

Contributed by: Hänel Nikolaus Valentin
The following snippet of code demonstrates the use of the function interface in the context of a workflow. Note the use of `import os` within the function as well as returning the absolute path from the Hello function. The *import* inside is necessary because functions are coded as strings and do not have to be on the PYTHONPATH. However any function called by this function has to be available on the PYTHONPATH. The *absolute path* is necessary because all workflow nodes are executed in their own directory and therefore there is no way of determining that the input file came from a different directory:

```
import nipype.pipeline.engine as pe
from nipype.interfaces.utility import Function

def Hello():
   import os
   from nipype import logging
   iflogger = logging.getLogger('interface')
   message = "Hello "
   file_name =  'hello.txt'
   iflogger.info(message)
   with open(file_name, 'w') as fp:
       fp.write(message)
   return os.path.abspath(file_name)

def World(in_file):
   from nipype import logging
```

```
        iflogger = logging.getLogger('interface')
        message = "World!"
        iflogger.info(message)
        with open(in_file, 'a') as fp:
            fp.write(message)

    hello = pe.Node(name='hello',
                    interface=Function(input_names=[],
                                       output_names=['out_file'],
                                       function=Hello))
    world = pe.Node(name='world',
                    interface=Function(input_names=['in_file'],
                                       output_names=[],
                                       function=World))

    pipeline = pe.Workflow(name='nipype_demo')
    pipeline.connect([(hello, world, [('out_file', 'in_file')])])
    pipeline.run()
    pipeline.write_graph(graph2use='flat')
```

1.10.4 Advanced Use

To use an existing function object (as we have been doing so far) with a Function interface, it must be passed to the constructor. However, it is also possible to dynamically set how a Function interface will process its inputs using the special `function_str` input.
This input takes not a function object, but actually a single string that can be parsed to define a function. In the equivalent case to our example above, the string would be

```
    add_two_str = "def add_two(val):\n    return val + 2\n"
```

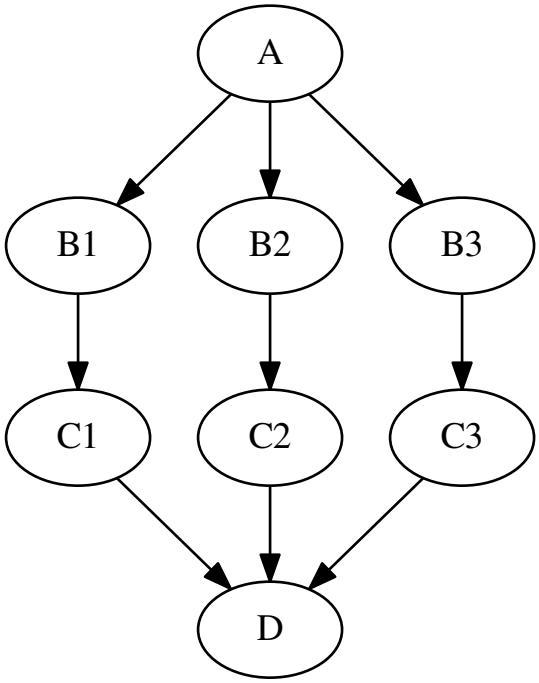
Unlike when using a function object, this input can be set like any other, meaning that you could write a function that outputs different function strings depending on some run-time contingencies, and connect that output the the `function_str` input of a downstream Function interface.

1.11 JoinNode, synchronize and itersource

The previous MapNode, iterfield, and iterables explained chapter described how to fork and join nodes using MapNode and iterables. In this chapter, we introduce features which build on these concepts to add workflow flexibility.

1.11.1 JoinNode, joinsource and joinfield

A `nipype.pipeline.engine.JoinNode` generalizes MapNode to operate in conjunction with an upstream iterable node to reassemble downstream results, e.g.:



The code to achieve this is as follows:

```
import nipype.pipeline.engine as pe
a = pe.Node(interface=A(), name="a")
b = pe.Node(interface=B(), name="b")
b.iterables = ("in_file", images)
c = pe.Node(interface=C(), name="c")
d = pe.JoinNode(interface=D(), joinsource="b",
                joinfield="in_files", name="d")

my_workflow = pe.Workflow(name="my_workflow")
my_workflow.connect([(a,b,[('subject','subject')]),
                     (b,c,[('out_file','in_file')])
                     (c,d,[('out_file','in_files')])
                     ])
```

This example assumes that interface "A" has one output *subject*, interface "B" has two inputs *subject* and *in_file* and one output *out_file*, interface "C" has one input *in_file* and one output *out_file*, and interface D has one list input *in_files*. The *images* variable is a list of three input image file names.
As with *iterables* and the MapNode *iterfield*, the *joinfield* can be a list of fields. Thus, the declaration in the previous example is equivalent to the following:

```
d = pe.JoinNode(interface=D(), joinsource="b",
                joinfield=["in_files"], name="d")
```

The *joinfield* defaults to all of the JoinNode input fields, so the declaration is also equivalent to the following:

```
d = pe.JoinNode(interface=D(), joinsource="b", name="d")
```

In this example, the node "c" *out_file* outputs are collected into the JoinNode "d" *in_files* input list. The *in_files* order is the same as the upstream "b" node iterables order.

The JoinNode input can be filtered for unique values by specifying the *unique* flag, e.g.:

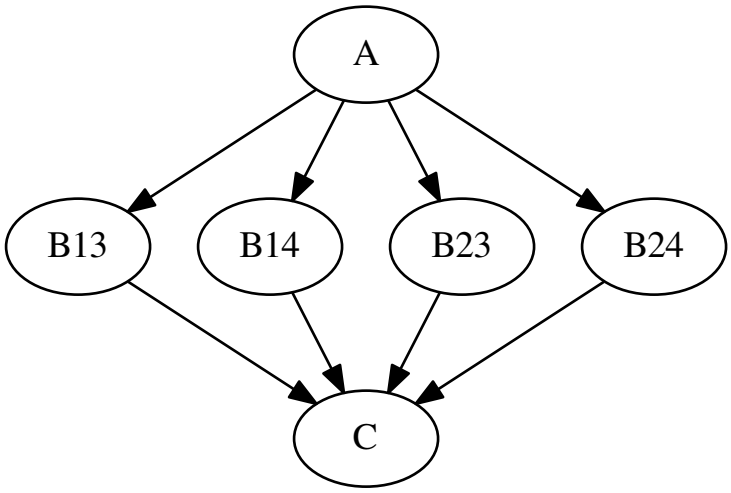
```
d = pe.JoinNode(interface=D(), joinsource="b", unique=True, name="d")
```

1.11.2 synchronize

The `nipype.pipeline.engine.Node` *iterables* parameter can be be a single field or a list of fields. If it is a list, then execution is performed over all permutations of the list items. For example:

```
b.iterables = [("m", [1, 2]), ("n", [3, 4])]
```

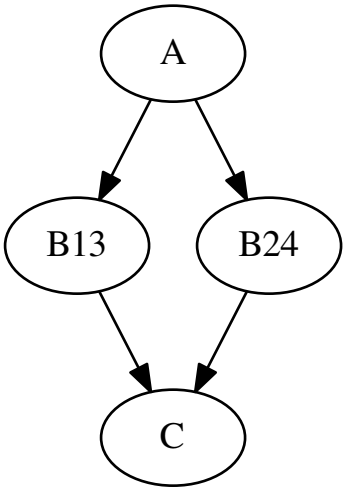
results in the execution graph:



where "B13" has inputs $m = 1$, $n = 3$, "B14" has inputs $m = 1$, $n = 4$, etc.
The *synchronize* parameter synchronizes the iterables lists, e.g.:

```
b.iterables = [("m", [1, 2]), ("n", [3, 4])]
b.synchronize = True
```

results in the execution graph:



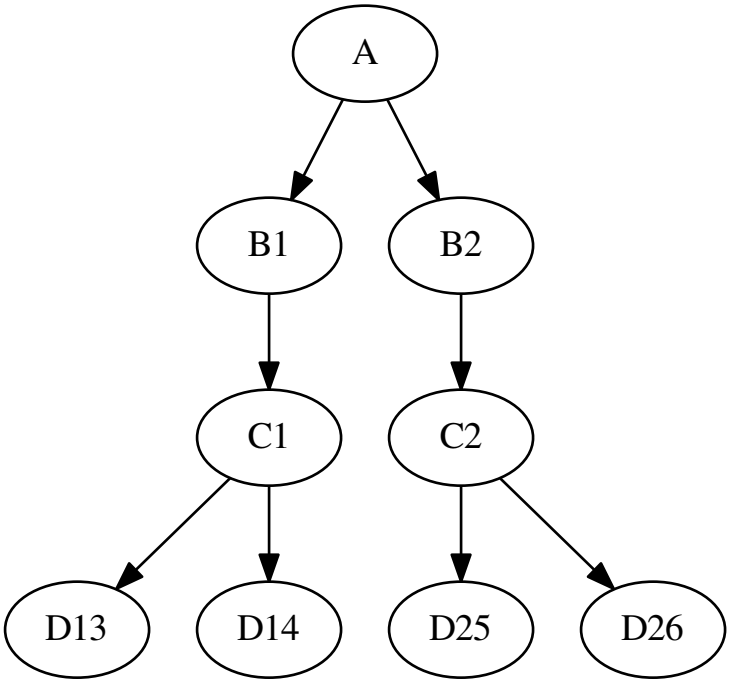
where the iterable inputs are selected in lock-step by index, i.e.:
(*m*, *n*) = (1, 3) and (2, 4)
for "B13" and "B24", resp.

1.11.3 itersource

The *itersource* feature allows you to expand a downstream iterable based on a mapping of an upstream iterable. For example:

```
a = pe.Node(interface=A(), name="a")
b = pe.Node(interface=B(), name="b")
b.iterables = ("m", [1, 2])
c = pe.Node(interface=C(), name="c")
d = pe.Node(interface=D(), name="d")
d.itersource = ("b", "m")
d.iterables = [("n", {1:[3,4], 2:[5,6]})]
my_workflow = pe.Workflow(name="my_workflow")
my_workflow.connect([(a,b,[('out_file','in_file')]),
                     (b,c,[('out_file','in_file')])
                     (c,d,[('out_file','in_file')])
                     ])
```

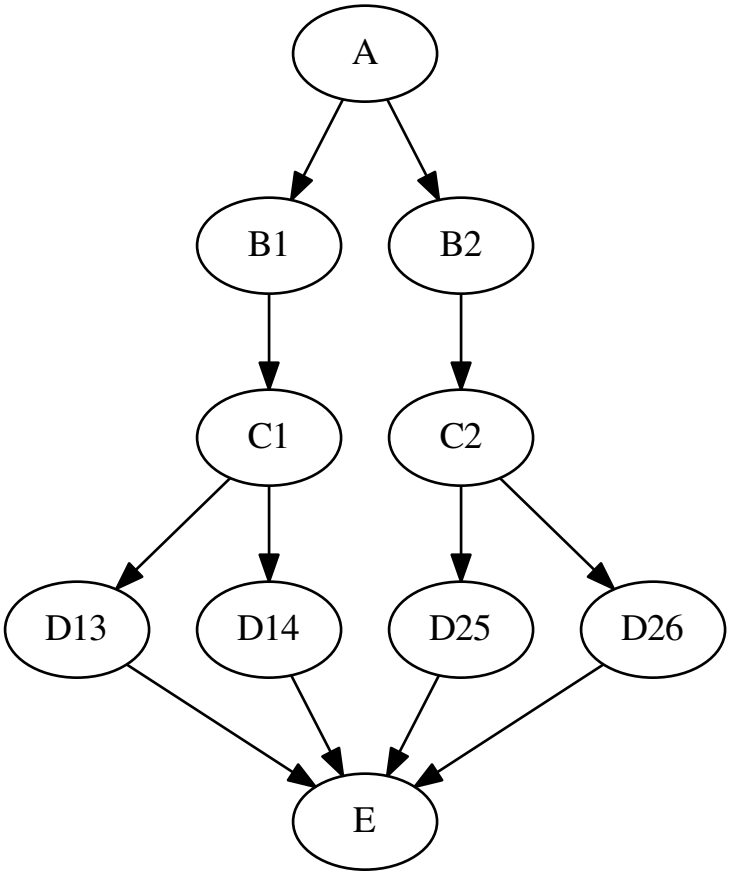
results in the execution graph:



In this example, all interfaces have input *in_file* and output *out_file*. In addition, interface "B" has input *m* and interface "D" has input *n*. A Python dictionary associates the "b" node input value with the downstream "d" node *n* iterable values.
This example can be extended with a summary JoinNode:

```
e = pe.JoinNode(interface=E(), joinsource="d",
                joinfield="in_files", name="e")
my_workflow.connect(d, 'out_file',
                    e, 'in_files')
```

resulting in the graph:



The combination of iterables, MapNode, JoinNode, synchronize and itersource enables the creation of arbitrarily complex workflow graphs. The astute workflow builder will recognize that this flexibility is both a blessing and a curse. These advanced features are handy additions to the Nipype toolkit when used judiciously.

1.12 Model Specification for First Level fMRI Analysis

Nipype provides a general purpose model specification mechanism with specialized subclasses for package specific extensions.

1.12.1 General purpose model specification

The `SpecifyModel` provides a generic mechanism for model specification. A mandatory input called subject_info provides paradigm specification for each run corresponding to a subject. This has to be in the form of a `Bunch` or a list of Bunch objects (one for each run). Each Bunch object contains the following attribules.

Required for most designs

- 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 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

An example Bunch definition:

```
from nipype.interfaces.base import Bunch
condnames = ['Tapping', 'Speaking', 'Yawning']
event_onsets = [[0, 10, 50], [20, 60, 80], [30, 40, 70]]
durations = [[0],[0],[0]]

subject_info = Bunch(conditions=condnames,
                                    onsets = event_onsets,
                                    durations = durations)
```

Alternatively, you can provide condition, onset, duration and amplitude 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.run<anything else> e.g.: Words.run001.txt. The event_name part will be used to create the condition names. Words.run001.txt may look like:

```
# Word Onsets Durations
 0   10
 20   10
 ...
```

or with amplitudes:

```
# Word Onsets Durations Amplitudes
0    10     1
20   10    1
...
```

Together with this information, one needs to specify:

- whether the durations and event onsets are specified in terms of scan volumes or secs.
- the high-pass filter cutoff,
- the repetition time per scan
- functional data files corresponding to each run.

Optionally you can specify realignment parameters, outlier indices. Outlier files should contain a list of numbers, one per row indicating which scans should not be included in the analysis. The numbers are 0-based.

1.12.2 SPM specific attributes

in addition to the generic specification options, several SPM specific options can be provided. In particular, the subject_info function can provide temporal and parametric modulators in the Bunch attributes tmod and pmod. The following example adds a linear parametric modulator for speaking rate for the events specified earlier:

```
pmod = [None, Bunch(name=['Rate'], param=[[.300, .500, .600]],
                                    poly=[1]), None]
```

```
subject_info = Bunch(conditions=condnames,
                                    onsets = event_onsets,
                                    durations = durations,
                                    pmod = pmod)
```

`SpecifySPMModel` also allows specifying additional components. If you have a study with multiple runs, you can choose to concatenate conditions from different runs. by setting the input option **concatenate_runs** to True. You can also choose to set the output options for this class to be in terms of 'scans'.

1.12.3 Sparse model specification

In addition to standard models, `SpecifySparseModel` allows model generation for sparse and sparse-clustered acquisition experiments. Details of the model generation and utility are provided in Ghosh et al. (2009) OHBM 2009.

1.13 Saving Workflows and Nodes to a file (experimental)

On top of the standard way of saving (i.e. serializing) objects in Python (see pickle) Nipype provides methods to turn Workflows and nodes into human readable code. This is useful if you want to save a Workflow that you have generated on the fly for future use.
To generate Python code for a Workflow use the export method:

```
from nipype.interfaces.fsl import BET, ImageMaths
from nipype.pipeline.engine import Workflow, Node, MapNode, format_node
from nipype.interfaces.utility import Function, IdentityInterface

bet = Node(BET(), name='bet')
bet.iterables = ('frac', [0.3, 0.4])

bet2 = MapNode(BET(), name='bet2', iterfield=['infile'])
bet2.iterables = ('frac', [0.4, 0.5])

maths = Node(ImageMaths(), name='maths')

def testfunc(in1):
    """dummy func
    """
    out = in1 + 'foo' + "out1"
    return out

funcnode = Node(Function(input_names=['a'], output_names=['output'], function=testfunc),
                name='testfunc')
funcnode.inputs.in1 = '-sub'
func = lambda x: x

inode = Node(IdentityInterface(fields=['a']), name='inode')

wf = Workflow('testsave')
wf.add_nodes([bet2])
wf.connect(bet, 'mask_file', maths, 'in_file')
wf.connect(bet2, ('mask_file', func), maths, 'in_file2')
wf.connect(inode, 'a', funcnode, 'in1')
wf.connect(funcnode, 'output', maths, 'op_string')

wf.export()
```

This will create a file "outputtestsave.py" with the following content:

```
from nipype.pipeline.engine import Workflow, Node, MapNode
from nipype.interfaces.utility import IdentityInterface
from nipype.interfaces.utility import Function
from nipype.utils.misc import getsource
from nipype.interfaces.fsl.preprocess import BET
from nipype.interfaces.fsl.utils import ImageMaths
# Functions
func = lambda x: x
# Workflow
testsave = Workflow("testsave")
# Node: testsave.inode
inode = Node(IdentityInterface(fields=['a'], mandatory_inputs=True), name="inode")
# Node: testsave.testfunc
testfunc = Node(Function(input_names=['a'], output_names=['output']), name="testfunc")
def testfunc_1(in1):
    """dummy func
    """
    out = in1 + 'foo' + "out1"
    return out

testfunc.inputs.function_str = getsource(testfunc_1)
testfunc.inputs.ignore_exception = False
testfunc.inputs.in1 = '-sub'
testsave.connect(inode, "a", testfunc, "in1")
# Node: testsave.bet2
bet2 = MapNode(BET(), iterfield=['infile'], name="bet2")
bet2.iterables = ('frac', [0.4, 0.5])
bet2.inputs.environ = {'FSLOUTPUTTYPE': 'NIFTI_GZ'}
bet2.inputs.ignore_exception = False
bet2.inputs.output_type = 'NIFTI_GZ'
bet2.inputs.terminal_output = 'stream'
# Node: testsave.bet
bet = Node(BET(), name="bet")
bet.iterables = ('frac', [0.3, 0.4])
bet.inputs.environ = {'FSLOUTPUTTYPE': 'NIFTI_GZ'}
bet.inputs.ignore_exception = False
bet.inputs.output_type = 'NIFTI_GZ'
bet.inputs.terminal_output = 'stream'
# Node: testsave.maths
maths = Node(ImageMaths(), name="maths")
maths.inputs.environ = {'FSLOUTPUTTYPE': 'NIFTI_GZ'}
maths.inputs.ignore_exception = False
maths.inputs.output_type = 'NIFTI_GZ'
maths.inputs.terminal_output = 'stream'
testsave.connect(bet2, ('mask_file', func), maths, "in_file2")
testsave.connect(bet, "mask_file", maths, "in_file")
testsave.connect(testfunc, "output", maths, "op_string")
```

The file is ready to use and includes all the necessary imports.

1.14 Using SPM with MATLAB Common Runtime

In order to use the standalone MCR version of spm, you need to ensure that the following commands are executed at the beginning of your script:

```
from nipype.interfaces import spm
matlab_cmd = '/path/to/run_spm8.sh /path/to/Compiler_Runtime/v713/ script'
spm.SPMCommand.set_mlab_paths(matlab_cmd=matlab_cmd, use_mcr=True)
```

you can test by calling:

```
spm.SPMCommand().version
```

If you want to enforce the standalone MCR version of spm for nipype globally, you can do so by setting the following environment variables:

SPMMCRCMD Specifies the command to use to run the spm standalone MCR version. You may still override the command as described above.

FORCE_SPMMCR Set this to any value in order to enforce the use of spm standalone MCR version in nipype globally. Technically, this sets the *use_mcr* flag of the spm interface to True.

Information about the MCR version of SPM8 can be found at:
http://en.wikibooks.org/wiki/SPM/Standalone

1.15 Using MIPAV, JIST, and CBS Tools

If you are trying to use MIPAV, JIST or CBS Tools interfaces you need to configure CLASSPATH environmental variable correctly. It needs to include extensions shipped with MIPAV, MIPAV itself and MIPAV plugins. For example:

In order to use the standalone MCR version of spm, you need to ensure that the following commands are executed at the beginning of your script:

```
# location of additional JAVA libraries to use
JAVALIB=/Applications/mipav/jre/Contents/Home/lib/ext/

# location of the MIPAV installation to use
MIPAV=/Applications/mipav
# location of the plugin installation to use
# please replace 'ThisUser' by your user name
PLUGINS=/Users/ThisUser/mipav/plugins

export CLASSPATH=$JAVALIB/*:$MIPAV:$MIPAV/lib/*:$PLUGINS
```

1.16 Running Nipype Interfaces from the command line (nipype_cmd)

The primary use of Nipype is to build automated non-interactive pipelines. However, sometimes there is a need to run some interfaces quickly from the command line. This is especially useful when running Interfaces wrapping code that does not have command line equivalents (nipy or SPM). Being able to run Nipype interfaces opens new possibilities such as inclusion of SPM processing steps in bash scripts.

To run Nipype Interafces you need to use the nipype_cmd tool that should already be installed. The tool allows you to list Interfaces available in a certain package:

```
$nipype_cmd nipype.interfaces.nipy

Available Interfaces:
    SpaceTimeRealigner
    Similarity
    ComputeMask
    FitGLM
    EstimateContrast
    FmriRealign4d
```

After selecting a particular Interface you can learn what inputs it requires:

```
$nipype_cmd nipype.interfaces.nipy ComputeMask --help
```

```
usage:nipype_cmd nipype.interfaces.nipy ComputeMask [-h] [--M M] [--cc CC]
                                                     [--ignore_exception IGNORE_EXCEPTION]
                                                     [--m M]
                                                     [--reference_volume REFERENCE_VOLUME]
                                                     mean_volume

Run ComputeMask

positional arguments:
  mean_volume           mean EPI image, used to compute the threshold for the
                        mask

optional arguments:
  -h, --help            show this help message and exit
  --M M                 upper fraction of the histogram to be discarded
  --cc CC               Keep only the largest connected component
  --ignore_exception IGNORE_EXCEPTION
                        Print an error message instead of throwing an
                        exception in case the interface fails to run
  --m M                 lower fraction of the histogram to be discarded
  --reference_volume REFERENCE_VOLUME
                        reference volume used to compute the mask. If none is
                        give, the mean volume is used.
```

Finally you can run run the Interface:

```
$nipype_cmd nipype.interfaces.nipy ComputeMask mean.nii.gz
```

All that from the command line without having to start python interpreter manually.

1.17 Using Nipype with Amazon Web Services (AWS)

Several groups have been successfully using Nipype on AWS. This procedure involves setting a temporary cluster using StarCluster and potentially transferring files to/from S3. The latter is supported by Nipype through DataSink and S3DataGrabber.

1.17.1 Using DataSink with S3

The DataSink class now supports sending output data directly to an AWS S3 bucket. It does this through the introduction of several input attributes to the DataSink interface and by parsing the *base_directory* attribute. This class uses the boto3 and botocore Python packages to interact with AWS. To configure the DataSink to write data to S3, the user must set the `base_directory` property to an S3-style filepath. For example:

```
import nipype.interfaces.io as nio
ds = nio.DataSink()
ds.inputs.base_directory = 's3://mybucket/path/to/output/dir'
```

With the "s3://" prefix in the path, the DataSink knows that the output directory to send files is on S3 in the bucket "mybucket". "path/to/output/dir" is the relative directory path within the bucket "mybucket" where output data will be uploaded to (NOTE: if the relative path specified contains folders that don't exist in the bucket, the DataSink will create them). The DataSink treats the S3 base directory exactly as it would a local directory, maintaining support for containers, substitutions, subfolders, "." notation, etc to route output data appropriately. There are four new attributes introduced with S3-compatibility: `creds_path`, `encrypt_bucket_keys`, `local_copy`, and `bucket`.

```
ds.inputs.creds_path = '/home/user/aws_creds/credentials.csv'
ds.inputs.encrypt_bucket_keys = True
ds.local_copy = '/home/user/workflow_outputs/local_backup'
```

`creds_path` is a file path where the user's AWS credentials file (typically a csv) is stored. This credentials file should contain the AWS access key id and secret access key and should be formatted as one of the following (these formats are how Amazon provides the credentials file by default when first downloaded).
Root-account user:

```
AWSAccessKeyID=ABCDEFGHIJKLMNOP
AWSSecretKey=zyx123wvu456/ABC890+gHiJk
```

IAM-user:

```
User Name,Access Key Id,Secret Access Key
"username",ABCDEFGHIJKLMNOP,zyx123wvu456/ABC890+gHiJk
```

The `creds_path` is necessary when writing files to a bucket that has restricted access (almost no buckets are publicly writable). If `creds_path` is not specified, the DataSink will check the `AWS_ACCESS_KEY_ID` and `AWS_SECRET_ACCESS_KEY` environment variables and use those values for bucket access.
`encrypt_bucket_keys` is a boolean flag that indicates whether to encrypt the output data on S3, using server-side AES-256 encryption. This is useful if the data being output is sensitive and one desires an extra layer of security on the data. By default, this is turned off.
`local_copy` is a string of the filepath where local copies of the output data are stored in addition to those sent to S3. This is useful if one wants to keep a backup version of the data stored on their local computer. By default, this is turned off.
`bucket` is a boto3 Bucket object that the user can use to overwrite the bucket specified in their `base_directory`. This can be useful if one has to manually create a bucket instance on their own using special credentials (or using a mock server like fakes3). This is typically used for developers unit-testing the DataSink class. Most users do not need to use this attribute for actual workflows. This is an optional argument.
Finally, the user needs only to specify the input attributes for any incoming data to the node, and the outputs will be written to their S3 bucket.

```
workflow.connect(inputnode, 'subject_id', ds, 'container')
workflow.connect(realigner, 'realigned_files', ds, 'motion')
```

So, for example, outputs for sub001's realigned_file1.nii.gz will be in: s3://mybucket/path/to/output/dir/sub001/motion/realigned_file1.nii.gz

1.17.2 Using S3DataGrabber

Coming soon...

CHAPTER 2

Changes in Nipype

2.1 Upcoming release 0.13

2.2 Release 0.12.1 (August 3, 2016)

- FIX: runtime profiling is optional and off by default (https://github.com/nipy/nipype/pull/1561)
- TST: circle CI tests run with docker (https://github.com/nipy/nipype/pull/1541)
- FIX: workflow export functions without import error (https://github.com/nipy/nipype/pull/1552)

2.3 Release 0.12.0 (July 12, 2016)

- ENH: New interface for Bruker to Nifti converter (https://github.com/nipy/nipype/pull/1523)
- FIX: output file naming for FIRST outputs (https://github.com/nipy/nipype/pull/1524)
- ENH: Adds *fslmaths -Tstd* to maths interfaces (https://github.com/nipy/nipype/pull/1518)
- FIX: Selecting "gamma" in FSL Level1Design now does what the name says (https://github.com/nipy/nipype/pull/1500)
- ENH: Added grad_dev input to fsl.dti.bedpostx5 interface(https://github.com/nipy/nipype/pull/1493)
- ENH: ResourceMultiProc plugin to support resource allocation (https://github.com/nipy/nipype/pull/1372)
- ENH: Added dcm2niix interface (https://github.com/nipy/nipype/pull/1435)
- ENH: Add nipype_crash_search command (https://github.com/nipy/nipype/pull/1422)
- ENH: Created interface for BrainSuite Cortical Surface Extraction command line tools (https://github.com/nipy/nipype/pull/1305)
- FIX: job execution on systems/approaches where locale is undefined (https://github.com/nipy/nipype/pull/1401)
- FIX: Clean up byte/unicode issues using subprocess (https://github.com/nipy/nipype/pull/1394)
- FIX: Prevent crash when tvtk is loaded - ETS_TOOLKIT=null (https://github.com/nipy/nipype/pull/973)
- **ENH: New interfaces in dipy: RESTORE, EstimateResponseSH, CSD and StreamlineTractography** (https://github.com/nipy/nipype/pull/1090)
- **ENH: Added interfaces of AFNI (https://github.com/nipy/nipype/pull/1360,** https://github.com/nipy/nipype/pull/1361, https://github.com/nipy/nipype/pull/1382)
- ENH: Provides a Nipype wrapper for antsJointFusion (https://github.com/nipy/nipype/pull/1351)
- ENH: Added support for PETPVC (https://github.com/nipy/nipype/pull/1335)
- ENH: Merge S3DataSink into DataSink, added AWS documentation (https://github.com/nipy/nipype/pull/1316)
- TST: Cache APT in CircleCI (https://github.com/nipy/nipype/pull/1333)
- ENH: Add new flags to the BRAINSABC for new features (https://github.com/nipy/nipype/pull/1322)
- ENH: Provides a Nipype wrapper for ANTs DenoiseImage (https://github.com/nipy/nipype/pull/1291)
- FIX: Minor bugfix logging hash differences (https://github.com/nipy/nipype/pull/1298)
- FIX: Use released Prov python library (https://github.com/nipy/nipype/pull/1279)
- ENH: Support for Python 3 (https://github.com/nipy/nipype/pull/1221)
- FIX: VTK version check missing when using tvtk (https://github.com/nipy/nipype/pull/1219)
- ENH: Added an OAR scheduler plugin (https://github.com/nipy/nipype/pull/1259)
- ENH: New ANTs interface: antsBrainExtraction (https://github.com/nipy/nipype/pull/1231)

- API: Default model level for the bedpostx workflow has been set to "2" following FSL 5.0.9 lead
- ENH: New interfaces for interacting with AWS S3: S3DataSink and S3DataGrabber (https://github.com/nipy/nipype/pull/1201)
- ENH: Interfaces for MINC tools (https://github.com/nipy/nipype/pull/1304)
- FIX: Use realpath to determine hard link source (https://github.com/nipy/nipype/pull/1388)
- FIX: Correct linking/copying fallback behavior (https://github.com/nipy/nipype/pull/1391)
- ENH: Nipype workflow and interfaces for FreeSurfer's recon-all (https://github.com/nipy/nipype/pull/1326)
- FIX: Permit relative path for concatenated_file input to Concatenate() (https://github.com/nipy/nipype/pull/1411)
- ENH: Makes ReconAll workflow backwards compatible with FreeSurfer 5.3.0 (https://github.com/nipy/nipype/pull/1434)
- **ENH: Added interfaces for AFNI 3dDegreeCentrality, 3dECM, 3dLFCD, 3dClipLevel, 3dmask_tool, and 3dSeg** (https://github.com/nipy/nipype/pull/1460)

2.4 Release 0.11.0 (September 15, 2015)

- API: Change how hash values are computed (https://github.com/nipy/nipype/pull/1174)
- **ENH: New algorithm: mesh.WarpPoints applies displacements fields to point sets** (https://github.com/nipy/nipype/pull/889).
- ENH: New interfaces for MRTrix3 (https://github.com/nipy/nipype/pull/1126)
- ENH: New option in afni.3dRefit - zdel, ydel, zdel etc. (https://github.com/nipy/nipype/pull/1079)
- FIX: ants.Registration composite transform outputs are no longer returned as lists (https://github.com/nipy/nipype/pull/1183)
- **BUG: ANTs Registration interface failed with multi-modal inputs** (https://github.com/nipy/nipype/pull/1176) (https://github.com/nipy/nipype/issues/1175)
- ENH: dipy.TrackDensityMap interface now accepts a reference image (https://github.com/nipy/nipype/pull/1091)
- FIX: Bug in XFibres5 (https://github.com/nipy/nipype/pull/1168)
- **ENH: Attempt to use hard links for data sink.** (https://github.com/nipy/nipype/pull/1161)
- **FIX: Updates to SGE Plugins** (https://github.com/nipy/nipype/pull/1129)
- **ENH: Add ants JointFusion() node with testing** (https://github.com/nipy/nipype/pull/1160)
- **ENH: Add –float option for antsRegistration calls** (https://github.com/nipy/nipype/pull/1159)
- **ENH: Added interface to simulate DWIs using the multi-tensor model** (https://github.com/nipy/nipype/pull/1085)
- ENH: New interface for FSL fslcpgeom utility (https://github.com/nipy/nipype/pull/1152)
- ENH: Added SLURMGraph plugin for submitting jobs to SLURM with dependencies (https://github.com/nipy/nipype/pull/1136)
- **FIX: Enable absolute path definitions in DCMStack (https://github.com/nipy/nipype/pull/1089,** replaced by https://github.com/nipy/nipype/pull/1093)
- **ENH: New mesh.MeshWarpMaths to operate on surface-defined warpings** (https://github.com/nipy/nipype/pull/1016)
- **FIX: Refactor P2PDistance, change name to ComputeMeshWarp, add regression tests,** fix bug in area weighted distance, and added optimizations (https://github.com/nipy/nipype/pull/1016)
- ENH: Add an option not to resubmit Nodes that finished running when using SGEGraph (https://github.com/nipy/nipype/pull/1002)
- FIX: FUGUE is now properly listing outputs. (https://github.com/nipy/nipype/pull/978)
- **ENH: Improved FieldMap-Based (FMB) workflow for correction of susceptibility distortions in EPI seqs.** (https://github.com/nipy/nipype/pull/1019)
- FIX: In the FSLXcommand _list_outputs function fixed for loop range (https://github.com/nipy/nipype/pull/1071)
- ENH: Dropped support for now 7 years old Python 2.6 (https://github.com/nipy/nipype/pull/1069)
- FIX: terminal_output is not mandatory anymore (https://github.com/nipy/nipype/pull/1070)
- ENH: Added "nipype_cmd" tool for running interfaces from the command line (https://github.com/nipy/nipype/pull/795)

- FIX: Fixed Camino output naming (https://github.com/nipy/nipype/pull/1061)
- ENH: Add the average distance to ErrorMap (https://github.com/nipy/nipype/pull/1039)
- ENH: Inputs with name_source can be now chained in cascade (https://github.com/nipy/nipype/pull/938)
- **ENH: Improve JSON interfaces: default settings when reading and consistent output creation** when writing (https://github.com/nipy/nipype/pull/1047)
- FIX: AddCSVRow problems when using infields (https://github.com/nipy/nipype/pull/1028)
- FIX: Removed unused ANTS registration flag (https://github.com/nipy/nipype/pull/999)
- FIX: Amend create_tbss_non_fa() workflow to match FSL's tbss_non_fa command. (https://github.com/nipy/nipype/pull/1033)
- FIX: remove unused mandatory flag from spm normalize (https://github.com/nipy/nipype/pull/1048)
- ENH: Update ANTSCorticalThickness interface (https://github.com/nipy/nipype/pull/1013)
- FIX: Edge case with sparsemodels and PEP8 cleanup (https://github.com/nipy/nipype/pull/1046)
- ENH: New io interfaces for JSON files reading/writing (https://github.com/nipy/nipype/pull/1020)
- ENH: Enhanced openfmri script to support freesurfer linkage (https://github.com/nipy/nipype/pull/1037)
- BUG: matplotlib is supposed to be optional (https://github.com/nipy/nipype/pull/1003)
- FIX: Fix split_filename behaviour when path has no file component (https://github.com/nipy/nipype/pull/1035)
- ENH: Updated FSL dtifit to include option for grad non-linearities (https://github.com/nipy/nipype/pull/1032)
- **ENH: Updated Camino tracking interfaces, which can now use FSL bedpostx output.** New options also include choice of tracker, interpolator, stepsize and curveinterval for angle threshold (https://github.com/nipy/nipype/pull/1029)
- FIX: Interfaces redirecting X crashed if $DISPLAY not defined (https://github.com/nipy/nipype/pull/1027)
- FIX: Bug crashed 'make api' (https://github.com/nipy/nipype/pull/1026)
- ENH: Updated antsIntroduction to handle RA and RI registrations (https://github.com/nipy/nipype/pull/1009)
- **ENH: Updated N4BiasCorrection input spec to include weight image and spline order. Made** argument formatting consistent. Cleaned ants.segmentation according to PEP8. (https://github.com/nipy/nipype/pull/990/files)
- ENH: SPM12 Normalize interface (https://github.com/nipy/nipype/pull/986)
- FIX: Utility interface test dir (https://github.com/nipy/nipype/pull/986)
- FIX: IPython engine directory reset after crash (https://github.com/nipy/nipype/pull/987)
- ENH: Resting state fMRI example with NiPy realignment and no SPM (https://github.com/nipy/nipype/pull/992)
- **FIX: Corrected Freesurfer SegStats _list_outputs to avoid error if summary_file is** undefined (issue #994)(https://https://github.com/nipy/nipype/pull/996)
- FIX: OpenfMRI support and FSL 5.0.7 changes (https://github.com/nipy/nipype/pull/1006)
- FIX: Output prefix in SPM Normalize with modulation (https://github.com/nipy/nipype/pull/1023)
- ENH: Usability improvements in cluster environments (https://github.com/nipy/nipype/pull/1025)
- ENH: ANTs JointFusion() (https://github.com/nipy/nipype/pull/1042)
- ENH: Added csvReader() utility (https://github.com/nipy/nipype/pull/1044)
- FIX: typo in nipype.interfaces.freesurfer.utils.py Tkregister2 (https://github.com/nipy/nipype/pull/1083)
- FIX: SSHDataGrabber outputs now return full path to the grabbed/downloaded files. (https://github.com/nipy/nipype/pull/1086)
- FIX: Add QA output for TSNR to resting workflow (https://github.com/nipy/nipype/pull/1088)
- FIX: Change N4BiasFieldCorrection to use short tag for dimensionality (backward compatible) (https://github.com/nipy/nipype/pull/1096)
- ENH: Added -newgrid input to Warp in AFNI (3dWarp wrapper) (https://github.com/nipy/nipype/pull/1128)
- FIX: Fixed AFNI Copy interface to use positional inputs as required (https://github.com/nipy/nipype/pull/1131)
- ENH: Added a check in Dcm2nii to check if nipype created the config.ini file and remove if true (https://github.com/nipy/nipype/pull/1132)
- **ENH: Use a while loop to wait for Xvfb (up to a max wait time "xvfb_max_wait" in config file, default 10)** (https://github.com/nipy/nipype/pull/1142)

2.5 Release 0.10.0 (October 10, 2014)

- **ENH: New miscelaneous interfaces: SplitROIs (mapper), MergeROIs (reducer)** to enable parallel processing of very large images.
- **ENH: Updated FSL interfaces: BEDPOSTX and XFibres, former interfaces are still** available with the version suffix: BEDPOSTX4 and XFibres4. Added gpu versions of BEDPOSTX: BEDPOSTXGPU, BEDPOSTX5GPU, and BEDPOSTX4GPU
- ENH: Added experimental support for MIPAV algorithms thorugh JIST plugins
- ENH: New dipy interfaces: Denoise, Resample
- ENH: New Freesurfer interfaces: Tkregister2 (for conversion of fsl style matrices to freesurfer format), MRIPretess
- ENH: New FSL interfaces: WarpPoints, WarpPointsToStd, EpiReg, ProbTrackX2, WarpUtils, ConvertWarp
- ENH: New miscelaneous interfaces: AddCSVRow, NormalizeProbabilityMapSet, AddNoise
- ENH: New AFNI interfaces: Eval, Means, SVMTest, SVMTrain
- **ENH: FUGUE interface has been refactored to use the name_template system, 3 examples** added to doctests, some bugs solved.
- **API: Interfaces to external packages are no longer available in the top-level** `nipype` namespace, and must be imported directly (e.g. `from nipype.interfaces import fsl`).
- **ENH: Support for elastix via a set of new interfaces: Registration, ApplyWarp,** AnalyzeWarp, PointsWarp, and EditTransform
- ENH: New ANTs interface: ApplyTransformsToPoints, LaplacianThickness
- ENH: New Diffusion Toolkit interface: TrackMerge
- ENH: New MRtrix interface: FilterTracks
- **ENH: New metrics group in algorithms. Now Distance, Overlap, and FuzzyOverlap** are found in nipype.algorithms.metrics instead of misc. Overlap interface extended to allow files containing multiple ROIs and volume physical units.
- ENH: New interface in algorithms.metrics: ErrorMap (a voxel-wise diff map).
- ENH: New FreeSurfer workflow: create_skullstripped_recon_flow()
- **ENH: Deep revision of workflows for correction of dMRI artifacts. New dmri_preprocessing** example.
- ENH: New data grabbing interface that works over SSH connections, SSHDataGrabber
- ENH: New color mode for write_graph
- ENH: You can now force MapNodes to be run serially
- ENH: Added ANTS based openfmri workflow
- ENH: MapNode now supports flattening of nested lists
- ENH: Support for headless mode using Xvfb
- ENH: nipype_display_crash has a debugging mode
- FIX: MRTrix tracking algorithms were ignoring mask parameters.
- FIX: FNIRT registration pathway and associated OpenFMRI example script
- FIX: spm12b compatibility for Model estimate
- FIX: Batch scheduler controls the number of maximum jobs properly
- FIX: Update for FSL 5.0.7 which deprecated Contrast Manager

2.6 Release 0.9.2 (January 31, 2014)

- FIX: DataFinder was broken due to a typo
- FIX: Order of DataFinder outputs was not guaranteed, it's human sorted now
- ENH: New interfaces: Vnifti2Image, VtoMat

2.7 Release 0.9.1 (December 25, 2013)

- FIX: installation issues

2.8 Release 0.9.0 (December 20, 2013)

- ENH: SelectFiles: a streamlined version of DataGrabber
- ENH: new tools for defining workflows: JoinNode, synchronize and itersource
- ENH: W3C PROV support with optional RDF export built into Nipype
- ENH: Added support for Simple Linux Utility Resource Management (SLURM)
- **ENH: AFNI interfaces refactor, prefix, suffix are replaced by** "flexible_%s_templates"
- **ENH: New SPM interfaces:**
  spm.ResliceToReference,
  spm.DicomImport
- **ENH: New AFNI interfaces:**
  afni.AFNItoNIFTI
  afni.TCorr1D
- **ENH: Several new interfaces related to Camino were added:**
  camino.SFPICOCalibData
  camino.Conmat
  camino.QBallMX
  camino.LinRecon
  camino.SFPeaks
  One outdated interface no longer part of Camino was removed: - camino.Conmap
- **ENH: Three new mrtrix interfaces were added:**
  mrtrix.GenerateDirections
  mrtrix.FindShPeaks
  mrtrix.Directions2Amplitude
- **ENH: New FSL interfaces:**
  fsl.PrepareFieldmap
  fsl.TOPUP
  fsl.ApplyTOPUP
  fsl.Eddy
- **ENH: New misc interfaces:**
  FuzzyOverlap,
  P2PDistance
- ENH: New workflows: nipype.workflows.dmri.fsl.epi.[fieldmap_correction&topup_correction]
- ENH: Added simplified outputname generation for command line interfaces.
- ENH: Allow ants use a single mask image
- ENH: Create configuration option for parameterizing directories with hashes
- ENH: arrange nodes by topological sort with disconnected subgraphs
- ENH: uses the nidm iri namespace for uuids
- ENH: remove old reporting webpage
- ENH: Added support for Vagrant
- API: 'name' is now a positional argument for Workflow, Node, and MapNode constructors
- API: SPM now defaults to SPM8 or SPM12b job format
- API: DataGrabber and SelectFiles use human (or natural) sort now
- **FIX: Several fixes related to Camino interfaces:**
  ProcStreamlines would ignore many arguments silently (target, waypoint, exclusion ROIS, etc.)
  DTLUTGen would silently round the "step", "snr" and "trace" parameters to integers
  PicoPDFs would not accept more than one lookup table
  PicoPDFs default pdf did not correspond to Camino default
  Track input model names were outdated (and would generate an error)
  Track numpds parameter could not be set for deterministic tractography
  FA created output files with erroneous extension
- FIX: Deals properly with 3d files in SPM Realign
- FIX: SPM with MCR fixed
- FIX: Cleaned up input and output spec metadata

- FIX: example openfmri script now makes the contrast spec a hashed input
- FIX: FILMGLS compatibility with FSL 5.0.5
- FIX: Freesurfer recon-all resume now avoids setting inputs
- FIX: File removal from node respects file associations img/hdr/mat, BRIK/HEAD

2.9 Release 0.8.0 (May 8, 2013)

- **ENH: New interfaces: nipy.Trim, fsl.GLM, fsl.SigLoss, spm.VBMSegment, fsl.InvWarp,** dipy.TensorMode
- ENH: Allow control over terminal output for commandline interfaces
- ENH: Added preliminary support for generating Python code from Workflows.
- **ENH: New workflows for dMRI and fMRI pre-processing: added motion artifact correction** with rotation of the B-matrix, and susceptibility correction for EPI imaging using fieldmaps. Updated eddy_correct pipeline to support both dMRI and fMRI, and new parameters.
- ENH: Minor improvements to FSL's FUGUE and FLIRT interfaces
- ENH: Added optional dilation of parcels in cmtk.Parcellate
- ENH: Interpolation mode added to afni.Resample
- **ENH: Function interface can accept a list of strings containing import statements** that allow external functions to run without their imports defined in the function body
- ENH: Allow node configurations to override master configuration
- FIX: SpecifyModel works with 3D files correctly now.

2.10 Release 0.7.0 (Dec 18, 2012)

- ENH: Add basic support for LSF plugin.
- **ENH: New interfaces: ICC, Meshfix, ants.Register, C3dAffineTool, ants.JacobianDeterminant,** afni.AutoTcorrelate, DcmStack
- ENH: New workflows: ants template building (both using 'ANTS' and the new 'antsRegistration')
- **ENH: New examples: how to use ANTS template building workflows (smri_ants_build_tmeplate),** how to set SGE specific options (smri_ants_build_template_new)
- ENH: added no_flatten option to Merge
- ENH: added versioning option and checking to traits
- ENH: added deprecation metadata to traits
- ENH: Slicer interfaces were updated to version 4.1

2.11 Release 0.6.0 (Jun 30, 2012)

- API: display variable no longer encoded as inputs in commandline interfaces
- ENH: input hash not modified when environment DISPLAY is changed
- ENH: support for 3d files for TSNR calculation
- ENH: Preliminary support for graph submission with SGE, PBS and Soma Workflow
- **ENH: New interfaces: MySQLSink, nipy.Similarity, WatershedBEM, MRIsSmooth,** NetworkBasedStatistic, Atropos, N4BiasFieldCorrection, ApplyTransforms, fs.MakeAverageSubject, epidewarp.fsl, WarpTimeSeriesImageMultiTransform, AVScale, mri_ms_LDA
- ENH: simple interfaces for spm
- FIX: CompCor component calculation was erroneous
- FIX: filename generation for AFNI and PRELUDE
- FIX: improved slicer module autogeneration
- FIX: added missing options for BBRegsiter
- FIX: functionality of remove_unnecessary_ouputs cleaned up
- FIX: local hash check works with appropriate inputs
- FIX: Captures all stdout from commandline programs

- FIX: Afni outputs should inherit from TraitedSpec

2.12 Release 0.5.3 (Mar 23, 2012)

- FIX: SPM model generation when output units is in scans

2.13 Release 0.5.2 (Mar 14, 2012)

- API: Node now allows specifying node level configuration for SGE/PBS clusters
- API: Logging to file is disabled by default
- API: New location of log file -> .nipype/nipype.cfg
- ENH: Changing logging options via config works for distributed processing
- FIX: Unittests on debian (logging and ipython)

2.14 Release 0.5 (Mar 10, 2012)

- API: FSL defaults to Nifti when OUTPUTTYPE environment variable not found
- API: By default inputs are removed from Node working directory
- API: InterfaceResult class is now versioned and stores class type not instance
- API: Added FIRST interface
- **API: Added max_jobs paramter to plugin_args. limits the number of jobs** executing at any given point in time
- API: crashdump_dir is now a config execution option
- **API: new config execution options for controlling hash checking, execution and** logging behavior when running in distributed mode.
- API: Node/MapNode has new attribute that allows it to run on master thread.
- API: IPython plugin now invokes IPython 0.11 or greater
- API: Canned workflows are now all under a different package structure
- API: SpecifyModel event_info renamed to event_files
- **API: DataGrabber is always being rerun (unless overwrite is set to False on** Node level)
- **API: "stop_on_first_rerun" does not stop for DataGrabber (unless overwrite is** set to True on Node level)
- **API: Output prefix can be set for spm nodes (SliceTiming, Realign, Coregister,** Normalize, Smooth)
- ENH: Added fsl resting state workflow based on behzadi 2007 CompCorr method.
- ENH: TSNR node produces mean and std-dev maps; allows polynomial detrending
- ENH: IdentityNodes are removed prior to execution
- ENH: Added Michael Notter's beginner's guide
- ENH: Added engine support for status callback functions
- ENH: SPM create warped node
- ENH: All underlying interfaces (including python ones) are now optional
- ENH: Added imperative programming option with Nodes and caching
- ENH: Added debug mode to configuration
- ENH: Results can be stored and loaded without traits exceptions
- ENH: Added concurrent log handler for distributed writing to log file
- ENH: Reporting can be turned off using config
- ENH: Added stats files to FreeSurferOutput
- ENH: Support for Condor through qsub emulation
- **ENH: IdentityNode with iterable expansion takes place after remaining Identity** Node removal
- ENH: Crashfile display script added
- ENH: Added FmriRealign4d node wrapped from nipy
- ENH: Added TBSS workflows and examples
- ENH: Support for openfmri data processing
- ENH: Package version check

- FIX: Fixed spm preproc workflow to cater to multiple functional runs
- FIX: Workflow outputs displays nodes with empty outputs
- FIX: SUSAN workflow works without usans
- FIX: SGE fixed for reading custom templates
- FIX: warping in SPM realign, Dartel and interpolation parameters
- FIX: Fixed voxel size parameter in freesurfer mri_convert
- FIX: 4D images in spm coregister
- FIX: Works around matlab tty bug
- FIX: Overwriting connection raises exception
- **FIX: Outputs are loaded from results and not stored in memory for during** distributed operation
- FIX: SPM threshold uses SPM.mat name and improved error detection
- FIX: Removing directory contents works even when a node has no outputs
- FIX: DARTEL workflows will run only when SPM 8 is available
- FIX: SPM Normalize estimate field fixed
- FIX: hashmethod argument now used for calculating hash of old file
- FIX: Modelgen now allows FSL style event files

2.15 Release 0.4.1 (Jun 16, 2011)

- Minor bugfixes

2.16 Release 0.4 (Jun 11, 2011)

- **API: Timestamp hashing does not use ctime anymore. Please update your hashes by** running workflows with updatehash=True option NOTE: THIS IS THE DEFAULT CONFIG NOW, so unless you updatehash, workflows will rerun
- **API: Workflow run function no longer supports (inseries, createdirsonly).** Functions used in connect string must be pickleable
- API: SPM EstimateContrast: ignore_derivs replaced by use_derivs
- API: All interfaces: added new config option ignore_exception
- **API: SpecifModel no longer supports (concatenate_runs, output_specs). high_pass_filter** cutoff is mandatory (even if its set to np.inf). Additional interfaces SpecifySPMModel and SpecifySparseModel support other types of data.
- API: fsl.DTIFit input "save" is now called "save_tensor"
- **API: All inputs of IdentityInterfaces are mandatory by default. You can turn** this off by specifying mandatory_inputs=False to the constructor.
- API: fsl FILMGLS input "autocorr_estimate" is now called "autocorr_estimate_only"
- **API: fsl ContrastMgr now requires access to specific files (no longer accepts** the result directory)
- **API: freesurfer.GLMFit input "surf" is now a boolean with three corresponding** inputs – subject_id, hemi, and surf_geo
- ENH: All commandline interfaces display stdout and stderr
- ENH: All interfaces raise exceptions on error with an option to suppress
- **ENH: Supports a plugin interface for execution (current support for multiprocessing,** IPython, SGE, PBS)
- ENH: MapNode runs in parallel under IPython, SGE, MultiProc, PBS
- ENH: Optionally allows keeping only required outputs
- **ENH: New interface: utility.Rename to change the name of files, optionally** using python string-formatting with inputs or regular expressions matching
- ENH: New interface: freesurfer.ApplyMask (mri_mask)
- ENH: New FSL interface – SwapDimensions (fslswapdim)
- ENH: Sparse models allow regressor scaling and temporal derivatives
- **ENH: Added support for the component parts of FSL's TBSS workflow (TBSSSkeleton** and DistanceMap)

- ENH: dcm2nii interface exposes bvals, bvecs, reoriented and cropped images
- **ENH: Added several higher-level interfaces to the fslmaths command:**
  ChangeDataType, Threshold, MeanImage, IsotropicSmooth, ApplyMask, TemporalFilter DilateImage, ErodeImage, SpatialFilter, UnaryMaths, BinaryMaths, MultiImageMaths
- ENH: added support for networx 1.4 and improved iterable expansion
- ENH: Replaced BEDPOSTX and EddyCurrent with nipype pipelines
- ENH: Ability to create a hierarchical dot file
- ENH: Improved debugging information for rerunning nodes
- ENH: Added 'stop_on_first_rerun' option
- ENH: Added support for Camino
- ENH: Added support for Camino2Trackvis
- ENH: Added support for Connectome Viewer
- BF: dcm2nii interface handles gzipped files correctly
- BF: FNIRT generates proper outputs
- BF: fsl.DTIFit now properly collects tensor volume
- BF: updatehash now removes old result hash file

2.17 Release 0.3.4 (Jan 12, 2011)

- API: hash values for float use a string conversion up to the 10th decimal place.
- API: Iterables in output path will always be generated as _var1_val1_var2_val2 pairs
- ENH: Added support to nipy: GLM fit, contrast estimation and calculating mask from EPI
- **ENH: Added support for manipulating surface files in Freesurfer:**
  projecting volume images onto the surface
  smoothing along the surface
  transforming a surface image from one subject to another
  using tksurfer to save pictures of the surface
- ENH: Added support for flash processing using FreeSurfer
- ENH: Added support for flirt matrix in BBRegister
- ENH: Added support for FSL convert_xfm
- ENH: hashes can be updated again without rerunning all nodes.
- ENH: Added multiple regression design for FSL
- ENH: Added SPM based Analyze to Nifti converter
- ENH: Added increased support for PyXNAT
- ENH: Added support for MCR-based binary version of SPM
- ENH: Added SPM node for calculating various threshold statistics
- ENH: Added distance and dissimilarity measurements
- BF: Diffusion toolkit gets installed
- **BF: Changed FNIRT interface to accept flexible lists (rather than 4-tuples)** on all options specific to different subsampling levels

2.18 Release 0.3.3 (Sep 16, 2010)

- API: subject_id in ModelSpec is now deprecated
- API: spm.Threshold - does not need mask, beta, RPV anymore - takes only one image (stat_image - mind the name change) - works with SPM2 SPM.mat - returns additional map - pre topological FDR
- ENH: Added support for Diffusion toolkit
- ENH: Added support for FSL slicer and overlay
- ENH: Added support for dcm2nii
- BF: DataSink properly handles lists of lists now
- BF: DataGrabber has option for raising Exception on getting empty lists
- BF: Traits logic for 'requires' metadata
- BF: allows workflows to be relocatable

- BF: nested workflows with connections don't raise connection not found error
- BF: multiple workflows with identical nodenames and iterables do not create nestsed workflows

2.19 Release 0.3.2 (Aug 03, 2010)

2.19.1 Enhancements

- all outputs from nodes are now pickled as part of workflow processing
- added git developer docs

2.19.2 Bugs fixed

- FreeSurfer
- Fixed bugs in SegStats doctest

2.20 Release 0.3.1 (Jul 29, 2010)

2.20.1 Bugs fixed

- FreeSurfer
- Fixed bugs in glmfit and concatenate
- Added group t-test to freesurfer tutorial

2.21 Release 0.3 (Jul 27, 2010)

2.21.1 Incompatible changes

- Complete redesign of the Interface class - heavy use of Traits.
- Changes in the engine API - added Workflow and MapNode. Compulsory name argument.

2.21.2 Features added

- General:
- Type checking of inputs and outputs using Traits from ETS.
- Support for nested workflows.
- Preliminary Slicer and AFNI support.
- New flexible DataGrabber node.
- AtlasPick and Threshold nodes.
- Preliminary support for XNAT.
- Doubled number of the tutorials.
- FSL:
- Added DTI processing nodes (note that TBSS nodes are still experimental).
- Recreated FEAT workflow.
- SPM:
- Added New Segment and many other nodes.
- Redesigned second level analysis.
- Developer

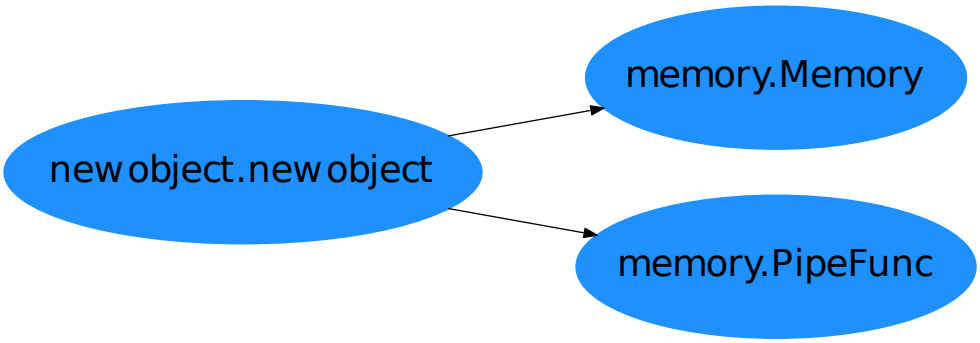
API

Release 0.12.1
Date August 04, 2016, 00:17 PDT

3.1 caching.memory

3.1.1 Module: caching.memory

Inheritance diagram for nipype.caching.memory:



Using nipype with persistence and lazy recomputation but without explicit name-steps pipeline: getting back scope in command-line based programming.

Change directory to provide relative paths for doctests >>> import os >>> filepath = os.path.dirname(os.path.realpath(__file__)) >>> datadir = os.path.realpath(os.path.join(filepath, '../testing/data')) >>> os.chdir(datadir)

3.1.2 Classes

Memory

class nipype.caching.memory.**Memory**(*base_dir*)

Bases: future.types.newobject.newobject

Memory context to provide caching for interfaces

Parameters **base_dir: string** :

The directory name of the location for the caching

Methods

cache(interface)	Returns a callable that caches the output of an interface
clear_previous_runs([warn])	Remove all the cache that where not used in the latest run of the memory object: i.e.
clear_previous_runs([warn])	Remove all the cache that where not used in the latest run of the memory object: i.e.

__init__(*base_dir*)

cache(*interface*)

Returns a callable that caches the output of an interface

Parameters **interface: nipype interface** :

The nipype 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 nipype.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')
```

We can retrieve the resulting file from the outputs: >>> results.outputs.merged_file # doctest: +SKIP '...'

clear_previous_runs(*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(*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

next()

PipeFunc

class nipype.caching.memory.**PipeFunc**(*interface*, *base_dir*, *callback=None*)

Bases: future.types.newobject.newobject

Callable interface to nipype.interface objects

Use this to wrap nipype.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

`__call__`(**kwargs)
next()

__init__ (*interface*, *base_dir*, *callback=None*)

Parameters **interface: a nipype 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.

next ()

3.1.3 Functions

nipype.caching.memory.**read_log** (*filename*, *run_dict=None*)

nipype.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

3.2 interfaces.base

3.2.1 Module: interfaces.base

Inheritance diagram for nipype.interfaces.base:

Package contains interfaces for using existing functionality in other packages
Exaples FSL, matlab/SPM , afni
Requires Packages to be installed

3.2.2 Classes

BaseInterface

class nipype.interfaces.base.**BaseInterface**(***inputs*)

Bases: *nipype.interfaces.base.Interface*

Implements common interface functionality.

Attributes

output_spec

Methods

aggregate_outputs([runtime, needed_outputs])	Collate expected outputs and check for existence
help([returnhelp])	Prints class help
input_spec	alias of *BaseInterfaceInputSpec*
next()	
run(**inputs)	Execute this interface.

__init__(***inputs*)

aggregate_outputs(*runtime=None*, *needed_outputs=None*)

Collate expected outputs and check for existence

always_run

can_resume

classmethod help(*returnhelp=False*)

Prints class help

input_spec

alias of *BaseInterfaceInputSpec*

next()

output_spec = None

run(***inputs*)

Execute this interface.

This interface will not raise an exception if runtime.returncode is non-zero.

Parameters 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** :

version

BaseInterfaceInputSpec

class nipype.interfaces.base.**BaseInterfaceInputSpec**(***kwargs*)

Bases: *nipype.interfaces.base.TraitedSpec*

Methods

add_class_trait(name, *trait)	Adds a named trait attribute to this class.
add_trait(name, *trait)	Adds a trait attribute to this object.
add_trait_category(category)	Adds a trait category to a class.
add_trait_listener(object[, prefix])	

Table 3.5 – continued from previous page

all_trait_names()	Returns the list of all trait names, including implicitly defined traits.
base_trait(name)	Returns the base trait definition for a trait attribute.
class_default_traits_view()	Returns the name of the default traits view for the class.
class_editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
class_trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
class_trait_view([name, view_element])	
class_trait_view_elements()	Returns the ViewElements object associated with the class.
class_traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
clone_traits([traits, memo, copy])	Clones a new object from this one, optionally copying only a specified set
configure_traits([filename, view, kind, ...])	Creates and displays a dialog box for editing values of trait attributes, as i
copy_traits(other[, traits, memo, copy])	Copies another object's trait attributes into this one.
copyable_trait_names(**metadata)	Returns the list of trait names to copy or clone by default.
default_traits_view()	Returns the name of the default traits view for the object's class.
edit_traits([view, parent, kind, context, ...])	Displays a user interface window for editing trait attribute values.
editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
get(**kwargs)	Returns traited class as a dict
get_hashval([hash_method])	Return a dictionary of our items with hashes for each file.
get_traitsfree(**kwargs)	Returns traited class as a dict
has_traits_interface(*interfaces)	Returns whether the object implements a specified traits interface.
items()	Name, trait generator for user modifiable traits
on_trait_change(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
on_trait_event(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
print_traits([show_help])	Prints the values of all explicitly-defined, non-event trait attributes on the
remove_trait(name)	Removes a trait attribute from this object.
remove_trait_listener(object[, prefix])	
reset_traits([traits])	Resets some or all of an object's trait attributes to their default values.
set([trait_change_notify])	Shortcut for setting object trait attributes.
set_trait_dispatch_handler(name, klass[, ...])	Sets a trait notification dispatch handler.
sync_trait(trait_name, object[, alias, ...])	Synchronizes the value of a trait attribute on this object with a trait attribu
trait(name[, force, copy])	Returns the trait definition for the *name* trait attribute.
trait_context()	Returns the default context to use for editing or configuring traits.
trait_get(*names, **metadata)	Shortcut for getting object trait attributes.
trait_items_event(event_trait,name,items_event)	
trait_monitor(handler[, remove])	Adds or removes the specified *handler* from the list of active monitors.
trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
trait_property_changed(...)	
trait_set([trait_change_notify])	Shortcut for setting object trait attributes.
trait_setq(**traits)	Shortcut for setting object trait attributes.
trait_subclasses([all])	Returns a list of the immediate (or all) subclasses of this class.
trait_view([name, view_element])	Gets or sets a ViewElement associated with an object's class.
trait_view_elements()	Returns the ViewElements object associated with the object's class.
trait_views([klass])	Returns a list of the names of all view elements associated with the curren
traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
traits_init()	
traits_inited([True])	
validate_trait(name, value)	Validates whether a value is legal for a trait.

__init__(***kwargs*)
Initialize handlers and inputs

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(*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().

add_trait_category(*category*)
Adds a trait category to a class.

add_trait_listener(*object*, *prefix=''*)

all_trait_names()
Returns the list of all trait names, including implicitly defined traits.

base_trait(*name*)
Returns the base trait definition for a trait attribute.
Parameters **name** : str
Name of the attribute whose trait definition is returned.

class_default_traits_view()
Returns the name of the default traits view for the class.

class_editable_traits()
Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current class.

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.

class_trait_view(*name=None*, *view_element=None*)

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.

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.

clone_traits(*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(*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.

copy_traits(*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(***metadata*)

Returns the list of trait names to copy or clone by default.

default_traits_view()

Returns the name of the default traits view for the object's class.

edit_traits(*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.

editable_traits()

Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current object.

get(***kwargs*)

Returns traited class as a dict

Augments the trait get function to return a dictionary without notification handles

get_hashval(*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 **dict_withhash** : dict

Copy of our dictionary with the new file hashes included with each file.

hashvalue : str

The md5 hash value of the traited spec

get_traitsfree(***kwargs*)

Returns traited 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_traits_interface(**interfaces*)

Returns whether the object implements a specified traits interface.

Parameters ***interfaces :** :

One or more traits Interface (sub)classes.

items()

Name, trait generator for user modifiable traits

on_trait_change(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

on_trait_event(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

print_traits(*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(*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(*object*, *prefix=''*)
reset_traits(*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(*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.
set_trait_dispatch_handler(*name*, *klass*, *override=False*)
Sets a trait notification dispatch handler.
sync_trait(*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(*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()
Returns the default context to use for editing or configuring traits.
trait_get(**names*, ***metadata*)
Shortcut for getting object trait attributes.
Parameters **names** : list of strings
A list of trait attribute names whose values are requested.
Returns **result** : dict

A dictionary whose keys are the names passed as arguments and whose values are the corresponding trait values.

trait_items_event(*event_trait*, *name*, *items_event*)

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(***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(*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(***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.

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(*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()

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(*klass=None*)

Returns a list of the names of all view elements associated with the current object's class.

Parameters **klass** : class
A class, such that all returned names must correspond to instances of this class. Possible values include:
Group
Item

View
ViewElement
ViewSubElement

traits(***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(*name*, *value*)
Validates whether a value is legal for a trait.
Returns the validated value if it is valid.

wrappers = {'new': <class 'traits.trait_notifiers.NewTraitChangeNotifyWrapper'>, 'ui': <class 'traits.trait_notifier

BaseTraitedSpec

class nipype.interfaces.base.**BaseTraitedSpec**(***kwargs*)
Bases: traits.has_traits.HasTraits
Provide a few methods necessary to support nipype interface api
The inputs attribute of interfaces call certain methods that are not available in traits.HasTraits. These are provided here.
new metadata:

usedefault : set this to True if the default value of the trait should be used. Unless this is set, the attributes are set to traits.Undefined
new attribute:

get_hashval : returns a tuple containing the state of the trait as a dict and hashvalue corresponding to dict.
XXX Reconsider this in the long run, but it seems like the best solution to move forward on the refactoring.

Methods

add_class_trait(name, *trait)	Adds a named trait attribute to this class.
add_trait(name, *trait)	Adds a trait attribute to this object.
add_trait_category(category)	Adds a trait category to a class.
add_trait_listener(object[, prefix])	
all_trait_names()	Returns the list of all trait names, including implicitly defined traits.
base_trait(name)	Returns the base trait definition for a trait attribute.
class_default_traits_view()	Returns the name of the default traits view for the class.
class_editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
class_trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
class_trait_view([name, view_element])	
class_trait_view_elements()	Returns the ViewElements object associated with the class.
class_traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
clone_traits([traits, memo, copy])	Clones a new object from this one, optionally copying only a specified set
configure_traits([filename, view, kind, ...])	Creates and displays a dialog box for editing values of trait attributes, as i
copy_traits(other[, traits, memo, copy])	Copies another object's trait attributes into this one.
copyable_trait_names(**metadata)	Returns the list of trait names to copy or clone by default.
default_traits_view()	Returns the name of the default traits view for the object's class.
edit_traits([view, parent, kind, context, ...])	Displays a user interface window for editing trait attribute values.
editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu

Table 3.6 – continued from previous page

get(**kwargs)	Returns traited class as a dict
get_hashval([hash_method])	Return a dictionary of our items with hashes for each file.
get_traitsfree(**kwargs)	Returns traited class as a dict
has_traits_interface(*interfaces)	Returns whether the object implements a specified traits interface.
items()	Name, trait generator for user modifiable traits
on_trait_change(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
on_trait_event(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
print_traits([show_help])	Prints the values of all explicitly-defined, non-event trait attributes on the
remove_trait(name)	Removes a trait attribute from this object.
remove_trait_listener(object[, prefix])	
reset_traits([traits])	Resets some or all of an object's trait attributes to their default values.
set([trait_change_notify])	Shortcut for setting object trait attributes.
set_trait_dispatch_handler(name, klass[, ...])	Sets a trait notification dispatch handler.
sync_trait(trait_name, object[, alias, ...])	Synchronizes the value of a trait attribute on this object with a trait attribu
trait(name[, force, copy])	Returns the trait definition for the *name* trait attribute.
trait_context()	Returns the default context to use for editing or configuring traits.
trait_get(*names, **metadata)	Shortcut for getting object trait attributes.
trait_items_event(event_trait,name,items_event)	
trait_monitor(handler[, remove])	Adds or removes the specified *handler* from the list of active monitors.
trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
trait_property_changed(...)	
trait_set([trait_change_notify])	Shortcut for setting object trait attributes.
trait_setq(**traits)	Shortcut for setting object trait attributes.
trait_subclasses([all])	Returns a list of the immediate (or all) subclasses of this class.
trait_view([name, view_element])	Gets or sets a ViewElement associated with an object's class.
trait_view_elements()	Returns the ViewElements object associated with the object's class.
trait_views([klass])	Returns a list of the names of all view elements associated with the curren
traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
traits_init()	
traits_inited([True])	
validate_trait(name, value)	Validates whether a value is legal for a trait.

__init__(***kwargs*)
Initialize handlers and inputs

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(*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().

add_trait_category(*category*)
Adds a trait category to a class.

add_trait_listener(*object*, *prefix=''*)

all_trait_names()

Returns the list of all trait names, including implicitly defined traits.

base_trait(*name*)

Returns the base trait definition for a trait attribute.

Parameters **name** : str

Name of the attribute whose trait definition is returned.

class_default_traits_view()

Returns the name of the default traits view for the class.

class_editable_traits()

Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current class.

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.

class_trait_view(*name=None*, *view_element=None*)

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.

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.

clone_traits(*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(*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.

copy_traits(*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(***metadata*)
Returns the list of trait names to copy or clone by default.

default_traits_view()
Returns the name of the default traits view for the object's class.

edit_traits(*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.

editable_traits()
Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current object.

get(***kwargs*)
Returns traited class as a dict
Augments the trait get function to return a dictionary without notification handles

get_hashval(*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 dict_withhash : dict
Copy of our dictionary with the new file hashes included with each file.

hashvalue : str
The md5 hash value of the traited spec

get_traitsfree(***kwargs*)
Returns traited 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_traits_interface(**interfaces*)
Returns whether the object implements a specified traits interface.

Parameters *interfaces : :
One or more traits Interface (sub)classes.

items()
Name, trait generator for user modifiable traits

on_trait_change(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

on_trait_event(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

print_traits(*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(*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(*object*, *prefix=''*)
reset_traits(*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(*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.

set_trait_dispatch_handler(*name*, *klass*, *override=False*)
Sets a trait notification dispatch handler.

sync_trait(*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(*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()
Returns the default context to use for editing or configuring traits.

trait_get(**names*, ***metadata*)
Shortcut for getting object trait attributes.

Parameters names : list of strings
A list of trait attribute names whose values are requested.

Returns result : dict
A dictionary whose keys are the names passed as arguments and whose values are the corresponding trait values.

trait_items_event(*event_trait*, *name*, *items_event*)

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(***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(*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(***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.

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(*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()

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(*klass=None*)

Returns a list of the names of all view elements associated with the current object's class.

Parameters **klass** : class
A class, such that all returned names must correspond to instances of this class. Possible values include:
Group
Item
View
ViewElement
ViewSubElement

traits(***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(*name*, *value*)

Validates whether a value is legal for a trait.

Returns the validated value if it is valid.

wrappers = {'new': <class 'traits.trait_notifiers.NewTraitChangeNotifyWrapper'>, 'ui': <class 'traits.trait_notifie

Bunch

class nipype.interfaces.base.**Bunch**(**args*, ***kwargs*)

Bases: future.types.newobject.newobject

Dictionary-like class that provides attribute-style access to it's items.

A *Bunch* is a simple container that stores it's items as class attributes. Internally all items are stored in a dictionary and the class exposes several of the dictionary methods.

Notes

The Bunch pattern came from the Python Cookbook:

Examples

```
>>> from nipype.interfaces.base import Bunch
>>> inputs = Bunch(infile='subj.nii', fwhm=6.0, register_to_mean=True)
>>> inputs
Bunch(fwhm=6.0, infile='subj.nii', register_to_mean=True)
>>> inputs.register_to_mean = False
>>> inputs
Bunch(fwhm=6.0, infile='subj.nii', register_to_mean=False)
```

Methods

dictcopy()	returns a deep copy of existing Bunch as a dictionary
get(*args)	Support dictionary get() functionality
items()	iterates over bunch attributes as key, value pairs
iteritems()	iterates over bunch attributes as key, value pairs
next()	
set(**kwargs)	Support dictionary get() functionality
update(*args, **kwargs)	update existing attribute, or create new attribute

__init__(**args*, ***kwargs*)

dictcopy()
: returns a deep copy of existing Bunch as a dictionary

get(**args*)
: Support dictionary get() functionality

items()
: iterates over bunch attributes as key, value pairs

iteritems()
: iterates over bunch attributes as key, value pairs

next()

set(***kwargs*)
: Support dictionary get() functionality

update(**args*, ***kwargs*)
: update existing attribute, or create new attribute
Note: update is very much like HasTraits.set

CommandLine

class nipype.interfaces.base.**CommandLine**(*command=None*, ***inputs*)

Bases: *nipype.interfaces.base.BaseInterface*

Implements functionality to interact with command line programs class must be instantiated with a com-

mand 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 nipype.interfaces.base import CommandLine
>>> cli = CommandLine(command='ls', environ={'DISPLAY': ':1'})
>>> cli.inputs.args = '-al'
>>> cli.cmdline
'ls -al'
```

```
>>> pprint.pprint(cli.inputs.trait_get())
{'args': '-al',
 'environ': {'DISPLAY': ':1'},
 'ignore_exception': False,
 'terminal_output': 'stream'}
```

```
>>> cli.inputs.get_hashval()
([('args', '-al')], '11c37f97649cd61627f4afe5136af8c0')
```

Attributes

output_spec

Methods

aggregate_outputs([runtime, needed_outputs])	Collate expected outputs and check for existence
help([returnhelp])	
input_spec	alias of *CommandLineInputSpec*
next()	
raise_exception(runtime)	
run(**inputs)	Execute this interface.
set_default_terminal_output(output_type)	Set the default terminal output for CommandLine Interfaces.
version_from_command([flag])	

__init__(*command=None*, ***inputs*)
aggregate_outputs(*runtime=None*, *needed_outputs=None*)
Collate expected outputs and check for existence
always_run
can_resume
cmd
sets base command, immutable
cmdline
command plus any arguments (args) validates arguments and generates command line
classmethod help(*returnhelp=False*)
input_spec
alias of *CommandLineInputSpec*
next()

output_spec = None
raise_exception(*runtime*)
run(***inputs*)
Execute this interface.
This interface will not raise an exception if runtime.returncode is non-zero.
Parameters 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 :
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>.inputs.terminal_output.
version
version_from_command(*flag='-v'*)

CommandLineInputSpec

class nipype.interfaces.base.**CommandLineInputSpec**(***kwargs*)
Bases: *nipype.interfaces.base.BaseInterfaceInputSpec*

Methods

add_class_trait(name, *trait)	Adds a named trait attribute to this class.
add_trait(name, *trait)	Adds a trait attribute to this object.
add_trait_category(category)	Adds a trait category to a class.
add_trait_listener(object[, prefix])	
all_trait_names()	Returns the list of all trait names, including implicitly defined traits.
base_trait(name)	Returns the base trait definition for a trait attribute.
class_default_traits_view()	Returns the name of the default traits view for the class.
class_editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
class_trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
class_trait_view([name, view_element])	
class_trait_view_elements()	Returns the ViewElements object associated with the class.
class_traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
clone_traits([traits, memo, copy])	Clones a new object from this one, optionally copying only a specified set
configure_traits([filename, view, kind, ...])	Creates and displays a dialog box for editing values of trait attributes, as i
copy_traits(other[, traits, memo, copy])	Copies another object's trait attributes into this one.
copyable_trait_names(**metadata)	Returns the list of trait names to copy or clone by default.
default_traits_view()	Returns the name of the default traits view for the object's class.
edit_traits([view, parent, kind, context, ...])	Displays a user interface window for editing trait attribute values.
editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
get(**kwargs)	Returns traited class as a dict
get_hashval([hash_method])	Return a dictionary of our items with hashes for each file.
get_traitsfree(**kwargs)	Returns traited class as a dict
has_traits_interface(*interfaces)	Returns whether the object implements a specified traits interface.
items()	Name, trait generator for user modifiable traits
on_trait_change(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
on_trait_event(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
print_traits([show_help])	Prints the values of all explicitly-defined, non-event trait attributes on the
remove_trait(name)	Removes a trait attribute from this object.

Table 3.10 – continued from previous page

remove_trait_listener(object[, prefix])	
reset_traits([traits])	Resets some or all of an object's trait attributes to their default values.
set([trait_change_notify])	Shortcut for setting object trait attributes.
set_trait_dispatch_handler(name, klass[, ...])	Sets a trait notification dispatch handler.
sync_trait(trait_name, object[, alias, ...])	Synchronizes the value of a trait attribute on this object with a trait attribu
trait(name[, force, copy])	Returns the trait definition for the *name* trait attribute.
trait_context()	Returns the default context to use for editing or configuring traits.
trait_get(*names, **metadata)	Shortcut for getting object trait attributes.
trait_items_event(event_trait,name,items_event)	
trait_monitor(handler[, remove])	Adds or removes the specified *handler* from the list of active monitors.
trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
trait_property_changed(...)	
trait_set([trait_change_notify])	Shortcut for setting object trait attributes.
trait_setq(**traits)	Shortcut for setting object trait attributes.
trait_subclasses([all])	Returns a list of the immediate (or all) subclasses of this class.
trait_view([name, view_element])	Gets or sets a ViewElement associated with an object's class.
trait_view_elements()	Returns the ViewElements object associated with the object's class.
trait_views([klass])	Returns a list of the names of all view elements associated with the curren
traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
traits_init()	
traits_inited([True])	
validate_trait(name, value)	Validates whether a value is legal for a trait.

__init__(***kwargs*)
Initialize handlers and inputs

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(*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().

add_trait_category(*category*)
Adds a trait category to a class.

add_trait_listener(*object*, *prefix=''*)

all_trait_names()
Returns the list of all trait names, including implicitly defined traits.

base_trait(*name*)
Returns the base trait definition for a trait attribute.

Parameters **name** : str
Name of the attribute whose trait definition is returned.

class_default_traits_view()
Returns the name of the default traits view for the class.

class_editable_traits()
Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current class.

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.

class_trait_view(*name=None*, *view_element=None*)

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.

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.

clone_traits(*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(*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.

copy_traits(*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(***metadata*)
Returns the list of trait names to copy or clone by default.

default_traits_view()
Returns the name of the default traits view for the object's class.

edit_traits(*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.

editable_traits()

Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current object.

get(***kwargs*)

Returns traited class as a dict

Augments the trait get function to return a dictionary without notification handles

get_hashval(*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 dict_withhash : dict

Copy of our dictionary with the new file hashes included with each file.

hashvalue : str

The md5 hash value of the traited spec

get_traitsfree(***kwargs*)

Returns traited 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_traits_interface(**interfaces*)

Returns whether the object implements a specified traits interface.

Parameters *interfaces : :

One or more traits Interface (sub)classes.

items()

Name, trait generator for user modifiable traits

on_trait_change(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

on_trait_event(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

print_traits(*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(*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(*object*, *prefix=''*)

reset_traits(*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(*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.

set_trait_dispatch_handler(*name*, *klass*, *override=False*)

Sets a trait notification dispatch handler.

sync_trait(*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(*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()

Returns the default context to use for editing or configuring traits.

trait_get(**names*, ***metadata*)

Shortcut for getting object trait attributes.

Parameters **names** : list of strings
A list of trait attribute names whose values are requested.
Returns **result** : dict
A dictionary whose keys are the names passed as arguments and whose values are the corresponding trait values.

trait_items_event(*event_trait*, *name*, *items_event*)

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(***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(*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(***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.

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(*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()
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(*klass=None*)
Returns a list of the names of all view elements associated with the current object's class.

Parameters **klass** : class
A class, such that all returned names must correspond to instances of this class. Possible values include:
Group
Item
View
ViewElement
ViewSubElement

traits(***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(*name*, *value*)
Validates whether a value is legal for a trait.
Returns the validated value if it is valid.

wrappers = {'new': <class 'traits.trait_notifiers.NewTraitChangeNotifyWrapper'>, 'ui': <class 'traits.trait_notifier

DynamicTraitedSpec

class nipype.interfaces.base.**DynamicTraitedSpec**(***kwargs*)
Bases: *nipype.interfaces.base.BaseTraitedSpec*
A subclass to handle dynamic traits
This class is a workaround for add_traits and clone_traits not functioning well together.

Methods

Table 3.11 – continued from previous page

add_class_trait(name, *trait)	Adds a named trait attribute to this class.
add_trait(name, *trait)	Adds a trait attribute to this object.
add_trait_category(category)	Adds a trait category to a class.
add_trait_listener(object[, prefix])	
all_trait_names()	Returns the list of all trait names, including implicitly defined traits.
base_trait(name)	Returns the base trait definition for a trait attribute.
class_default_traits_view()	Returns the name of the default traits view for the class.
class_editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
class_trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
class_trait_view([name, view_element])	
class_trait_view_elements()	Returns the ViewElements object associated with the class.
class_traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
clone_traits([traits, memo, copy])	Clones a new object from this one, optionally copying only a specified set
configure_traits([filename, view, kind, ...])	Creates and displays a dialog box for editing values of trait attributes, as i
copy_traits(other[, traits, memo, copy])	Copies another object's trait attributes into this one.
copyable_trait_names(**metadata)	Returns the list of trait names to copy or clone by default.
default_traits_view()	Returns the name of the default traits view for the object's class.
edit_traits([view, parent, kind, context, ...])	Displays a user interface window for editing trait attribute values.
editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
get(**kwargs)	Returns traited class as a dict
get_hashval([hash_method])	Return a dictionary of our items with hashes for each file.
get_traitsfree(**kwargs)	Returns traited class as a dict
has_traits_interface(*interfaces)	Returns whether the object implements a specified traits interface.
items()	Name, trait generator for user modifiable traits
on_trait_change(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
on_trait_event(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
print_traits([show_help])	Prints the values of all explicitly-defined, non-event trait attributes on the
remove_trait(name)	Removes a trait attribute from this object.
remove_trait_listener(object[, prefix])	
reset_traits([traits])	Resets some or all of an object's trait attributes to their default values.
set([trait_change_notify])	Shortcut for setting object trait attributes.
set_trait_dispatch_handler(name, klass[, ...])	Sets a trait notification dispatch handler.
sync_trait(trait_name, object[, alias, ...])	Synchronizes the value of a trait attribute on this object with a trait attribu
trait(name[, force, copy])	Returns the trait definition for the *name* trait attribute.
trait_context()	Returns the default context to use for editing or configuring traits.
trait_get(*names, **metadata)	Shortcut for getting object trait attributes.
trait_items_event(event_trait,name,items_event)	
trait_monitor(handler[, remove])	Adds or removes the specified *handler* from the list of active monitors.
trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
trait_property_changed(...)	
trait_set([trait_change_notify])	Shortcut for setting object trait attributes.
trait_setq(**traits)	Shortcut for setting object trait attributes.
trait_subclasses([all])	Returns a list of the immediate (or all) subclasses of this class.
trait_view([name, view_element])	Gets or sets a ViewElement associated with an object's class.
trait_view_elements()	Returns the ViewElements object associated with the object's class.
trait_views([klass])	Returns a list of the names of all view elements associated with the curren
traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
traits_init()	
traits_inited([True])	

Table 3.11 – continued from previous page

validate_trait(name, value)	Validates whether a value is legal for a trait.

__init__(***kwargs*)
Initialize handlers and inputs

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(*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().

add_trait_category(*category*)
Adds a trait category to a class.

add_trait_listener(*object*, *prefix=''*)

all_trait_names()
Returns the list of all trait names, including implicitly defined traits.

base_trait(*name*)
Returns the base trait definition for a trait attribute.

Parameters **name** : str
Name of the attribute whose trait definition is returned.

class_default_traits_view()
Returns the name of the default traits view for the class.

class_editable_traits()
Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current class.

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.

class_trait_view(*name=None*, *view_element=None*)

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.

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.

clone_traits(*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`(*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.

`copy_traits`(*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(***metadata*)

Returns the list of trait names to copy or clone by default.

default_traits_view()

Returns the name of the default traits view for the object's class.

edit_traits(*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.

editable_traits()

Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current object.

get(***kwargs*)

Returns traited class as a dict

Augments the trait get function to return a dictionary without notification handles

get_hashval(*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 **dict_withhash** : dict

Copy of our dictionary with the new file hashes included with each file.

hashvalue : str

The md5 hash value of the traited spec

get_traitsfree(***kwargs*)

Returns traited 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_traits_interface(**interfaces*)

Returns whether the object implements a specified traits interface.

Parameters ***interfaces :** :

One or more traits Interface (sub)classes.

items()

Name, trait generator for user modifiable traits

on_trait_change(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

on_trait_event(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

print_traits(*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(*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(*object*, *prefix=''*)

reset_traits(*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(*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.

set_trait_dispatch_handler(*name*, *klass*, *override=False*)

Sets a trait notification dispatch handler.

sync_trait(*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(*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()
Returns the default context to use for editing or configuring traits.

trait_get(**names*, ***metadata*)
Shortcut for getting object trait attributes.

Parameters **names** : list of strings
A list of trait attribute names whose values are requested.

Returns **result** : dict
A dictionary whose keys are the names passed as arguments and whose values are the corresponding trait values.

trait_items_event(*event_trait*, *name*, *items_event*)

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(***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(*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(***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.

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(*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()

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(*klass=None*)

Returns a list of the names of all view elements associated with the current object's class.

Parameters **klass** : class

A class, such that all returned names must correspond to instances of this class. Possible values include:

Group

Item

View

ViewElement

ViewSubElement

traits(***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(*name*, *value*)

Validates whether a value is legal for a trait.

Returns the validated value if it is valid.

wrappers = {'new': <class 'traits.trait_notifiers.NewTraitChangeNotifyWrapper'>, 'ui': <class 'traits.trait_notifier

InputMultiPath

class nipype.interfaces.base.**InputMultiPath**(*trait=None*, *value=None*, *minlen=0*, *maxlen=9223372036854775807*, *items=True*, ***metadata*)

Bases: *nipype.interfaces.base.MultiPath*

Implements a user friendly traits that accepts one or more paths to files or directories. This is the input version which always returns a list. Default value of this trait is _Undefined. It does not accept empty lists. XXX This should only be used as a final resort. We should stick to established Traits to the extent possible. XXX This needs to be vetted by somebody who understands traits

```
>>> from nipype.interfaces.base import InputMultiPath
>>> class A(TraitedSpec):
...     foo = InputMultiPath(File(exists=False))
>>> a = A()
>>> a.foo
<undefined>
```

```
>>> a.foo = '/software/temp/foo.txt'
>>> a.foo
['/software/temp/foo.txt']
```

```
>>> a.foo = ['/software/temp/foo.txt']
>>> a.foo
['/software/temp/foo.txt']
```

```
>>> a.foo = ['/software/temp/foo.txt', '/software/temp/goo.txt']
>>> a.foo
['/software/temp/foo.txt', '/software/temp/goo.txt']
```

Attributes

editor
info_trait

Methods

__call__(*args, **kw)	Allows a derivative trait to be defined from this one.
as_ctrait()	Returns a CTrait corresponding to the trait defined by this class.
clone([default_value])	Clones the contents of this object into a new instance of the same class, and then modifies the cl
create_editor()	Returns the default UI editor for the trait.
error(object, name, value)	Raises a TraitError exception.
full_info(object, name, value)	Returns a description of the trait.
get_default_value()	Returns a tuple of the form: (*default_value_type*, *default_value*) which describes the default valu
get_editor([trait])	Returns a trait editor that allows the user to modify the *trait* trait.
get_value(object, name[, trait])	Returns the current value of a property-based trait.
info()	Must return a string describing the type of value accepted by the trait handler.
init()	Allows the trait to perform any additional initialization needed.
inner_traits()	Returns the *inner trait* (or traits) for this trait.
is_valid(object, name, value)	
items_event()	
repr(value)	Returns a printable representation of a value along with its type.
set_value(object, name, value)	Sets the cached value of a property-based trait and fires the appropriate trait change event.
validate(object, name, value)	

__init__(*trait=None*, *value=None*, *minlen=0*, *maxlen=9223372036854775807*, *items=True*, ***metadata*)

Returns a List trait.

Parameters **trait** : a trait or value that can be converted to a trait using Trait()

The type of item that the list contains. If not specified, the list can contain items of any type.

value : list

Default value for the list.

minlen : integer

The minimum length of a list that can be assigned to the trait.

maxlen : integer

The maximum length of a list that can be assigned to the trait.

The length of the list assigned to the trait must be such that:: :

minlen <= len(list) <= maxlen

as_ctrait()

Returns a CTrait corresponding to the trait defined by this class.

clone(*default_value=<missing>*, ***metadata*)

Clones the contents of this object into a new instance of the same class, and then modifies the cloned copy using the specified *default_value* and *metadata*. Returns the cloned object as the result.

Note that subclasses can change the signature of this method if needed, but should always call the 'super' method if possible.

create_editor()

Returns the default UI editor for the trait.

default_value = <undefined>

default_value_type = 5

editor = None

error(*object*, *name*, *value*)
Raises a TraitError exception.
Parameters **object** : object
The object whose attribute is being assigned.
name : str
The name of the attribute being assigned.
value : object
The proposed new value for the attribute.
full_info(*object*, *name*, *value*)
Returns a description of the trait.
get_default_value()
Returns a tuple of the form: (*default_value_type*, *default_value*) which describes the default value for this trait. The default implementation analyzes the value of the trait's **default_value** attribute and determines an appropriate *default_value_type* for *default_value*. If you need to override this method to provide a different result tuple, the following values are valid values for *default_value_type*:

0, 1: The *default_value* item of the tuple is the default value.

2: The object containing the trait is the default value.

3: A new copy of the list specified by *default_value* is the default value.

4: A new copy of the dictionary specified by *default_value* is the default value.

5: A new instance of TraitListObject constructed using the *default_value* list is the default value.

6: A new instance of TraitDictObject constructed using the *default_value* dictionary is the default value.

7: *default_value* is a tuple of the form: (*callable*, *args*, *kw*), where *callable* is a callable, *args* is a tuple, and *kw* is either a dictionary or None. The default value is the result obtained by invoking callable(*args, **kw).

8: *default_value* is a callable. The default value is the result obtained by invoking *default_value*(*object*), where *object* is the object containing the trait. If the trait has a validate() method, the validate() method is also called to validate the result.

9: A new instance of TraitSetObject constructed using the *default_value* set is the default value.
get_editor(*trait=None*)
Returns a trait editor that allows the user to modify the *trait* trait.
Parameters **trait** : Trait
The trait to be edited.
get_value(*object*, *name*, *trait=None*)
Returns the current value of a property-based trait.
has_items = False
info()
Must return a string describing the type of value accepted by the trait handler.
The string should be a phrase describing the type defined by the TraitHandler subclass, rather than a complete sentence. For example, use the phrase, "a square sprocket" instead of the sentence, "The value must be a square sprocket." The value returned by info() is combined with other information whenever an error occurs and therefore makes more sense to the user if the result is a phrase. The info() method is similar in purpose and use to the **info** attribute of a validator function.
Note that the result can include information specific to the particular trait handler instance. For example, TraitRange instances return a string indicating the range of values acceptable to the handler

(e.g., "an integer in the range from 1 to 9"). If the info() method is not overridden, the default method returns the value of the 'info_text' attribute.

info_text = 'a legal value'

info_trait = None

init()

Allows the trait to perform any additional initialization needed.

inner_traits()

Returns the *inner trait* (or traits) for this trait.

is_mapped = False

is_valid(*object*, *name*, *value*)

items_event()

metadata = {}

repr(*value*)

Returns a printable representation of a value along with its type.

Deprecated since version 3.0.3: This functionality was only used to provide readable error messages. This functionality has been incorporated into TraitError itself.

Parameters **value** : object

The value to be printed.

set_value(*object*, *name*, *value*)

Sets the cached value of a property-based trait and fires the appropriate trait change event.

validate(*object*, *name*, *value*)

Interface

class nipype.interfaces.base.**Interface**(***inputs*)

Bases: future.types.newobject.newobject

This is an abstract definition for Interface objects.

It provides no functionality. It defines the necessary attributes and methods all Interface objects should have.

Attributes

input_spec
output_spec

Methods

aggregate_outputs([runtime, needed_outputs])	Called to populate outputs
help()	Prints class help
next()	
run()	Execute the command.

__init__(***inputs*)

Initialize command with given args and inputs.

aggregate_outputs(*runtime=None*, *needed_outputs=None*)

Called to populate outputs

always_run

can_resume

classmethod help()

Prints class help

input_spec = None

next()

output_spec = None
run()
Execute the command.
version

InterfaceResult

class nipype.interfaces.base.**InterfaceResult**(*interface*, *runtime*, *inputs=None*, *outputs=None*, *provenance=None*)
Bases: future.types.newobject.newobject
Object that contains the results of running a particular Interface.

Attributes

MpiCommandLine

class nipype.interfaces.base.**MpiCommandLine**(*command=None*, ***inputs*)
Bases: *nipype.interfaces.base.CommandLine*
Implements functionality to interact with command line programs that can be run with MPI (i.e. using 'mpiexec').

Examples

```
>>> from nipype.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'
```

Attributes

---

output_spec

Methods

aggregate_outputs([runtime, needed_outputs])	Collate expected outputs and check for existence
help([returnhelp])	
input_spec	alias of *MpiCommandLineInputSpec*
next()	
raise_exception(runtime)	
run(**inputs)	Execute this interface.
set_default_terminal_output(output_type)	Set the default terminal output for CommandLine Interfaces.
version_from_command([flag])	

__init__(*command=None*, ***inputs*)

aggregate_outputs(*runtime=None*, *needed_outputs=None*)
Collate expected outputs and check for existence
always_run
can_resume
cmd
sets base command, immutable
cmdline
Adds 'mpiexec' to begining of command
help(*returnhelp=False*)
input_spec
alias of *MpiCommandLineInputSpec*
next()
output_spec = None
raise_exception(*runtime*)
run(***inputs*)
Execute this interface.
This interface will not raise an exception if runtime.returncode is non-zero.
Parameters 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 :
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>.inputs.terminal_output.
version
version_from_command(*flag='-v'*)

MpiCommandLineInputSpec

class nipype.interfaces.base.**MpiCommandLineInputSpec**(***kwargs*)
Bases: *nipype.interfaces.base.CommandLineInputSpec*

Methods

add_class_trait(name, *trait)	Adds a named trait attribute to this class.
add_trait(name, *trait)	Adds a trait attribute to this object.
add_trait_category(category)	Adds a trait category to a class.
add_trait_listener(object[, prefix])	
all_trait_names()	Returns the list of all trait names, including implicitly defined traits.
base_trait(name)	Returns the base trait definition for a trait attribute.
class_default_traits_view()	Returns the name of the default traits view for the class.
class_editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
class_trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
class_trait_view([name, view_element])	
class_trait_view_elements()	Returns the ViewElements object associated with the class.
class_traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
clone_traits([traits, memo, copy])	Clones a new object from this one, optionally copying only a specified set
configure_traits([filename, view, kind, ...])	Creates and displays a dialog box for editing values of trait attributes, as i
copy_traits(other[, traits, memo, copy])	Copies another object's trait attributes into this one.
copyable_trait_names(**metadata)	Returns the list of trait names to copy or clone by default.
default_traits_view()	Returns the name of the default traits view for the object's class.

Table 3.19 – continued from previous page

edit_traits([view, parent, kind, context, ...])	Displays a user interface window for editing trait attribute values.
editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
get(**kwargs)	Returns traited class as a dict
get_hashval([hash_method])	Return a dictionary of our items with hashes for each file.
get_traitsfree(**kwargs)	Returns traited class as a dict
has_traits_interface(*interfaces)	Returns whether the object implements a specified traits interface.
items()	Name, trait generator for user modifiable traits
on_trait_change(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
on_trait_event(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
print_traits([show_help])	Prints the values of all explicitly-defined, non-event trait attributes on the
remove_trait(name)	Removes a trait attribute from this object.
remove_trait_listener(object[, prefix])	
reset_traits([traits])	Resets some or all of an object's trait attributes to their default values.
set([trait_change_notify])	Shortcut for setting object trait attributes.
set_trait_dispatch_handler(name, klass[, ...])	Sets a trait notification dispatch handler.
sync_trait(trait_name, object[, alias, ...])	Synchronizes the value of a trait attribute on this object with a trait attribu
trait(name[, force, copy])	Returns the trait definition for the *name* trait attribute.
trait_context()	Returns the default context to use for editing or configuring traits.
trait_get(*names, **metadata)	Shortcut for getting object trait attributes.
trait_items_event(event_trait,name,items_event)	
trait_monitor(handler[, remove])	Adds or removes the specified *handler* from the list of active monitors.
trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
trait_property_changed(...)	
trait_set([trait_change_notify])	Shortcut for setting object trait attributes.
trait_setq(**traits)	Shortcut for setting object trait attributes.
trait_subclasses([all])	Returns a list of the immediate (or all) subclasses of this class.
trait_view([name, view_element])	Gets or sets a ViewElement associated with an object's class.
trait_view_elements()	Returns the ViewElements object associated with the object's class.
trait_views([klass])	Returns a list of the names of all view elements associated with the curren
traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
traits_init()	
traits_inited([True])	
validate_trait(name, value)	Validates whether a value is legal for a trait.

__init__(***kwargs*)
Initialize handlers and inputs

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(*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().

add_trait_category(*category*)
Adds a trait category to a class.
add_trait_listener(*object*, *prefix=''*)
all_trait_names()
Returns the list of all trait names, including implicitly defined traits.
base_trait(*name*)
Returns the base trait definition for a trait attribute.
Parameters **name** : str
Name of the attribute whose trait definition is returned.
class_default_traits_view()
Returns the name of the default traits view for the class.
class_editable_traits()
Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current class.
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.
class_trait_view(*name=None*, *view_element=None*)
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.
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.
clone_traits(*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(*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.

copy_traits(*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(***metadata*)
Returns the list of trait names to copy or clone by default.

default_traits_view()
Returns the name of the default traits view for the object's class.

edit_traits(*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.

editable_traits()
Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current object.

get(***kwargs*)
Returns traited class as a dict
Augments the trait get function to return a dictionary without notification handles

get_hashval(*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 dict_withhash : dict
Copy of our dictionary with the new file hashes included with each file.

hashvalue : str
The md5 hash value of the traited spec

get_traitsfree(***kwargs*)
Returns traited 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_traits_interface(**interfaces*)
Returns whether the object implements a specified traits interface.

Parameters *interfaces : :
One or more traits Interface (sub)classes.

items()
Name, trait generator for user modifiable traits

on_trait_change(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

on_trait_event(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

print_traits(*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(*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(*object*, *prefix=''*)

reset_traits(*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(*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.

set_trait_dispatch_handler(*name*, *klass*, *override=False*)

Sets a trait notification dispatch handler.

sync_trait(*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(*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()

Returns the default context to use for editing or configuring traits.

trait_get(**names*, ***metadata*)

Shortcut for getting object trait attributes.

Parameters **names** : list of strings

A list of trait attribute names whose values are requested.

Returns **result** : dict

A dictionary whose keys are the names passed as arguments and whose values are the corresponding trait values.

trait_items_event(*event_trait*, *name*, *items_event*)

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(***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(*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(***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.
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(*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()
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(*klass=None*)
Returns a list of the names of all view elements associated with the current object's class.
Parameters **klass** : class
A class, such that all returned names must correspond to instances of this class. Possible values include:
Group
Item
View
ViewElement
ViewSubElement
traits(***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(*name*, *value*)
Validates whether a value is legal for a trait.
Returns the validated value if it is valid.
wrappers = {'new': <class 'traits.trait_notifiers.NewTraitChangeNotifyWrapper'>, 'ui': <class 'traits.trait_notifie

MultiPath

class nipype.interfaces.base.**MultiPath**(*trait=None*, *value=None*, *minlen=0*, *maxlen=9223372036854775807*, *items=True*, ***metadata*)

Bases: traits.trait_types.List

Abstract class - shared functionality of input and output MultiPath

Attributes

editor
info_trait

Methods

__call__(*args, **kw)	Allows a derivative trait to be defined from this one.
as_ctrait()	Returns a CTrait corresponding to the trait defined by this class.
clone([default_value])	Clones the contents of this object into a new instance of the same class, and then modifies the cl
create_editor()	Returns the default UI editor for the trait.
error(object, name, value)	Raises a TraitError exception.
full_info(object, name, value)	Returns a description of the trait.
get_default_value()	Returns a tuple of the form: (*default_value_type*, *default_value*) which describes the default valu
get_editor([trait])	Returns a trait editor that allows the user to modify the *trait* trait.
get_value(object, name[, trait])	Returns the current value of a property-based trait.
info()	Must return a string describing the type of value accepted by the trait handler.
init()	Allows the trait to perform any additional initialization needed.
inner_traits()	Returns the *inner trait* (or traits) for this trait.
is_valid(object, name, value)	
items_event()	
repr(value)	Returns a printable representation of a value along with its type.
set_value(object, name, value)	Sets the cached value of a property-based trait and fires the appropriate trait change event.
validate(object, name, value)	

__init__(*trait=None*, *value=None*, *minlen=0*, *maxlen=9223372036854775807*, *items=True*, ***metadata*)

Returns a List trait.

Parameters **trait** : a trait or value that can be converted to a trait using Trait()
The type of item that the list contains. If not specified, the list can contain items of any type.
value : list
Default value for the list.
minlen : integer
The minimum length of a list that can be assigned to the trait.
maxlen : integer
The maximum length of a list that can be assigned to the trait.
The length of the list assigned to the trait must be such that:: :
minlen <= len(list) <= maxlen

as_ctrait()

Returns a CTrait corresponding to the trait defined by this class.

clone(*default_value=<missing>*, ***metadata*)

Clones the contents of this object into a new instance of the same class, and then modifies the cloned copy using the specified *default_value* and *metadata*. Returns the cloned object as the result.

Note that subclasses can change the signature of this method if needed, but should always call the 'super' method if possible.

create_editor()
Returns the default UI editor for the trait.

default_value = <undefined>

default_value_type = 5

editor = None

error(*object*, *name*, *value*)
Raises a TraitError exception.
Parameters object : object
The object whose attribute is being assigned.
name : str
The name of the attribute being assigned.
value : object
The proposed new value for the attribute.

full_info(*object*, *name*, *value*)
Returns a description of the trait.

get_default_value()
Returns a tuple of the form: (*default_value_type*, *default_value*) which describes the default value for this trait. The default implementation analyzes the value of the trait's **default_value** attribute and determines an appropriate *default_value_type* for *default_value*. If you need to override this method to provide a different result tuple, the following values are valid values for *default_value_type*:

0, 1: The *default_value* item of the tuple is the default value.

2: The object containing the trait is the default value.

3: A new copy of the list specified by *default_value* is the default value.

4: A new copy of the dictionary specified by *default_value* is the default value.

5: A new instance of TraitListObject constructed using the *default_value* list is the default value.

6: A new instance of TraitDictObject constructed using the *default_value* dictionary is the default value.

7: *default_value* is a tuple of the form: (*callable*, *args*, *kw*), where *callable* is a callable, *args* is a tuple, and *kw* is either a dictionary or None. The default value is the result obtained by invoking callable(*args, **kw).

8: *default_value* is a callable. The default value is the result obtained by invoking *default_value*(*object*), where *object* is the object containing the trait. If the trait has a validate() method, the validate() method is also called to validate the result.

9: A new instance of TraitSetObject constructed using the *default_value* set is the default value.

get_editor(*trait=None*)
Returns a trait editor that allows the user to modify the *trait* trait.
Parameters trait : Trait
The trait to be edited.

get_value(*object*, *name*, *trait=None*)
Returns the current value of a property-based trait.

has_items = False

info()
Must return a string describing the type of value accepted by the trait handler.

The string should be a phrase describing the type defined by the TraitHandler subclass, rather than a complete sentence. For example, use the phrase, "a square sprocket" instead of the sentence, "The value must be a square sprocket." The value returned by info() is combined with other information whenever an error occurs and therefore makes more sense to the user if the result is a phrase. The info() method is similar in purpose and use to the **info** attribute of a validator function.

Note that the result can include information specific to the particular trait handler instance. For example, TraitRange instances return a string indicating the range of values acceptable to the handler (e.g., "an integer in the range from 1 to 9"). If the info() method is not overridden, the default method returns the value of the 'info_text' attribute.

info_text = 'a legal value'

info_trait = None

init()

Allows the trait to perform any additional initialization needed.

inner_traits()

Returns the *inner trait* (or traits) for this trait.

is_mapped = False

is_valid(*object*, *name*, *value*)

items_event()

metadata = {}

repr(*value*)

Returns a printable representation of a value along with its type.

Deprecated since version 3.0.3: This functionality was only used to provide readable error messages. This functionality has been incorporated into TraitError itself.

Parameters **value** : object

The value to be printed.

set_value(*object*, *name*, *value*)

Sets the cached value of a property-based trait and fires the appropriate trait change event.

validate(*object*, *name*, *value*)

NipypeInterfaceError

class nipype.interfaces.base.**NipypeInterfaceError**(*value*)

Bases: exceptions.Exception

__init__(*value*)

args

message

OutputMultiPath

class nipype.interfaces.base.**OutputMultiPath**(*trait=None*, *value=None*, *minlen=0*, *maxlen=9223372036854775807*, *items=True*, ***metadata*)

Bases: *nipype.interfaces.base.MultiPath*

Implements a user friendly traits that accepts one or more paths to files or directories. This is the output version which return a single string whenever possible (when it was set to a single value or a list of length 1). Default value of this trait is _Undefined. It does not accept empty lists.

XXX This should only be used as a final resort. We should stick to established Traits to the extent possible.

XXX This needs to be vetted by somebody who understands traits

```
>>> from nipype.interfaces.base import OutputMultiPath
>>> class A(TraitedSpec):
...     foo = OutputMultiPath(File(exists=False))
>>> a = A()
>>> a.foo
<undefined>
```

```
>>> a.foo = '/software/temp/foo.txt'
>>> a.foo
'/software/temp/foo.txt'
```

```
>>> a.foo = ['/software/temp/foo.txt']
>>> a.foo
'/software/temp/foo.txt'
```

```
>>> a.foo = ['/software/temp/foo.txt', '/software/temp/goo.txt']
>>> a.foo
['/software/temp/foo.txt', '/software/temp/goo.txt']
```

Attributes

editor
info_trait

Methods

__call__(*args, **kw)	Allows a derivative trait to be defined from this one.
as_ctrait()	Returns a CTrait corresponding to the trait defined by this class.
clone([default_value])	Clones the contents of this object into a new instance of the same class, and then modifies the cl
create_editor()	Returns the default UI editor for the trait.
error(object, name, value)	Raises a TraitError exception.
full_info(object, name, value)	Returns a description of the trait.
get(object, name)	
get_default_value()	Returns a tuple of the form: (*default_value_type*, *default_value*) which describes the default valu
get_editor([trait])	Returns a trait editor that allows the user to modify the *trait* trait.
get_value(object, name[, trait])	Returns the current value of a property-based trait.
info()	Must return a string describing the type of value accepted by the trait handler.
init()	Allows the trait to perform any additional initialization needed.
inner_traits()	Returns the *inner trait* (or traits) for this trait.
is_valid(object, name, value)	
items_event()	
repr(value)	Returns a printable representation of a value along with its type.
set(object, name, value)	
set_value(object, name, value)	Sets the cached value of a property-based trait and fires the appropriate trait change event.
validate(object, name, value)	

__init__(*trait=None*, *value=None*, *minlen=0*, *maxlen=9223372036854775807*, *items=True*, ***metadata*)

Returns a List trait.

Parameters **trait** : a trait or value that can be converted to a trait using Trait()
The type of item that the list contains. If not specified, the list can contain items of any type.

value : list
Default value for the list.

minlen : integer
The minimum length of a list that can be assigned to the trait.

maxlen : integer
The maximum length of a list that can be assigned to the trait.

The length of the list assigned to the trait must be such that:: :
minlen <= len(list) <= maxlen

as_ctrait()
Returns a CTrait corresponding to the trait defined by this class.

clone(*default_value=<missing>*, ***metadata*)
Clones the contents of this object into a new instance of the same class, and then modifies the cloned copy using the specified *default_value* and *metadata*. Returns the cloned object as the result.
Note that subclasses can change the signature of this method if needed, but should always call the 'super' method if possible.

create_editor()
Returns the default UI editor for the trait.

default_value = <undefined>

default_value_type = 5

editor = None

error(*object*, *name*, *value*)
Raises a TraitError exception.

Parameters object : object
The object whose attribute is being assigned.
name : str
The name of the attribute being assigned.
value : object
The proposed new value for the attribute.

full_info(*object*, *name*, *value*)
Returns a description of the trait.

get(*object*, *name*)

get_default_value()
Returns a tuple of the form: (*default_value_type*, *default_value*) which describes the default value for this trait. The default implementation analyzes the value of the trait's **default_value** attribute and determines an appropriate *default_value_type* for *default_value*. If you need to override this method to provide a different result tuple, the following values are valid values for *default_value_type*:

0, 1: The *default_value* item of the tuple is the default value.

2: The object containing the trait is the default value.

3: A new copy of the list specified by *default_value* is the default value.

4: A new copy of the dictionary specified by *default_value* is the default value.

5: A new instance of TraitListObject constructed using the *default_value* list is the default value.

6: A new instance of TraitDictObject constructed using the *default_value* dictionary is the default value.

7: *default_value* is a tuple of the form: (*callable*, *args*, *kw*), where *callable* is a callable, *args* is a tuple, and *kw* is either a dictionary or None. The default value is the result obtained by invoking callable(*args, **kw).

8: *default_value* is a callable. The default value is the result obtained by invoking *default_value*(*object*), where *object* is the object containing the trait. If the trait has a validate() method, the validate() method is also called to validate the result.

9: A new instance of TraitSetObject constructed using the *default_value* set is the default value.

get_editor(*trait=None*)

Returns a trait editor that allows the user to modify the *trait* trait.

Parameters **trait** : Trait
The trait to be edited.

get_value(*object*, *name*, *trait=None*)
Returns the current value of a property-based trait.

has_items = False

info()
Must return a string describing the type of value accepted by the trait handler.
The string should be a phrase describing the type defined by the TraitHandler subclass, rather than a complete sentence. For example, use the phrase, "a square sprocket" instead of the sentence, "The value must be a square sprocket." The value returned by info() is combined with other information whenever an error occurs and therefore makes more sense to the user if the result is a phrase. The info() method is similar in purpose and use to the **info** attribute of a validator function.
Note that the result can include information specific to the particular trait handler instance. For example, TraitRange instances return a string indicating the range of values acceptable to the handler (e.g., "an integer in the range from 1 to 9"). If the info() method is not overridden, the default method returns the value of the 'info_text' attribute.

info_text = 'a legal value'

info_trait = None

init()
Allows the trait to perform any additional initialization needed.

inner_traits()
Returns the *inner trait* (or traits) for this trait.

is_mapped = False

is_valid(*object*, *name*, *value*)

items_event()

metadata = {}

repr(*value*)
Returns a printable representation of a value along with its type.
Deprecated since version 3.0.3: This functionality was only used to provide readable error messages. This functionality has been incorporated into TraitError itself.

Parameters **value** : object
The value to be printed.

set(*object*, *name*, *value*)

set_value(*object*, *name*, *value*)
Sets the cached value of a property-based trait and fires the appropriate trait change event.

validate(*object*, *name*, *value*)

SEMLikeCommandLine

class nipype.interfaces.base.**SEMLikeCommandLine**(*command=None*, ***inputs*)
Bases: *nipype.interfaces.base.CommandLine*
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.

Attributes

output_spec

Methods

aggregate_outputs([runtime, needed_outputs])	Collate expected outputs and check for existence
help([returnhelp])	
input_spec	alias of *CommandLineInputSpec*
next()	
raise_exception(runtime)	
run(**inputs)	Execute this interface.
set_default_terminal_output(output_type)	Set the default terminal output for CommandLine Interfaces.
version_from_command([flag])	

__init__ (*command=None*, ***inputs*)
aggregate_outputs (*runtime=None*, *needed_outputs=None*)
Collate expected outputs and check for existence
always_run
can_resume
cmd
sets base command, immutable
cmdline
command plus any arguments (args) validates arguments and generates command line
help (*returnhelp=False*)
input_spec
alias of *CommandLineInputSpec*
next ()
output_spec = None
raise_exception (*runtime*)
run (***inputs*)
Execute this interface.
This interface will not raise an exception if runtime.returncode is non-zero.
Parameters 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 :
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>.inputs.terminal_output.
version
version_from_command (*flag='-v'*)

StdOutCommandLine

class nipype.interfaces.base.**StdOutCommandLine** (*command=None*, ***inputs*)
Bases: *nipype.interfaces.base.CommandLine*

Attributes

output_spec

Methods

aggregate_outputs([runtime, needed_outputs])	Collate expected outputs and check for existence

Continued on next page

Table 3.27 – continued from previous page

help([returnhelp])	
input_spec	alias of *StdOutCommandLineInputSpec*
next()	
raise_exception(runtime)	
run(**inputs)	Execute this interface.
set_default_terminal_output(output_type)	Set the default terminal output for CommandLine Interfaces.
version_from_command([flag])	

__init__ (*command=None*, ***inputs*)
aggregate_outputs (*runtime=None*, *needed_outputs=None*)
Collate expected outputs and check for existence
always_run
can_resume
cmd
sets base command, immutable
cmdline
command plus any arguments (args) validates arguments and generates command line
help (*returnhelp=False*)
input_spec
alias of *StdOutCommandLineInputSpec*
next ()
output_spec = None
raise_exception (*runtime*)
run (***inputs*)
Execute this interface.
This interface will not raise an exception if runtime.returncode is non-zero.
Parameters 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 :
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>.inputs.terminal_output.
version
version_from_command (*flag='-v'*)

StdOutCommandLineInputSpec

class nipype.interfaces.base.**StdOutCommandLineInputSpec** (***kwargs*)
Bases: *nipype.interfaces.base.CommandLineInputSpec*

Methods

add_class_trait(name, *trait)	Adds a named trait attribute to this class.
add_trait(name, *trait)	Adds a trait attribute to this object.
add_trait_category(category)	Adds a trait category to a class.
add_trait_listener(object[, prefix])	
all_trait_names()	Returns the list of all trait names, including implicitly defined traits.
base_trait(name)	Returns the base trait definition for a trait attribute.
class_default_traits_view()	Returns the name of the default traits view for the class.

Table 3.28 – continued from previous page

class_editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
class_trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
class_trait_view([name, view_element])	
class_trait_view_elements()	Returns the ViewElements object associated with the class.
class_traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
clone_traits([traits, memo, copy])	Clones a new object from this one, optionally copying only a specified set
configure_traits([filename, view, kind, ...])	Creates and displays a dialog box for editing values of trait attributes, as i
copy_traits(other[, traits, memo, copy])	Copies another object's trait attributes into this one.
copyable_trait_names(**metadata)	Returns the list of trait names to copy or clone by default.
default_traits_view()	Returns the name of the default traits view for the object's class.
edit_traits([view, parent, kind, context, ...])	Displays a user interface window for editing trait attribute values.
editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
get(**kwargs)	Returns traited class as a dict
get_hashval([hash_method])	Return a dictionary of our items with hashes for each file.
get_traitsfree(**kwargs)	Returns traited class as a dict
has_traits_interface(*interfaces)	Returns whether the object implements a specified traits interface.
items()	Name, trait generator for user modifiable traits
on_trait_change(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
on_trait_event(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
print_traits([show_help])	Prints the values of all explicitly-defined, non-event trait attributes on the
remove_trait(name)	Removes a trait attribute from this object.
remove_trait_listener(object[, prefix])	
reset_traits([traits])	Resets some or all of an object's trait attributes to their default values.
set([trait_change_notify])	Shortcut for setting object trait attributes.
set_trait_dispatch_handler(name, klass[, ...])	Sets a trait notification dispatch handler.
sync_trait(trait_name, object[, alias, ...])	Synchronizes the value of a trait attribute on this object with a trait attribu
trait(name[, force, copy])	Returns the trait definition for the *name* trait attribute.
trait_context()	Returns the default context to use for editing or configuring traits.
trait_get(*names, **metadata)	Shortcut for getting object trait attributes.
trait_items_event(event_trait,name,items_event)	
trait_monitor(handler[, remove])	Adds or removes the specified *handler* from the list of active monitors.
trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
trait_property_changed(...)	
trait_set([trait_change_notify])	Shortcut for setting object trait attributes.
trait_setq(**traits)	Shortcut for setting object trait attributes.
trait_subclasses([all])	Returns a list of the immediate (or all) subclasses of this class.
trait_view([name, view_element])	Gets or sets a ViewElement associated with an object's class.
trait_view_elements()	Returns the ViewElements object associated with the object's class.
trait_views([klass])	Returns a list of the names of all view elements associated with the curren
traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
traits_init()	
traits_inited([True])	
validate_trait(name, value)	Validates whether a value is legal for a trait.

__init__(***kwargs*)
Initialize handlers and inputs

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(*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().

add_trait_category(*category*)

Adds a trait category to a class.

add_trait_listener(*object*, *prefix=''*)

all_trait_names()

Returns the list of all trait names, including implicitly defined traits.

base_trait(*name*)

Returns the base trait definition for a trait attribute.

Parameters **name** : str

Name of the attribute whose trait definition is returned.

class_default_traits_view()

Returns the name of the default traits view for the class.

class_editable_traits()

Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current class.

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.

class_trait_view(*name=None*, *view_element=None*)

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.

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.

clone_traits(*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(*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.

copy_traits(*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(***metadata*)
Returns the list of trait names to copy or clone by default.

default_traits_view()
Returns the name of the default traits view for the object's class.

edit_traits(*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.

editable_traits()

Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current object.

get(***kwargs*)

Returns traited class as a dict

Augments the trait get function to return a dictionary without notification handles

get_hashval(*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 **dict_withhash** : dict

Copy of our dictionary with the new file hashes included with each file.

hashvalue : str

The md5 hash value of the traited spec

get_traitsfree(***kwargs*)

Returns traited 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_traits_interface(**interfaces*)

Returns whether the object implements a specified traits interface.

Parameters ***interfaces :** :

One or more traits Interface (sub)classes.

items()

Name, trait generator for user modifiable traits

on_trait_change(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

on_trait_event(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

print_traits(*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(*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(*object*, *prefix=''*)

reset_traits(*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(*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.

set_trait_dispatch_handler(*name*, *klass*, *override=False*)

Sets a trait notification dispatch handler.

sync_trait(*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(*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()

Returns the default context to use for editing or configuring traits.

trait_get(**names*, ***metadata*)

Shortcut for getting object trait attributes.

Parameters **names** : list of strings
A list of trait attribute names whose values are requested.

Returns **result** : dict
A dictionary whose keys are the names passed as arguments and whose values are the corresponding trait values.

trait_items_event(*event_trait*, *name*, *items_event*)

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(***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(*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(***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.

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(*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()
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(*klass=None*)
Returns a list of the names of all view elements associated with the current object's class.
Parameters **klass** : class
A class, such that all returned names must correspond to instances of this class. Possible values include:
Group
Item
View
ViewElement
ViewSubElement

traits(***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(*name*, *value*)

Validates whether a value is legal for a trait.

Returns the validated value if it is valid.

wrappers = {'new': <class 'traits.trait_notifiers.NewTraitChangeNotifyWrapper'>, 'ui': <class 'traits.trait_notifier

Stream

class nipype.interfaces.base.**Stream**(*name*, *impl*)

Bases: future.types.newobject.newobject

Function to capture stdout and stderr streams with timestamps

stackoverflow.com/questions/4984549/merge-and-sync-stdout-and-stderr/5188359

Methods

fileno()	Pass-through for file descriptor.
next()	
read([drain])	Read from the file descriptor.

__init__(*name*, *impl*)

fileno()

Pass-through for file descriptor.

next()

read(*drain=0*)

Read from the file descriptor. If 'drain' set, read until EOF.

TraitedSpec

class nipype.interfaces.base.**TraitedSpec**(***kwargs*)

Bases: *nipype.interfaces.base.BaseTraitedSpec*

Create a subclass with strict traits.

This is used in 90% of the cases.

Methods

add_class_trait(name, *trait)	Adds a named trait attribute to this class.
add_trait(name, *trait)	Adds a trait attribute to this object.
add_trait_category(category)	Adds a trait category to a class.
add_trait_listener(object[, prefix])	
all_trait_names()	Returns the list of all trait names, including implicitly defined traits.
base_trait(name)	Returns the base trait definition for a trait attribute.
class_default_traits_view()	Returns the name of the default traits view for the class.
class_editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
class_trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
class_trait_view([name, view_element])	
class_trait_view_elements()	Returns the ViewElements object associated with the class.
class_traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes

Table 3.30 – continued from previous page

clone_traits([traits, memo, copy])	Clones a new object from this one, optionally copying only a specified set
configure_traits([filename, view, kind, ...])	Creates and displays a dialog box for editing values of trait attributes, as i
copy_traits(other[, traits, memo, copy])	Copies another object's trait attributes into this one.
copyable_trait_names(**metadata)	Returns the list of trait names to copy or clone by default.
default_traits_view()	Returns the name of the default traits view for the object's class.
edit_traits([view, parent, kind, context, ...])	Displays a user interface window for editing trait attribute values.
editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
get(**kwargs)	Returns traited class as a dict
get_hashval([hash_method])	Return a dictionary of our items with hashes for each file.
get_traitsfree(**kwargs)	Returns traited class as a dict
has_traits_interface(*interfaces)	Returns whether the object implements a specified traits interface.
items()	Name, trait generator for user modifiable traits
on_trait_change(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
on_trait_event(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
print_traits([show_help])	Prints the values of all explicitly-defined, non-event trait attributes on the
remove_trait(name)	Removes a trait attribute from this object.
remove_trait_listener(object[, prefix])	
reset_traits([traits])	Resets some or all of an object's trait attributes to their default values.
set([trait_change_notify])	Shortcut for setting object trait attributes.
set_trait_dispatch_handler(name, klass[, ...])	Sets a trait notification dispatch handler.
sync_trait(trait_name, object[, alias, ...])	Synchronizes the value of a trait attribute on this object with a trait attribu
trait(name[, force, copy])	Returns the trait definition for the *name* trait attribute.
trait_context()	Returns the default context to use for editing or configuring traits.
trait_get(*names, **metadata)	Shortcut for getting object trait attributes.
trait_items_event(event_trait,name,items_event)	
trait_monitor(handler[, remove])	Adds or removes the specified *handler* from the list of active monitors.
trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
trait_property_changed(...)	
trait_set([trait_change_notify])	Shortcut for setting object trait attributes.
trait_setq(**traits)	Shortcut for setting object trait attributes.
trait_subclasses([all])	Returns a list of the immediate (or all) subclasses of this class.
trait_view([name, view_element])	Gets or sets a ViewElement associated with an object's class.
trait_view_elements()	Returns the ViewElements object associated with the object's class.
trait_views([klass])	Returns a list of the names of all view elements associated with the curren
traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
traits_init()	
traits_inited([True])	
validate_trait(name, value)	Validates whether a value is legal for a trait.

__init__(***kwargs*)
Initialize handlers and inputs

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(*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().

add_trait_category(*category*)
Adds a trait category to a class.

add_trait_listener(*object*, *prefix=''*)

all_trait_names()
Returns the list of all trait names, including implicitly defined traits.

base_trait(*name*)
Returns the base trait definition for a trait attribute.

Parameters **name** : str
Name of the attribute whose trait definition is returned.

class_default_traits_view()
Returns the name of the default traits view for the class.

class_editable_traits()
Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current class.

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.

class_trait_view(*name=None*, *view_element=None*)

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.

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.

clone_traits(*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(*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.

copy_traits(*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(***metadata*)
Returns the list of trait names to copy or clone by default.

default_traits_view()
Returns the name of the default traits view for the object's class.

edit_traits(*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.

editable_traits()
Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current object.

get(***kwargs*)
Returns traited class as a dict
Augments the trait get function to return a dictionary without notification handles

get_hashval(*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 dict_withhash : dict
Copy of our dictionary with the new file hashes included with each file.

hashvalue : str
The md5 hash value of the traited spec

get_traitsfree(***kwargs*)
Returns traited 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_traits_interface(**interfaces*)
Returns whether the object implements a specified traits interface.

Parameters *interfaces : :
One or more traits Interface (sub)classes.

items()
Name, trait generator for user modifiable traits

on_trait_change(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

on_trait_event(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

print_traits(*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(*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(*object*, *prefix=''*)
reset_traits(*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 (*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.

set_trait_dispatch_handler (*name*, *klass*, *override=False*)

Sets a trait notification dispatch handler.

sync_trait (*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 (*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 ()

Returns the default context to use for editing or configuring traits.

trait_get (**names*, ***metadata*)

Shortcut for getting object trait attributes.

Parameters **names** : list of strings

A list of trait attribute names whose values are requested.

Returns **result** : dict

A dictionary whose keys are the names passed as arguments and whose values are the corresponding trait values.

trait_items_event (*event_trait*, *name*, *items_event*)

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(***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(*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(***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.
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(*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()
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(*klass=None*)
Returns a list of the names of all view elements associated with the current object's class.
Parameters **klass** : class
A class, such that all returned names must correspond to instances of this class. Possible values include:
Group
Item
View
ViewElement
ViewSubElement
traits(***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(*name*, *value*)
Validates whether a value is legal for a trait.
Returns the validated value if it is valid.
wrappers = {'new': <class 'traits.trait_notifiers.NewTraitChangeNotifyWrapper'>, 'ui': <class 'traits.trait_notifier

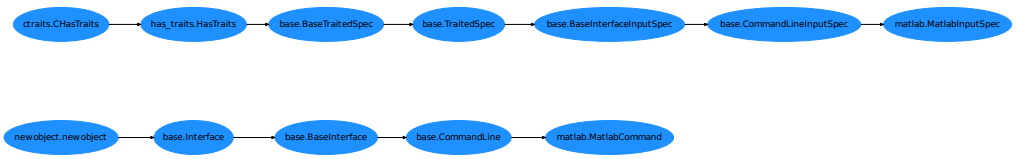
3.2.3 Functions

nipype.interfaces.base.**get_dependencies**(*name*, *environ*)
Return library dependencies of a dynamically linked executable
Uses otool on darwin, ldd on linux. Currently doesn't support windows.
nipype.interfaces.base.**get_max_resources_used**(*pid*, *mem_mb*, *num_threads*, *py-func=False*)
Function to get the RAM and threads usage of a process
Returns **mem_mb** : float
the new high memory watermark of process (MB)
num_threads : float
the new high thread watermark of process
nipype.interfaces.base.**load_template**(*name*)
Load a template from the script_templates directory
Parameters **name** : str
The name of the file to load
Returns **template** : string.Template
nipype.interfaces.base.**run_command**(*runtime*, *output=None*, *timeout=0.01*, *redirect_x=False*)
Run a command, read stdout and stderr, prefix with timestamp.
The returned runtime contains a merged stdout+stderr log with timestamps

3.3 interfaces.matlab

3.3.1 Module: interfaces.matlab

Inheritance diagram for nipype.interfaces.matlab:



General matlab interface code

3.3.2 Classes

MatlabCommand

class nipype.interfaces.matlab.**MatlabCommand**(*matlab_cmd=None*, ***inputs*)
Bases: *nipype.interfaces.base.CommandLine*
Interface that runs matlab code

```
>>> import nipype.interfaces.matlab as matlab
>>> mlab = matlab.MatlabCommand(mfile=False)  # don't write script file
```

```
>>> mlab.inputs.script = "which('who')"
>>> out = mlab.run()
```

Attributes

output_spec

Methods

aggregate_outputs([runtime, needed_outputs])	Collate expected outputs and check for existence
help([returnhelp])	
input_spec	alias of *MatlabInputSpec*
next()	
raise_exception(runtime)	
run(**inputs)	Execute this interface.
set_default_matlab_cmd(matlab_cmd)	Set the default MATLAB command line for MATLAB classes.
set_default_mfile(mfile)	Set the default MATLAB script file format for MATLAB classes.
set_default_paths(paths)	Set the default MATLAB paths for MATLAB classes.
set_default_terminal_output(output_type)	Set the default terminal output for CommandLine Interfaces.
version_from_command([flag])	

__init__ (*matlab_cmd=None*, ***inputs*)
initializes interface to matlab (default 'matlab -nodesktop -nosplash')

aggregate_outputs (*runtime=None*, *needed_outputs=None*)
Collate expected outputs and check for existence

always_run

can_resume

cmd
sets base command, immutable

cmdline
command plus any arguments (args) validates arguments and generates command line

help (*returnhelp=False*)

input_spec
alias of *MatlabInputSpec*

next ()

output_spec = None

raise_exception (*runtime*)

run (***inputs*)
Execute this interface.
This interface will not raise an exception if runtime.returncode is non-zero.
Parameters 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 :

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.

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>.inputs.terminal_output.

version

version_from_command(*flag='-v'*)

MatlabInputSpec

class nipype.interfaces.matlab.**MatlabInputSpec**(***kwargs*)
Bases: *nipype.interfaces.base.CommandLineInputSpec*
Basic expected inputs to Matlab interface

Methods

add_class_trait(name, *trait)	Adds a named trait attribute to this class.
add_trait(name, *trait)	Adds a trait attribute to this object.
add_trait_category(category)	Adds a trait category to a class.
add_trait_listener(object[, prefix])	
all_trait_names()	Returns the list of all trait names, including implicitly defined traits.
base_trait(name)	Returns the base trait definition for a trait attribute.
class_default_traits_view()	Returns the name of the default traits view for the class.
class_editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
class_trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
class_trait_view([name, view_element])	
class_trait_view_elements()	Returns the ViewElements object associated with the class.
class_traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
clone_traits([traits, memo, copy])	Clones a new object from this one, optionally copying only a specified set
configure_traits([filename, view, kind, ...])	Creates and displays a dialog box for editing values of trait attributes, as i
copy_traits(other[, traits, memo, copy])	Copies another object's trait attributes into this one.
copyable_trait_names(**metadata)	Returns the list of trait names to copy or clone by default.
default_traits_view()	Returns the name of the default traits view for the object's class.
edit_traits([view, parent, kind, context, ...])	Displays a user interface window for editing trait attribute values.
editable_traits()	Returns an alphabetically sorted list of the names of non-event trait attribu
get(**kwargs)	Returns traited class as a dict
get_hashval([hash_method])	Return a dictionary of our items with hashes for each file.
get_traitsfree(**kwargs)	Returns traited class as a dict
has_traits_interface(*interfaces)	Returns whether the object implements a specified traits interface.
items()	Name, trait generator for user modifiable traits
on_trait_change(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
on_trait_event(handler[, name, remove, ...])	Causes the object to invoke a handler whenever a trait attribute matching a
print_traits([show_help])	Prints the values of all explicitly-defined, non-event trait attributes on the
remove_trait(name)	Removes a trait attribute from this object.
remove_trait_listener(object[, prefix])	
reset_traits([traits])	Resets some or all of an object's trait attributes to their default values.
set([trait_change_notify])	Shortcut for setting object trait attributes.

Table 3.33 – continued from previous page

set_trait_dispatch_handler(name, klass[, ...])	Sets a trait notification dispatch handler.
sync_trait(trait_name, object[, alias, ...])	Synchronizes the value of a trait attribute on this object with a trait attribu
trait(name[, force, copy])	Returns the trait definition for the *name* trait attribute.
trait_context()	Returns the default context to use for editing or configuring traits.
trait_get(*names, **metadata)	Shortcut for getting object trait attributes.
trait_items_event(event_trait,name,items_event)	
trait_monitor(handler[, remove])	Adds or removes the specified *handler* from the list of active monitors.
trait_names(**metadata)	Returns a list of the names of all trait attributes whose definitions match th
trait_property_changed(...)	
trait_set([trait_change_notify])	Shortcut for setting object trait attributes.
trait_setq(**traits)	Shortcut for setting object trait attributes.
trait_subclasses([all])	Returns a list of the immediate (or all) subclasses of this class.
trait_view([name, view_element])	Gets or sets a ViewElement associated with an object's class.
trait_view_elements()	Returns the ViewElements object associated with the object's class.
trait_views([klass])	Returns a list of the names of all view elements associated with the curren
traits(**metadata)	Returns a dictionary containing the definitions of all of the trait attributes
traits_init()	
traits_inited([True])	
validate_trait(name, value)	Validates whether a value is legal for a trait.

__init__(***kwargs*)
Initialize handlers and inputs

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(*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().

add_trait_category(*category*)
Adds a trait category to a class.

add_trait_listener(*object*, *prefix=''*)

all_trait_names()
Returns the list of all trait names, including implicitly defined traits.

base_trait(*name*)
Returns the base trait definition for a trait attribute.

Parameters **name** : str
Name of the attribute whose trait definition is returned.

class_default_traits_view()
Returns the name of the default traits view for the class.

class_editable_traits()
Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current class.

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.
class_trait_view(*name=None*, *view_element=None*)
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.
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.
clone_traits(*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(*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.

copy_traits(*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(***metadata*)
Returns the list of trait names to copy or clone by default.

default_traits_view()
Returns the name of the default traits view for the object's class.

edit_traits(*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.

editable_traits()
Returns an alphabetically sorted list of the names of non-event trait attributes associated with the current object.

get(***kwargs*)
Returns traited class as a dict
Augments the trait get function to return a dictionary without notification handles

get_hashval(*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 dict_withhash : dict
Copy of our dictionary with the new file hashes included with each file.

hashvalue : str
The md5 hash value of the traited spec

get_traitsfree(***kwargs*)
Returns traited 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_traits_interface(**interfaces*)
Returns whether the object implements a specified traits interface.

Parameters *interfaces : :
One or more traits Interface (sub)classes.

items()
Name, trait generator for user modifiable traits

on_trait_change(*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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

on_trait_event(*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 modi-

fied, 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_ui`	Alias for `ui`.
`new`	Run notifications in a new thread.

print_traits(*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(*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(*object*, *prefix=''*)

reset_traits(*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(*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.

set_trait_dispatch_handler(*name*, *klass*, *override=False*)

Sets a trait notification dispatch handler.

sync_trait(*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(*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()
Returns the default context to use for editing or configuring traits.

trait_get(**names*, ***metadata*)
Shortcut for getting object trait attributes.
Parameters **names** : list of strings
A list of trait attribute names whose values are requested.
Returns **result** : dict
A dictionary whose keys are the names passed as arguments and whose values are the corresponding trait values.

trait_items_event(*event_trait*, *name*, *items_event*)

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(***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(*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(***traits*)
Shortcut for setting object trait attributes.
Parameters ****traits :** :
Key/value pairs, the trait attributes and their values to be set. No trait change notifica-

tions will be generated for any values assigned (see also: trait_set).

Returns **self :** :
The method returns this object, after setting attributes.

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(*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()
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(*klass=None*)
Returns a list of the names of all view elements associated with the current object's class.

Parameters **klass** : class
A class, such that all returned names must correspond to instances of this class. Possible values include:
Group
Item
View
ViewElement
ViewSubElement

traits(***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(*name*, *value*)
Validates whether a value is legal for a trait.
Returns the validated value if it is valid.

wrappers = {'new': <class 'traits.trait_notifiers.NewTraitChangeNotifyWrapper'>, 'ui': <class 'traits.trait_notifie

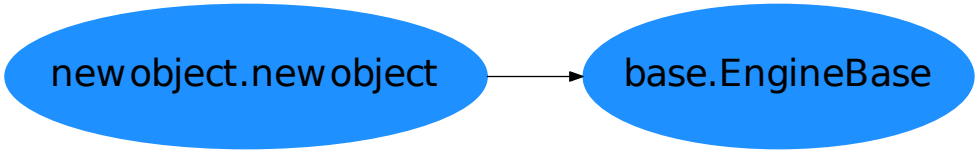
3.3.3 Function

nipype.interfaces.matlab.**get_matlab_command**()

3.4 pipeline.engine.base

3.4.1 Module: pipeline.engine.base

Inheritance diagram for nipype.pipeline.engine.base:



Defines functionality for pipelined execution of interfaces
The *EngineBase* class implements the more general view of a task.

3.4.2 EngineBase

class nipype.pipeline.engine.base.**EngineBase**(*name=None*, *base_dir=None*)
Bases: future.types.newobject.newobject
Defines common attributes and functions for workflows and nodes.

Methods

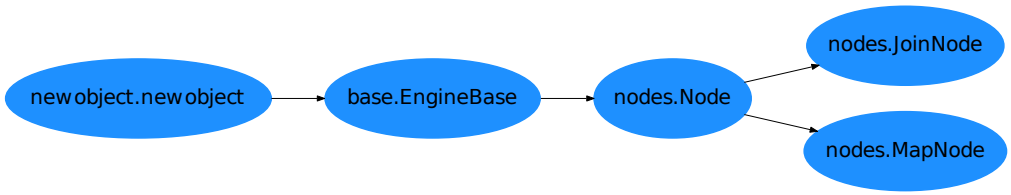
clone(name)	Clone an EngineBase object
load(filename)	
next()	
save([filename])	

__init__(*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(*name*)
Clone an EngineBase object
Parameters **name** : string (mandatory)
A clone of node or workflow must have a new name
fullname
inputs
load(*filename*)
next()
outputs
save(*filename=None*)

3.5 pipeline.engine.nodes

3.5.1 Module: pipeline.engine.nodes

Inheritance diagram for nipype.pipeline.engine.nodes:



Defines functionality for pipelined execution of interfaces
The *Node* class provides core functionality for batch processing.

3.5.2 Classes

JoinNode

class nipype.pipeline.engine.nodes.**JoinNode**(*interface*, *name*, *joinsource*, *joinfield=None*, *unique=False*, ***kwargs*)

Bases: *nipype.pipeline.engine.nodes.Node*

Wraps interface objects that join inputs into a list.

Examples

```
>>> import nipype.pipeline.engine as pe
>>> from nipype import Node, JoinNode, Workflow
>>> from nipype.interfaces.utility import IdentityInterface
>>> from nipype.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')
```

Methods

clone(name)	Clone an EngineBase object
get_output(parameter)	Retrieve a particular output of the node
hash_exists([updatehash])	

Continued on next page

Table 3.35 – continued from previous page

help()	Print interface help
load(filename)	
next()	
output_dir()	Return the location of the output directory for the node
run([updatehash])	Execute the node in its directory.
save([filename])	
set_input(parameter, val)	Set interface input value
update(**opts)	
write_report([report_type, cwd])	

__init__(*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(*name*)

Clone an EngineBase object

Parameters **name** : string (mandatory)
A clone of node or workflow must have a new name

fullname

get_output(*parameter*)

Retrieve a particular output of the node

hash_exists(*updatehash=False*)

help()

Print interface help

inputs

The JoinNode inputs include the join field overrides.

interface

Return the underlying interface object

joinfield = None

the fields to join

joinsource

the join predecessor iterable node

load(*filename*)

next()

output_dir()

Return the location of the output directory for the node

outputs

Return the output fields of the underlying interface

result

run(*updatehash=False*)

Execute the node in its directory.

Parameters **updatehash: boolean** :
Update the hash stored in the output directory

save(*filename=None*)

set_input(*parameter*, *val*)

Set interface input value

update(***opts*)

write_report(*report_type=None*, *cwd=None*)

MapNode

class nipype.pipeline.engine.nodes.**MapNode**(*interface*, *iterfield*, *name*, *serial=False*, *nested=False*, ***kwargs*)

Bases: *nipype.pipeline.engine.nodes.Node*

Wraps interface objects that need to be iterated on a list of inputs.

Examples

```
>>> from nipype import MapNode
>>> from nipype.interfaces import fsl
>>> realign = MapNode(fsl.MCFLIRT(), 'in_file', 'realign')
>>> realign.inputs.in_file = ['functional.nii',
...                           'functional2.nii',
...                           'functional3.nii']
>>> realign.run()
```

Methods

clone(name)	Clone an EngineBase object
get_output(parameter)	Retrieve a particular output of the node
get_subnodes()	
hash_exists([updatehash])	
help()	Print interface help
load(filename)	
next()	
num_subnodes()	
output_dir()	Return the location of the output directory for the node
run([updatehash])	Execute the node in its directory.
save([filename])	
set_input(parameter, val)	Set interface input value or nodewrapper attribute
update(**opts)	
write_report([report_type, cwd])	

__init__(*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 : boolea
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 Node docstring for additional keyword arguments. :

clone (*name*)

Clone an EngineBase object

Parameters **name** : string (mandatory)

A clone of node or workflow must have a new name

fullname

get_output (*parameter*)

Retrieve a particular output of the node

get_subnodes ()

hash_exists (*updatehash=False*)

help ()

Print interface help

inputs

interface

Return the underlying interface object

load (*filename*)

next ()

num_subnodes ()

output_dir ()

Return the location of the output directory for the node

outputs

result

run (*updatehash=False*)

Execute the node in its directory.

Parameters **updatehash: boolean** :

Update the hash stored in the output directory

save (*filename=None*)

set_input (*parameter*, *val*)

Set interface input value or nodewrapper attribute

Priority goes to interface.

update (**opts*)

write_report (*report_type=None*, *cwd=None*)

Node

class nipype.pipeline.engine.nodes.**Node** (*interface*, *name*, *iterables=None*, *iterfield=None*, *synchronize=False*, *overwrite=None*, *needed_outputs=None*, *run_without_submitting=False*, **kwargs*)

Bases: *nipype.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 nipype import Node
>>> from nipype.interfaces import spm
>>> realign = Node(spm.Realign(), 'realign')
>>> realign.inputs.in_files = 'functional.nii'
>>> realign.inputs.register_to_mean = True
>>> realign.run()
```

Methods

clone(name)	Clone an EngineBase object
get_output(parameter)	Retrieve a particular output of the node
hash_exists([updatehash])	
help()	Print interface help
load(filename)	
next()	
output_dir()	Return the location of the output directory for the node
run([updatehash])	Execute the node in its directory.
save([filename])	
set_input(parameter, val)	Set interface input value
update(**opts)	
write_report([report_type, cwd])	

__init__(*interface*, *name*, *iterables=None*, *itersource=None*, *synchronize=False*, *overwrite=None*, *needed_outputs=None*, *run_without_submitting=False*, ***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(*name*)

Clone an EngineBase object

Parameters name : string (mandatory)

A clone of node or workflow must have a new name

fullname

get_output(*parameter*)

Retrieve a particular output of the node

hash_exists(*updatehash=False*)

help()

Print interface help

inputs

Return the inputs of the underlying interface

interface

Return the underlying interface object

load(*filename*)

next()

output_dir()

Return the location of the output directory for the node

outputs

Return the output fields of the underlying interface

result

run(*updatehash=False*)

Execute the node in its directory.

Parameters updatehash: boolean :

Update the hash stored in the output directory

save(*filename=None*)

set_input(*parameter*, *val*)

Set interface input value

update(***opts*)

write_report(*report_type=None*, *cwd=None*)

3.6 pipeline.engine.utils

3.6.1 Module: pipeline.engine.utils

Utility routines for workflow graphs

3.6.2 Functions

nipype.pipeline.engine.utils.**clean_working_directory**(*outputs*, *cwd*, *inputs*, *needed_outputs*, *config*, *files2keep=None*, *dirs2keep=None*)

Removes all files not needed for further analysis from the directory

nipype.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.

nipype.pipeline.engine.utils.**evaluate_connect_function**(*function_source*, *args*, *first_arg*)

nipype.pipeline.engine.utils.**expand_iterables**(*iterables*, *synchronize=False*)

nipype.pipeline.engine.utils.**export_graph**(*graph_in*, *base_dir=None*, *show=False*, *use_execgraph=False*, *show_connectinfo=False*, *dotfilename='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] :

nipype.pipeline.engine.utils.**format_dot**(*dotfilename*, *format=None*)

Dump a directed graph (Linux only; install via *brew* on OSX)

nipype.pipeline.engine.utils.**format_node**(*node*, *format='python'*, *include_config=False*)

Format a node in a given output syntax.

nipype.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).

nipype.pipeline.engine.utils.**get_all_files**(*infile*)

nipype.pipeline.engine.utils.**get_levels**(*G*)

nipype.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

nipype.pipeline.engine.utils.**make_output_dir**(*outdir*)

Make the output_dir if it doesn't exist.

Parameters **outdir** : output directory to create

nipype.pipeline.engine.utils.**merge_bundles**(*g1*, *g2*)

nipype.pipeline.engine.utils.**merge_dict**(*d1*, *d2*, *merge=<function <lambda>>*)

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]
```

nipype.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

nipype.pipeline.engine.utils.**synchronize_iterables**(*iterables*)

Synchronize the given iterables in item-wise order.

Return: the {field: value} dictionary list

Examples

```
>>> from nipype.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
```

nipype.pipeline.engine.utils.**topological_sort**(*graph*, *depth_first=False*)

Returns a depth first sorted order if depth_first is True

nipype.pipeline.engine.utils.**walk**(*children*, *level=0*, *path=None*, *usename=True*)

Generate all the full paths in a tree, as a dict.

Examples

```
>>> from nipype.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]
```

nipype.pipeline.engine.utils.**walk_files**(*cwd*)

nipype.pipeline.engine.utils.**walk_outputs**(*object*)

Extract every file and directory from a python structure

nipype.pipeline.engine.utils.**write_workflow_prov**(*graph*, *filename=None*, *format='all'*)

Write W3C PROV Model JSON file

3.7 pipeline.engine.workflows

3.7.1 Module: pipeline.engine.workflows

Inheritance diagram for nipype.pipeline.engine.workflows:

Defines functionality for pipelined execution of interfaces
The *Workflow* class provides core functionality for batch processing.

3.7.2 Workflow

class nipype.pipeline.engine.workflows.**Workflow**(*name*, *base_dir=None*)

Bases: *nipype.pipeline.engine.base.EngineBase*

Controls the setup and execution of a pipeline of processes.

Methods

add_nodes(nodes)	Add nodes to a workflow
clone(name)	Clone a workflow
connect(*args, **kwargs)	Connect nodes in the pipeline.
disconnect(*args)	Disconnect nodes See the docstring for connect for format.
export([filename, prefix, format, ...])	Export object into a different format
get_node(name)	Return an internal node by name
list_node_names()	List names of all nodes in a workflow
load(filename)	
next()	
remove_nodes(nodes)	Remove nodes from a workflow
run([plugin, plugin_args, updatehash])	Execute the workflow
save([filename])	
write_graph([dotfilename, graph2use, ...])	Generates a graphviz dot file and a png file
write_hierarchical_dotfile([dotfilename, ...])	

__init__(*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(*nodes*)

Add nodes to a workflow

Parameters **nodes** : list
A list of EngineBase-based objects

clone(*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(**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:

```
connect(source, sourceoutput, dest, destinput)
```

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 ot 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(**args*)

Disconnect nodes See the docstring for connect for format.

export(*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(*name*)

Return an internal node by name

inputs

list_node_names()

List names of all nodes in a workflow

load(*filename*)

next()

outputs

remove_nodes(*nodes*)

Remove nodes from a workflow

Parameters **nodes** : list

A list of EngineBase-based objects

run(*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(*filename=None*)

write_graph(*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 hierarchy; 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(*dotfilename=None*, *colored=False*, *simple_form=True*)

CHAPTER 4

Developer Guide

Release 0.12.1
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Since nipype 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

4.1 Interface Specifications

4.1.1 Before you start

Nipype is a young project maintained by an enthusiastic group of developers. Even though the documentation might be sparse or cryptic at times we strongly encourage you to contact us on the official nipype developers mailing list in case of any troubles: nipy-devel@neuroimaging.scipy.org (we are sharing a mailing list with the nipy community therefore please add `[nipype]` to the messsage title).

4.1.2 Overview

We're using the 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 though 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 3.x which can be install as part of EPD or from pypi

More documentation

Not everything is documented in the User Manual, in those cases the enthought-dev mailing list or the API docs is your next place to look.

4.1.3 Nipype 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. If you are familiar with the Nipype 0.2 code-base, these attributes are the same as the keys in the opt_map dictionaries. 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 nipype.interfaces import fsl
>>> bet = fsl.BET()
>>> type(bet.inputs)
<class 'nipype.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.__getattribute__       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.FSLTraitedSpec. FSLTraitedSpec 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).:

`TraitedSpec`: Nipype's primary base class for all Specs. Provides initialization, some nipype-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 (`sbjects_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.

4.1.4 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 us traits metadata. These are keyword arguments supplied in the initialization of the attributes. The base classes `BaseInterface` and `CommandLine` (defined in `nipype.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 `nipype.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/nipype/interfaces/base.py", line 76
    self.error( object, name, value )
  File "/Users/cburns/local/lib/python2.5/site-packages/enthought/traits/trait_handlers.py"
    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)
...     y = traits.Int
...
>>> foo = Foo()
>>> foo.x
12
>>> foo.y
0
```

Nipype 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 nipype.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',
                          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 Nipype 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 nipype 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 witch 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 refered by the SPM job manager

Required: This metadata is required by all SPM-mediated interface classes.

4.1.5 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
  commandlines that spawn a graphical user interface.
- `_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(TraitedSpec):
    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 `outfile` 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 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.

4.1.6 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 `isdefiend` function (comparing to None will not work).

4.1.7 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 nipype.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)
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/nipype/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`.

4.2 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.

4.2.1 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(TraitedSpec):
        input_volume = File(desc = "Input volume", exists = True,
                            mandatory = True)
        parameter = traits.Int(desc = "some parameter")

class ExampleOutputSpec(TraitedSpec):
        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 TraitedSpec (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.

4.2.2 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 formated) 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 *nipype.interfaces.base.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 nipype.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()
```

4.2.3 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 trigerred 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.'))
```

4.3 How to wrap a MATLAB script

This is minimal script for wrapping MATLAB code. You should replace the MATLAB code template, and define approriate inputs and outputs.

4.3.1 Example 1

```
    from nipype.interfaces.matlab import MatlabCommand
    from nipype.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)

            # 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
```

4.3.2 Example 2

By subclassing **MatlabCommand** for your main class, and **MatlabInputSpec** for your input and output spec, you gain access to some useful MATLAB hooks

```
import os
from nipype.interfaces.base import File, traits
from nipype.interfaces.matlab import MatlabCommand, MatlabInputSpec


class HelloWorldInputSpec( MatlabInputSpec):
    name = traits.Str( mandatory = True,
                       desc = 'Name of person to say hello to')

class HelloWorldOutputSpec( MatlabInputSpec):
    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()
    >>> 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
```

4.4 How to wrap a Python script

This is a minimal pure python interface. As you can see all you need to do is to do is to define inputs, outputs, _run_interface() (not run()), and _list_outputs.

```
from nipype.interfaces.base import BaseInterface, \
    BaseInterfaceInputSpec, traits, File, TraitedSpec
from nipype.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(TraitedSpec):
    thresholded_volume = File(exists=True, desc="thresholded volume")


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
```

4.5 Working with *nipype* source code

Contents:

4.5.1 Introduction

These pages describe a git and github workflow for the nipype project.

There are several different workflows here, for different ways of working with *nipype*.
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*.

4.5.2 Install git

Overview

Debian / Ubuntu	`sudo apt-get install git-core`
Fedora	`sudo yum install git-core`
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

4.5.3 Following the latest source

These are the instructions if you just want to follow the latest *nipype* 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/nipype.git
```

You now have a copy of the code tree in the new `nipype` directory.

Updating the code

From time to time you may want to pull down the latest code. Do this with:

```
cd nipype
git pull
```

The tree in `nipype` will now have the latest changes from the initial repository.

4.5.4 Making a patch

You've discovered a bug or something else you want to change in nipype .. — 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/nipype.git
# make a branch for your patching
cd nipype
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'
# make the patch files
git format-patch -M -C master
```

Then, send the generated patch files to the nipype 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 nipype repository:

```
git clone git://github.com/nipy/nipype.git
cd nipype
```

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 nipype 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 nipype repository on github — *Making your own copy (fork) of nipype*. 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/nipype.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*.

4.5.5 Git for development

Contents:

Making your own copy (fork) of nipype

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 nipype project, and to suggest some default names.

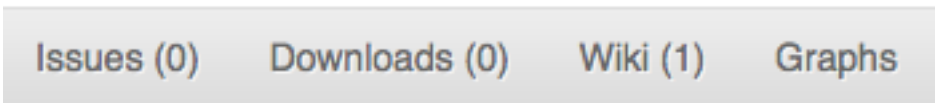
Set up and configure a github account

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 nipype

1. Log into your github account.
2. Go to the nipype github home at nipype 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 nipype.

Set up your fork

First you follow the instructions for *Making your own copy (fork) of nipype*.

Overview

```
git clone git@github.com:your-user-name/nipype.git
cd nipype
git remote add upstream git://github.com/nipy/nipype.git
```

In detail

Clone your fork

1. Clone your fork to the local computer with `git clone git@github.com:your-user-name/nipype.git`
2. Investigate. Change directory to your new repo: `cd nipype`. 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 nipype github repository, so you can merge in changes from trunk.

Linking your repository to the upstream repo

```
cd nipype
git remote add upstream git://github.com/nipy/nipype.git
```

`upstream` here is just the arbitrary name we're using to refer to the main nipype repository at nipype 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/nipype.git (fetch)
upstream     git://github.com/nipy/nipype.git (push)
origin       git@github.com:your-user-name/nipype.git (fetch)
origin       git@github.com:your-user-name/nipype.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

[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
        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 nipype repository, by following *Making your own copy (fork) of nipype*, *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 nipype development repo. Your `master` then will follow the main nipype 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 nipype. 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:

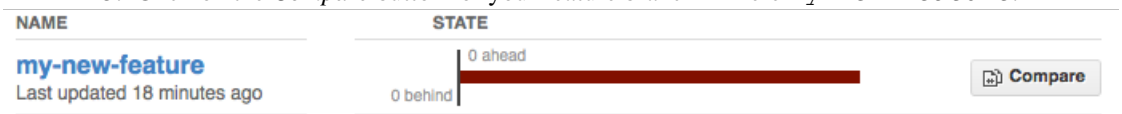
```
# On branch ny-new-feature
# Changed but not updated:
#   (use "git add <file>..." to update what will be committed)
#   (use "git checkout -- <file>..." to discard changes in working directory)
#
#  modified:   README
#
# Untracked files:
#   (use "git add <file>..." to include in what will be committed)
#
#  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/nipype`.
2. Click on the *Branch list* button:

3. Click on the *Compare* button for your feature branch — here `my-new-feature`:



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).
5. At this point you should get a nice summary of the changes. Copy the URL for this, and post it to the nipype mailing list, asking for review. The URL will look something like: `http://github.com/your-user-name/nipype/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:

1. Go to the URL of your forked repo, say `http://github.com/your-user-name/nipype.git`.
2. Click on the 'Pull request' button:

Enter a message; we suggest you select only `nipype` as the recipient. The message will go to the nipype mailing list. Please feel free to add others from the list as you like.

Merging from trunk

This updates your code from the upstream nipype github repo.

Overview

```
# go to your master branch
git checkout master
# pull changes from github
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:

[1] Thanks to Yarik Halchenko for this explanation.

```
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 nipype into your account, as from *Making your own copy (fork) of nipype*.
Then, go to your forked repository github page, say `http://github.com/your-user-name/nipype`
Click on the 'Admin' button, and add anyone else to the repo as a collaborator:

Now all those people can do:

```
git clone git@githhub.com:your-user-name/nipype.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.

4.5.6 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

4.6 Architecture (discussions from 2009)

This section reflects notes and discussion between developers during the start of the nipype project in 2009.

4.6.1 Design Guidelines

These are guidelines that the core nipype 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 maintinence 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.

4.6.2 Providing for Provenance

The following is a specific discussion that should be thought out an 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.

4.6.3 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 pypeline.
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.

4.6.4 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 nipype.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/nipype/trunk/nipype/interfaces/tests/foo_brain.n

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/nipype/trunk/nipype/interfaces/tests/foo_brain.n

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.n

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.n
```

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'))

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 absolue path, so the absolue 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/nipype/trunk/nipype/interfaces/tests/bar.nii'

In [77]: res = mybet.run()

In [78]: res.runtime.cmdline
Out[78]: 'bet foo.nii /Users/cburns/src/nipy-sf/nipype/trunk/nipype/interfaces/tests/bar.nii'

In [80]: res.interface.inputs.outfile
Out[80]: 'bar.nii'
```

4.7 W3C PROV support

4.7.1 Overview

We're using the the W3C PROV data model to capture and represent provenance in Nipype.
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 nipype import config
>>> config.enable_provenance()
```

4.8 Software using Nipype

4.8.1 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 Nipype Workflows and Interfaces.

4.8.2 BRAINSTools

BRAINSTools is a suite of tools for medical image processing focused on brain analysis.

4.8.3 Brain Imaging Pipelines (BIPs)

BIPs is a set of predefined Nipype workflows coupled with a graphical interface and ability to save and share workflow configurations. It provides both Nipype Workflows and Interfaces.

4.8.4 BROCCOLI

BROCCOLI is a piece of software for fast fMRI analysis on many core CPUs and GPUs. It provides Nipype Interfaces.

4.8.5 Forward

Forward is set of tools simplifying the preparation of accurate electromagnetic head models for EEG forward modeling. It uses Nipype Workflows and Interfaces.

4.8.6 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 Nipype Interfaces and Workflows.

4.8.7 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 Nipype Workflows and Interfaces.

4.8.8 Medimsight

Medimsight is a commercial service medical imaging cloud platform. It uses Nipype to interface with various neuroimaging software.

4.8.9 MIA

MIA MIA is a a toolkit for gray scale medical image analysis. It provides Nipype interfaces for easy integration with other software.

4.8.10 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 Nipype pipeline framework.

4.8.11 OpenfMRI

OpenfMRI is a repository for task based fMRI datasets. It uses Nipype for automated analysis of the deposited data.

4.8.12 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 Nipype to process the data.

4.8.13 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.

4.8.14 tract_querier

tract_querier is a White Matter Query Language tool. It provides Nipype interfaces.

Interfaces, Workflows and Examples

- Workflows

CHAPTER 5

workflows.data

5.1 get_flirt_schedule()

Link to code

CHAPTER 6

workflows.dmri.camino.connectivity_mapping

6.1 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).

6.1.1 Example

```
>>> from nipype.workflows.dmri.camino.connectivity_mapping import create_connectivity_pipeline
>>> conmapper = create_connectivity_pipeline("nipype_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()
```

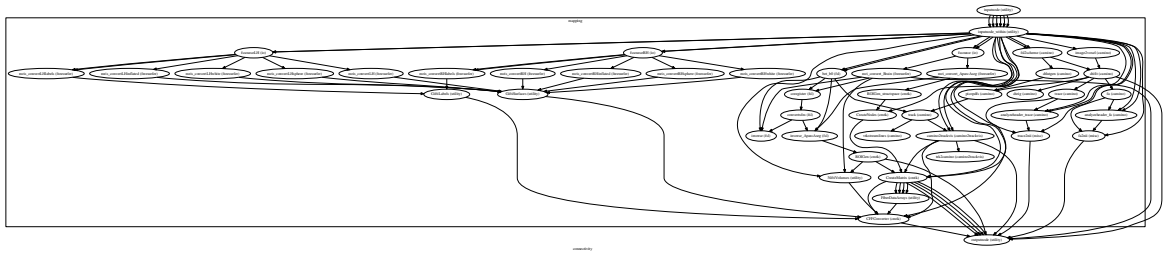
Inputs:

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

Outputs:

```
outputnode.connectome
outputnode.cmatrix
outputnode.gpickled_network
outputnode.fa
outputnode.struct
outputnode.trace
outputnode.tracts
outputnode.tensors
```

6.1.2 Graph



CHAPTER 7

workflows.dmri.camino.diffusion

7.1 create_camino_dti_pipeline()

Link to code

Creates a pipeline that does the same diffusion processing as in the 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.

7.1.1 Example

```
>>> import os
>>> nipype_camino_dti = create_camino_dti_pipeline("nipype_camino_dti")
>>> nipype_camino_dti.inputs.inputnode.dwi = os.path.abspath('dwi.nii')
>>> nipype_camino_dti.inputs.inputnode.bvecs = os.path.abspath('bvecs')
>>> nipype_camino_dti.inputs.inputnode.bvals = os.path.abspath('bvals')
>>> nipype_camino_dti.run()
```

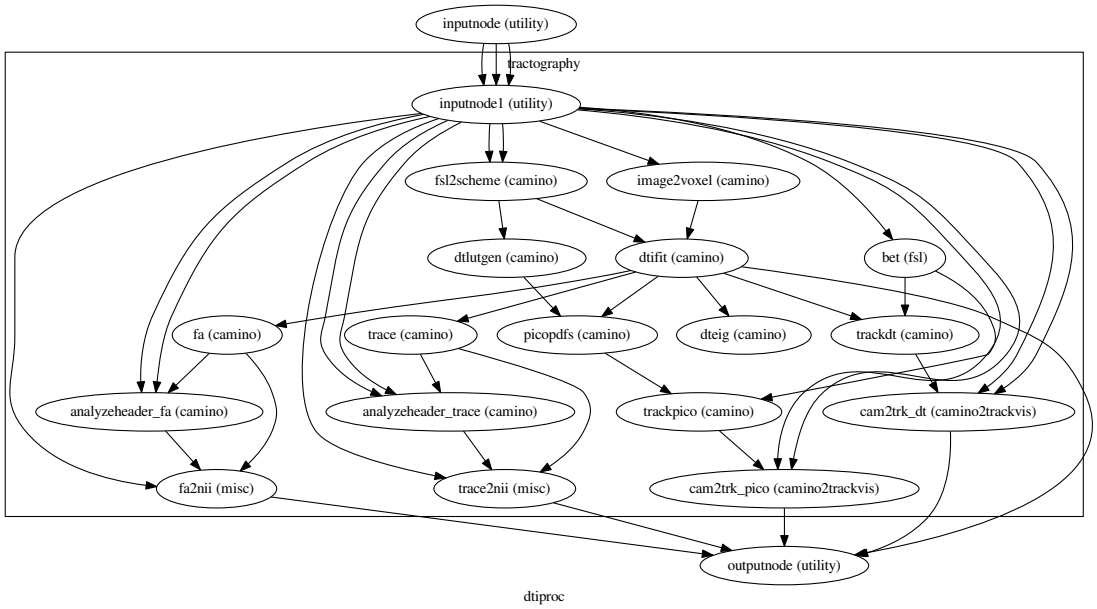
Inputs:

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

Outputs:

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

7.1.2 Graph



dtiproc

CHAPTER 8

workflows.dmri.camino.group_connectivity

8.1 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).

8.1.1 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=[['
>>> group_id = 'group1'
>>> l1pipeline = groupwork.create_group_connectivity_pipeline(group_list, group_id, data_dir, su
>>> l1pipeline.run()
```

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']])
```

CHAPTER 9

workflows.dmri.connectivity.group_connectivity

9.1 concatcsv()

Link to code

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

9.2 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.

9.2.1 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']
>>> l4pipeline = groupwork.create_average_networks_by_group_workflow(group_list, data_dir, subje
>>> l4pipeline.run()
```

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')
```

9.3 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.

9.3.1 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, sub
>>> l3pipeline.run()
```

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')
```

9.4 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.

9.4.1 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_d
>>> l3pipeline.run()
```

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')
```

9.5 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 MRtrix structural connectivity processing pipeline into a single CFF file for each group.

9.5.1 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,
>>> l2pipeline.run()
```

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
```

9.6 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 MRtrix structural connectivity processing pipeline into a single CFF file for each group.

9.6.1 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_di
>>> l2pipeline.run()
```

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
```

9.7 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

CHAPTER 10

workflows.dmri.connectivity.nx

10.1 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.

10.1.1 Example

```
>>> from nipype.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.ma
>>> csv.run()
```

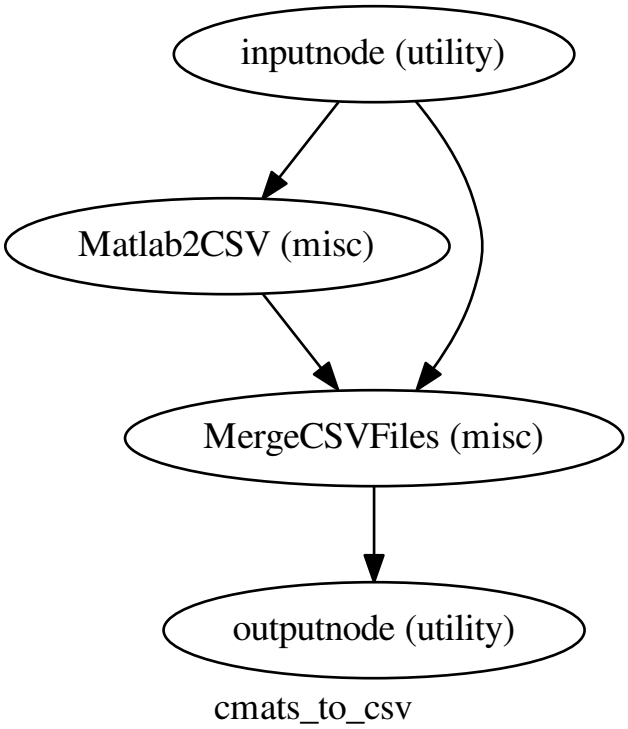
Inputs:

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

Outputs:

```
outputnode.csv_file
```

10.1.2 Graph



10.2 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.

10.2.1 Example

```
>>> from nipype.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()
```

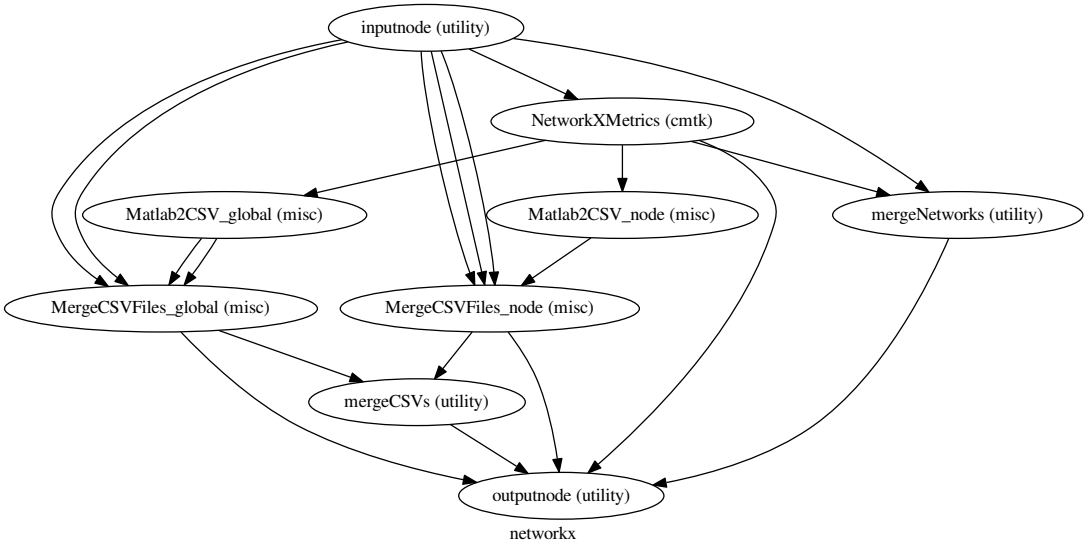
Inputs:

```
inputnode.extra_field
inputnode.network_file
```

Outputs:

```
    outputnode.network_files
    outputnode.csv_files
    outputnode.matlab_files
```

10.2.2 Graph



10.3 add_global_to_filename()

Link to code

10.4 add_nodal_to_filename()

Link to code

CHAPTER 11

workflows.dmri.dipy.denoise

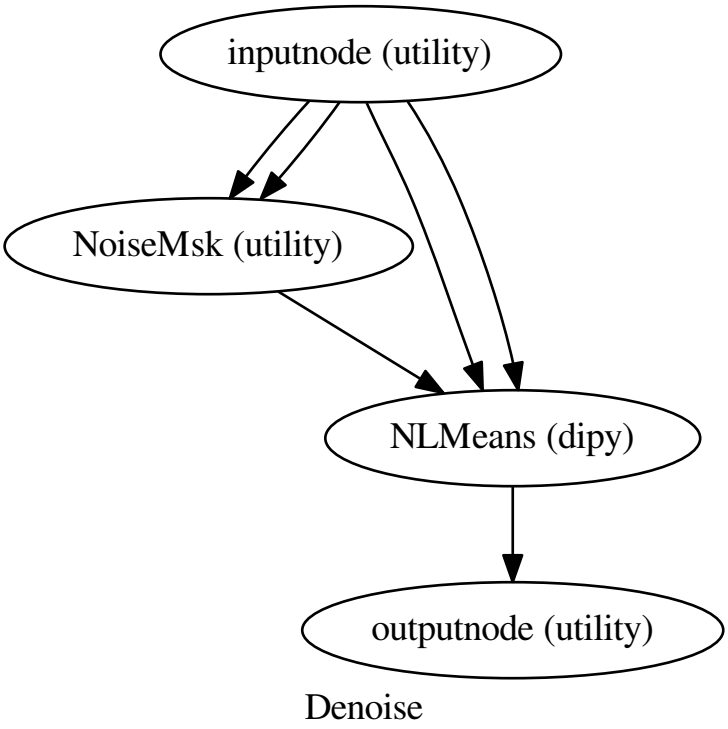
11.1 nlmeans_pipeline()

Link to code
Workflow that performs nlmeans denoising

11.1.1 Example

```
>>> from nipype.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()
```

11.1.2 Graph



11.2 bg_mask()

Link to code
Rough mask of background from brain masks

11.3 csf_mask()

Link to code
Artesanal mask of csf in T2w-like images

CHAPTER 12

workflows.dmri.fsl.artifacts

12.1 all_fmb_pipeline()

Link to code

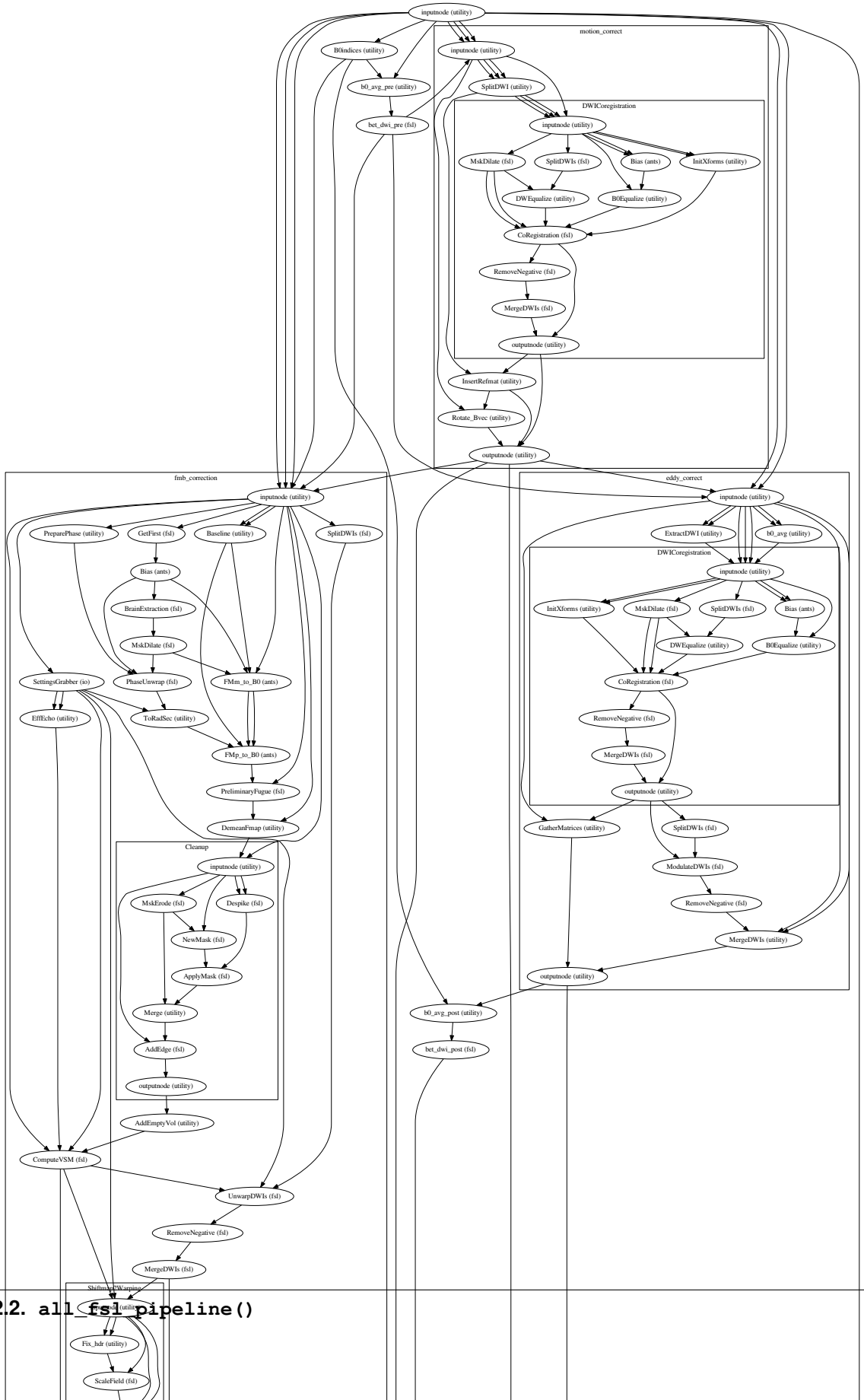
Builds a pipeline including three artifact corrections: head-motion correction (HMC), susceptibility-derived distortion correction (SDC), and Eddy currents-derived distortion correction (ECC).
The displacement fields from each kind of distortions are combined. Thus, only one interpolation occurs between input data and result.

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

12.1.1 Examples

```
>>> from nipype.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()
```

12.1.2 Graph


inputnode (utility)
motion_correct
B0indices (utility)
inputnode (utility)
b0_avg_pre (utility)
SplitDWI (utility)
DWICoregistration
bet_dwi_pre (fsl)
inputnode (utility)
MskDilate (fsl)
SplitDWIs (fsl)
Bias (ants)
InitXforms (utility)
DWEqualize (utility)
B0Equalize (utility)
CoRegistration (fsl)
RemoveNegative (fsl)
MergeDWIs (fsl)
outputnode (utility)
InsertRefmat (utility)
Rotate_Bvec (utility)
outputnode (utility)
fmb_correction
eddy_correct
inputnode (utility)
inputnode (utility)
PrepareFMap (utility)
GetFirst (fsl)
Baseline (utility)
SplitDWIs (fsl)
ExtractDWI (utility)
b0_avg (utility)
DWICoregistration
Bias (ants)
inputnode (utility)
BrainExtraction (fsl)
InitXforms (utility)
MskDilate (fsl)
SplitDWIs (fsl)
Bias (ants)
MskDilate (fsl)
DWEqualize (utility)
B0Equalize (utility)
SettingsGrabber (io)
PhaseUnwrap (fsl)
FMm_to_B0 (ants)
CoRegistration (fsl)
EffEcho (utility)
ToRadSec (utility)
RemoveNegative (fsl)
FMp_to_B0 (ants)
MergeDWIs (fsl)
PreliminaryFugue (fsl)
outputnode (utility)
DemeanFmap (utility)
GatherMatrices (utility)
SplitDWIs (fsl)
Cleanup
inputnode (utility)
ModulateDWIs (fsl)
MskErode (fsl)
Despike (fsl)
RemoveNegative (fsl)
NewMask (fsl)
MergeDWIs (utility)
ApplyMask (fsl)
outputnode (utility)
Merge (utility)
b0_avg_post (utility)
AddEdge (fsl)
bet_dwi_post (fsl)
outputnode (utility)
AddEmptyVol (utility)
ComputeVSM (fsl)
UnwarpDWIs (fsl)
RemoveNegative (fsl)
MergeDWIs (fsl)
ShiftmapDWarping
Fix_hdr (utility)
ScaleField (fsl)

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]*.

12.2.1 Examples

```
>>> from nipype.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()
```

12.2.2 Graph

12.3 `all_peb_pipeline()`

Link to code

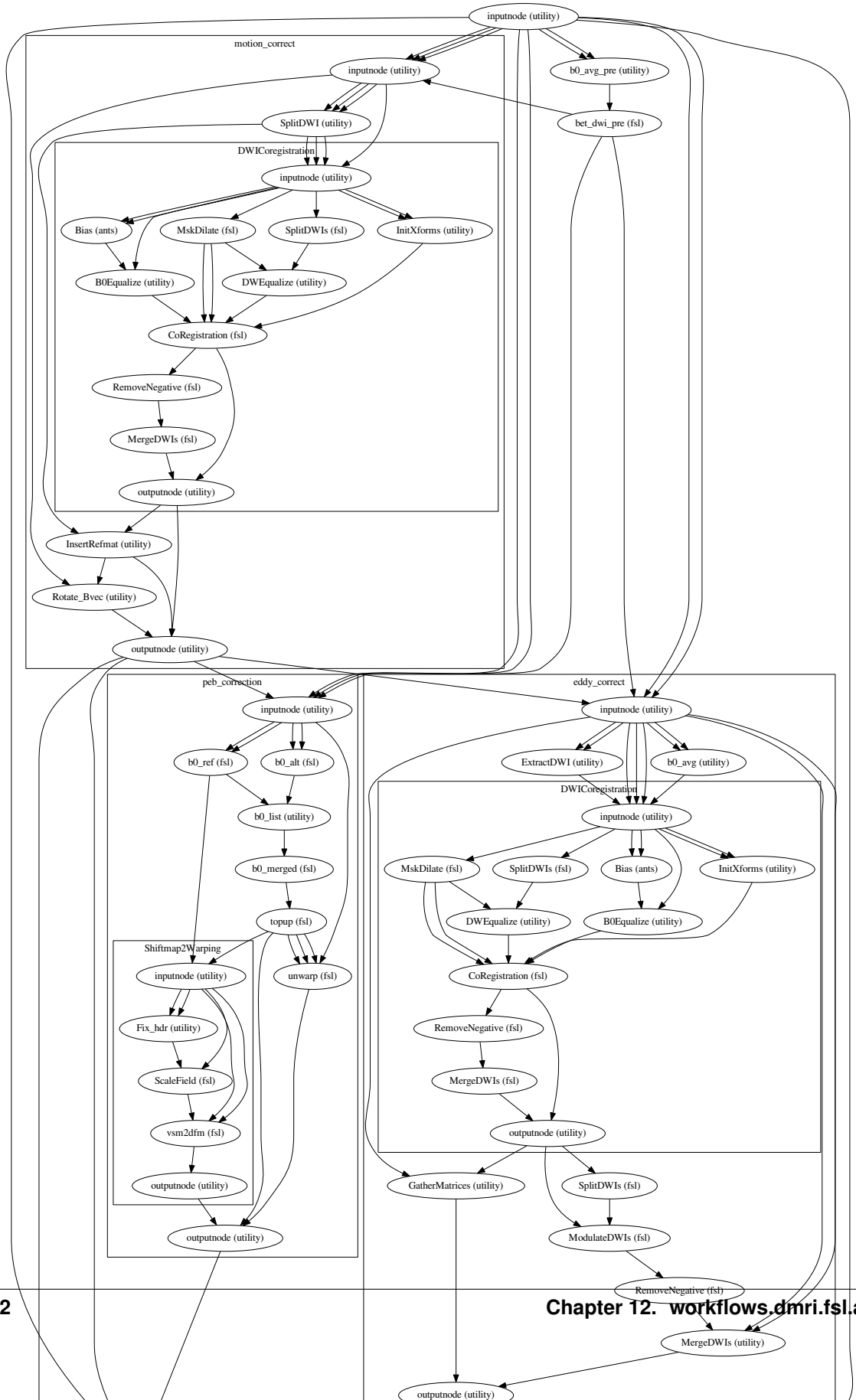
Builds a pipeline including three artifact corrections: head-motion correction (HMC), susceptibility-derived distortion correction (SDC), and Eddy currents-derived distortion correction (ECC).

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

12.3.1 Examples

```
>>> from nipype.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'
>>> allcorr.inputs.inputnode.in_bval = 'diffusion.bval'
>>> allcorr.inputs.inputnode.in_bvec = 'diffusion.bvec'
>>> allcorr.run()
```

12.3.2 Graph


inputnode (utility)
motion_correct
inputnode (utility)
b0_avg_pre (utility)
SplitDWI (utility)
bet_dwi_pre (fsl)
DWICoregistration
inputnode (utility)
Bias (ants)
MskDilate (fsl)
SplitDWIs (fsl)
InitXforms (utility)
B0Equalize (utility)
DWEqualize (utility)
CoRegistration (fsl)
RemoveNegative (fsl)
MergeDWIs (fsl)
outputnode (utility)
InsertRefmat (utility)
Rotate_Bvec (utility)
outputnode (utility)
peb_correction
inputnode (utility)
b0_ref (fsl)
b0_alt (fsl)
b0_list (utility)
b0_merged (fsl)
topup (fsl)
Shiftmap2Warping
inputnode (utility)
Fix_hdr (utility)
ScaleField (fsl)
vsm2dfm (fsl)
outputnode (utility)
unwarp (fsl)
outputnode (utility)
eddy_correct
inputnode (utility)
ExtractDWI (utility)
b0_avg (utility)
DWICoregistration
inputnode (utility)
MskDilate (fsl)
SplitDWIs (fsl)
Bias (ants)
InitXforms (utility)
DWEqualize (utility)
B0Equalize (utility)
CoRegistration (fsl)
RemoveNegative (fsl)
MergeDWIs (fsl)
outputnode (utility)
GatherMatrices (utility)
SplitDWIs (fsl)
ModulateDWIs (fsl)
RemoveNegative (fsl)
MergeDWIs (utility)
outputnode (utility)

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

12.4.1 Example

```
>>> from nipype.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()
```

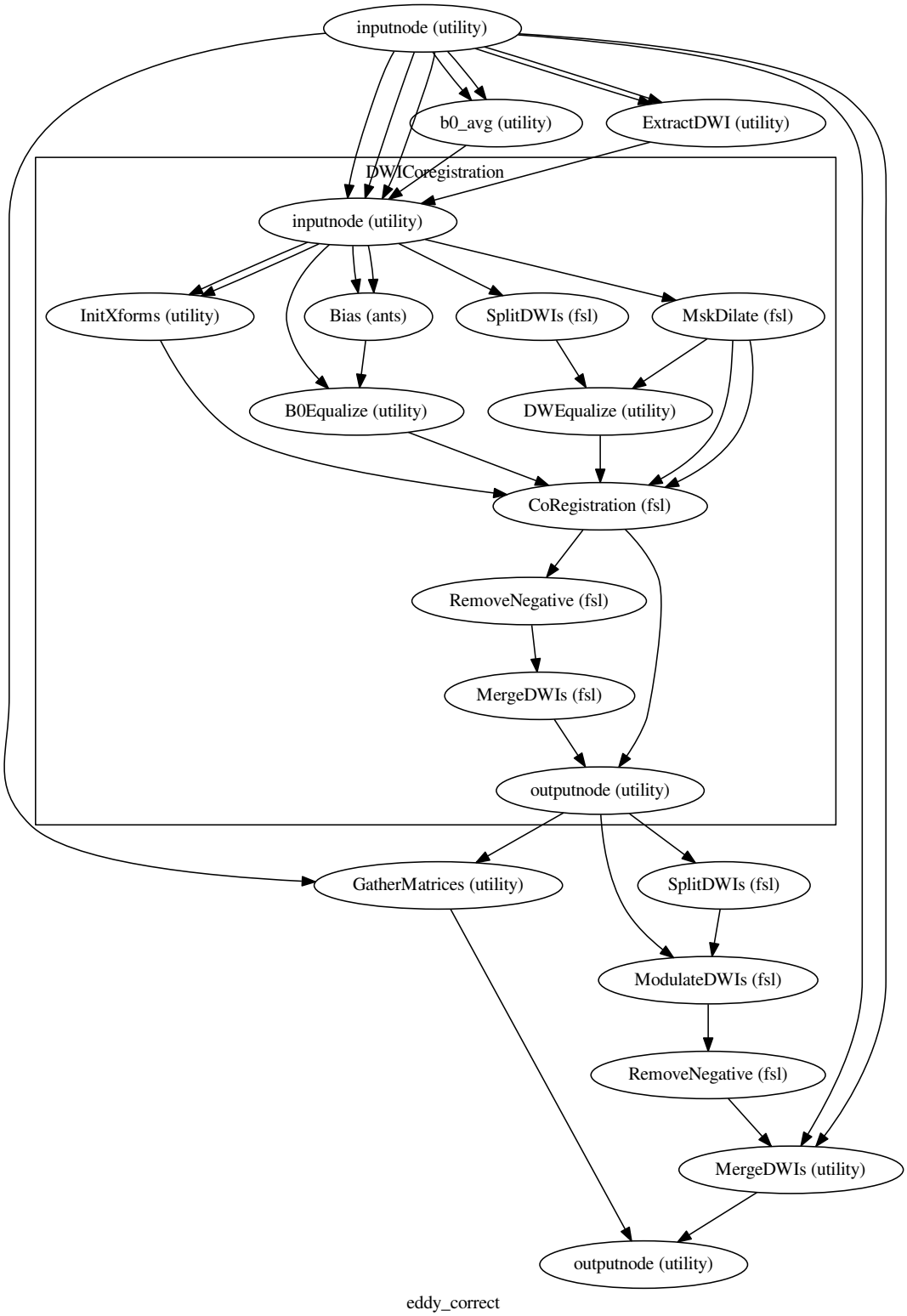
Inputs:

```
inputnode.in_file - input dwi file
inputnode.in_mask - weights mask of reference image (a file with data range sin [0.0, 1.0], indi
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
```

12.4.2 Graph



eddy_correct

12.5 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

12.5.1 Example

```
>>> from nipype.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()
```

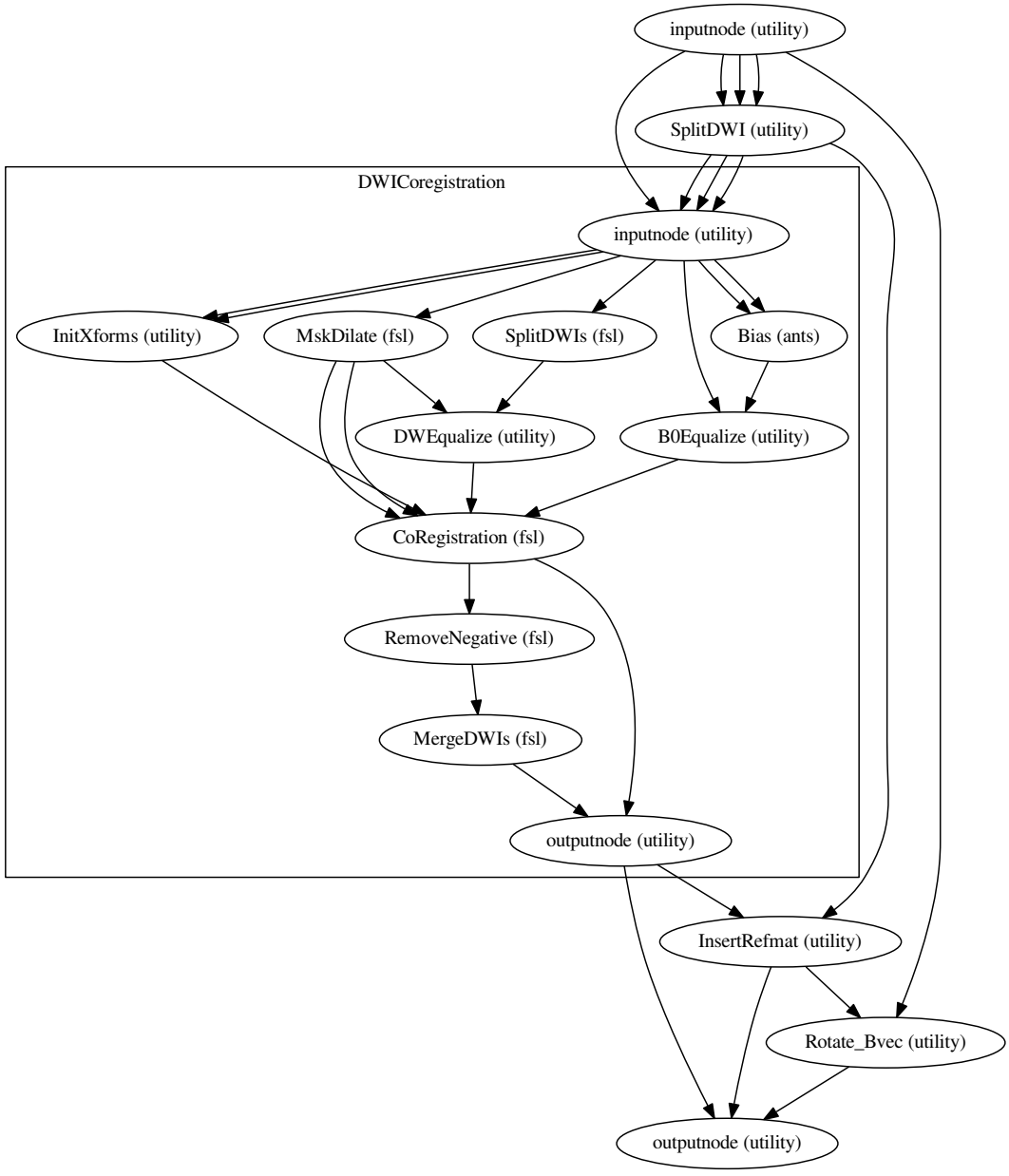
Inputs:

```
inputnode.in_file - input dwi file
inputnode.in_mask - weights mask of reference image (a file with data range in [0.0, 1.0], indic
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
```

12.5.2 Graph



12.6 `remove_bias()`

Link to code

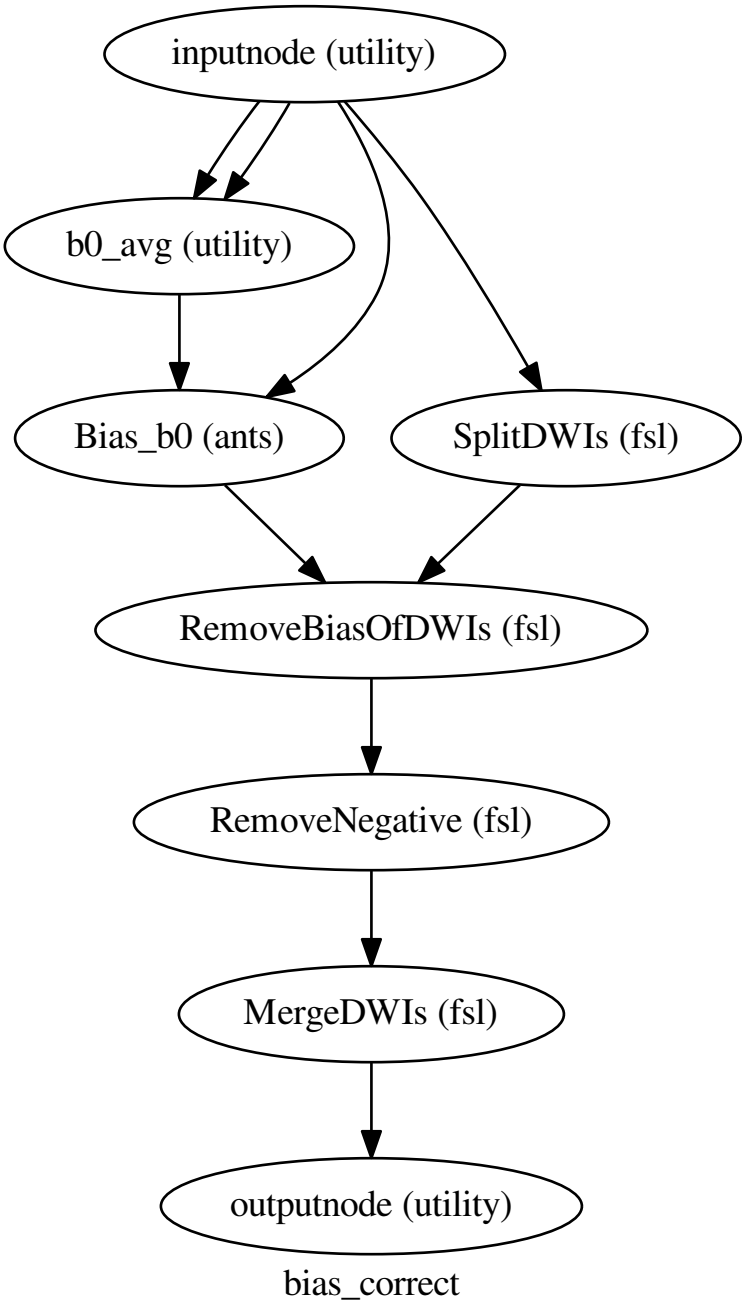
This workflow estimates a single multiplicative bias field from the averaged *b0* image, as suggested in *[Jeurissen2014]*.

References

12.6.1 Example

```
>>> from nipype.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()
```

12.6.2 Graph



12.7 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.

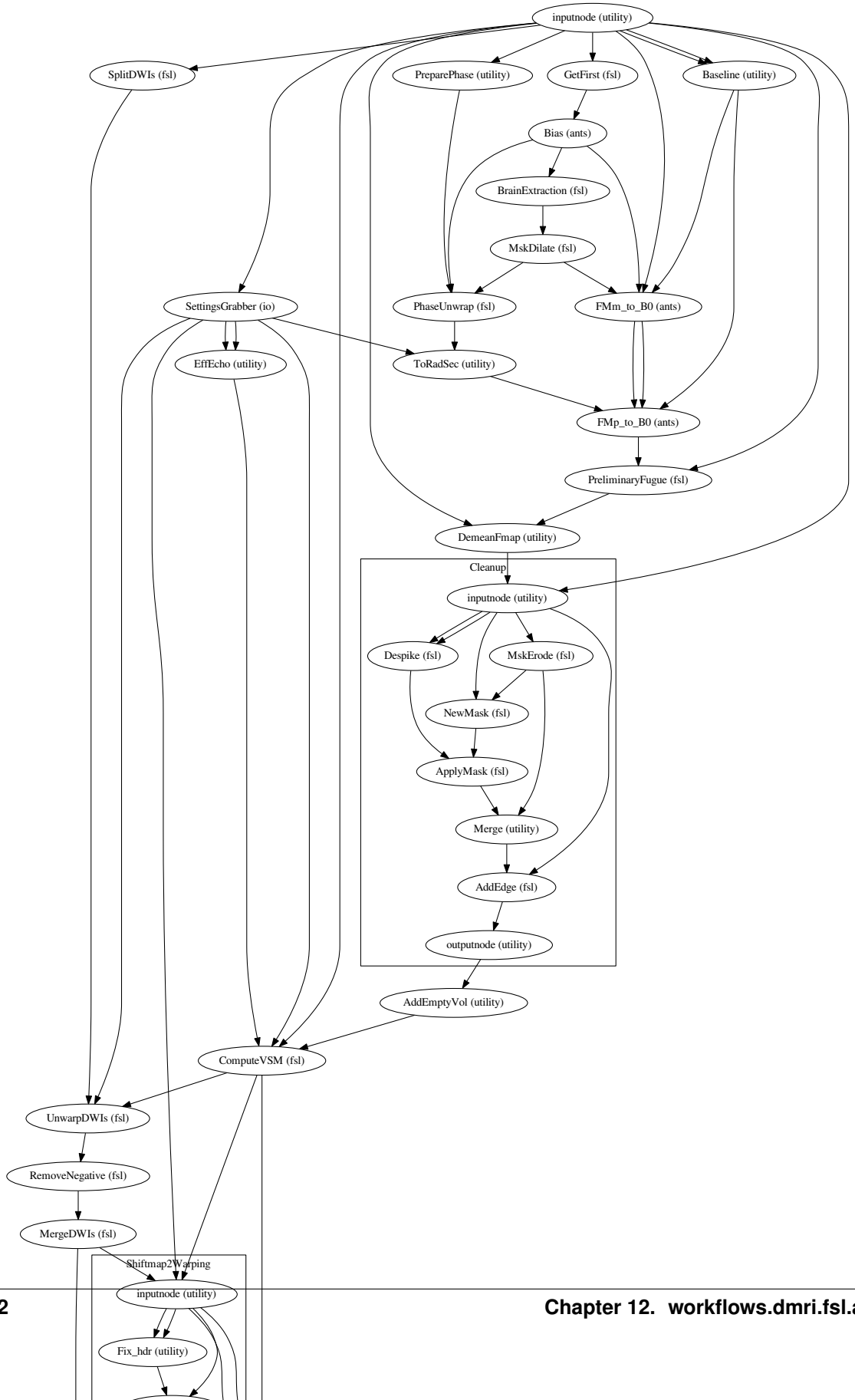
12.7.1 Example

```
>>> from nipype.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()
```

Warning: Only SIEMENS format fieldmaps are supported.

References

12.7.2 Graph


inputnode (utility)
SplitDWIs (fsl)
PreparePhase (utility)
GetFirst (fsl)
Baseline (utility)
Bias (ants)
BrainExtraction (fsl)
MskDilate (fsl)
SettingsGrabber (io)
PhaseUnwrap (fsl)
FMm_to_B0 (ants)
EffEcho (utility)
ToRadSec (utility)
FMp_to_B0 (ants)
PreliminaryFugue (fsl)
DemeanFmap (utility)
Cleanup
inputnode (utility)
Despike (fsl)
MskErode (fsl)
NewMask (fsl)
ApplyMask (fsl)
Merge (utility)
AddEdge (fsl)
outputnode (utility)
AddEmptyVol (utility)
ComputeVSM (fsl)
UnwarpDWIs (fsl)
RemoveNegative (fsl)
MergeDWIs (fsl)
Shiftmap2Warping
inputnode (utility)
Fix_hdr (utility)

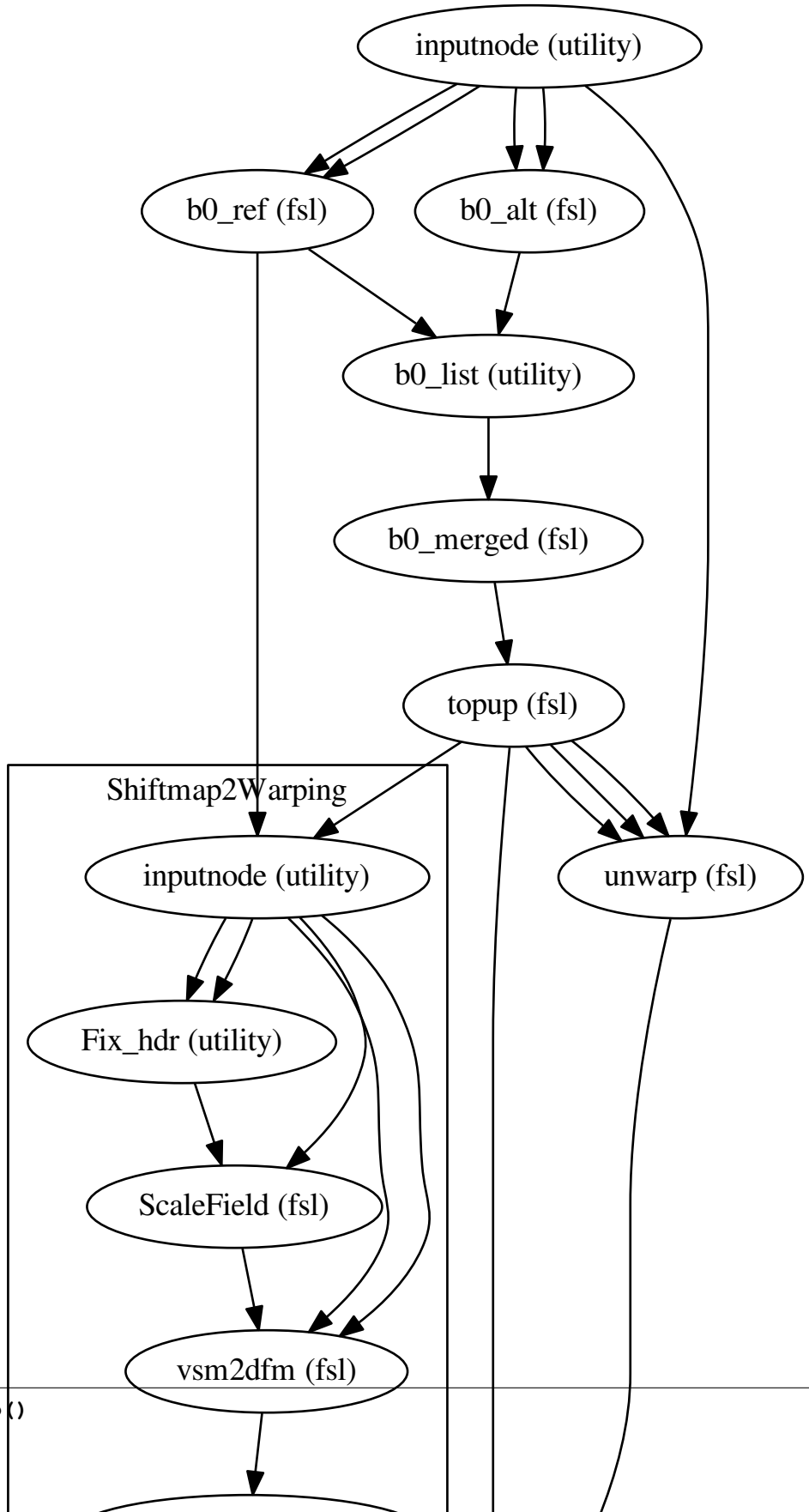
SDC stands for susceptibility distortion correction. PEB stands for phase-encoding-based.
The phase-encoding-based (PEB) method implements SDC by acquiring diffusion images with two different enconding directions *[Andersson2003]*. The most typical case is acquiring with opposed phase-gradient blips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

12.8.1 Example

```
>>> from nipype.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()
```

References

12.8.2 Graph


inputnode (utility)
b0_ref (fsl)
b0_alt (fsl)
b0_list (utility)
b0_merged (fsl)
topup (fsl)
Shiftmap2Warping
inputnode (utility)
unwarp (fsl)
Fix_hdr (utility)
ScaleField (fsl)
vsm2dfm (fsl)

CHAPTER 13

workflows.dmri.fsl.dti

13.1 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).

13.1.1 Example

```
>>> from nipype.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('nipype_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')
```

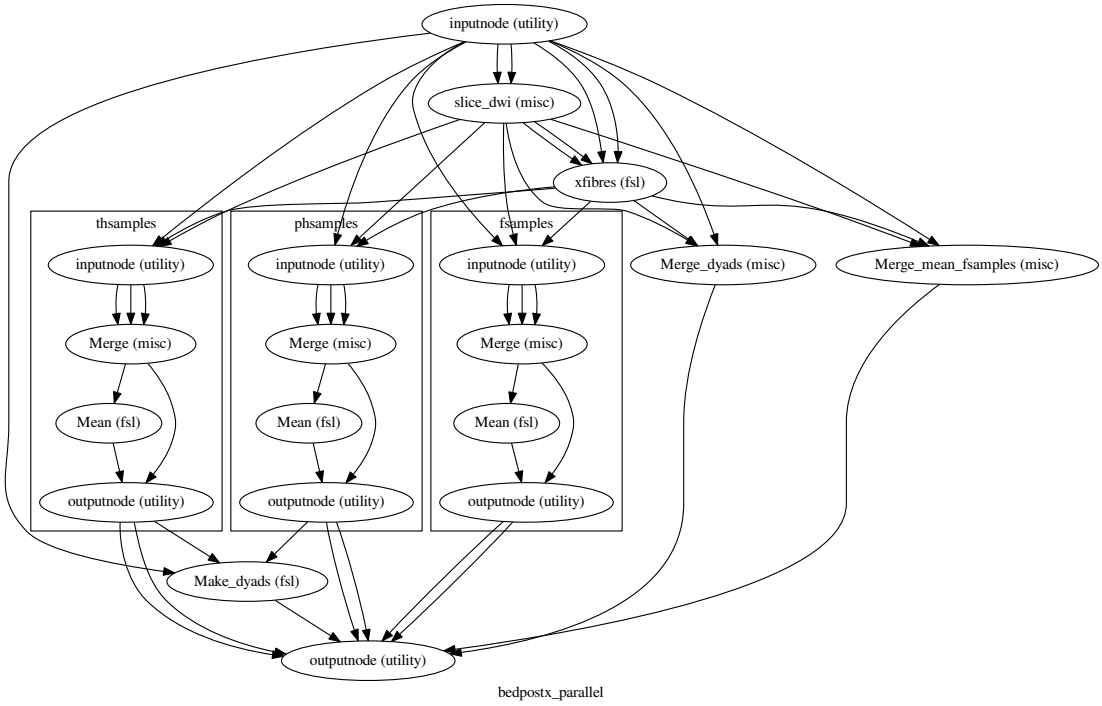
Inputs:

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

Outputs:

```
outputnode wraps all XFibres outputs
```

13.1.2 Graph



13.2 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).

13.2.1 Example

```
>>> from nipype.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('nipype_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()
```

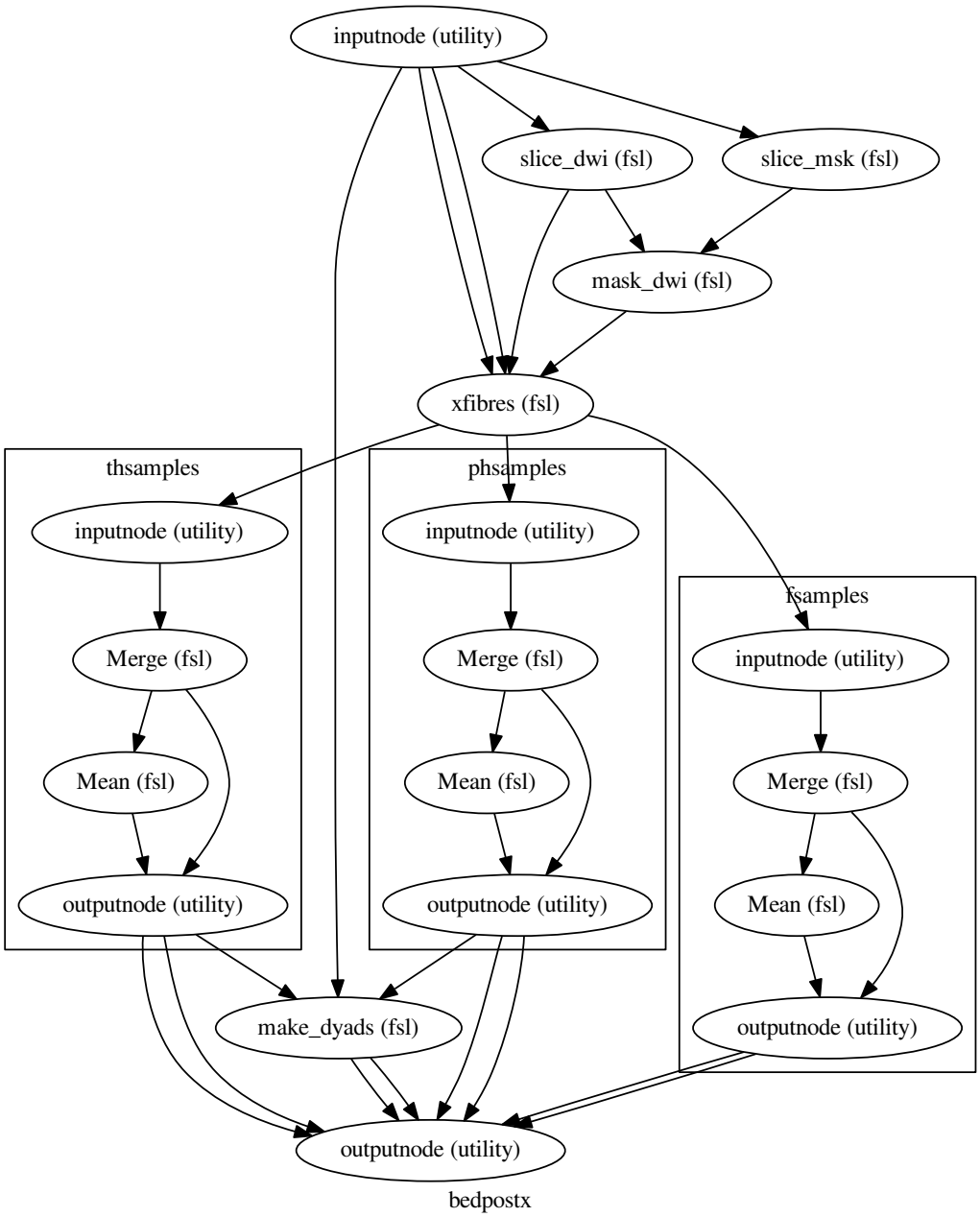
Inputs:

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

Outputs:

```
outputnode wraps all XFibres outputs
```

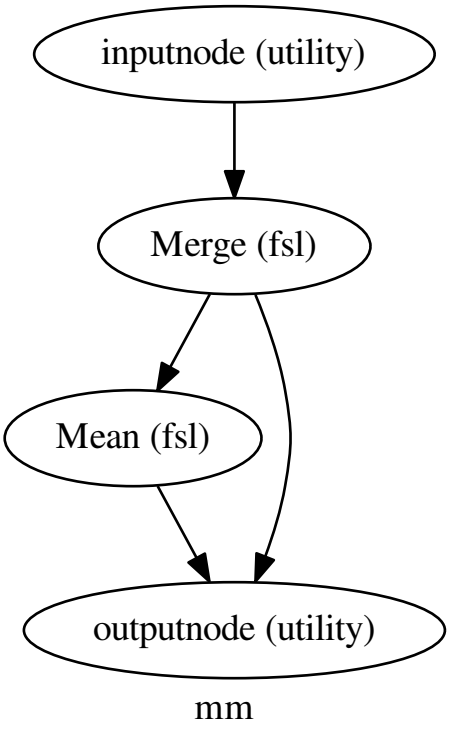
13.2.2 Graph



13.3 `merge_and_mean()`

Link to code

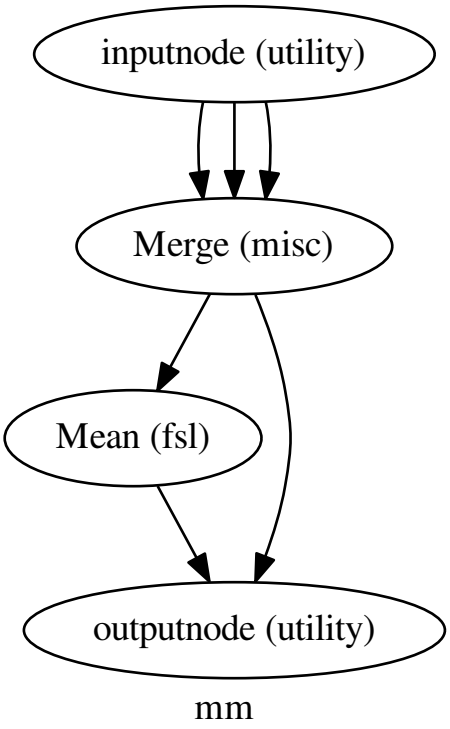
13.3.1 Graph



13.4 `merge_and_mean_parallel()`

Link to code

13.4.1 Graph



13.5 `transpose()`

Link to code

workflows.dmri.fsl.epi

14.1 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 `nipype.workflows.dmri.preprocess.epi.all_fmb_pipeline()` or `nipype.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).

14.1.1 Example

```
>>> nipype_dmri_preprocess = create_dmri_preprocessing('nipype_dmri_prep')
>>> nipype_dmri_preprocess.inputs.inputnode.in_file = 'diffusion.nii'
>>> nipype_dmri_preprocess.inputs.inputnode.in_bvec = 'diffusion.bvec'
>>> nipype_dmri_preprocess.inputs.inputnode.ref_num = 0
>>> nipype_dmri_preprocess.inputs.inputnode.fieldmap_mag = 'magnitude.nii'
>>> nipype_dmri_preprocess.inputs.inputnode.fieldmap_pha = 'phase.nii'
>>> nipype_dmri_preprocess.inputs.inputnode.te_diff = 2.46
>>> nipype_dmri_preprocess.inputs.inputnode.epi_echospacing = 0.77
>>> nipype_dmri_preprocess.inputs.inputnode.epi_rev_encoding = False
>>> nipype_dmri_preprocess.inputs.inputnode.pi_accel_factor = True
>>> nipype_dmri_preprocess.run()
```

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 f
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 d
```

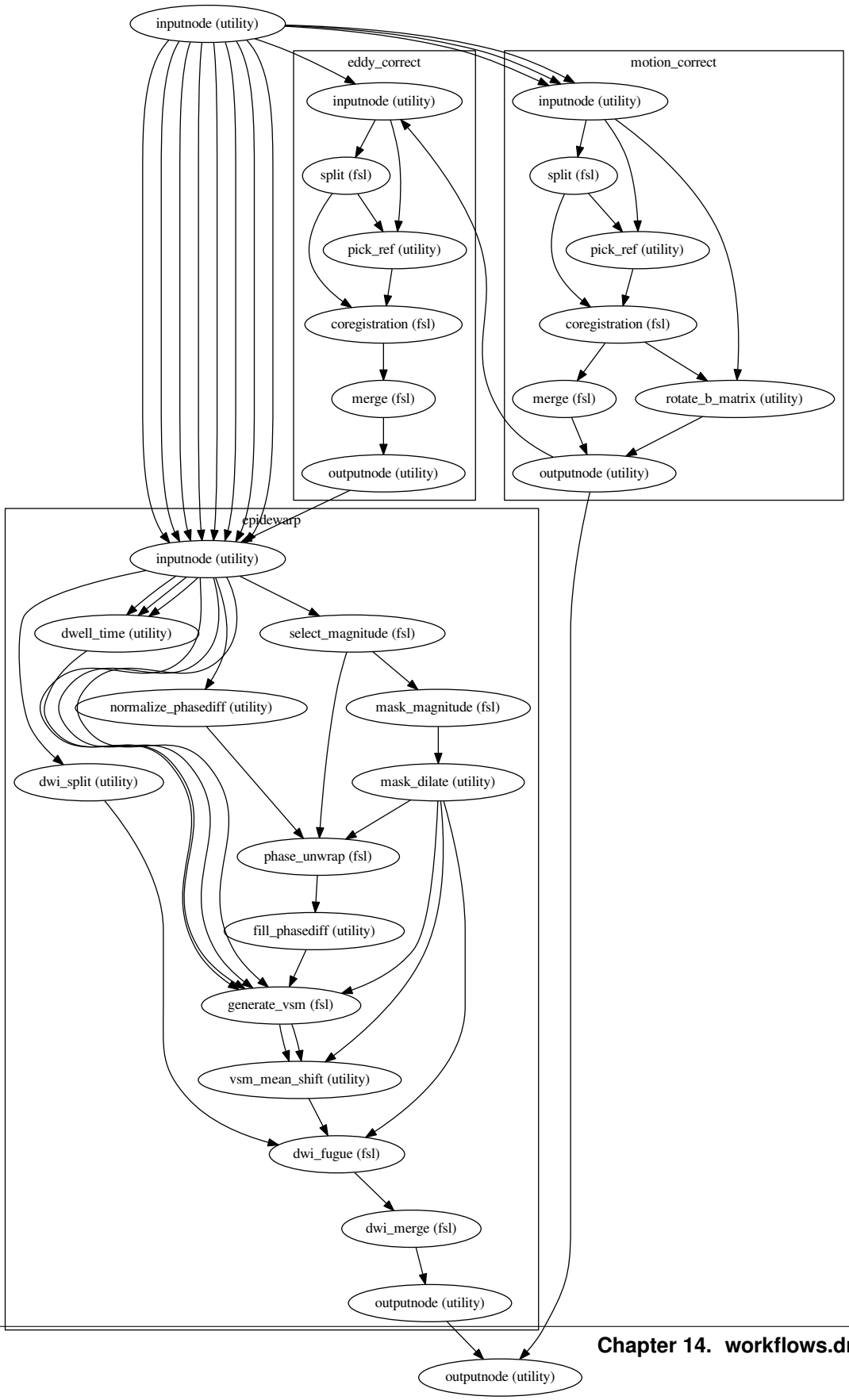
Outputs:

```
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)
```

14.1.2 Graph



dMRI_preprocessing

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.

14.2.1 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()
```

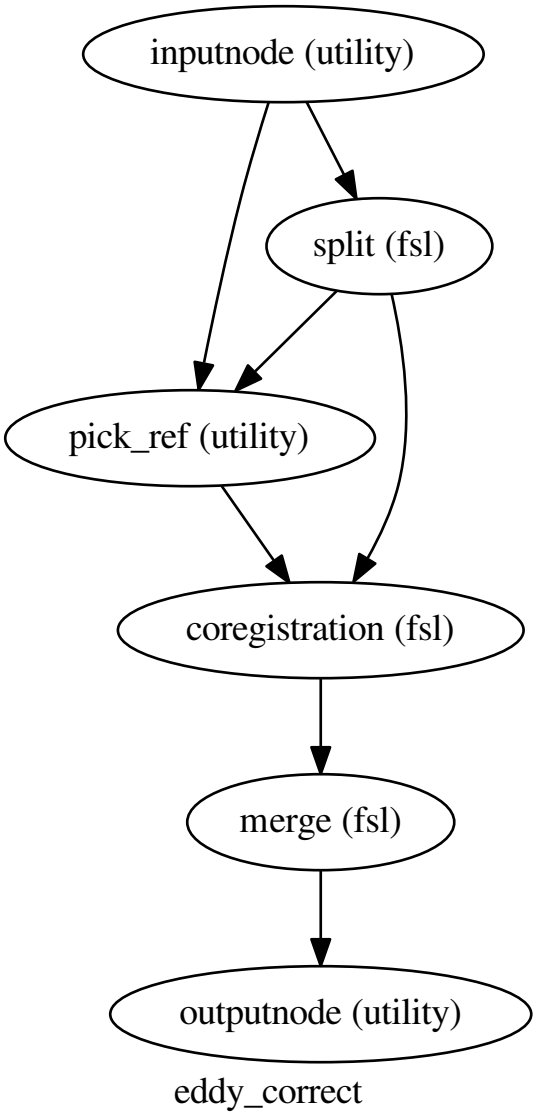
Inputs:

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

Outputs:

```
outputnode.eddy_corrected
```

14.2.2 Graph



14.3 `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 `nipype.workflows.dmri.preprocess.epi.sdc_fmb()` instead.

14.3.1 Example

```
>>> nipype_epicorrect = create_epidewarp_pipeline('nipype_epidewarp', fieldmap_registration=Fals
>>> nipype_epicorrect.inputs.inputnode.in_file = 'diffusion.nii'
>>> nipype_epicorrect.inputs.inputnode.fieldmap_mag = 'magnitude.nii'
>>> nipype_epicorrect.inputs.inputnode.fieldmap_pha = 'phase.nii'
>>> nipype_epicorrect.inputs.inputnode.te_diff = 2.46
>>> nipype_epicorrect.inputs.inputnode.epi_echospacing = 0.77
>>> nipype_epicorrect.inputs.inputnode.epi_rev_encoding = False
>>> nipype_epicorrect.inputs.inputnode.ref_num = 0
>>> nipype_epicorrect.inputs.inputnode.pi_accel_factor = 1.0
>>> nipype_epicorrect.run()
```

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 shi
inputnode.ref_num - The reference volume (B=0 in dMRI or a central frame in fMRI)
```

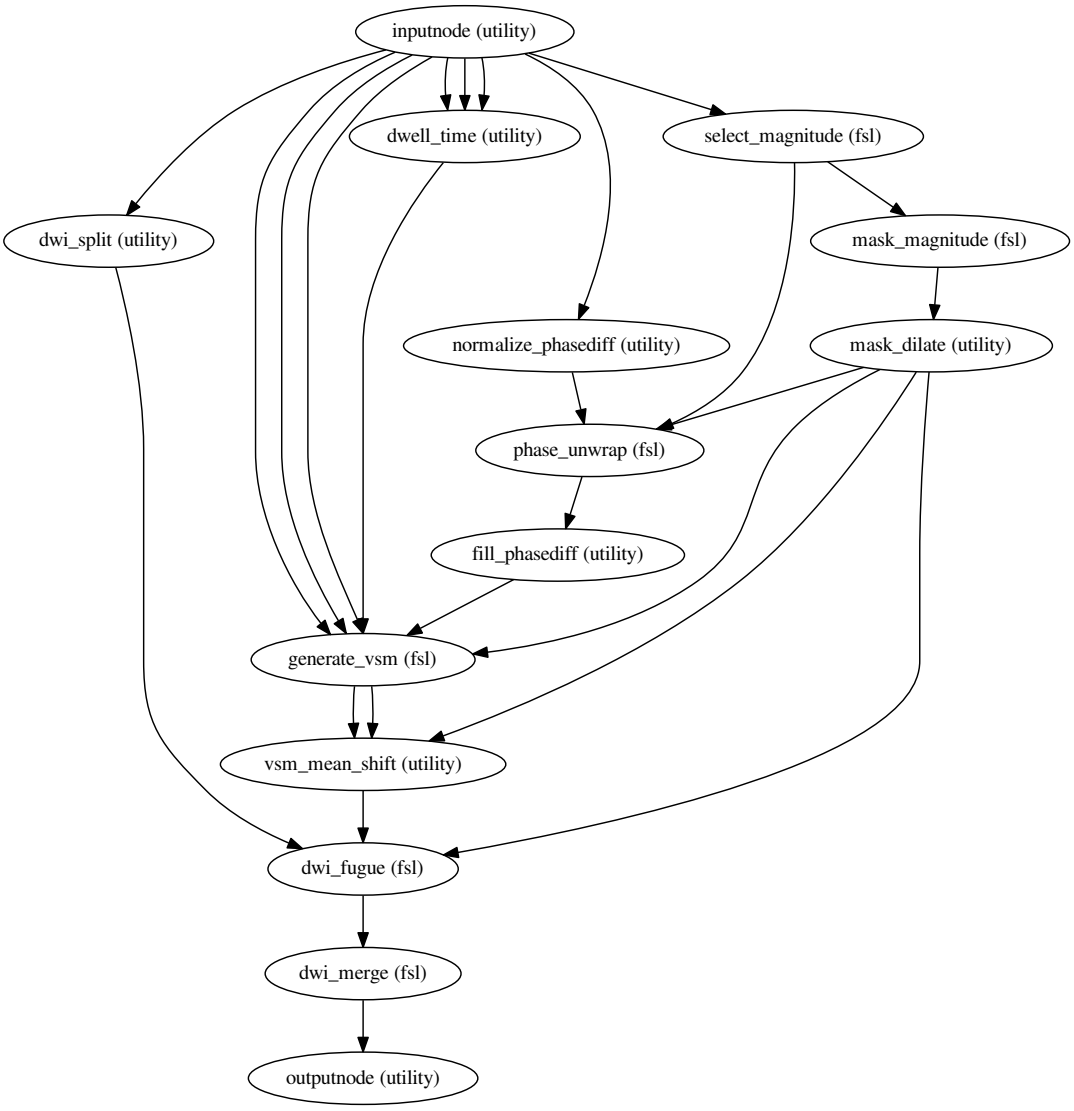
Outputs:

```
outputnode.epi_corrected
```

Optional arguments:

```
fieldmap_registration - True if registration to fieldmap should be done (default False)
```

14.3.2 Graph



epidewarp

14.4 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 (Leemans 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 `nipype.workflows.dmri.preprocess.epi.hmc_pipeline()` instead.

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

14.4.1 Example

```
>>> nipype_motioncorrect = create_motion_correct_pipeline('nipype_motioncorrect')
>>> nipype_motioncorrect.inputs.inputnode.in_file = 'diffusion.nii'
>>> nipype_motioncorrect.inputs.inputnode.in_bvec = 'diffusion.bvec'
>>> nipype_motioncorrect.inputs.inputnode.ref_num = 0
>>> nipype_motioncorrect.run()
```

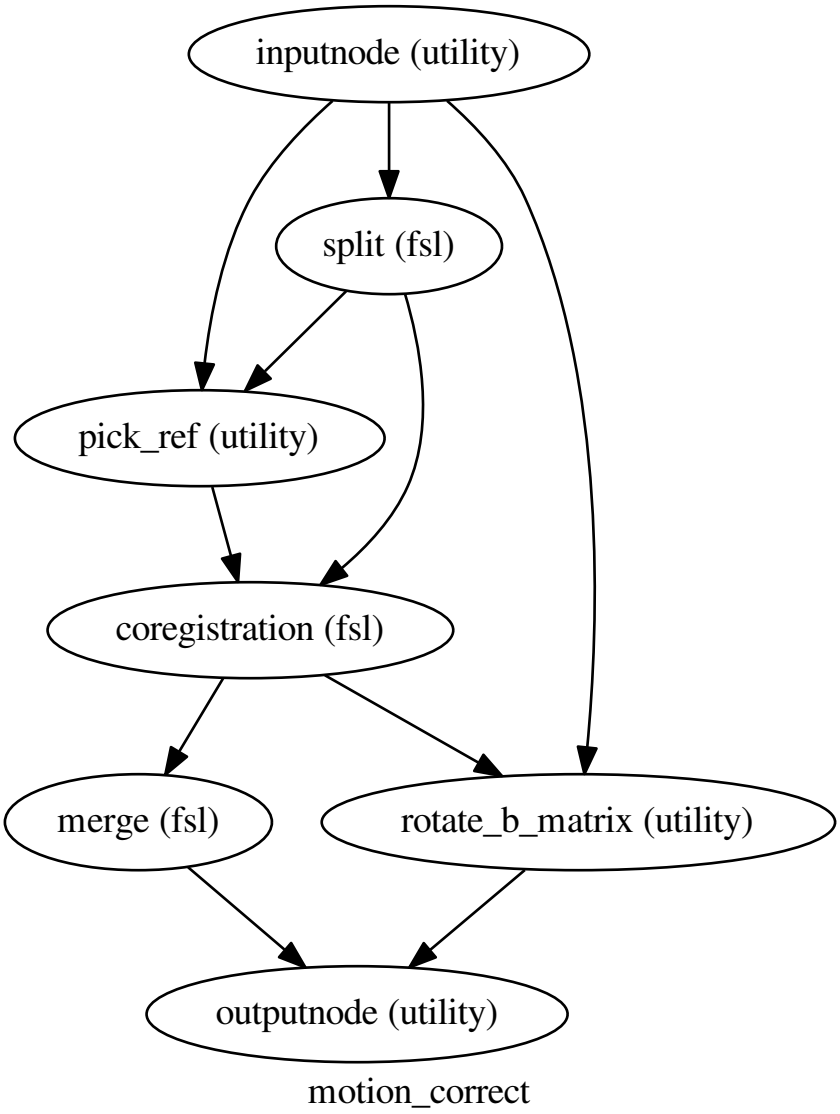
Inputs:

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

Outputs:

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

14.4.2 Graph



14.5 fieldmap_correction()

Link to code

Deprecated since version 0.9.3: Use `nipype.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.

14.5.1 Example

```
>>> nipype_epicorrect = fieldmap_correction('nipype_epidewarp')
>>> nipype_epicorrect.inputs.inputnode.in_file = 'diffusion.nii'
>>> nipype_epicorrect.inputs.inputnode.in_mask = 'brainmask.nii'
>>> nipype_epicorrect.inputs.inputnode.fieldmap_pha = 'phase.nii'
>>> nipype_epicorrect.inputs.inputnode.fieldmap_mag = 'magnitude.nii'
>>> nipype_epicorrect.inputs.inputnode.te_diff = 2.46
>>> nipype_epicorrect.inputs.inputnode.epi_echospacing = 0.77
>>> nipype_epicorrect.inputs.inputnode.encoding_direction = 'y'
>>> nipype_epicorrect.run()
```

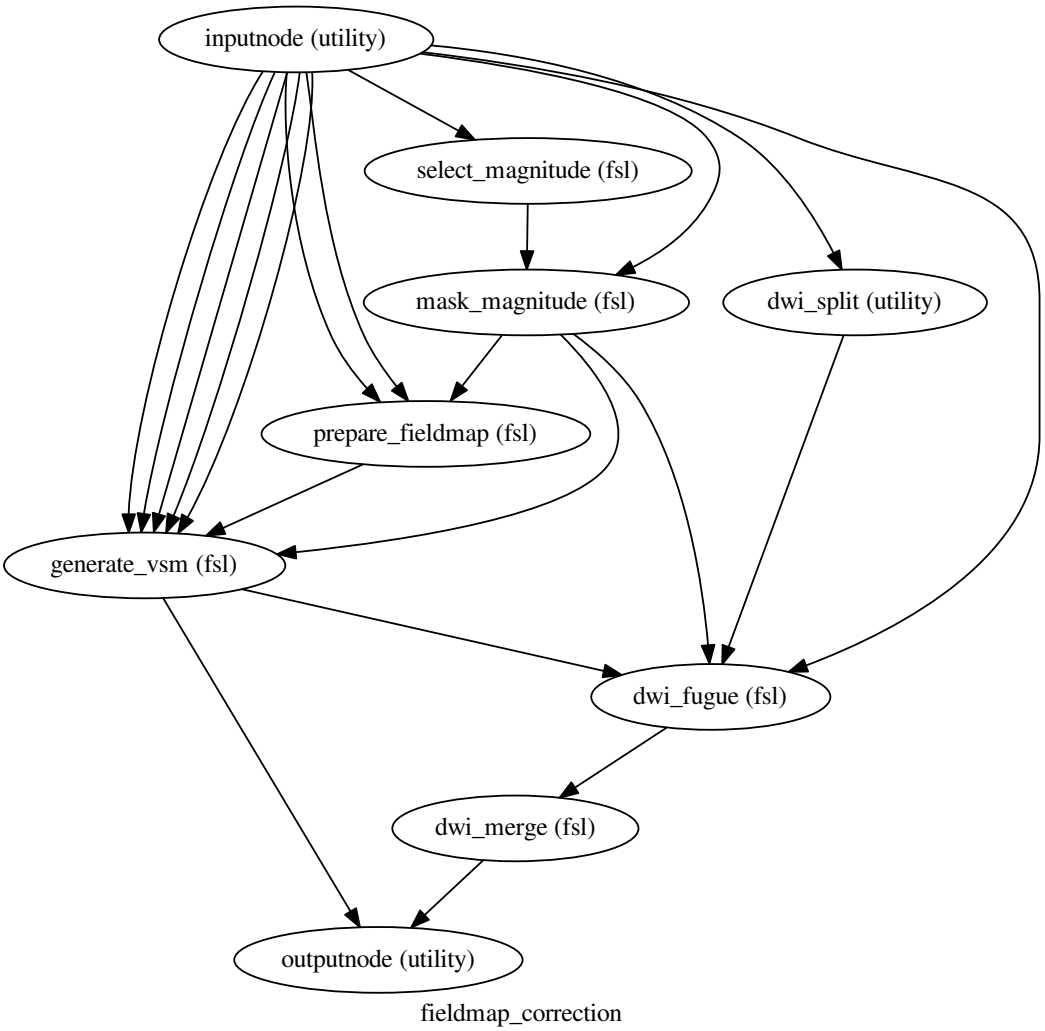
Inputs:

```
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 magnitud 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
inputnode.epi_echospacing - The effective echo spacing (aka dwell time) in msec. of the EPI sequ
                            EPI was acquired with parallel imaging, then the effective echo spac
                            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 shi
```

Outputs:

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

14.5.2 Graph



fieldmap_correction

14.6 topup_correction()

Link to code

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

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

14.6.1 Example

```
>>> nipype_epicorrect = topup_correction('nipype_topup')
>>> nipype_epicorrect.inputs.inputnode.in_file_dir = 'epi.nii'
>>> nipype_epicorrect.inputs.inputnode.in_file_rev = 'epi_rev.nii'
>>> nipype_epicorrect.inputs.inputnode.encoding_direction = ['y', 'y-']
>>> nipype_epicorrect.inputs.inputnode.ref_num = 0
>>> nipype_epicorrect.run()
```

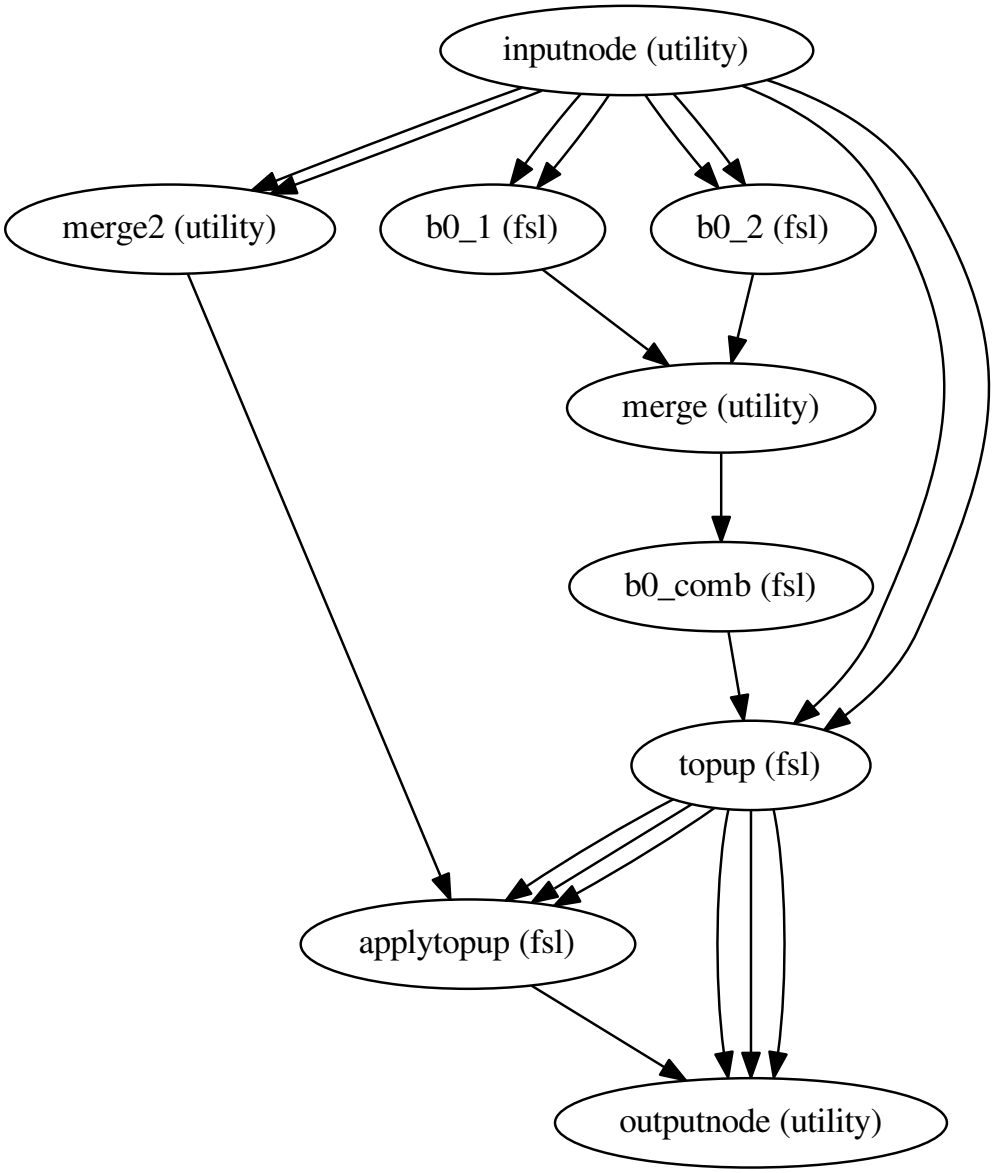
Inputs:

```
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
```

14.6.2 Graph



topup_correction

CHAPTER 15

workflows.dmri.fsl.tbss

15.1 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

15.1.1 Example

```
>>> from nipype.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']
```

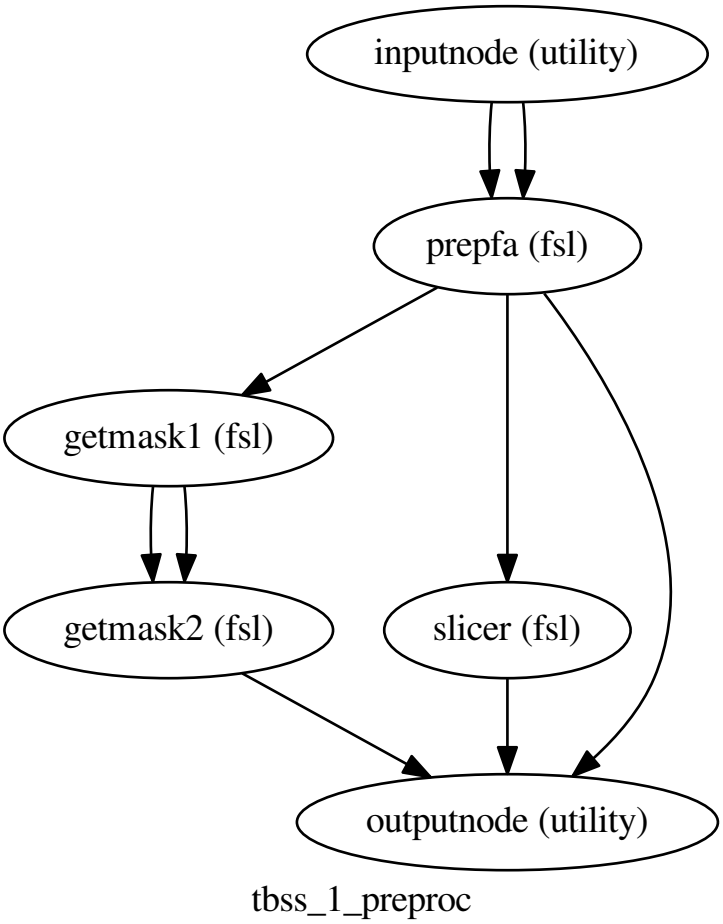
Inputs:

```
inputnode.fa_list
```

Outputs:

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

15.1.2 Graph



15.2 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.

15.2.1 Example

```
>>> from nipype.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']
```

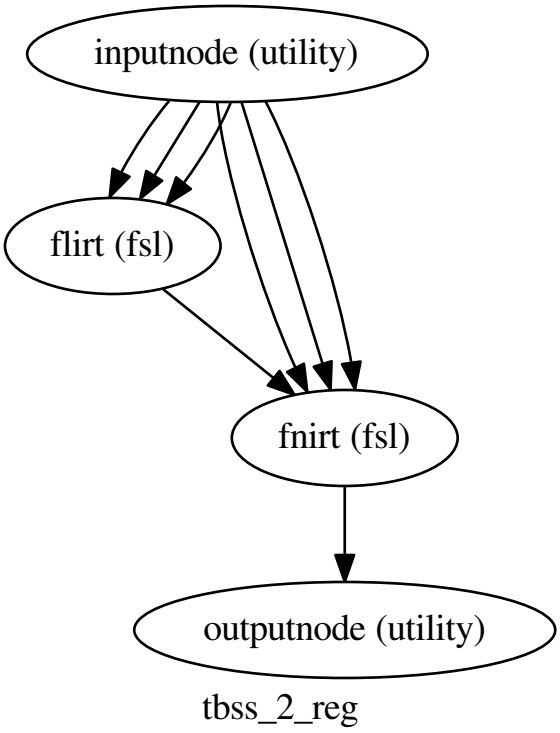
Inputs:

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

Outputs:

```
outputnode.field_list
```

15.2.2 Graph



15.3 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').

15.3.1 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.n
```

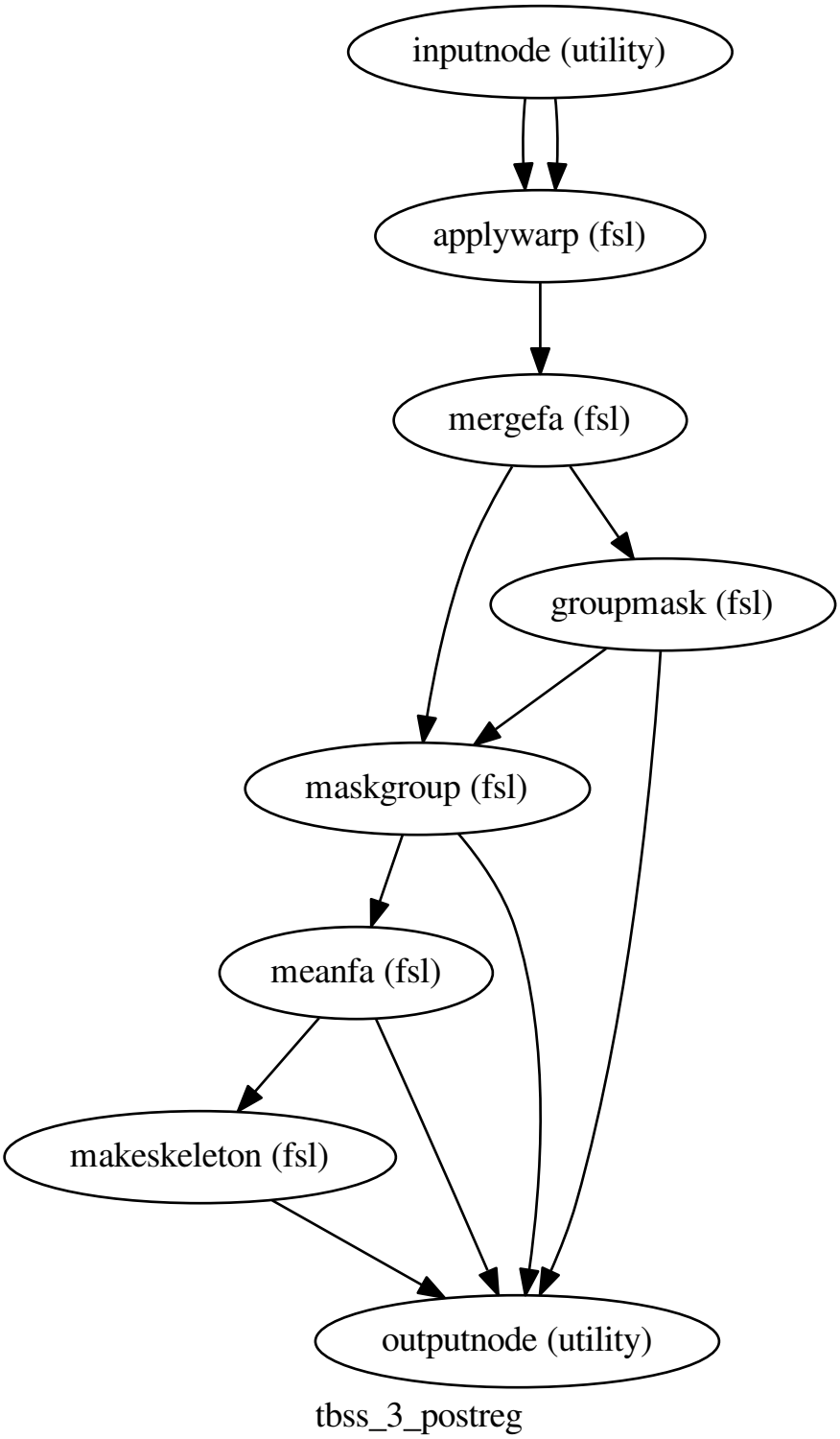
Inputs:

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

Outputs:

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

15.3.2 Graph


inputnode (utility)
applywarp (fsl)
mergefa (fsl)
groupmask (fsl)
maskgroup (fsl)
meanfa (fsl)
makeskeleton (fsl)
outputnode (utility)
tbss_3_postreg

15.4 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

15.4.1 Example

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

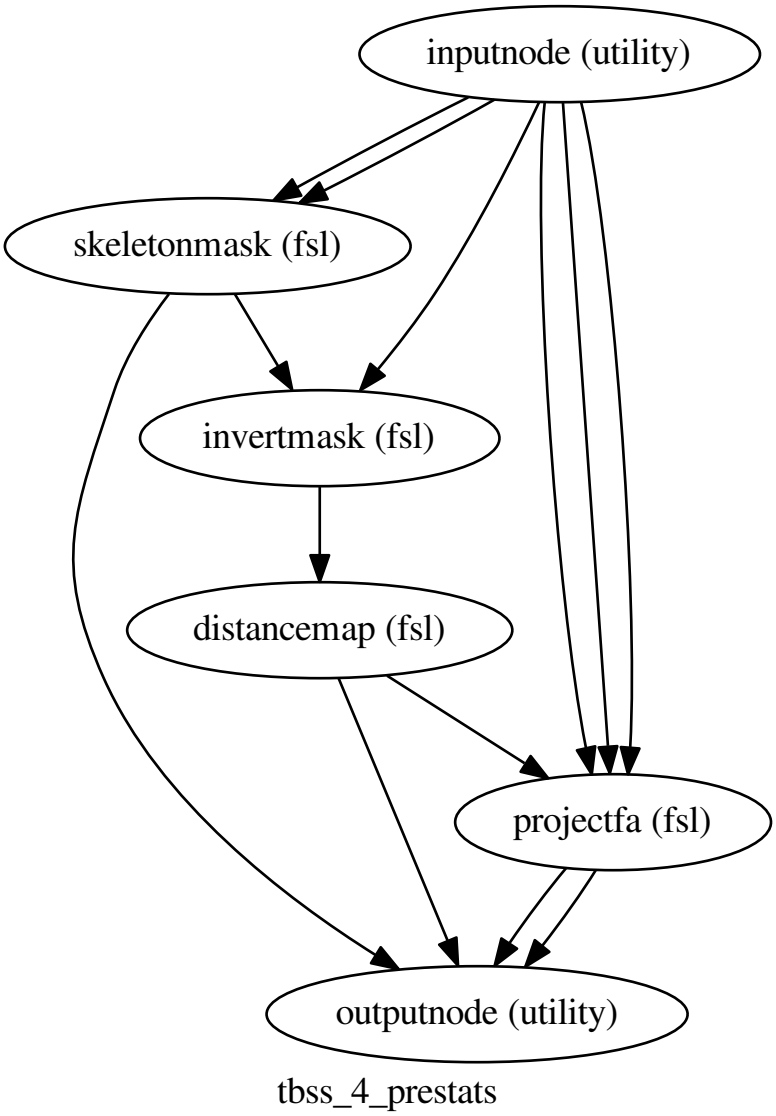
Inputs:

```
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
```

15.4.2 Graph



15.5 `create_tbss_all()`

Link to code
Create a pipeline that combines create_tbss_* pipelines

15.5.1 Example

```
>>> from nipype.workflows.dmri.fsl import tbss
>>> tbss = tbss.create_tbss_all('tbss')
>>> tbss.inputs.inputnode.skeleton_thresh = 0.2
```

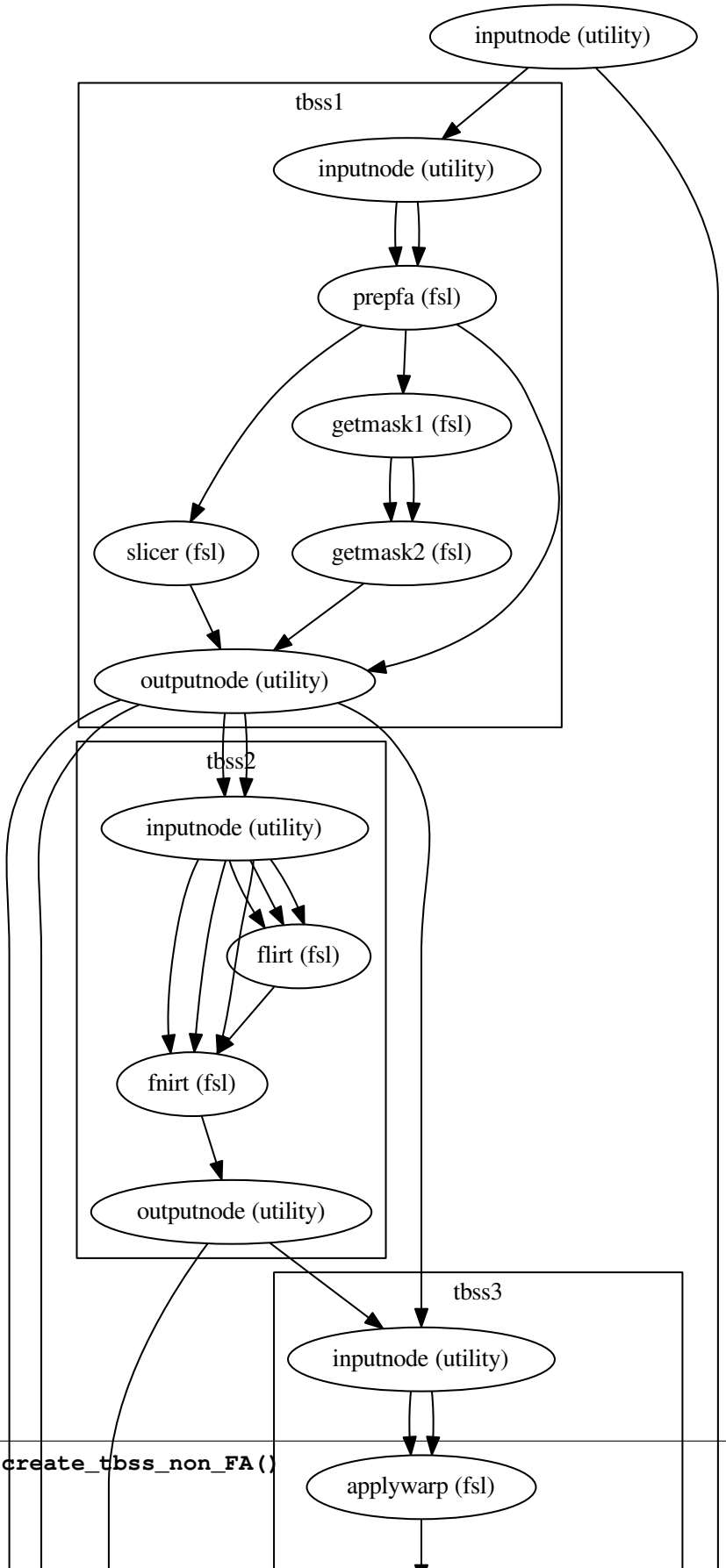
Inputs:

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

Outputs:

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

15.5.2 Graph


inputnode (utility)
tbss1
inputnode (utility)
prepfa (fsl)
getmask1 (fsl)
slicer (fsl)
getmask2 (fsl)
outputnode (utility)
tbss2
inputnode (utility)
flirt (fsl)
fnirt (fsl)
outputnode (utility)
tbss3
inputnode (utility)
applywarp (fsl)

A pipeline that implement tbss_non_FA in FSL

15.6.1 Example

```
>>> from nipype.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'
```

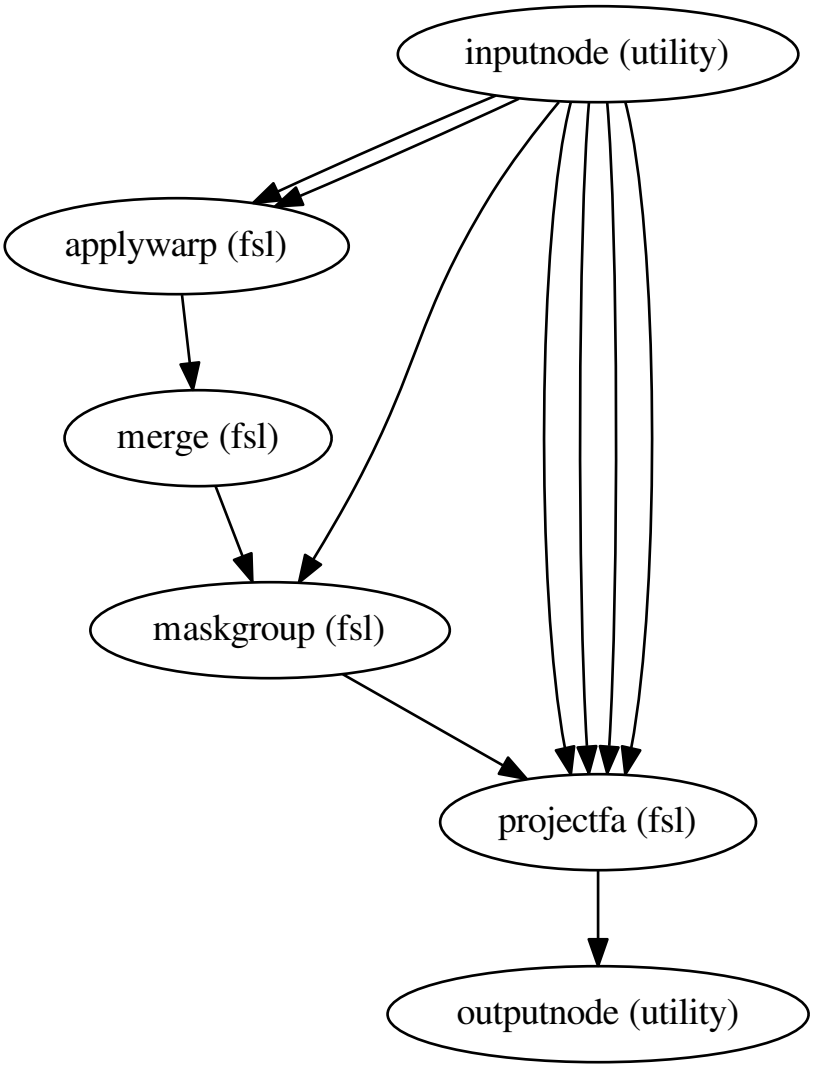
Inputs:

```
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
```

15.6.2 Graph



15.7 `tbss1_op_string()`

Link to code

15.8 `tbss4_op_string()`

Link to code

CHAPTER 16

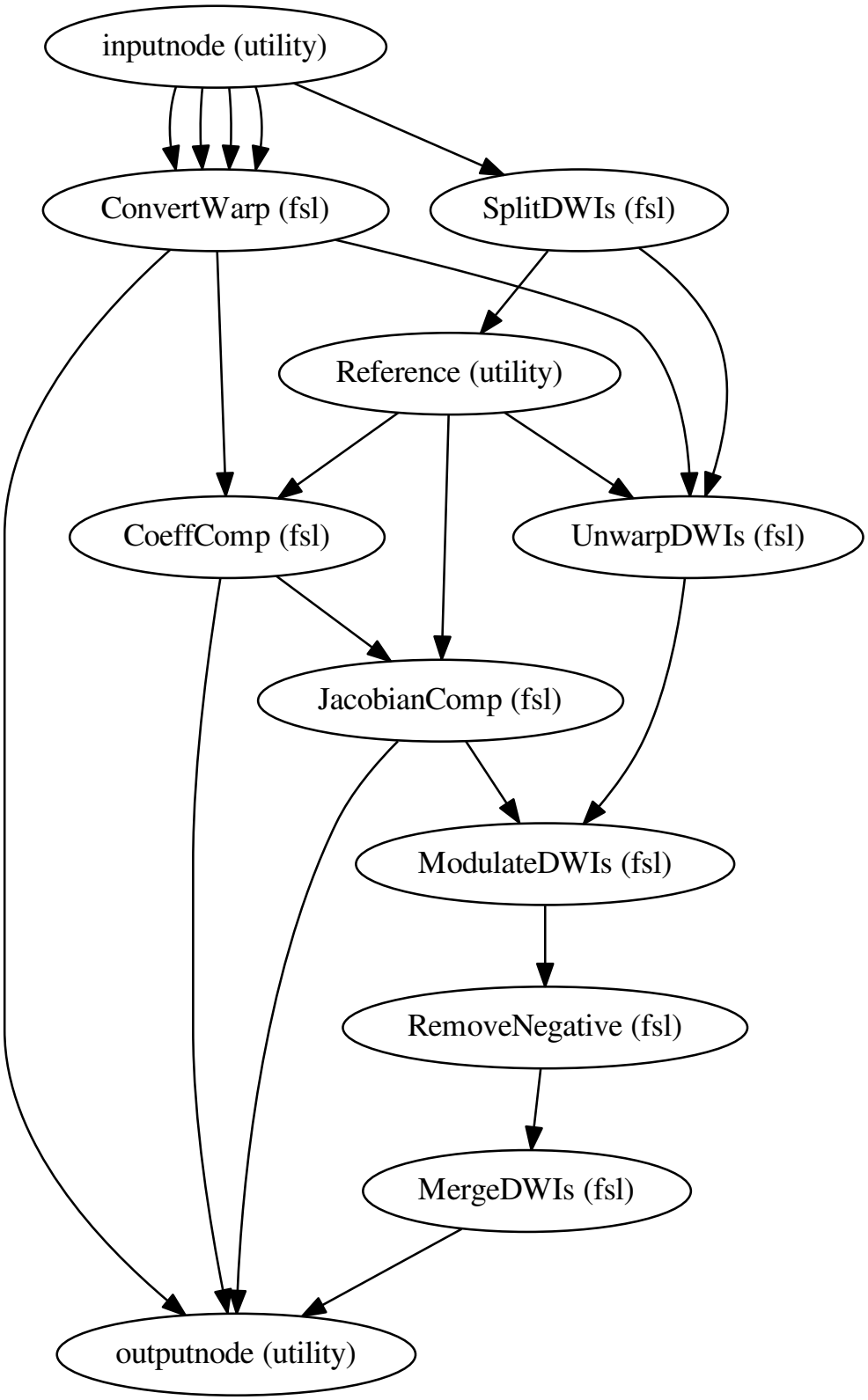
workflows.dmri.fsl.utils

16.1 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.

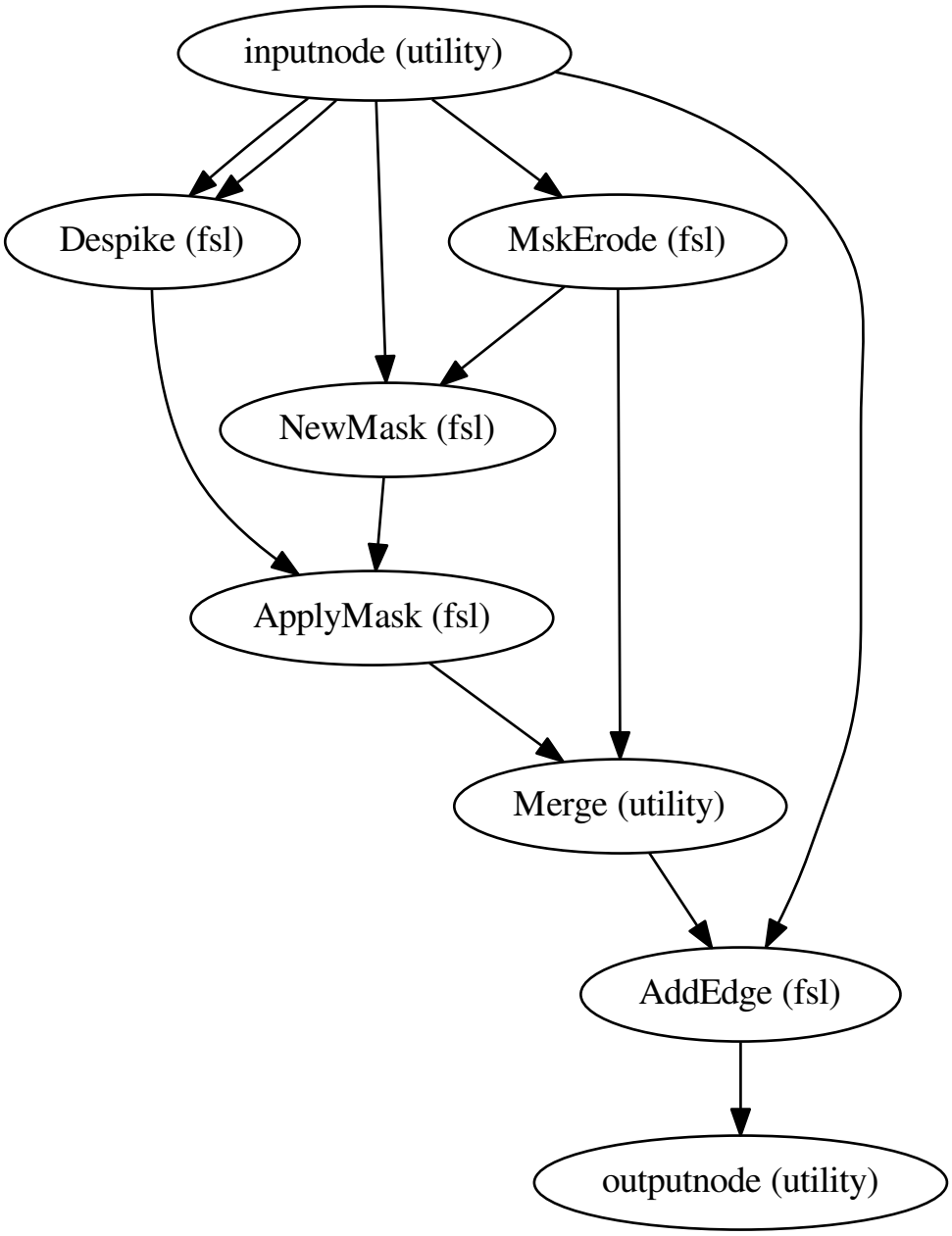
16.1.1 Graph



UnwarpArtifacts

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

16.2.1 Graph

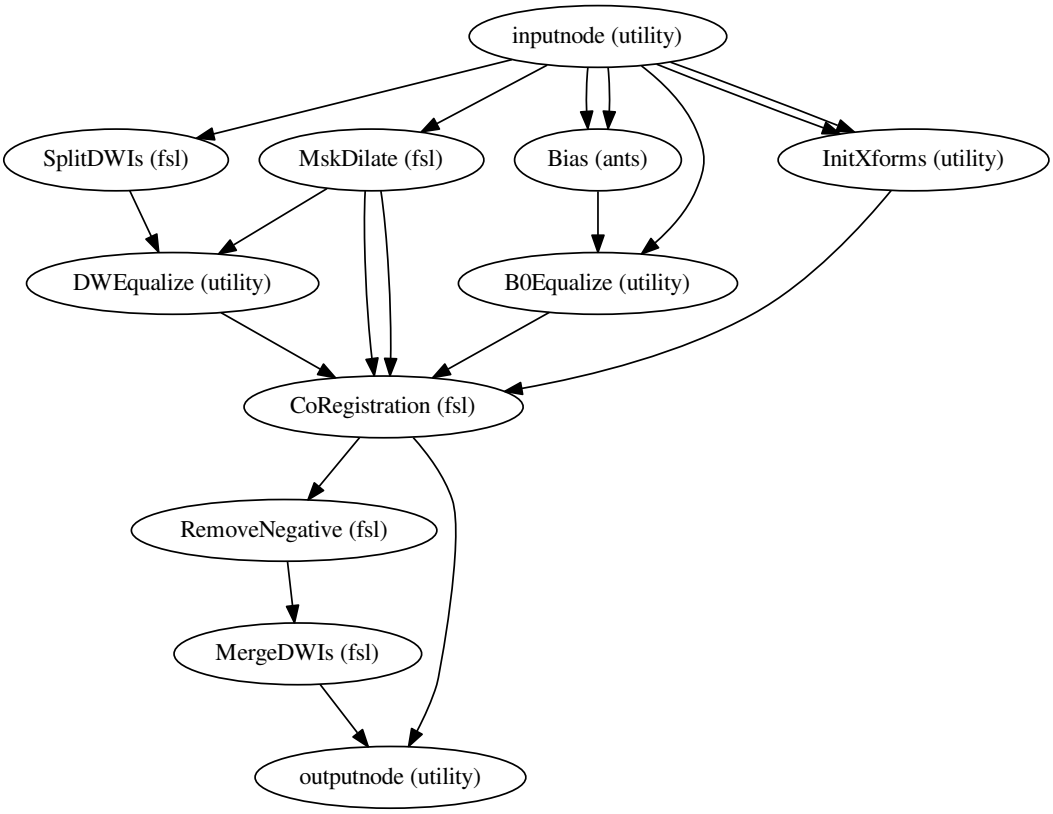


Cleanup

16.3 dwi_flirt()

Link to code
Generates a workflow for linear registration of dwi volumes

16.3.1 Graph

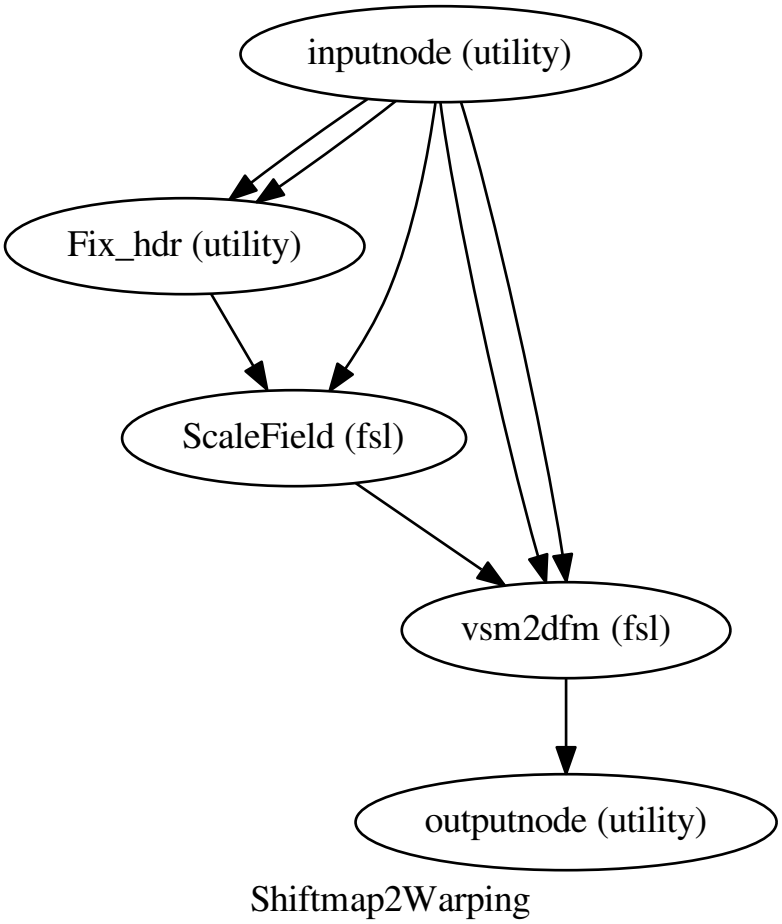


DWICoregistration

16.4 vsm2warp()

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

16.4.1 Graph



16.5 add_empty_vol()

Link to code
Adds an empty vol to the phase difference image

16.6 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).

16.7 b0_indices()

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

16.8 compute_readout()

Link to code
Computes readout time from epi params (see eddy documentation).

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

16.9 copy_hdr()

Link to code

16.10 demean_image()

Link to code
Demean image data inside mask

16.11 eddy_rotate_bvecs()

Link to code
Rotates the input bvec file accordingly with a list of parameters sourced from `eddy`, as explained here.

16.12 enhance()

Link to code

16.13 extract_bval()

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

16.14 hmc_split()

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

16.15 insert_mat()

Link to code

16.16 rads2radsec()

Link to code
Converts input phase difference map to rads

16.17 recompose_dwi()

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

16.18 recompose_xfm()

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

16.19 remove_comp()

Link to code
Removes the volume `volid` from the 4D nifti file

16.20 reorient_bvecs()

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

16.21 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 $\vec{r}$.

16.22 siemens2rads()

Link to code
Converts input phase difference map to rads

16.23 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).

CHAPTER 17

workflows.dmri.mrtrix.connectivity_mapping

17.1 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).

17.1.1 Example

```
>>> from nipype.workflows.dmri.mrtrix.connectivity_mapping import create_connectivity_pipeline
>>> conmapper = create_connectivity_pipeline("nipype_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()
```

Inputs:

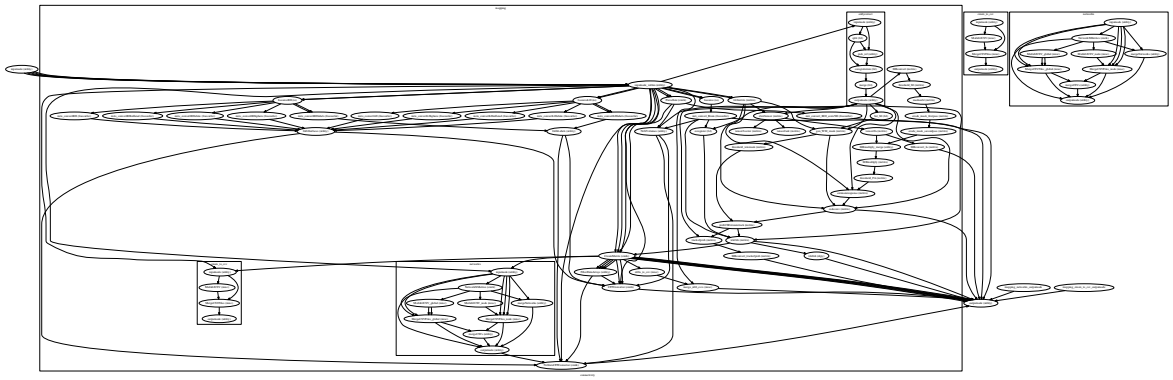
```
inputnode.subject_id
inputnode.subjects_dir
inputnode.dwi
inputnode.bvecs
inputnode.bvals
inputnode.resolution_network_file
```

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
```

17.1.2 Graph



CHAPTER 18

workflows.dmri.mrtrix.diffusion

18.1 create_mrtrix_dti_pipeline()

Link to code

Creates a pipeline that does the same diffusion processing as in the dMRI: DTI - MRtrix, FSL 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

18.1.1 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()
```

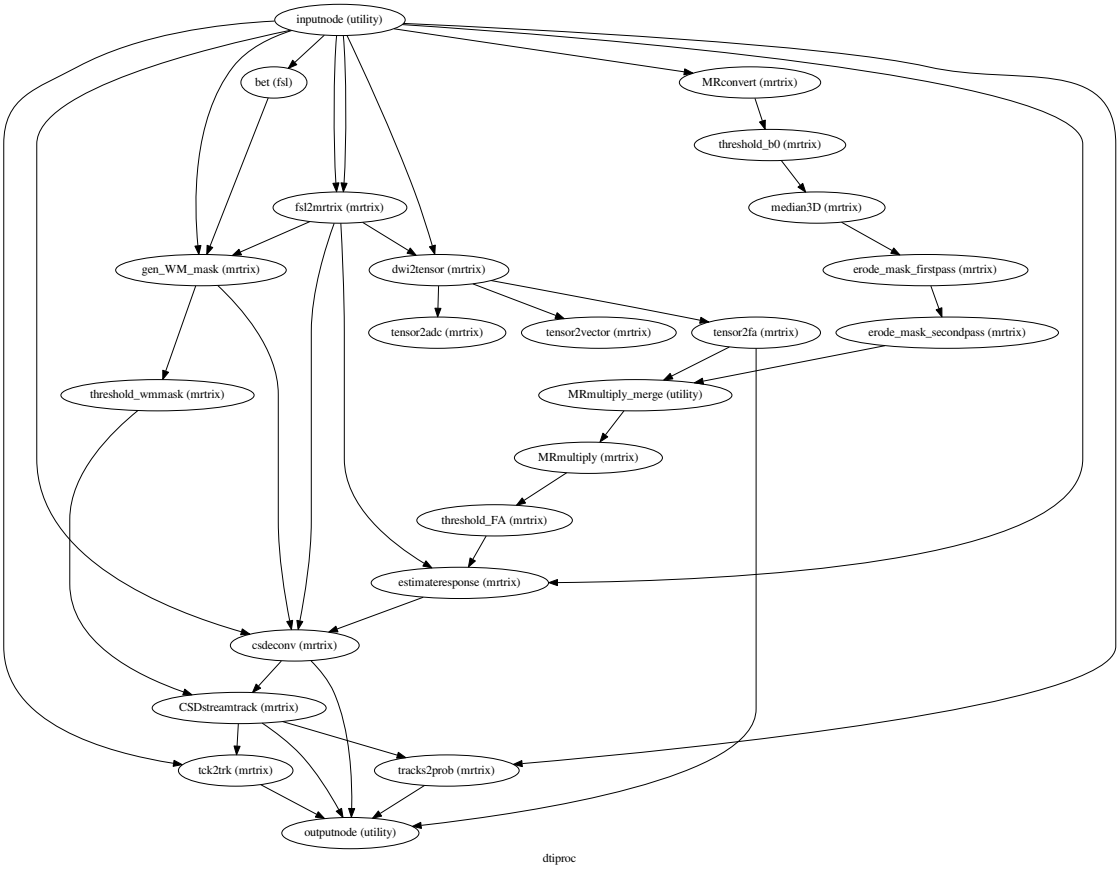
Inputs:

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

Outputs:

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

18.1.2 Graph



dtiproc

CHAPTER 19

workflows.dmri.mrtrix.group_connectivity

19.1 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).

19.1.1 Example

```
>>> import nipype.interfaces.freesurfer as fs
>>> import nipype.workflows.dmri.mrtrix.group_connectivity as groupwork
>>> import cmp
>>> 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=[['
>>> group_id = 'group1'
>>> l1pipeline = groupwork.create_group_connectivity_pipeline(group_list, group_id, data_dir, su
>>> 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
>>> l1pipeline.run()
```

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']])
```

CHAPTER 20

workflows.fmri.fsl.estimate

20.1 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

20.1.1 Example

```
>>> fixedfx = create_fixed_effects_flow()
>>> fixedfx.base_dir = '.'
>>> fixedfx.inputs.inputspec.copes = [['cope1run1.nii.gz', 'cope1run2.nii.gz'], ['cope2run1.nii.
>>> fixedfx.inputs.inputspec.varcopes = [['varcope1run1.nii.gz', 'varcope1run2.nii.gz'], ['varcc
>>> fixedfx.inputs.inputspec.dof_files = ['dofrun1', 'dofrun2'] # per run
>>> fixedfx.run()
```

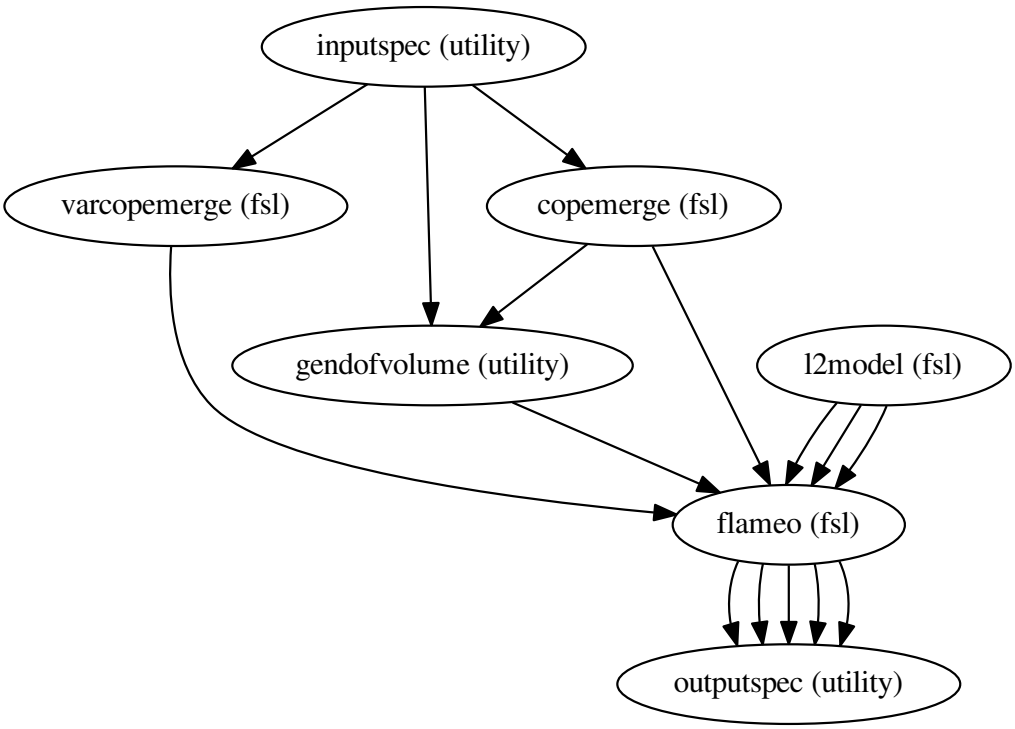
Inputs:

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

Outputs:

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

20.1.2 Graph



fixedfx

20.2 create_modelfit_workflow()

Link to code

Create an FSL individual modelfitting workflow

20.2.1 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()
```

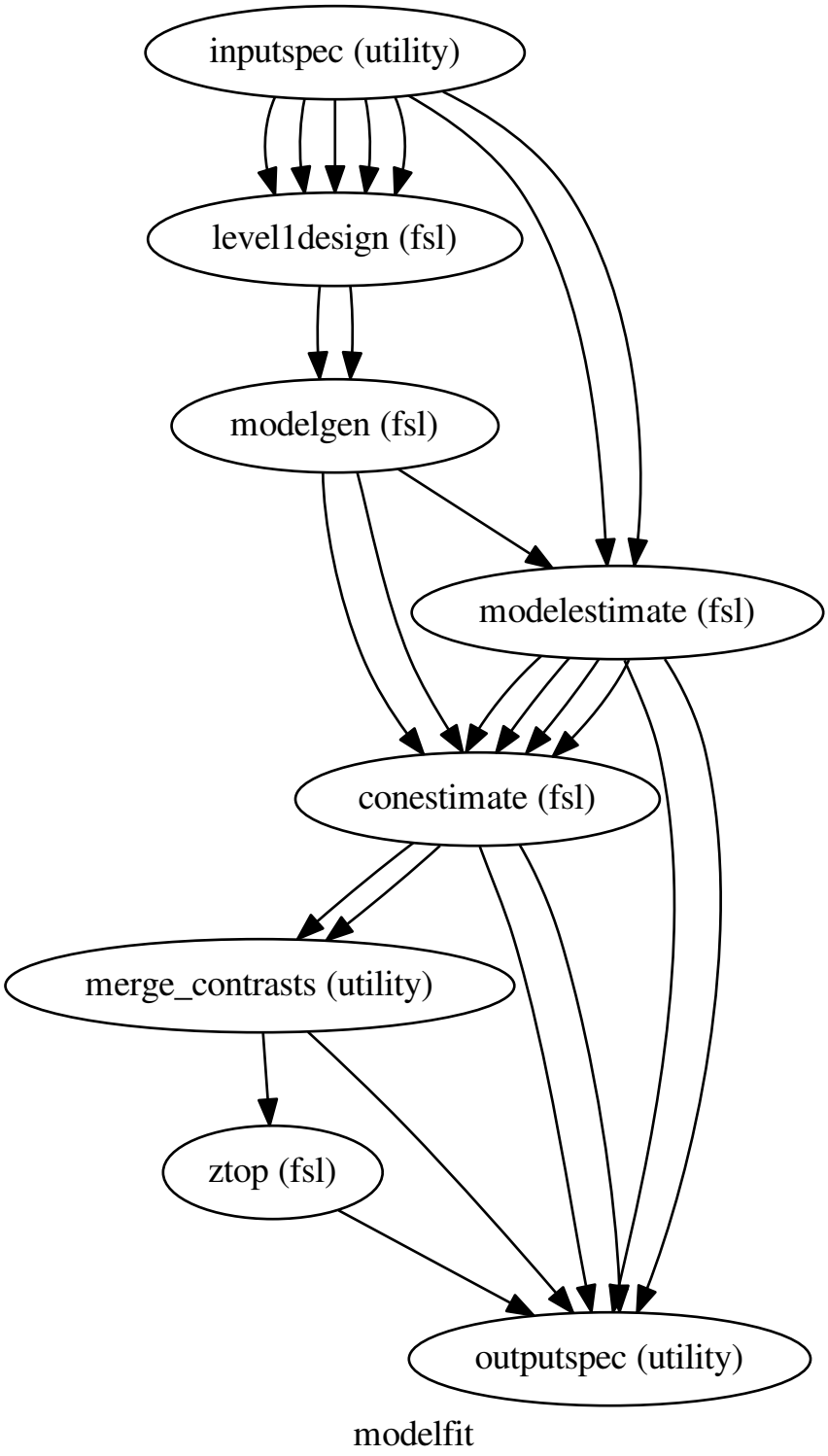
Inputs:

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

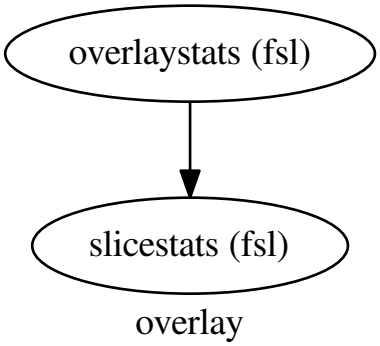
20.2.2 Graph


inputspec (utility)
level1design (fsl)
modelgen (fsl)
modelestimate (fsl)
conestimate (fsl)
merge_contrasts (utility)
ztop (fsl)
outputspec (utility)
modelfit

20.3 create_overlay_workflow()

Link to code
Setup overlay workflow

20.3.1 Graph



CHAPTER 21

workflows.fmri.fsl.preprocess

21.1 create_featreg_preproc()

Link to code

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

21.1.1 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')
```

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:

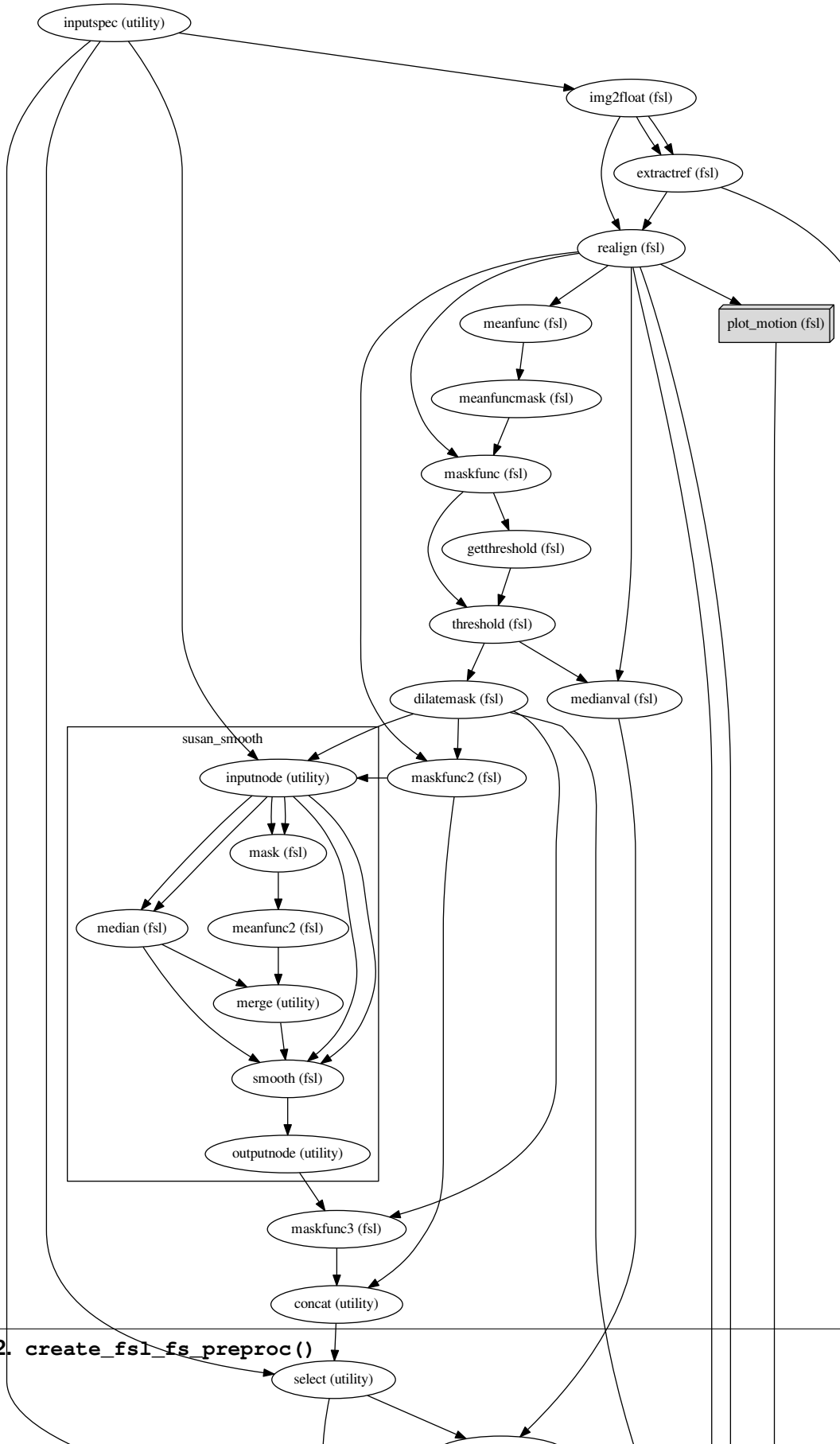
```
outputspec.reference : volume to which runs are realigned
outputspec.motion_parameters : motion correction parameters
outputspec.realigned_files : motion corrected files
outputspec.motion_plots : plots of motion correction parameters
outputspec.mask : mask file used to mask the brain
outputspec.smoothed_files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

21.1.2 Example

```
>>> preproc = create_featreg_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()
```

```
>>> preproc = create_featreg_preproc(highpass=False, whichvol='mean')
>>> preproc.inputs.inputspec.func = 'f3.nii'
>>> preproc.inputs.inputspec.fwhm = 5
>>> preproc.base_dir = '/tmp'
>>> preproc.run()
```

21.1.3 Graph


inputspec (utility)
img2float (fsl)
extractref (fsl)
realign (fsl)
meanfunc (fsl)
plot_motion (fsl)
meanfuncmask (fsl)
maskfunc (fsl)
getthreshold (fsl)
threshold (fsl)
dilatemask (fsl)
medianval (fsl)
susan_smooth
inputnode (utility)
maskfunc2 (fsl)
mask (fsl)
median (fsl)
meanfunc2 (fsl)
merge (utility)
smooth (fsl)
outputnode (utility)
maskfunc3 (fsl)
concat (utility)
select (utility)

Create a FEAT preprocessing workflow together with freesurfer

21.2.1 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
```

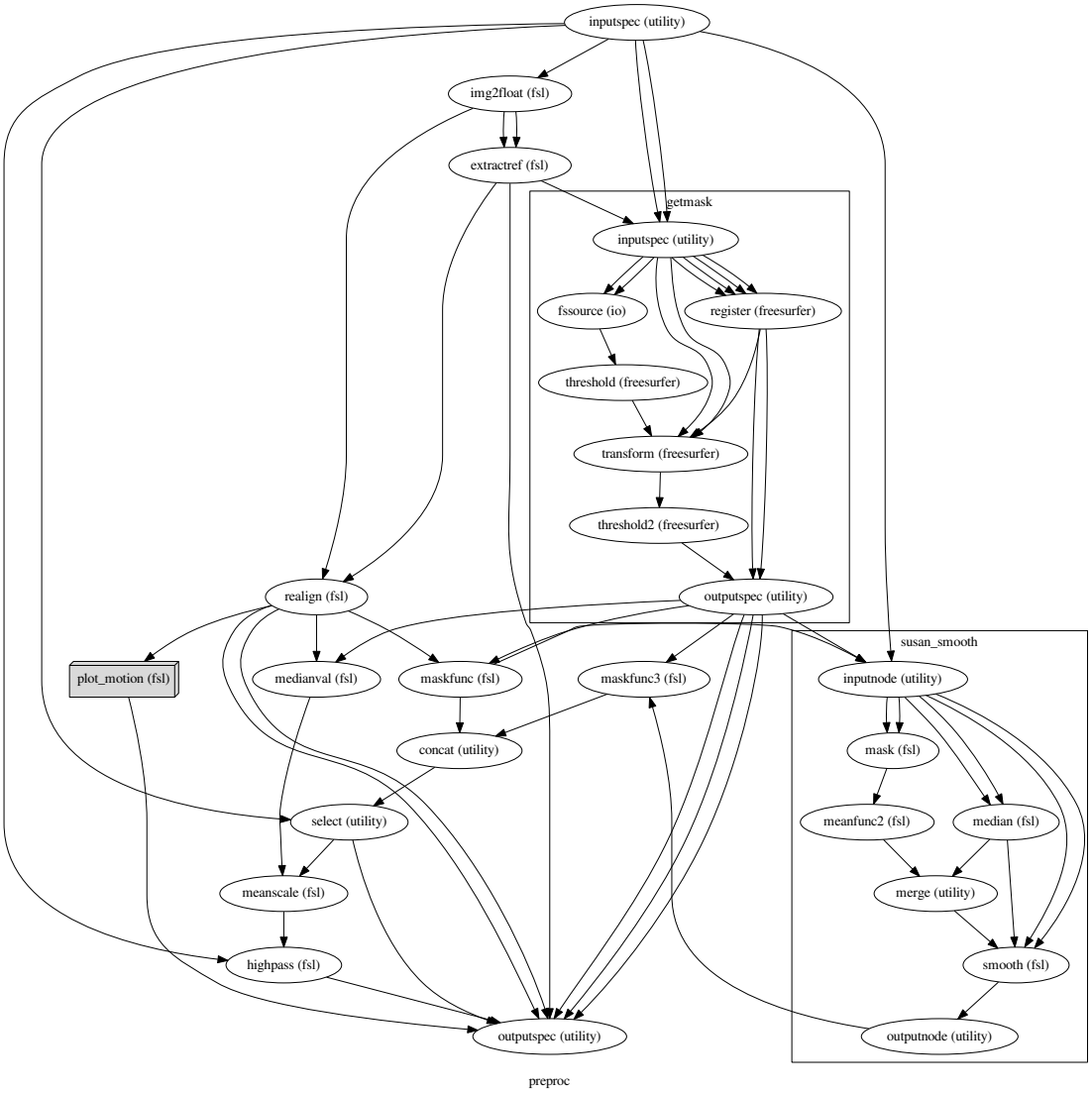
Outputs:

```
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 : bbregister registration files
outputspec.reg_cost : bbregister registration cost files
```

21.2.2 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()
```

21.2.3 Graph



21.3 create_parallelfeat_preproc()

Link to code

Preprocess each run with FSL independently of the others

21.3.1 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:

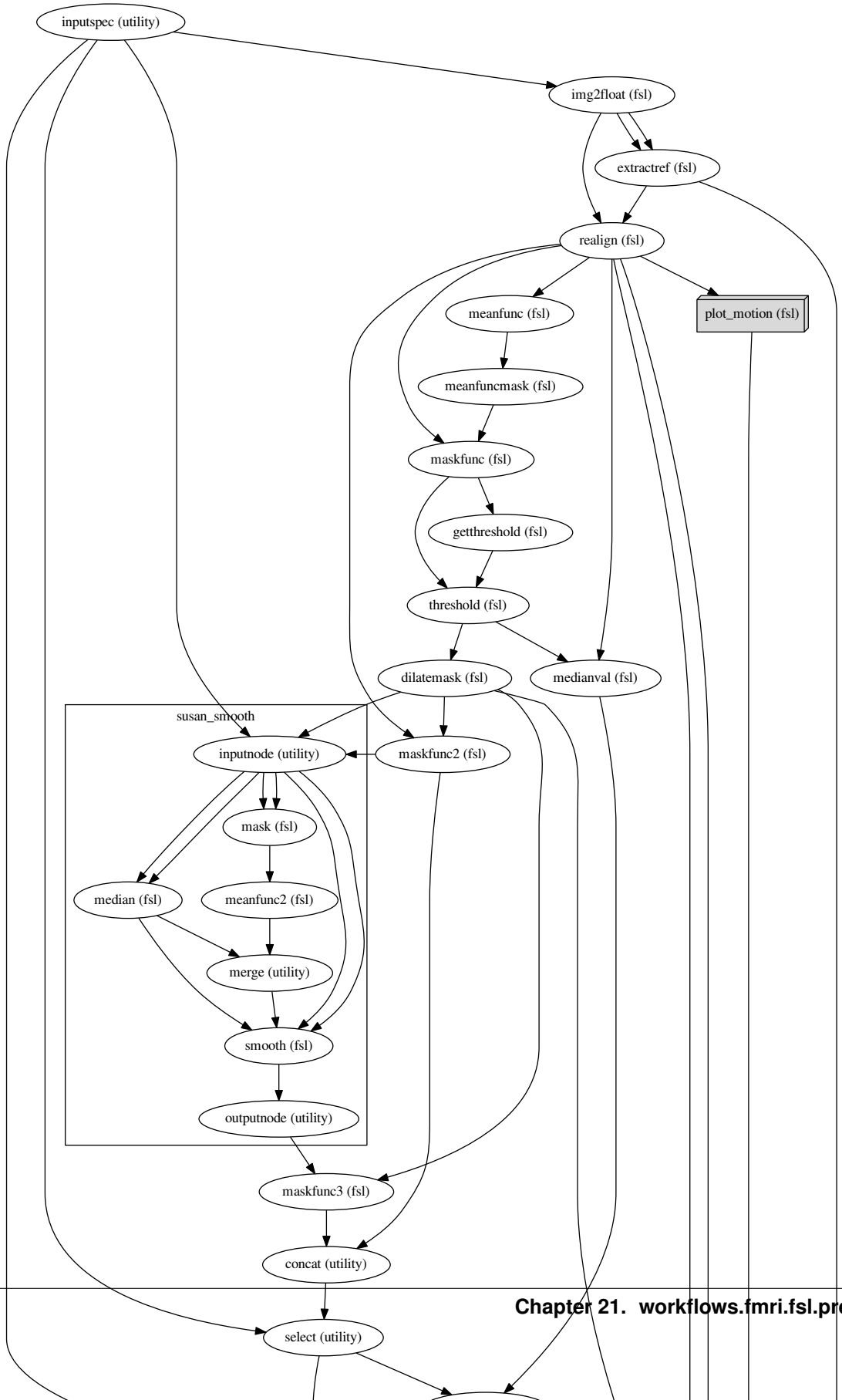
```
outputspec.reference : volume to which runs are realigned
outputspec.motion_parameters : motion correction parameters
outputspec.realigned_files : motion corrected files
outputspec.motion_plots : plots of motion correction parameters
outputspec.mask : mask file used to mask the brain
outputspec.smoothed_files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

21.3.2 Example

```
>>> preproc = create_parallelfeat_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()
```

```
>>> preproc = create_parallelfeat_preproc(highpass=False)
>>> preproc.inputs.inputspec.func = 'f3.nii'
>>> preproc.inputs.inputspec.fwhm = 5
>>> preproc.base_dir = '/tmp'
>>> preproc.run()
```

21.3.3 Graph


inputspec (utility)
img2float (fsl)
extractref (fsl)
realign (fsl)
meanfunc (fsl)
plot_motion (fsl)
meanfuncmask (fsl)
maskfunc (fsl)
getthreshold (fsl)
threshold (fsl)
dilatemask (fsl)
medianval (fsl)
susan_smooth
inputnode (utility)
maskfunc2 (fsl)
mask (fsl)
median (fsl)
meanfunc2 (fsl)
merge (utility)
smooth (fsl)
outputnode (utility)
maskfunc3 (fsl)
concat (utility)
select (utility)

Create a SUSAN smoothing workflow

21.4.1 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
inputnode.mask_file : mask used for estimating SUSAN thresholds (but not for smoothing)
```

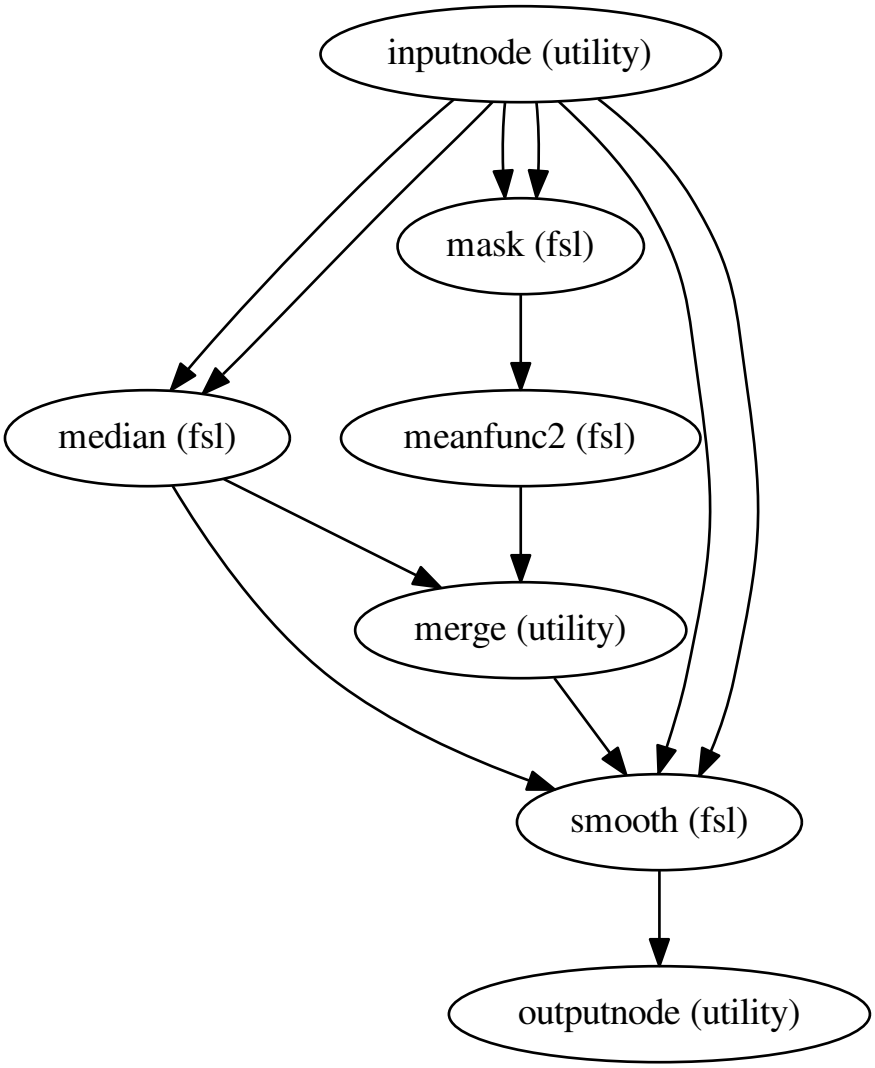
Outputs:

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

21.4.2 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()
```

21.4.3 Graph



susan_smooth

21.5 chooseindex()

Link to code

21.6 create_reg_workflow()

Link to code
Create a FEAT preprocessing workflow

21.6.1 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
```

21.6.2 Example

21.7 getbtthresh()

Link to code

21.8 getmeanscale()

Link to code

21.9 getthreshop()

Link to code

21.10 getusans()

Link to code

21.11 pickfirst()

Link to code

21.12 pickmiddle()

Link to code

21.13 pickvol()

Link to code

CHAPTER 22

workflows.fmri.spm.preprocess

22.1 create_DARTEL_template()

Link to code
Create a vbm workflow that generates DARTEL-based template

22.1.1 Example

```
>>> preproc = create_DARTEL_template()
>>> preproc.inputs.inputspec.structural_files = [os.path.abspath('s1.nii'), os.path.abspath('s3.
>>> preproc.inputs.inputspec.template_prefix = 'Template'
>>> preproc.run()
```

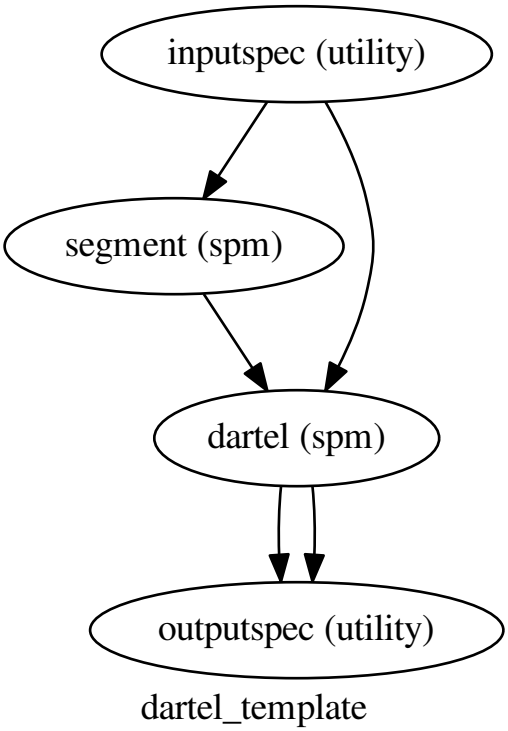
Inputs:

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

Outputs:

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

22.1.2 Graph



22.2 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.

22.2.1 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:

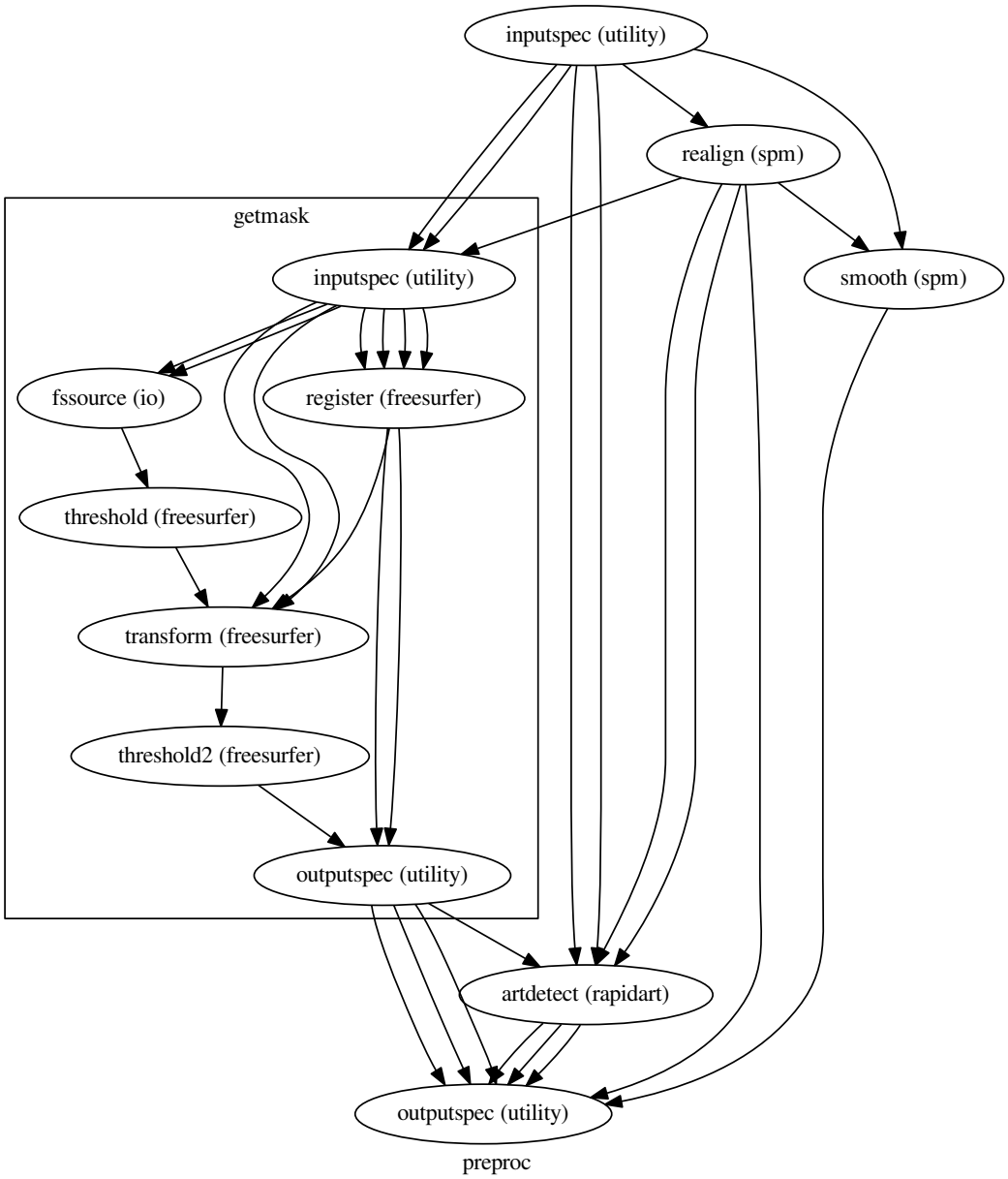
```
inputspec.functionals : functional runs use 4d nifti
inputspec.subject_id : freesurfer subject id
inputspec.subjects_dir : freesurfer subjects dir
```

```
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)
```

22.2.2 Graph



22.3 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

22.3.1 Example

```
>>> preproc = create_vbm_preproc()
>>> preproc.inputs.inputspec.fwhm = 8
>>> preproc.inputs.inputspec.structural_files = [os.path.abspath('s1.nii'), os.path.abspath('s3.
>>> preproc.inputs.inputspec.template_prefix = 'Template'
>>> preproc.run()
```

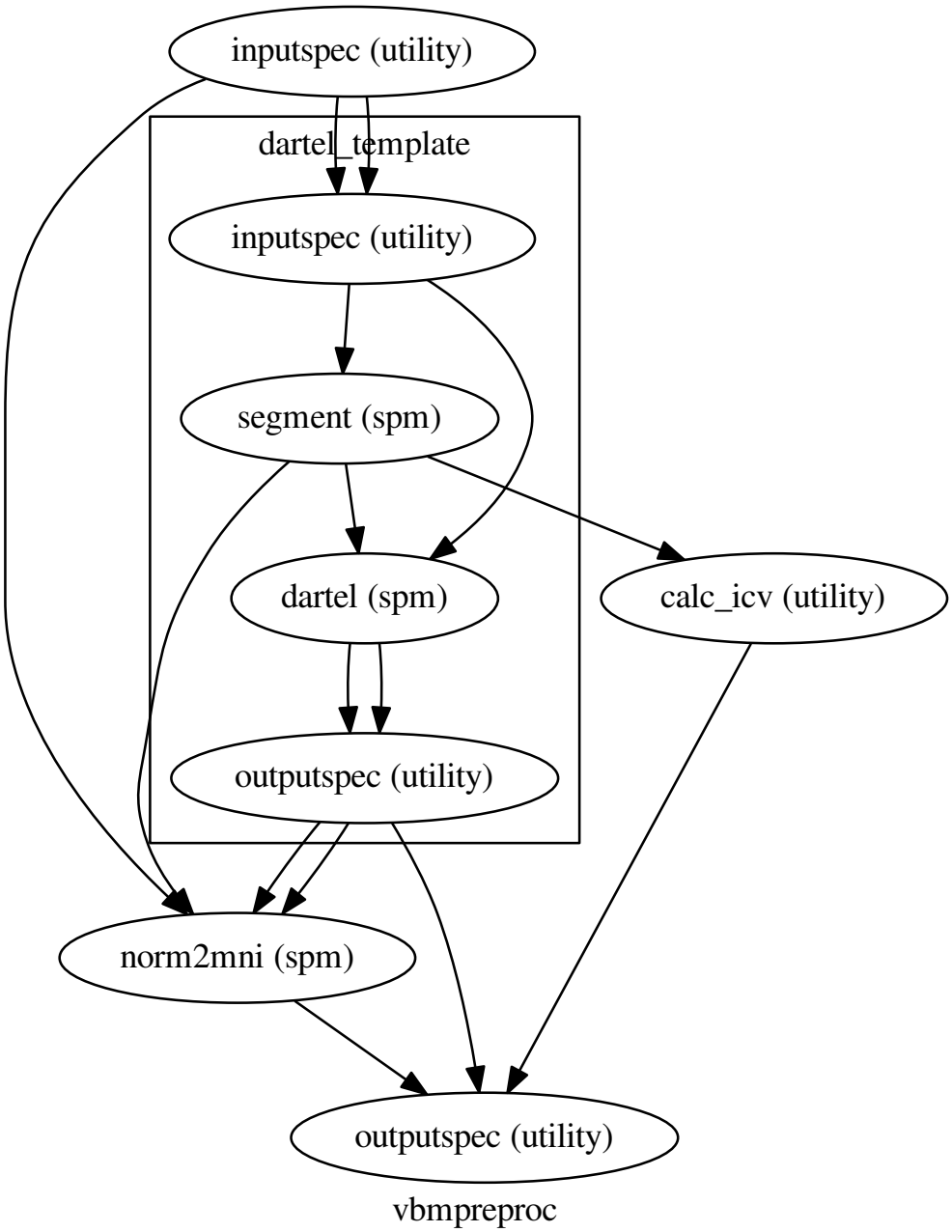
Inputs:

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

Outputs:

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

22.3.2 Graph


inputspec (utility)
dartel_template
inputspec (utility)
segment (spm)
dartel (spm)
calc_icv (utility)
outputspec (utility)
norm2mni (spm)
outputspec (utility)
vbmpreproc

CHAPTER 23

workflows.misc.utils

23.1 get_affine()

Link to code

23.2 get_data_dims()

Link to code

23.3 get_vox_dims()

Link to code

23.4 id_list_from_lookup_table()

Link to code

23.5 region_list_from_volume()

Link to code

23.6 select_aparc()

Link to code

23.7 select_aparc_annot()

Link to code

CHAPTER 24

workflows.rsfmri.fsl.resting

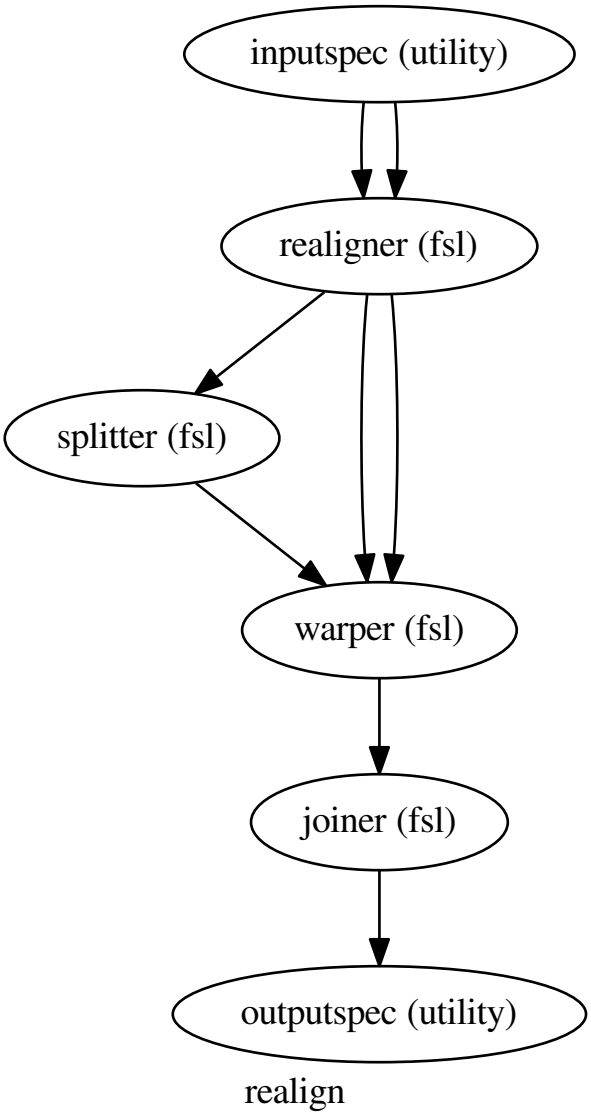
24.1 create_realign_flow()

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).

24.1.1 Example

```
>>> wf = create_realign_flow()
>>> wf.inputs.inputspec.func = 'f3.nii'
>>> wf.run()
```

24.1.2 Graph



24.2 create_resting_preproc()

Link to code
Create a "resting" time series preprocessing workflow
The noise removal is based on Behzadi et al. (2007)

24.2.1 Parameters

name : name of workflow (default: restpreproc)

Inputs:

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

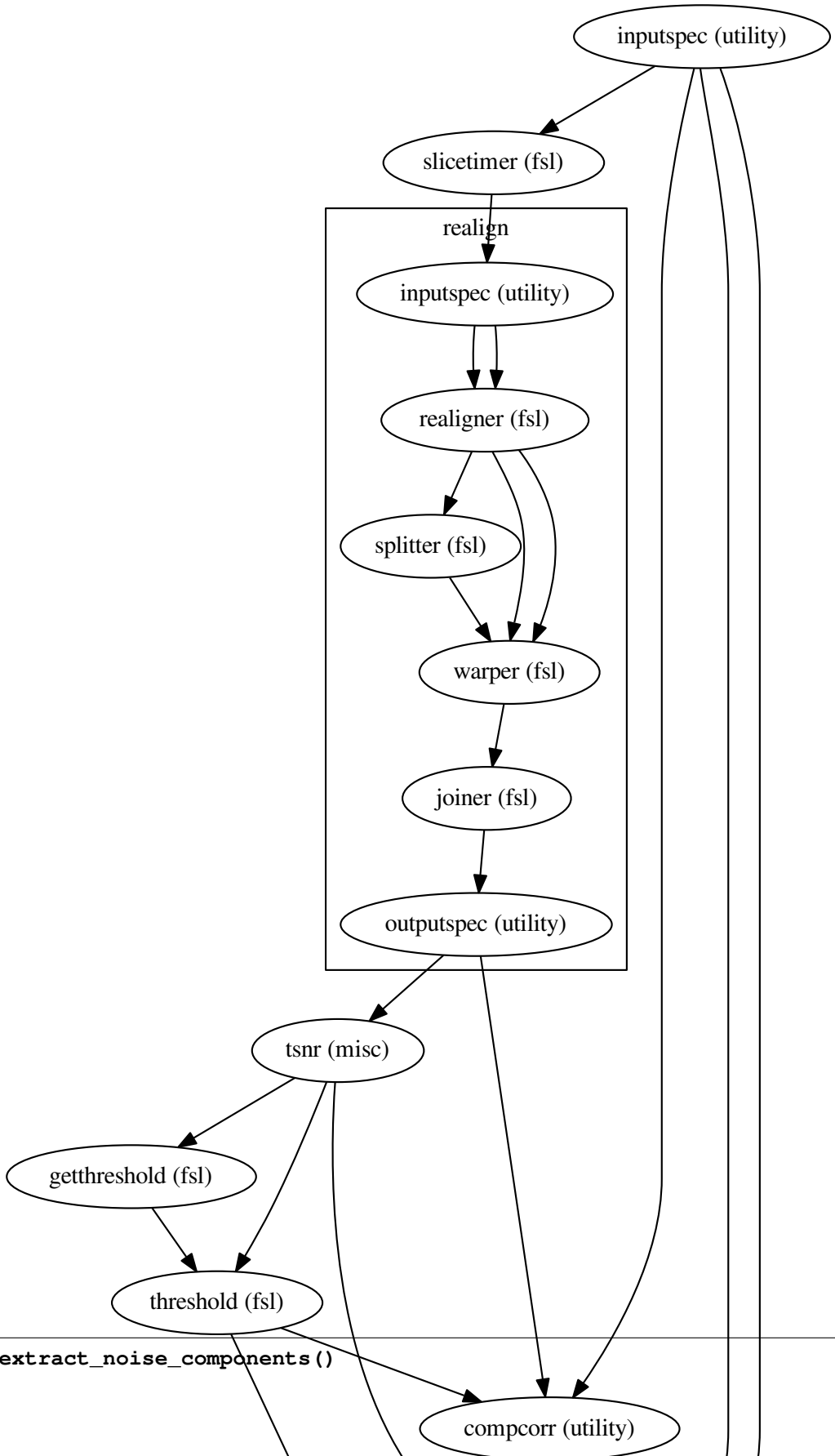
Outputs:

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

24.2.2 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()
```

24.2.3 Graph


inputspec (utility)
slicetimer (fsl)
realign
inputspec (utility)
realigner (fsl)
splitter (fsl)
warper (fsl)
joiner (fsl)
outputspec (utility)
tsnr (misc)
getthreshold (fsl)
threshold (fsl)
compcorr (utility)

Derive components most reflective of physiological noise

24.4 select_volume()

Link to code
Return the middle index of a file

CHAPTER 25

workflows.smri.ants.ANTSBuildTemplate

25.1 ANTSTemplateBuildSingleIterationWF()

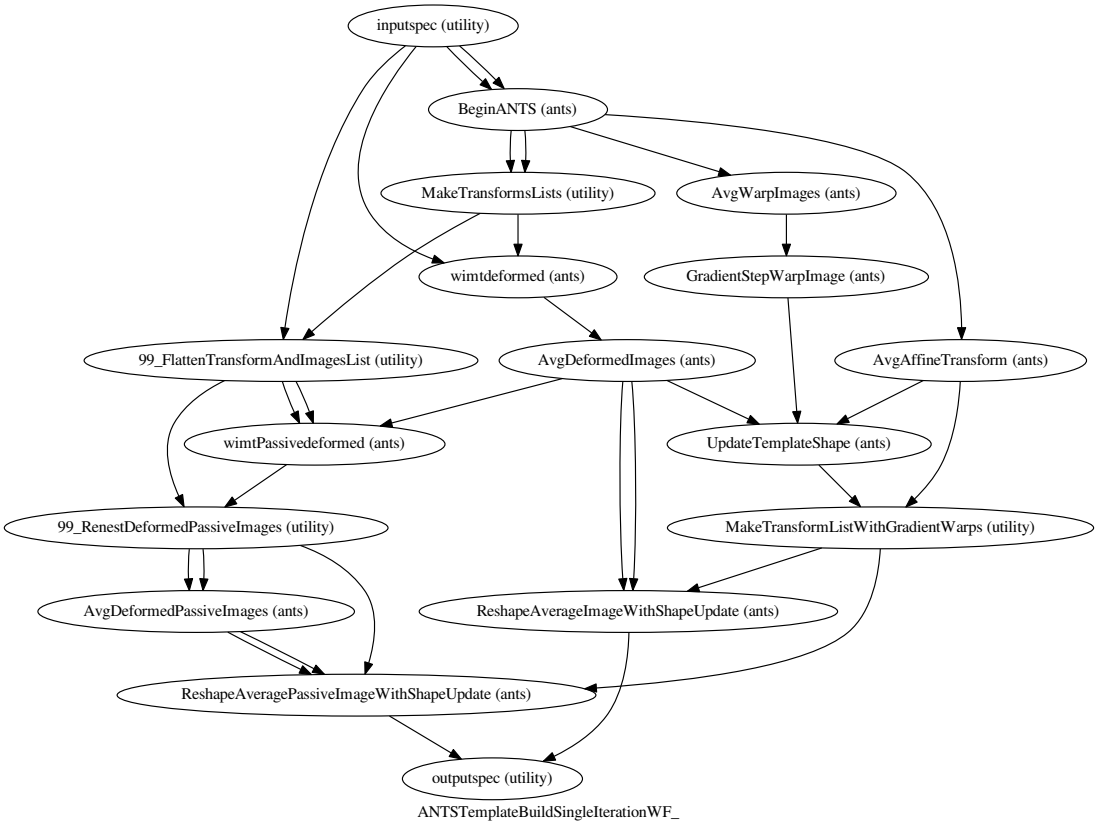
Link to code
Inputs:

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

Outputs:

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

25.1.1 Graph



25.2 FlattenTransformAndImagesList()

Link to code

25.3 GetFirstListElement()

Link to code

25.4 MakeListsOfTransformLists()

Link to code

25.5 MakeTransformListWithGradientWarps()

Link to code

25.6 RenestDeformedPassiveImages()

Link to code

CHAPTER 26

workflows.smri.ants.antsRegistrationBuildTemplate

26.1 antsRegistrationTemplateBuildSingleIterationWF()

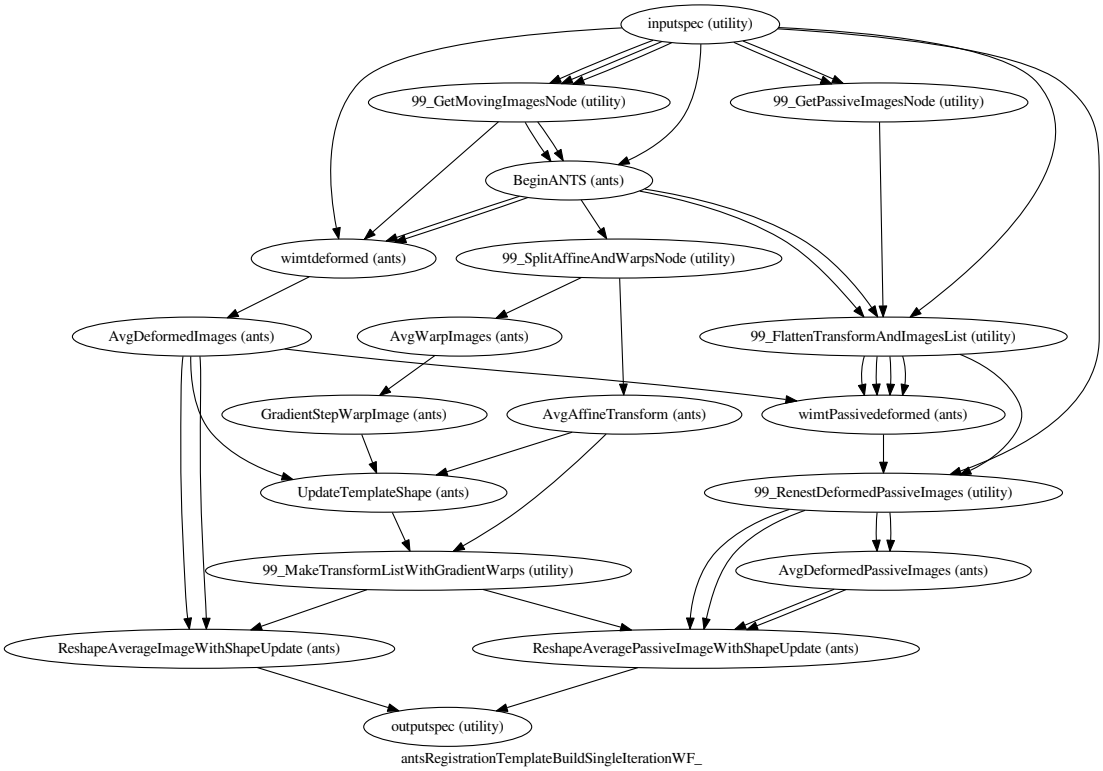
Link to code
Inputs:

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

Outputs:

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

26.1.1 Graph



antsRegistrationTemplateBuildSingleIterationWF_

26.2 FlattenTransformAndImagesList()

Link to code

26.3 GetFirstListElement()

Link to code

26.4 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.

26.5 GetPassiveImages()

Link to code

26.6 MakeTransformListWithGradientWarps()

Link to code

26.7 RenestDeformedPassiveImages()

Link to code

26.8 SplitAffineAndWarpComponents()

Link to code

26.9 makeListOfOneElement()

Link to code

CHAPTER 27

workflows.smri.freesurfer.autorecon1

27.1 checkT1s()

Link to code
Verifying size of inputs and setting workflow parameters

27.2 create_AutoRecon1()

Link to code
Creates the AutoRecon1 workflow in nipype.
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)
Outpus:

CHAPTER 28

workflows.smri.freesurfer.autorecon2

28.1 copy_ltas()

Link to code

CHAPTER 29

workflows.smri.freesurfer.bem

29.1 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.

29.1.1 Example

```
>>> from nipype.workflows.smri.freesurfer import create_bem_flow
>>> bemflow = create_bem_flow()
>>> bemflow.inputs.inputspec.subject_id = 'subj1'
>>> bemflow.inputs.inputspec.subjects_dir = '.'
>>> bemflow.run()
```

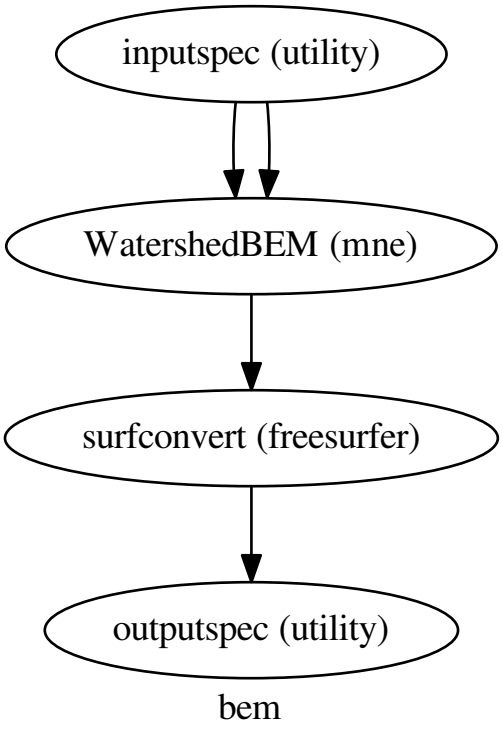
Inputs:

```
inputspec.subject_id : freesurfer subject id
inputspec.subjects_dir : freesurfer subjects directory
```

Outputs:

```
outputspec.meshes : output boundary element meshes in (by default) stereolithographic (.stl) for
```

29.1.2 Graph


inputspec (utility)
WatershedBEM (mne)
surfconvert (freesurfer)
outputspec (utility)
bem

CHAPTER 30

workflows.smri.freesurfer.recon

30.1 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.

30.1.1 Example

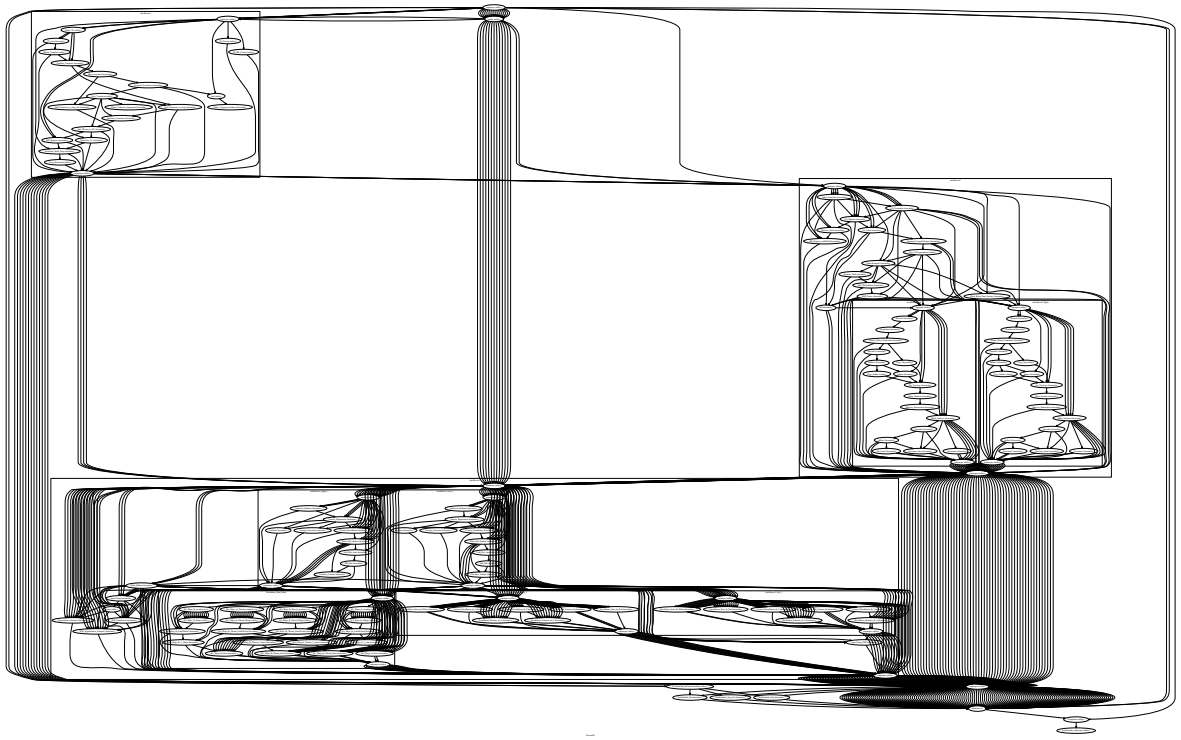
```
>>> from nipype.workflows.smri.freesurfer import create_reconall_workflow
>>> recon_all = create_reconall_workflow()
>>> recon_all.inputs.inputspec.subject_id = 'subj1'
>>> recon_all.inputs.inputspec.subjects_dir = '.'
>>> recon_all.inputs.inputspec.T1_files = 'T1.nii.gz'
>>> recon_flow.run()
```

Inputs:: inputspec.subjects_dir : subjects directory (mandatory) inputspec.subject_id : name of subject (mandatory) 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 on nodes that utilize OpenMP (default=1) plugin_args : Dictionary of plugin args to set to nodes that utilize OpenMP (optional)

Outpus:: postdatasink_outputspec.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}.

30.1.2 Graph



30.2 create_skullstripped_recon_flow()

Link to code

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

30.2.1 Example

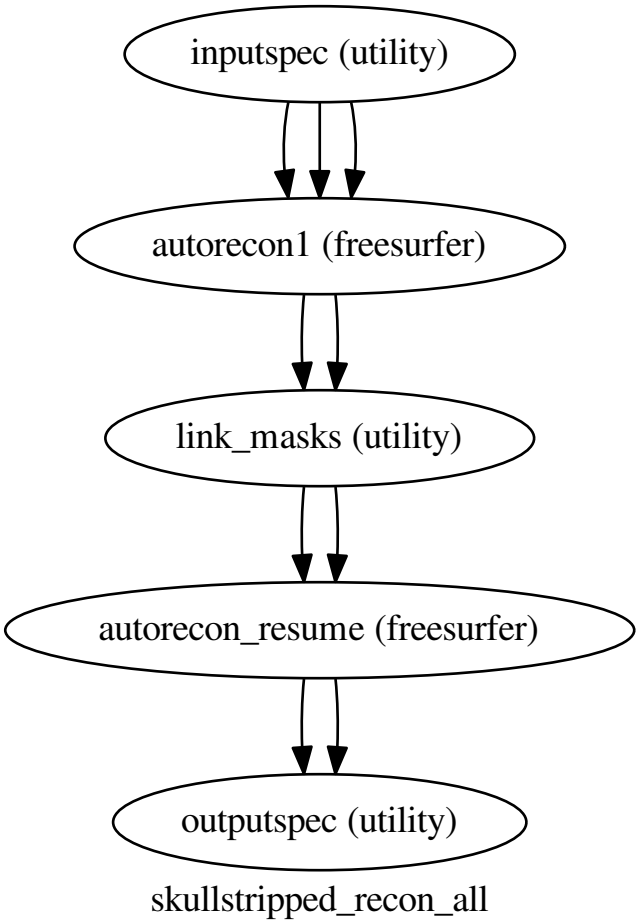
```
>>> from nipype.workflows.smri.freesurfer import create_skullstripped_recon_flow
>>> recon_flow = create_skullstripped_recon_flow()
>>> recon_flow.inputs.inputspec.subject_id = 'subj1'
>>> recon_flow.inputs.inputspec.T1_files = 'T1.nii.gz'
>>> recon_flow.run()
```

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

Outputs:

```
outputspec.subject_id : freesurfer subject id
outputspec.subjects_dir : freesurfer subjects directory
```

30.2.2 Graph


inputspec (utility)
autorecon1 (freesurfer)
link_masks (utility)
autorecon_resume (freesurfer)
outputspec (utility)
skullstripped_recon_all

CHAPTER 31

workflows.smri.freesurfer.utils

31.1 create_get_stats_flow()

Link to code
Retrieves stats from labels

31.1.1 Parameters

name [string] name of workflow
withreg [boolean] indicates whether to register source to label

31.1.2 Example

Inputs:

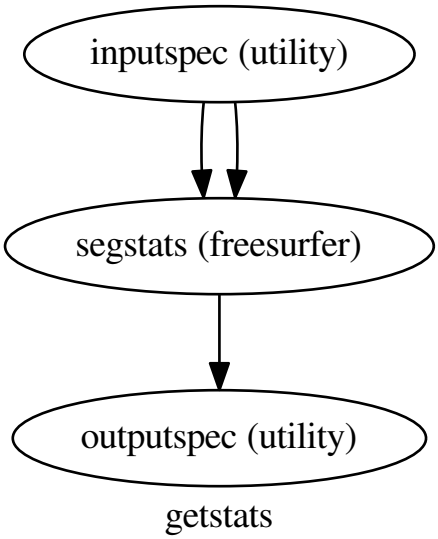
```
inputspec.source_file : reference image for mask generation
inputspec.label_file : label file from which to get ROIs

(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
```

31.1.3 Graph



31.2 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

31.2.1 Parameters

name [string] name of workflow
dilate_mask [boolean] indicates whether to dilate mask or not

31.2.2 Example

```
>>> getmask = create_getmask_flow()
>>> getmask.inputs.inputspec.source_file = 'mean.nii'
>>> getmask.inputs.inputspec.subject_id = 's1'
>>> getmask.inputs.inputspec.subjects_dir = '.'
>>> getmask.inputs.inputspec.contrast_type = 't2'
```

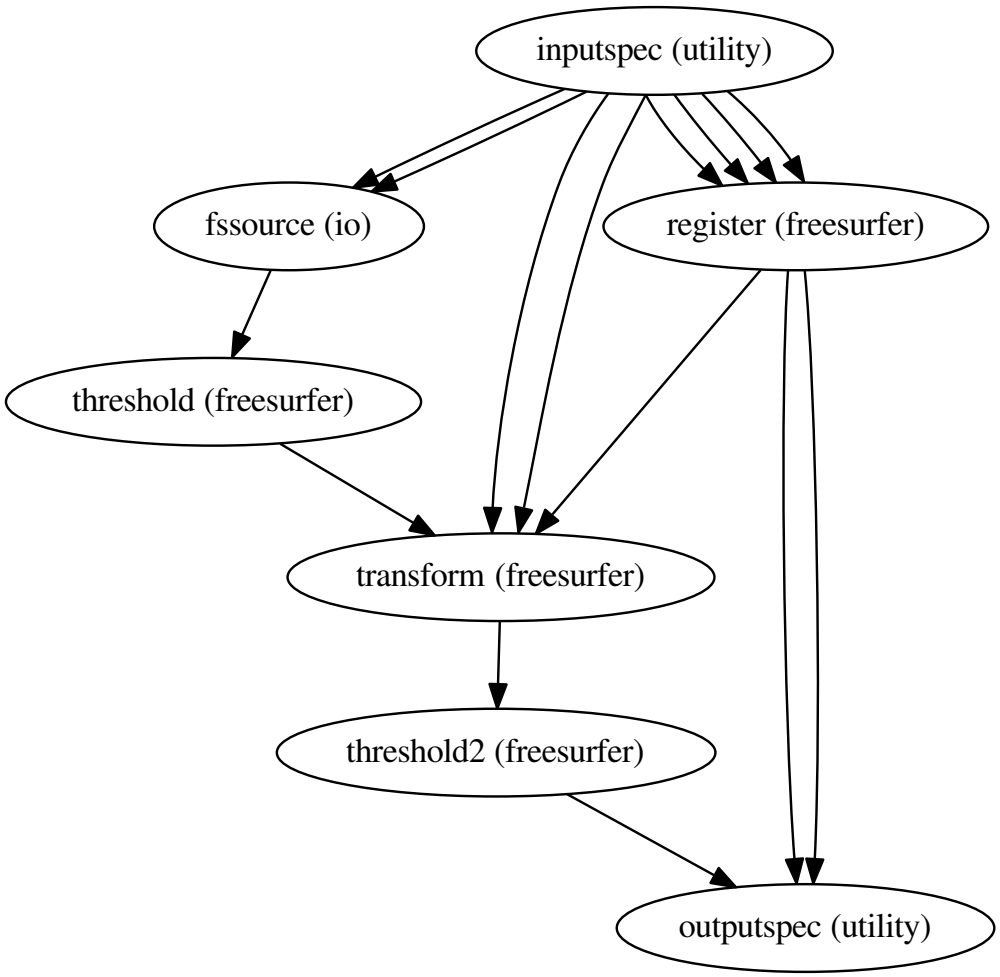
Inputs:

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

Outputs:

```
    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)
```

31.2.3 Graph



getmask

31.3 `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

31.3.1 Example

```
>>> from nipype.workflows.smri.freesurfer import create_tessellation_flow
>>> tessflow = create_tessellation_flow()
>>> tessflow.inputs.inputspec.subject_id = 'subj1'
>>> tessflow.inputs.inputspec.subjects_dir = '.'
>>> tessflow.inputs.inputspec.lookup_file = 'FreeSurferColorLUT.txt'
>>> tessflow.run()
```

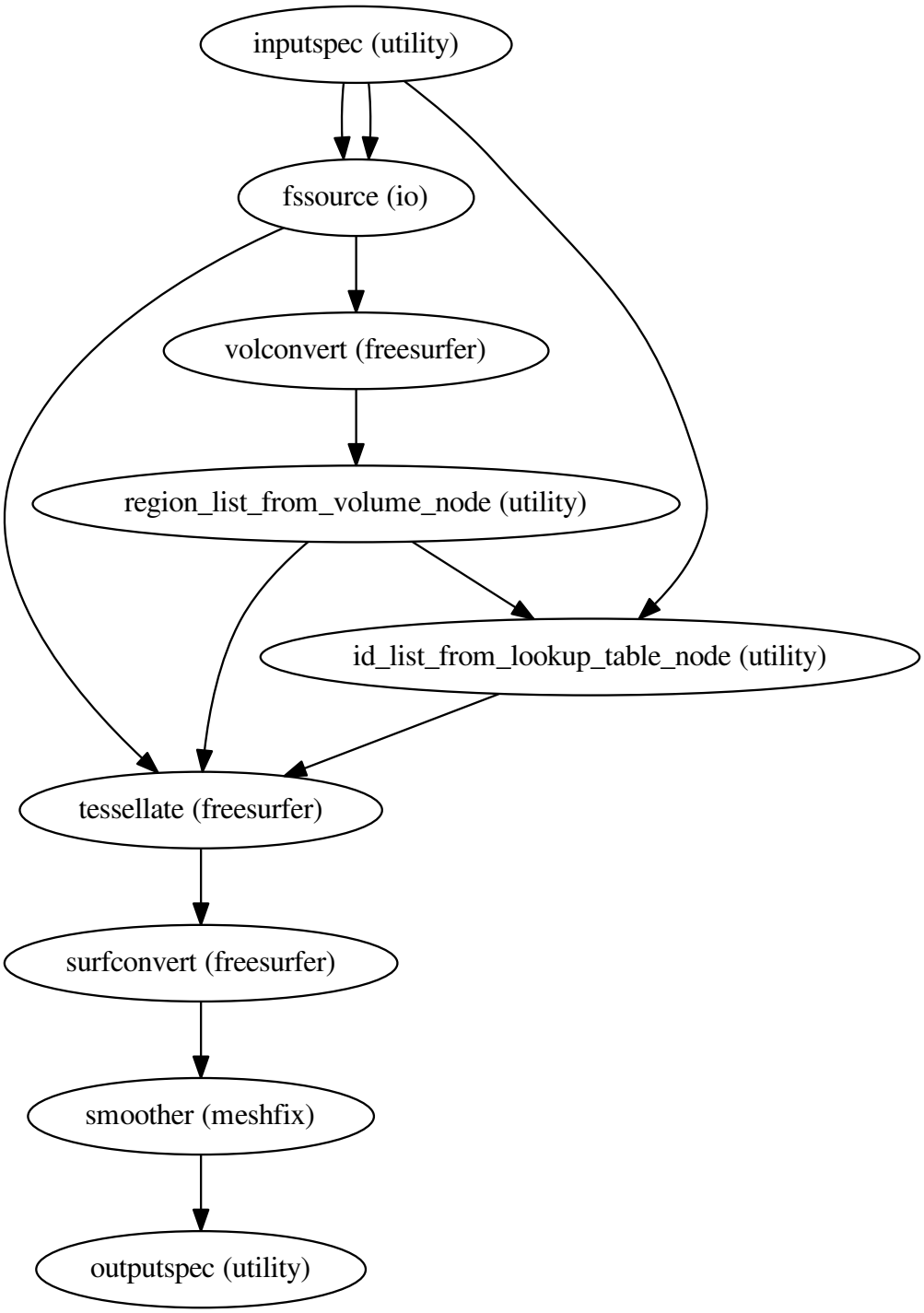
Inputs:

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

Outputs:

```
outputspec.meshes : output region meshes in (by default) stereolithographic (.stl) format
```

31.3.2 Graph



tessellate

31.4 copy_file()

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

31.5 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

31.6 get_aparc_aseg()

Link to code
Return the aparc+aseg.mgz file

31.7 getdefaultconfig()

Link to code

31.8 mkdir_p()

Link to code
- Examples
- Interfaces

algorithms.icc

32.1 ICC

Link to code

Calculates Interclass Correlation Coefficient (3,1) as defined in P. E. Shrout & Joseph L. Fleiss (1979). “Intraclass Correlations: Uses in Assessing Rater Reliability”. Psychological Bulletin 86 (2): 420-428. This particular implementation is aimed at relaibility (test-retest) studies.

Inputs:

```
[Mandatory]
mask: (an existing file name)
subjects_sessions: (a list of items which are a list of items which
         are an existing file name)
        n subjects m sessions 3D stat files

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
icc_map: (an existing file name)
session_var_map: (an existing file name)
        variance between sessions
subject_var_map: (an existing file name)
        variance between subjects
```

32.2 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 = [FaTor / Subjects]

CHAPTER 33

algorithms.mesh

33.1 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 nipype.algorithms.mesh as m
dist = m.ComputeMeshWarp()
dist.inputs.surface1 = 'surf1.vtk'
dist.inputs.surface2 = 'surf2.vtk'
res = dist.run()
```

Inputs:

```
[Mandatory]
surface1: (an existing file name)
        Reference surface (vtk format) to which compute distance.
surface2: (an existing file name)
        Test surface (vtk format) from which compute distance.

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
metric: ('euclidean' or 'sqeuclidean', nipype default value:
         euclidean)
        norm used to report distance
out_file: (a file name, nipype default value: distance.npy)
        numpy file keeping computed distances and weights
out_warp: (a file name, nipype default value: surfwarp.vtk)
        vtk file based on surface1 and warpings mapping it to surface2
weighting: ('none' or 'area', nipype default value: none)
        "none": no weighting is performed, surface": edge distance is
        weighted by the corresponding surface area
```

Outputs:

```
distance: (a float)
        computed distance
out_file: (an existing file name)
        numpy file keeping computed distances and weights
out_warp: (an existing file name)
        vtk file with the vertex-wise mapping of surface1 to surface2
```

33.2 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 nipype.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: (an existing file name)
        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 an existing file name)
        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))
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
operation: ('sum' or 'sub' or 'mul' or 'div', nipype default value:
         sum)
        operation to be performed
out_file: (a file name, nipype default value: warped_surf.vtk)
        vtk with surface warped
out_warp: (a file name, nipype default value: warp_maths.vtk)
        vtk file based on in_surf and warpings mapping it to out_file
```

Outputs:

```
out_file: (an existing file name)
        vtk with surface warped
out_warp: (an existing file name)
        vtk file with the vertex-wise mapping of surface1 to surface2
```

33.3 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: (an existing file name)
        Reference surface (vtk format) to which compute distance.
surface2: (an existing file name)
        Test surface (vtk format) from which compute distance.
```

```
[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
metric: ('euclidean' or 'sqeuclidean', nipype default value:
         euclidean)
        norm used to report distance
out_file: (a file name, nipype default value: distance.npy)
        numpy file keeping computed distances and weights
out_warp: (a file name, nipype default value: surfwarp.vtk)
        vtk file based on surface1 and warpings mapping it to surface2
weighting: ('none' or 'area', nipype default value: none)
        "none": no weighting is performed, surface": edge distance is
        weighted by the corresponding surface area
```

Outputs:

```
distance: (a float)
        computed distance
out_file: (an existing file name)
        numpy file keeping computed distances and weights
out_warp: (an existing file name)
        vtk file with the vertex-wise mapping of surface1 to surface2
```

33.4 TVTKBaseInterface

Link to code

A base class for interfaces using VTK

Inputs:

```
[Mandatory]

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
None
```

33.5 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 `nipype.interfaces.fsl.utils.ConvertWarp`.

Example:

```
from nipype.algorithms.mesh import WarpPoints
wp = WarpPoints()
wp.inputs.points = 'surf1.vtk'
wp.inputs.warp = 'warpfield.nii'
res = wp.run()
```

Inputs:

```
    [Mandatory]
    interp: ('cubic' or 'nearest' or 'linear', nipype default value:
             cubic)
            interpolation
    points: (an existing file name)
            file containing the point set
    warp: (an existing file name)
            dense deformation field to be applied

    [Optional]
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    out_points: (a file name)
            the warped point set
```

Outputs:

```
    out_points: (a file name)
            the warped point set
```

CHAPTER 34

algorithms.metrics

34.1 Distance

Link to code
Calculates distance between two volumes.
Inputs:

```
[Mandatory]
volume1: (an existing file name)
        Has to have the same dimensions as volume2.
volume2: (an existing file name)
        Has to have the same dimensions as volume1.

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask_volume: (an existing file name)
        calculate overlap only within this mask.
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)
```

Outputs:

```
distance: (a float)
histogram: (a file name)
point1: (an array with shape (3,))
point2: (an array with shape (3,))
```

34.2 ErrorMap

Link to code
Calculates the error (distance) map between two input volumes.

34.2.1 Example

```
>>> errormap = ErrorMap()
>>> errormap.inputs.in_ref = 'cont1.nii'
>>> errormap.inputs.in_tst = 'cont2.nii'
>>> res = errormap.run()
```

Inputs:

```
[Mandatory]
in_ref: (an existing file name)
        Reference image. Requires the same dimensions as in_tst.
in_tst: (an existing file name)
        Test image. Requires the same dimensions as in_ref.
metric: ('sqeuclidean' or 'euclidean', nipype default value:
         sqeuclidean)
        error map metric (as implemented in scipy cdist)

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        calculate overlap only within this mask.
out_map: (a file name)
        Name for the output file
```

Outputs:

```
distance: (a float)
        Average distance between volume 1 and 2
out_map: (an existing file name)
        resulting error map
```

34.3 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.

34.3.1 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()
```

Inputs:

```
[Mandatory]
in_ref: (a list of items which are an existing file name)
        Reference image. Requires the same dimensions as in_tst.
in_tst: (a list of items which are an existing file name)
        Test image. Requires the same dimensions as in_ref.
```

```
    [Optional]
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    out_file: (a file name, nipype default value: diff.nii)
            alternative name for resulting difference-map
    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
```

Outputs:

```
    class_fdi: (a list of items which are a float)
            Array containing the fDIs of each computed class
    class_fji: (a list of items which are a float)
            Array containing the fJIs of each computed class
    dice: (a float)
            Fuzzy Dice Index (fDI), all the classes
    diff_file: (an existing file name)
            resulting difference-map of all classes, using the chosen weighting
    jaccard: (a float)
            Fuzzy Jaccard Index (fJI), all the classes
```

34.4 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.

34.4.1 Example

```
>>> overlap = Overlap()
>>> overlap.inputs.volume1 = 'cont1.nii'
>>> overlap.inputs.volume2 = 'cont2.nii'
>>> res = overlap.run()
```

Inputs:

```
    [Mandatory]
    bg_overlap: (a boolean, nipype default value: False)
            consider zeros as a label
    vol_units: ('voxel' or 'mm', nipype default value: voxel)
            units for volumes
    volume1: (an existing file name)
            Has to have the same dimensions as volume2.
    volume2: (an existing file name)
            Has to have the same dimensions as volume1.

    [Optional]
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    mask_volume: (an existing file name)
```

```
        calculate overlap only within this mask.
out_file: (a file name, nipype default value: diff.nii)
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
```

Outputs:

```
dice: (a float)
        averaged dice index
diff_file: (an existing file name)
        error map of differences
jaccard: (a float)
        averaged jaccard index
labels: (a list of items which are an integer (int or long))
        detected labels
roi_di: (a list of items which are a float)
        the Dice index (DI) per ROI
roi_ji: (a list of items which are a float)
        the Jaccard index (JI) per ROI
roi_voldiff: (a list of items which are a float)
        volume differences of ROIs
volume_difference: (a float)
        averaged volume difference
```

34.5 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 `nipype.interfaces.nipy.utils.Similarity` to support 4D files. Requires `nipy`

34.5.1 Example

```
>>> from nipype.algorithms.metrics import Similarity
>>> similarity = Similarity()
>>> similarity.inputs.volume1 = 'rc1s1.nii'
>>> similarity.inputs.volume2 = 'rc1s2.nii'
>>> similarity.inputs.mask1 = 'mask.nii'
>>> similarity.inputs.mask2 = 'mask.nii'
>>> similarity.inputs.metric = 'cr'
>>> res = similarity.run()
```

Inputs:

```
[Mandatory]
volume1: (an existing file name)
        3D/4D volume
volume2: (an existing file name)
        3D/4D volume

[Optional]
```

```
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    mask1: (an existing file name)
            3D volume
    mask2: (an existing file name)
            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)
```

CHAPTER 35

algorithms.misc

35.1 AddCSVColumn

Link to code
Short interface to add an extra column and field to a text file

35.1.1 Example

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Input comma-separated value (CSV) files

[Optional]
extra_column_heading: (a string)
        New heading to add for the added field.
extra_field: (a string)
        New field to add to each row. This is useful for saving the group or
        subject ID in the file.
out_file: (a file name, nipype default value: extra_heading.csv)
        Output filename for merged CSV file
```

Outputs:

```
csv_file: (a file name)
        Output CSV file containing columns
```

35.2 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.

35.2.1 Example

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (a file name)
        Input comma-separated value (CSV) files

[Optional]
_outputs: (a dictionary with keys which are any value and with values
         which are any value, nipype default value: {})
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
csv_file: (a file name)
        Output CSV file containing rows
```

35.3 AddNoise

Link to code
Corrupts with noise the input image

35.3.1 Example

```
>>> from nipype.algorithms.misc import AddNoise
>>> noise = AddNoise()
>>> noise.inputs.in_file = 'T1.nii'
>>> noise.inputs.in_mask = 'mask.nii'
>>> noise.snr = 30.0
>>> noise.run()
```

Inputs:

```
[Mandatory]
bg_dist: ('normal' or 'rayleigh', nipype default value: normal)
        desired noise distribution, currently only normal is implemented
dist: ('normal' or 'rician', nipype default value: normal)
        desired noise distribution
in_file: (an existing file name)
        input image that will be corrupted with noise
```

```
[Optional]
in_mask: (an existing file name)
        input mask, voxels outside this mask will be considered background
out_file: (a file name)
        desired output filename
snr: (a float, nipype default value: 10.0)
        desired output SNR in dB
```

Outputs:

```
out_file: (an existing file name)
        corrupted image
```

35.4 CalculateNormalizedMoments

Link to code
Calculates moments of timeseries.

35.4.1 Example

```
>>> from nipype.algorithms import misc
>>> skew = misc.CalculateNormalizedMoments()
>>> skew.inputs.moment = 3
>>> skew.inputs.timeseries_file = 'timeseries.txt'
>>> skew.run()
```

Inputs:

```
[Mandatory]
moment: (an integer (int or long))
        Define which moment should be calculated, 3 for skewness, 4 for
        kurtosis.
timeseries_file: (an existing file name)
        Text file with timeseries in columns and timepoints in rows,
        whitespace separated

[Optional]
```

Outputs:

```
moments: (a list of items which are a float)
        Moments
```

35.5 CreateNifti

Link to code
Creates a nifti volume
Inputs:

```
[Mandatory]
data_file: (an existing file name)
        ANALYZE img file
header_file: (an existing file name)
        corresponding ANALYZE hdr file

[Optional]
affine: (an array)
```

```
        affine transformation array
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
nifti_file: (an existing file name)
```

35.6 Distance

Link to code

Calculates distance between two volumes.

Deprecated since version 0.10.0: Use `nipype.algorithms.metrics.Distance` instead.

Inputs:

```
[Mandatory]
volume1: (an existing file name)
        Has to have the same dimensions as volume2.
volume2: (an existing file name)
        Has to have the same dimensions as volume1.

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask_volume: (an existing file name)
        calculate overlap only within this mask.
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)
```

Outputs:

```
distance: (a float)
histogram: (a file name)
point1: (an array with shape (3,))
point2: (an array with shape (3,))
```

35.7 FuzzyOverlap

Link to code

Calculates various overlap measures between two maps, using a fuzzy definition.

Deprecated since version 0.10.0: Use `nipype.algorithms.metrics.FuzzyOverlap` instead.

Inputs:

```
[Mandatory]
in_ref: (a list of items which are an existing file name)
        Reference image. Requires the same dimensions as in_tst.
in_tst: (a list of items which are an existing file name)
```

```
        Test image. Requires the same dimensions as in_ref.

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name, nipype default value: diff.nii)
        alternative name for resulting difference-map
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
```

Outputs:

```
class_fdi: (a list of items which are a float)
        Array containing the fDIs of each computed class
class_fji: (a list of items which are a float)
        Array containing the fJIs of each computed class
dice: (a float)
        Fuzzy Dice Index (fDI), all the classes
diff_file: (an existing file name)
        resulting difference-map of all classes, using the chosen weighting
jaccard: (a float)
        Fuzzy Jaccard Index (fJI), all the classes
```

35.8 Gunzip

Link to code

Gunzip wrapper

Inputs:

```
[Mandatory]
in_file: (an existing file name)

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
out_file: (an existing file name)
```

35.9 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

35.9.1 Example

```
>>> from nipype.algorithms import misc
>>> mat2csv = misc.Matlab2CSV()
>>> mat2csv.inputs.in_file = 'cmatrix.mat'
>>> mat2csv.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Input MATLAB .mat file

[Optional]
reshape_matrix: (a boolean, nipype default value: True)
        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 file name)
```

35.10 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

35.10.1 Example

```
>>> from nipype.algorithms import misc
>>> mat2csv = misc.MergeCSVFiles()
>>> mat2csv.inputs.in_files = ['degree.mat','clustering.mat']
>>> mat2csv.inputs.column_headings = ['degree','clustering']
>>> mat2csv.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        Input comma-separated value (CSV) files

[Optional]
column_headings: (a list of items which are a 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.
extra_column_heading: (a string)
        New heading to add for the added field.
extra_field: (a string)
        New field to add to each row. This is useful for saving the group or
        subject ID in the file.
out_file: (a file name, nipype default value: merged.csv)
        Output filename for merged CSV file
row_heading_title: (a string, nipype default value: label)
```

```
        Column heading for the row headings added
row_headings: (a list of items which are a string)
        List of row headings to save in merged CSV file (must be equal to
        number of rows in the input files).
```

Outputs:

```
csv_file: (a file name)
        Output CSV file containing columns
```

35.11 MergeROIs

Link to code

Splits a 3D image in small chunks to enable parallel processing. ROIs keep time series structure in 4D images.

35.11.1 Example

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]

[Optional]
in_files: (a list of items which are an existing file name)
in_index: (a list of items which are an existing file name)
        array keeping original locations
in_reference: (an existing file name)
        reference file
```

Outputs:

```
merged_file: (an existing file name)
        the recomposed file
```

35.12 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 an existing file name)
        volumes which affine matrices will be modified

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
transformation_matrix: (an array with shape (4, 4), nipype default
         value: (<bound method Array.copy_default_value of
         <traits.trait_numeric.Array object at 0x7fc86b2c0a50>>, (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 file name)
```

35.13 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

35.13.1 Example

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]

[Optional]
in_files: (a list of items which are an existing file name)
in_mask: (an existing file name)
        Masked voxels must sum up 1.0, 0.0 otherwise.
```

Outputs:

```
out_files: (a list of items which are an existing file name)
        normalized maps
```

35.14 Overlap

Link to code

Calculates various overlap measures between two maps.
Deprecated since version 0.10.0: Use `nipype.algorithms.metrics.Overlap` instead.
Inputs:

```
[Mandatory]
bg_overlap: (a boolean, nipype default value: False)
        consider zeros as a label
vol_units: ('voxel' or 'mm', nipype default value: voxel)
        units for volumes
volume1: (an existing file name)
        Has to have the same dimensions as volume2.
volume2: (an existing file name)
        Has to have the same dimensions as volume1.
```

```
[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask_volume: (an existing file name)
        calculate overlap only within this mask.
out_file: (a file name, nipype default value: diff.nii)
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
```

Outputs:

```
dice: (a float)
        averaged dice index
diff_file: (an existing file name)
        error map of differences
jaccard: (a float)
        averaged jaccard index
labels: (a list of items which are an integer (int or long))
        detected labels
roi_di: (a list of items which are a float)
        the Dice index (DI) per ROI
roi_ji: (a list of items which are a float)
        the Jaccard index (JI) per ROI
roi_voldiff: (a list of items which are a float)
        volume differences of ROIs
volume_difference: (a float)
        averaged volume difference
```

35.15 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: (an existing file name)
        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]
dilation_size: (an integer (int or long), nipype default value: 0)
        Defines how much the mask will be dilated (expanded in 3D).
hemi: ('both' or 'left' or 'right', nipype default value: both)
        Restrict the mask to only one hemisphere: left or right
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_file: (a file name)
        Where to store the output mask.
```

Outputs:

```
mask_file: (an existing file name)
        output mask file
```

35.16 SimpleThreshold

Link to code

Applies a threshold to input volumes
Inputs:

```
[Mandatory]
threshold: (a float)
        volumes to be thresholdedeverything below this value will be set to
        zero
volumes: (a list of items which are an existing file name)
        volumes to be thresholded

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
thresholded_volumes: (a list of items which are an existing file
         name)
        thresholded volumes
```

35.17 SplitROIs

Link to code

Splits a 3D image in small chunks to enable parallel processing. ROIs keep time series structure in 4D images. >>> from nipype.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: (an existing file name)
        file to be splitted

[Optional]
in_mask: (an existing file name)
        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 an existing file name)
        the resulting ROIs
out_index: (a list of items which are an existing file name)
        arrays keeping original locations
out_masks: (a list of items which are an existing file name)
        a mask indicating valid values
```

35.18 TSNR

Link to code
Computes the time-course SNR for a time series
Typically you want to run this on a realigned time-series.

35.18.1 Example

```
>>> tsnr = TSNR()
>>> tsnr.inputs.in_file = 'functional.nii'
>>> res = tsnr.run()
```

Inputs:

```
[Mandatory]
in_file: (a list of items which are an existing file name)
        realigned 4D file or a list of 3D files

[Optional]
detrended_file: (a file name, nipype default value: detrend.nii.gz)
        input file after detrending
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mean_file: (a file name, nipype default value: mean.nii.gz)
        output mean file
regress_poly: (an integer >= 1)
        Remove polynomials
stddev_file: (a file name, nipype default value: stdev.nii.gz)
        output tSNR file
tsnr_file: (a file name, nipype default value: tsnr.nii.gz)
        output tSNR file
```

Outputs:

```
detrended_file: (a file name)
        detrended input file
mean_file: (an existing file name)
        mean image file
stddev_file: (an existing file name)
        std dev image file
tsnr_file: (an existing file name)
        tsnr image file
```

35.19 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

35.20 makefmtlist()

Link to code

35.21 maketypelist()

Link to code

35.22 matlab2csv()

Link to code

35.23 merge_csvs()

Link to code

35.24 merge_rois()

Link to code
Re-builds an image resulting from a parallelized processing

35.25 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.

35.26 remove_identical_paths()

Link to code

35.27 replaceext()

Link to code

35.28 split_rois()

Link to code
Splits an image in ROIs for parallel processing

CHAPTER 36

algorithms.modelgen

36.1 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.

36.1.1 Examples

```
>>> from nipype.interfaces.base import Bunch
>>> s = 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.
>>> info = [Bunch(conditions=['cond1'], onsets=[[2, 50, 100, 180]],                    duratic
>>> s.inputs.subject_info = info
```

Using pmod:

```
>>> info = [Bunch(conditions=['cond1', 'cond2'],                          onsets=[[2, 50],[100, 180
>>> s.inputs.subject_info = info
```

Inputs:

```
[Mandatory]
event_files: (a list of items which are a list of items which are an
         existing file name)
        list of event description files 1, 2 or 3 column format
        corresponding to onsets, durations and amplitudes
        mutually_exclusive: subject_info, event_files
functional_runs: (a list of items which are a list of items which are
         an existing file name or an existing file name)
        Data files for model. List of 4D files or list of list of 3D files
        per session
high_pass_filter_cutoff: (a float)
        High-pass filter cutoff in secs
input_units: ('secs' or 'scans')
        Units of event onsets and durations (secs or scans). Output units
        are always in secs
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
time_repetition: (a float)
        Time between the start of one volume to the start of the next image
        volume.

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
outlier_files: (a list of items which are an existing file name)
        Files containing scan outlier indices that should be tossed
realignment_parameters: (a list of items which are an existing file
         name)
        Realignment parameters returned by motion correction algorithm
```

Outputs:

```
session_info: (any value)
        session info for level1designs
```

36.2 SpecifySPMModel

Link to code

Adds SPM specific options to SpecifyModel

adds:

concatenate_runs
output_units

36.2.1 Examples

```
>>> from nipype.interfaces.base import Bunch
>>> s = 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
>>> info = [Bunch(conditions=['cond1'], onsets=[[2, 50, 100, 180]],                    durati
>>> s.inputs.subject_info = info
```

Inputs:

```
[Mandatory]
event_files: (a list of items which are a list of items which are an
         existing file name)
        list of event description files 1, 2 or 3 column format
        corresponding to onsets, durations and amplitudes
        mutually_exclusive: subject_info, event_files
functional_runs: (a list of items which are a list of items which are
         an existing file name or an existing file name)
        Data files for model. List of 4D files or list of list of 3D files
        per session
high_pass_filter_cutoff: (a float)
        High-pass filter cutoff in secs
input_units: ('secs' or 'scans')
        Units of event onsets and durations (secs or scans). Output units
        are always in secs
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
time_repetition: (a float)
        Time between the start of one volume to the start of the next image
        volume.

[Optional]
concatenate_runs: (a boolean, nipype default value: False)
        Concatenate all runs to look like a single session.
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
outlier_files: (a list of items which are an existing file name)
        Files containing scan outlier indices that should be tossed
output_units: ('secs' or 'scans', nipype default value: secs)
        Units of design event onsets and durations (secs or scans)
realignment_parameters: (a list of items which are an existing file
         name)
        Realignment parameters returned by motion correction algorithm
```

Outputs:

```
session_info: (any value)
        session info for level1designs
```

36.3 SpecifySparseModel

Link to code
Specify a sparse model that is compatible with spm/fsl designers

36.3.1 References

sparse-sampling fMRI experiments. Front. Neurosci. 7:55 http://journal.frontiersin.org/Journal/10.3389/fnins.2013.00055/abstrac

36.3.2 Examples

```
>>> from nipype.interfaces.base import Bunch
>>> s = 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
>>> info = [Bunch(conditions=['cond1'], onsets=[[2, 50, 100, 180]],                    durati
>>> s.inputs.subject_info = info
```

Inputs:

```
[Mandatory]
event_files: (a list of items which are a list of items which are an
         existing file name)
        list of event description files 1, 2 or 3 column format
        corresponding to onsets, durations and amplitudes
        mutually_exclusive: subject_info, event_files
functional_runs: (a list of items which are a list of items which are
         an existing file name or an existing file name)
        Data files for model. List of 4D files or list of list of 3D files
        per session
high_pass_filter_cutoff: (a float)
        High-pass filter cutoff in secs
input_units: ('secs' or 'scans')
        Units of event onsets and durations (secs or scans). Output units
        are always in secs
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
time_acquisition: (a float)
        Time in seconds to acquire a single image volume
time_repetition: (a float)
        Time between the start of one volume to the start of the next image
        volume.

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
model_hrf: (a boolean)
        model sparse events with hrf
outlier_files: (a list of items which are an existing file name)
        Files containing scan outlier indices that should be tossed
realignment_parameters: (a list of items which are an existing file
```

```
            name)
           Realignment parameters returned by motion correction algorithm
    save_plot: (a boolean)
           save plot of sparse design calculation (Requires matplotlib)
    scale_regressors: (a boolean, nipype default value: True)
           Scale regressors by the peak
    scan_onset: (a float, nipype default value: 0.0)
           Start of scanning relative to onset of run in secs
    stimuli_as_impulses: (a boolean, nipype 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
    volumes_in_cluster: (an integer >= 1, nipype default value: 1)
           Number of scan volumes in a cluster
```

Outputs:

```
    session_info: (any value)
           session info for level1designs
    sparse_png_file: (a file name)
           PNG file showing sparse design
    sparse_svg_file: (a file name)
           SVG file showing sparse design
```

36.4 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)
    ~~
```

36.5 gen_info()

Link to code

Generate subject_info structure from a list of event files

36.6 orth()

Link to code

Orthoganlize y_in with respect to x_in

```
    >>> orth_expected = np.array([1.7142857142857144, 0.42857142857142883,
    >>> err = np.abs(np.array(orth([1, 2, 3],[4, 5, 6]) - orth_expected))
    >>> all(err < np.finfo(float).eps)
    True
```

36.7 scale_timings()

Link to code
Scales timings given input and output units (scans/secs)

36.7.1 Parameters

timelist: list of times to scale input_units: 'secs' or 'scans' output_units: Ibid. time_repetition: float in seconds

36.8 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]
```

CHAPTER 37

algorithms.rapidart

37.1 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.

37.1.1 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()
```

Inputs:

```
[Mandatory]
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 voxelsare used, unless one of these mask types
        are defined.
norm_threshold: (a float)
        Threshold to use to detect motion-related outliers when composite
        motion is being used
        mutually_exclusive: rotation_threshold, translation_threshold
parameter_source: ('SPM' or 'FSL' or 'AFNI' or 'NiPy' or 'FSFAST')
        Source of movement parameters
realigned_files: (a list of items which are an existing file name)
        Names of realigned functional data files
realignment_parameters: (a list of items which are an existing file
         name)
        Names of realignment parameterscorresponding to the functional data
        files
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

[Optional]
bound_by_brainmask: (a boolean, nipype default value: False)
        use the brain mask to determine bounding boxfor composite norm
        (worksfor SPM and Nipy - currentlyinaccurate for FSL, AFNI
global_threshold: (a float, nipype default value: 8.0)
        use this threshold when mask type equal's spm_global
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
intersect_mask: (a boolean)
        Intersect the masks when computed from spm_global.
mask_file: (an existing file name)
        Mask file to be used if mask_type is 'file'.
mask_threshold: (a float)
        Mask threshold to be used if mask_type is 'thresh'.
plot_type: ('png' or 'svg' or 'eps' or 'pdf', nipype default value:
         png)
        file type of the outlier plot
save_plot: (a boolean, nipype default value: True)
        save plots containing outliers
use_differences: (a list of items which are a bool or None, nipype
         default value: [True, False])
        Use differences between successive motion (first element)and
        intensity paramter (second element) estimates in orderto determine
        outliers. (default is [True, False])
use_norm: (a boolean, nipype default value: True)
        Uses a composite of the motion parameters in order to determine
        outliers.
        requires: norm_threshold
```

Outputs:

```
displacement_files: (a list of items which are a file name)
        One image file for each functional run containing the
        voxeldisplacement timeseries
intensity_files: (a list of items which are an existing file name)
        One file for each functional run containing the global intensity
        values determined from the brainmask
mask_files: (a list of items which are a file name)
        One image file for each functional run containing the maskused for
        global signal calculation
norm_files: (a list of items which are a file name)
        One file for each functional run containing the composite norm
outlier_files: (a list of items which are an existing file name)
        One file for each functional run containing a list of 0-based
        indices corresponding to outlier volumes
plot_files: (a list of items which are a file name)
        One image file for each functional run containing the detected
        outliers
statistic_files: (a list of items which are an existing file name)
        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.
```

37.2 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.

37.2.1 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()
```

Inputs:

```
[Mandatory]
concatenated_design: (a boolean)
        state if the design matrix contains concatenated sessions
intensity_values: (a list of items which are an existing file name)
        Name of file containing intensity values
realignment_parameters: (a list of items which are an existing file
         name)
        Names of realignment parameters corresponding to the functional data
        files
spm_mat_file: (an existing file name)
        SPM mat file (use pre-estimate SPM.mat file)

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
stimcorr_files: (a list of items which are an existing file name)
        List of files containing correlation values
```

CHAPTER 38

interfaces.afni.preprocess

38.1 Allineate

Link to code
Wraps command **3dAllineate**
Program to align one dataset (the 'source') to a base dataset
For complete details, see the 3dAllineate Documentation.

38.1.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> allineate = afni.Allineate()
>>> allineate.inputs.in_file = 'functional.nii'
>>> allineate.inputs.out_file= 'functional_allineate.nii'
>>> allineate.inputs.in_matrix= 'cmatrix.mat'
>>> res = allineate.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dAllineate
        flag: -source %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
autobox: (a boolean)
        Expand the -automask function to enclose a rectangular
         box that holds the irregular mask.
        flag: -autobox
automask: (an integer (int or long))
        Compute a mask function, set a value for dilation or 0.
        flag: -automask+%d
autoweight: (a string)
        Compute a weight function using the 3dAutomask
         algorithm plus some blurring of the base image.
        flag: -autoweight%s
center_of_mass: (a string)
        Use the center-of-mass calculation to bracket the shifts.
        flag: -cmass%s
check: (a list of items which are '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 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.
        flag: -check %s
convergence: (a float)
        Convergence test in millimeters (default 0.05mm).
        flag: -conv %f
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
        flag: -cost %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
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.
        flag: -EPI
final_interpolation: ('nearestneighbour' or 'linear' or 'cubic' or
         'quintic' or 'wsinc5')
        Defines interpolation method used to create the output dataset
        flag: -final %s
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]
        flag: -fineblur %f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_matrix: (a file name)
        matrix to align input file
        flag: -1Dmatrix_apply %s, position: -3
in_param_file: (an existing file name)
        Read warp parameters from file and apply them to
         the source dataset, and produce a new dataset
        flag: -1Dparam_apply %s
interpolation: ('nearestneighbour' or 'linear' or 'cubic' or
         'quintic')
        Defines interpolation method to use during matching
        flag: -interp %s
master: (an existing file name)
        Write the output dataset on the same grid as this file
        flag: -master %s
newgrid: (a float)
        Write the output dataset using isotropic grid spacing in mm
        flag: -newgrid %f
nmatch: (an integer (int or long))
```

```
        Use at most n scattered points to match the datasets.
        flag: -nmatch %d
no_pad: (a boolean)
        Do not use zero-padding on the base image.
        flag: -nopad
nomask: (a boolean)
        Don't compute the autoweight/mask; if -weight is not
         also used, then every voxel will be counted equally.
        flag: -nomask
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.
        flag: -nwarp %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.
        flag: -nwarp_fixdep%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.
        flag: -nwarp_fixmot%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.
        flag: -onepass
out_file: (a file name)
        output file from 3dAllineate
        flag: -prefix %s, position: -2
out_matrix: (a file name)
        Save the transformation matrix for each volume.
        flag: -1Dmatrix_save %s
out_param_file: (a file name)
        Save the warp parameters in ASCII (.1D) format.
        flag: -1Dparam_save %s
out_weight_file: (a file name)
        Write the weight volume to disk as a dataset
        flag: -wtprefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
reference: (an existing file name)
        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.
        flag: -base %s
replacebase: (a boolean)
        If the source has more than one volume, then after the first
         volume is aligned to the base
        flag: -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'.
        flag: -replacemeth %s
source_automask: (an integer (int or long))
        Automatically mask the source dataset with dilation or 0.
        flag: -source_automask+%d
```

```
    source_mask: (an existing file name)
            mask the input dataset
            flag: -source_mask %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    two_best: (an integer (int or long))
            In the coarse pass, use the best 'bb' set of initial
             points to search for the starting point for the fine
             pass. If bb==0, then no search is made for the best
             starting point, and the identity transformation is
             used as the starting point. [Default=5; min=0 max=11]
            flag: -twobest %d
    two_blur: (a float)
            Set the blurring radius for the first pass in mm.
            flag: -twoblur
    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.
            flag: -twofirst
    two_pass: (a boolean)
            Use a two pass alignment strategy for all volumes, searching
             for a large rotation+shift and then refining the alignment.
            flag: -twopass
    usetemp: (a boolean)
            temporary file use
            flag: -usetemp
    warp_type: ('shift_only' or 'shift_rotate' or 'shift_rotate_scale' or
             'affine_general')
            Set the warp type.
            flag: -warp %s
    warpfreeze: (a boolean)
            Freeze the non-rigid body parameters after first volume.
            flag: -warpfreeze
    weight_file: (an existing file name)
            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
            flag: -weight %s
    zclip: (a boolean)
            Replace negative values in the input datasets (source & base) with
            zero.
            flag: -zclip
```

Outputs:

```
    matrix: (a file name)
            matrix to align input file
    out_file: (a file name)
            output image file name
```

38.2 AutoTcorrelate

Link to code
Wraps 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].

38.2.1 Examples

```
>>> from nipype.interfaces import afni as 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
'3dAutoTcorrelate -eta2 -mask mask.nii -mask_only_targets -prefix functional_similarity_matrix.1
>>> res = corr.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        timeseries x space (volume or surface) file
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
eta2: (a boolean)
        eta^2 similarity
        flag: -eta2
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        mask of voxels
        flag: -mask %s
mask_only_targets: (a boolean)
        use mask only on targets voxels
        flag: -mask_only_targets
        mutually_exclusive: mask_source
mask_source: (an existing file name)
        mask for source voxels
        flag: -mask_source %s
        mutually_exclusive: mask_only_targets
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
polort: (an integer (int or long))
        Remove polynomical trend of order m or -1 for no detrending
        flag: -polort %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
```

```
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.3 Autobox

Link to code

Wraps 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. <http://afni.nimh.nih.gov/pub/dist/doc/program_help/3dAutobox.html>

38.3.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> abox = afni.Autobox()
>>> abox.inputs.in_file = 'structural.nii'
>>> abox.inputs.padding = 5
>>> res = abox.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file
        flag: -input %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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.
        flag: -noclust
out_file: (a file name)
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
padding: (an integer (int or long))
        Number of extra voxels to pad on each side of box
        flag: -npad %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        output file
x_max: (an integer (int or long))
x_min: (an integer (int or long))
y_max: (an integer (int or long))
y_min: (an integer (int or long))
z_max: (an integer (int or long))
z_min: (an integer (int or long))
```

38.4 Automask

Link to code
Wraps command **3dAutomask**
Create a brain-only mask of the image using AFNI 3dAutomask command
For complete details, see the 3dAutomask Documentation.

38.4.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> automask = afni.Automask()
>>> automask.inputs.in_file = 'functional.nii'
>>> automask.inputs.dilate = 1
>>> automask.inputs.outputtype = "NIFTI"
>>> automask.cmdline
'3dAutomask -apply_prefix functional_masked.nii -dilate 1 -prefix functional_mask.nii functional
>>> res = automask.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dAutomask
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
brain_file: (a file name)
        output file from 3dAutomask
        flag: -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].
        flag: -clfrac %s
dilate: (an integer (int or long))
        dilate the mask outwards
        flag: -dilate %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
erode: (an integer (int or long))
        erode the mask inwards
        flag: -erode %s
```

```
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
brain_file: (an existing file name)
        brain file (skull stripped)
out_file: (an existing file name)
        mask file
```

38.5 Bandpass

Link to code

Wraps 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 Documentation.

38.5.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> from nipype.testing import  example_data
>>> bandpass = afni.Bandpass()
>>> bandpass.inputs.in_file = example_data('functional.nii')
>>> bandpass.inputs.highpass = 0.005
>>> bandpass.inputs.lowpass = 0.1
>>> res = bandpass.run()
```

Inputs:

```
[Mandatory]
highpass: (a float)
        highpass
        flag: %f, position: -3
in_file: (an existing file name)
        input file to 3dBandpass
        flag: %s, position: -1
lowpass: (a float)
        lowpass
        flag: %f, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
automask: (a boolean)
        Create a mask from the input dataset
```

```
        flag: -automask
blur: (a float)
        Blur (inside the mask only) with a filter
         width (FWHM) of 'fff' millimeters.
        flag: -blur %f
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.
        flag: -despike
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
localPV: (a float)
        Replace each vector by the local Principal Vector
         (AKA first singular vector) from a neighborhood
         of radius 'rrr' millimiters.
         ++ Note that the PV time series is L2 normalized.
         ++ This option is mostly for Bob Cox to have fun with.
        flag: -localPV %f
mask: (an existing file name)
        mask file
        flag: -mask %s, position: 2
nfft: (an integer (int or long))
        set the FFT length [must be a legal value]
        flag: -nfft %d
no_detrend: (a boolean)
        Skip the quadratic detrending of the input that
         occurs before the FFT-based bandpassing.
         ++ You would only want to do this if the dataset
         had been detrended already in some other program.
        flag: -nodetrend
normalize: (a boolean)
        Make all output time series have L2 norm = 1
         ++ i.e., sum of squares = 1
        flag: -norm
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.
        flag: -notrans
orthogonalize_dset: (an existing file name)
        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.
        flag: -dsort %s
orthogonalize_file: (a list of items which are an existing file name)
        Also orthogonalize input to columns in f.1D
         ++ Multiple '-ort' options are allowed.
        flag: -ort %s
out_file: (a file name)
        output file from 3dBandpass
```

```
        flag: -prefix %s, position: 1
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tr: (a float)
        set time step (TR) in sec [default=from dataset header]
        flag: -dt %f
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.6 BlurInMask

Link to code

Wraps command **3dBlurInMask**

Blurs a dataset spatially inside a mask. That's all. Experimental.

For complete details, see the '3dBlurInMask Documentation. <http://afni.nimh.nih.gov/pub/dist/doc/program_help/3dBlurInMask

38.6.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> bim = afni.BlurInMask()
>>> bim.inputs.in_file = 'functional.nii'
>>> bim.inputs.mask = 'mask.nii'
>>> bim.inputs.fwhm = 5.0
>>> bim.cmdline
'3dBlurInMask -input functional.nii -FWHM 5.000000 -mask mask.nii -prefix functional_blur'
>>> res = bim.run()
```

Inputs:

```
[Mandatory]
fwhm: (a float)
        fwhm kernel size
        flag: -FWHM %f
in_file: (an existing file name)
        input file to 3dSkullStrip
        flag: -input %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
automask: (a boolean)
        Create an automask from the input dataset.
        flag: -automask
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
float_out: (a boolean)
        Save dataset as floats, no matter what the input data type is.
```

```
        flag: -float
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (a file name)
        Mask dataset, if desired. Blurring will occur only within the mask.
        Voxels NOT in the mask will be set to zero in the output.
        flag: -mask %s
multimask: (a file name)
        Multi-mask dataset -- each distinct nonzero value in dataset will be
        treated as a separate mask for blurring purposes.
        flag: -Mmask %s
options: (a string)
        options
        flag: %s, position: 2
out_file: (a file name)
        output to the file
        flag: -prefix %s, position: -1
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
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.
        flag: -preserve
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.7 BlurToFWHM

Link to code

Wraps command **3dBlurToFWHM**

Blurs a 'master' dataset until it reaches a specified FWHM smoothness (approximately).

For complete details, see the to3d Documentation

38.7.1 Examples

```
>>> from nipype.interfaces import afni
>>> blur = afni.preprocess.BlurToFWHM()
>>> blur.inputs.in_file = 'epi.nii'
>>> blur.inputs.fwhm = 2.5
>>> blur.cmdline
'3dBlurToFWHM -FWHM 2.500000 -input epi.nii -prefix epi_afni'
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        The dataset that will be smoothed
        flag: -input %s
```

```
    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    automask: (a boolean)
            Create an automask from the input dataset.
            flag: -automask
    blurmaster: (an existing file name)
            The dataset whose smoothness controls the process.
            flag: -blurmaster %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    fwhm: (a float)
            Blur until the 3D FWHM reaches this value (in mm)
            flag: -FWHM %f
    fwhmxy: (a float)
            Blur until the 2D (x,y)-plane FWHM reaches this value (in mm)
            flag: -FWHMxy %f
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    mask: (an existing file name)
            Mask dataset, if desired. Voxels NOT in mask will be set to zero in
            output.
            flag: -blurmaster %s
    out_file: (a file name)
            output image file name
            flag: -prefix %s
    outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
            AFNI output filetype
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
            output file
```

38.8 BrickStat

Link to code

Wraps command **3dBrickStat**

Compute maximum and/or minimum voxel values of an input dataset

For complete details, see the 3dBrickStat Documentation.

38.8.1 Examples

```
    >>> from nipype.interfaces import afni as afni
    >>> brickstat = afni.BrickStat()
    >>> brickstat.inputs.in_file = 'functional.nii'
    >>> brickstat.inputs.mask = 'skeleton_mask.nii.gz'
    >>> brickstat.inputs.min = True
```

```
>>> res = brickstat.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dmaskave
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        -mask dset = use dset as mask to include/exclude voxels
        flag: -mask %s, position: 2
min: (a boolean)
        print the minimum value in dataset
        flag: -min, position: 1
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
min_val: (a float)
        output
```

38.9 Calc

Link to code

Wraps command **3dcalc**

This program does voxel-by-voxel arithmetic on 3D datasets

For complete details, see the 3dcalc Documentation.

38.9.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> calc = afni.Calc()
>>> calc.inputs.in_file_a = 'functional.nii'
>>> calc.inputs.in_file_b = 'functional2.nii'
>>> calc.inputs.expr='a*b'
>>> calc.inputs.out_file =  'functional_calc.nii.gz'
>>> calc.inputs.outputtype = "NIFTI"
```

```
>>> calc.cmdline
'3dcalc -a functional.nii  -b functional2.nii -expr "a*b" -prefix functional_calc.nii.gz'
```

Inputs:

```
[Mandatory]
expr: (a string)
        expr
        flag: -expr "%s", position: 3
in_file_a: (an existing file name)
        input file to 3dcalc
        flag: -a %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_file_b: (an existing file name)
        operand file to 3dcalc
        flag:  -b %s, position: 1
in_file_c: (an existing file name)
        operand file to 3dcalc
        flag:  -c %s, position: 2
other: (a file name)
        other options
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
single_idx: (an integer (int or long))
        volume index for in_file_a
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
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.10 ClipLevel

Link to code
Wraps 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.

38.10.1 Examples

```
>>> from nipype.interfaces.afni import preprocess
>>> cliplevel = preprocess.ClipLevel()
>>> cliplevel.inputs.in_file = 'anatomical.nii'
>>> res = cliplevel.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dClipLevel
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
doall: (a boolean)
        Apply the algorithm to each sub-brick separately
        flag: -doall, position: 3
        mutually_exclusive: g, r, a, d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
grad: (a file name)
        also compute a 'gradual' clip level as a function of voxel position,
        and output that to a dataset
        flag: -grad %s, position: 3
        mutually_exclusive: d, o, a, l, l
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mfrac: (a float)
        Use the number ff instead of 0.50 in the algorithm
        flag: -mfrac %s, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
clip_val: (a float)
        output
```

38.11 Copy

Link to code
Wraps 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 Documentation.

38.11.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> copy3d = afni.Copy()
>>> copy3d.inputs.in_file = 'functional.nii'
>>> copy3d.cmdline
'3dcopy functional.nii functional_copy'
```

```
>>> from copy import deepcopy
>>> copy3d_2 = deepcopy(copy3d)
>>> copy3d_2.inputs.outputtype = 'NIFTI'
>>> copy3d_2.cmdline
'3dcopy functional.nii functional_copy.nii'
```

```
>>> copy3d_3 = deepcopy(copy3d)
>>> copy3d_3.inputs.outputtype = 'NIFTI_GZ'
>>> copy3d_3.cmdline
'3dcopy functional.nii functional_copy.nii.gz'
```

```
>>> copy3d_4 = deepcopy(copy3d)
>>> copy3d_4.inputs.out_file = 'new_func.nii'
>>> copy3d_4.cmdline
'3dcopy functional.nii new_func.nii'
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dcopy
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output image file name
        flag: %s, position: -1
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.12 DegreeCentrality

Link to code
Wraps command **3dDegreeCentrality**
Performs degree centrality on a dataset using a given maskfile via 3dDegreeCentrality
For complete details, see the '3dDegreeCentrality Documentation. <http://afni.nimh.nih.gov/pub/dist/doc/program_help/3dDegree

38.12.1 Examples

```
>>> from nipype.interfaces import afni as 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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dDegreeCentrality
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
autoclip: (a boolean)
        Clip off low-intensity regions in the dataset
        flag: -autoclip
automask: (a boolean)
        Mask the dataset to target brain-only voxels
        flag: -automask
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        mask file to mask input data
        flag: -mask %s
oned_file: (a string)
        output filepath to text dump of correlation matrix
        flag: -out1D %s
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
polort: (an integer (int or long))
        flag: -polort %d
sparsity: (a float)
        only take the top percent of connections
```

```
        flag: -sparsity %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
thresh: (a float)
        threshold to exclude connections where corr <= thresh
        flag: -thresh %f
```

Outputs:

```
oned_file: (a file name)
        The text output of the similarity matrix computedafter thresholding
        with one-dimensional and ijk voxel indices, correlations, image
        extents, and affine matrix
out_file: (an existing file name)
        output file
```

38.13 Despike

Link to code
Wraps command **3dDespike**
Removes 'spikes' from the 3D+time input dataset
For complete details, see the 3dDespike Documentation.

38.13.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> despike = afni.Despike()
>>> despike.inputs.in_file = 'functional.nii'
>>> despike.cmdline
'3dDespike -prefix functional_despike functional.nii'
>>> res = despike.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dDespike
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
```

```
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.14 Detrend

Link to code
Wraps command **3dDetrend**
This program removes components from voxel time series using linear least squares
For complete details, see the 3dDetrend Documentation.

38.14.1 Examples

```
>>> from nipype.interfaces import afni as 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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dDetrend
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
            output file
```

38.15 ECM

Link to code
Wraps command **3dECM**
Performs degree centrality on a dataset using a given maskfile via the 3dLFCD command
For complete details, see the '3dECM Documentation. <http://afni.nimh.nih.gov/pub/dist/doc/program_help/3dECM.html>

38.15.1 Examples

```
>>> from nipype.interfaces import afni as 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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dECM
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
autoclip: (a boolean)
        Clip off low-intensity regions in the dataset
        flag: -autoclip
automask: (a boolean)
        Mask the dataset to target brain-only voxels
        flag: -automask
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
eps: (a float)
        sets the stopping criterion for the power iteration; l2|v_old -
        v_new| < eps*|v_old|; default = 0.001
        flag: -eps %f
fecm: (a boolean)
        Fast centrality method; substantial speed increase but cannot
        accomodate thresholding; automatically selected if -thresh or
        -sparsity are not set
        flag: -fecm
full: (a boolean)
        Full power method; enables thresholding; automatically selected if
        -thresh or -sparsity are set
        flag: -full
ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        mask file to mask input data
        flag: -mask %s
max_iter: (an integer (int or long))
        sets the maximum number of iterations to use in the power iteration;
        default = 1000
        flag: -max_iter %d
memory: (a float)
        Limit memory consumption on system by setting the amount of GB to
        limit the algorithm to; default = 2GB
        flag: -memory %f
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
polort: (an integer (int or long))
        flag: -polort %d
scale: (a float)
        scale correlation coefficients in similarity matrix to after
        shifting, x >= 0.0; default = 1.0 for -full, 0.5 for -fecm
        flag: -scale %f
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
        flag: -shift %f
sparsity: (a float)
        only take the top percent of connections
        flag: -sparsity %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
thresh: (a float)
        threshold to exclude connections where corr <= thresh
        flag: -thresh %f
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.16 Eval

Link to code

Wraps command **1deval**

Evaluates an expression that may include columns of data from one or more text files

see AFNI Documentation: <http://afni.nimh.nih.gov/pub/dist/doc/program_help/1deval.html>

38.16.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> eval = afni.Eval()
>>> eval.inputs.in_file_a = 'seed.1D'
>>> eval.inputs.in_file_b = 'resp.1D'
```

```
>>> eval.inputs.expr='a*b'
>>> eval.inputs.out1D = True
>>> eval.inputs.out_file =  'data_calc.1D'
>>> calc.cmdline
'3deval -a timeseries1.1D  -b timeseries2.1D -expr "a*b" -1D -prefix data_calc.1D'
```

Inputs:

```
[Mandatory]
expr: (a string)
        expr
        flag: -expr "%s", position: 3
in_file_a: (an existing file name)
        input file to 1deval
        flag: -a %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_file_b: (an existing file name)
        operand file to 1deval
        flag:  -b %s, position: 1
in_file_c: (an existing file name)
        operand file to 1deval
        flag:  -c %s, position: 2
other: (a file name)
        other options
out1D: (a boolean)
        output in 1D
        flag: -1D
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
single_idx: (an integer (int or long))
        volume index for in_file_a
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
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.17 FWHMx

Link to code

Wraps 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.)

38.17.1 Examples

```
>>> from nipype.interfaces import afni as afp
>>> fwhm = afp.FWHMx()
>>> fwhm.inputs.in_file = 'functional.nii'
>>> fwhm.cmdline
'3dFWHMx -input functional.nii -out functional_subbricks.out > functional_fwhmx.out'
```

(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 -demend

- 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: (an existing file name)
        input dataset
        flag: -input %s

[Optional]
acf: (a boolean or a file name or a tuple of the form: (an existing
         file name, a float), nipype default value: False)
        computes the spatial autocorrelation
        flag: -acf
args: (a string)
        Additional parameters to the command
        flag: %s
arith: (a boolean)
        if in_file has more than one sub-brick, compute the final estimate
        asthe arithmetic mean of the individual sub-brick FWHM estimates
        flag: -arith
        mutually_exclusive: geom
automask: (a boolean, nipype default value: False)
        compute a mask from THIS dataset, a la 3dAutomask
        flag: -automask
combine: (a boolean)
        combine the final measurements along each axis
        flag: -combine
compat: (a boolean)
        be compatible with the older 3dFWHM
        flag: -compat
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.
        flag: -demed
        mutually_exclusive: detrend
detrend: (a boolean or an integer (int or long), nipype 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.
```

```
        flag: -detrend
        mutually_exclusive: demed
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
geom: (a boolean)
        if in_file has more than one sub-brick, compute the final estimate
        asthe geometric mean of the individual sub-brick FWHM estimates
        flag: -geom
        mutually_exclusive: arith
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        use only voxels that are nonzero in mask
        flag: -mask %s
out_detrend: (a file name)
        Save the detrended file into a dataset
        flag: -detprefix %s
out_file: (a file name)
        output file
        flag: > %s, position: -1
out_subbricks: (a file name)
        output file listing the subbricks FWHM
        flag: -out %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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.
        flag: -unif
```

Outputs:

```
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
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
out_acf: (an existing file name)
        output acf file
out_detrend: (a file name)
        output file, detrended
out_file: (an existing file name)
        output file
out_subbricks: (an existing file name)
        output file (subbricks)
```

38.18 Fim

Link to code

Wraps 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+ Documentation.

38.18.1 Examples

```
>>> from nipype.interfaces import afni as 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
>>> res = fim.run()
```

Inputs:

```
[Mandatory]
ideal_file: (an existing file name)
        ideal time series file name
        flag: -ideal_file %s, position: 2
in_file: (an existing file name)
        input file to 3dfim+
        flag:  -input %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fim_thr: (a float)
        fim internal mask threshold value
        flag: -fim_thr %f, position: 3
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out: (a string)
        Flag to output the specified parameter
        flag: -out %s, position: 4
out_file: (a file name)
        output image file name
        flag: -bucket %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.19 Fourier

Link to code
Wraps command **3dFourier**
Program to lowpass and/or highpass each voxel time series in a dataset, via the FFT
For complete details, see the 3dFourier Documentation.

38.19.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> fourier = afni.Fourier()
>>> fourier.inputs.in_file = 'functional.nii'
>>> fourier.inputs.args = '-retrend'
>>> fourier.inputs.highpass = 0.005
>>> fourier.inputs.lowpass = 0.1
>>> res = fourier.run()
```

Inputs:

```
[Mandatory]
highpass: (a float)
        highpass
        flag: -highpass %f, position: 1
in_file: (an existing file name)
        input file to 3dFourier
        flag: %s, position: -1
lowpass: (a float)
        lowpass
        flag: -lowpass %f, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.20 Hist

Link to code
Wraps 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 Documentation.

38.20.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> hist = afni.Hist()
>>> hist.inputs.in_file = 'functional.nii'
>>> hist.cmdline
'3dHist -input functional.nii -prefix functional_hist'
>>> res = hist.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dHist
        flag: -input %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
bin_width: (a float)
        bin width
        flag: -binwidth %f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        matrix to align input file
        flag: -mask %s
max_value: (a float)
        maximum intensity value
        flag: -max %f
min_value: (a float)
        minimum intensity value
        flag: -min %f
nbin: (an integer (int or long))
        number of bins
        flag: -nbin %d
out_file: (a file name)
        Write histogram to niml file with this prefix
        flag: -prefix %s
out_show: (a file name)
        output image file name
        flag: > %s, position: -1
showhist: (a boolean, nipype default value: False)
        write a text visual histogram
        flag: -showhist
```

```
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
out_show: (a file name)
        output visual histogram
```

38.21 LFCD

Link to code
Wraps command **3dLFCD**
Performs degree centrality on a dataset using a given maskfile via the 3dLFCD command
For complete details, see the '3dLFCD Documentation. <http://afni.nimh.nih.gov/pub/dist/doc/program_help/3dLFCD.html>

38.21.1 Examples

```
>>> from nipype.interfaces import afni as 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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dLFCD
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
autoclip: (a boolean)
        Clip off low-intensity regions in the dataset
        flag: -autoclip
automask: (a boolean)
        Mask the dataset to target brain-only voxels
        flag: -automask
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        mask file to mask input data
```

```
        flag: -mask %s
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
polort: (an integer (int or long))
        flag: -polort %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
thresh: (a float)
        threshold to exclude connections where corr <= thresh
        flag: -thresh %f
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.22 MaskTool

Link to code
Wraps command **3dmask_tool**
3dmask_tool - for combining/dilating/eroding/filling masks
For complete details, see the 3dmask_tool Documentation.

38.22.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> automask = afni.Automask()
>>> automask.inputs.in_file = 'functional.nii'
>>> automask.inputs.dilate = 1
>>> automask.inputs.outputtype = "NIFTI"
>>> automask.cmdline
'3dAutomask -apply_prefix functional_masked.nii -dilate 1 -prefix functional_mask.nii functional
>>> res = automask.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file or files to 3dmask_tool
        flag: -input %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %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.
        flag: -count, position: 2
datum: ('byte' or 'short' or 'float')
        specify data type for output. Valid types are 'byte', 'short' and
```

```
        'float'.
        flag: -datum %s
dilate_inputs: (a string)
        Use this option to dilate and/or erode datasets as they are read.
        ex. '5 -5' to dilate and erode 5 times
        flag: -dilate_inputs %s
dilate_results: (a string)
        dilate and/or erode combined mask at the given levels.
        flag: -dilate_results %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fill_dirs: (a 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}.
        flag: -fill_dirs %s
        requires: fill_holes
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.
        flag: -fill_holes
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
        flag: -frac %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inter: (a boolean)
        intersection, this means -frac 1.0
        flag: -inter
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
union: (a boolean)
        union, this means -frac 0
        flag: -union
```

Outputs:

```
out_file: (an existing file name)
        mask file
```

38.23 Maskave

Link to code

Wraps 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.

38.23.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> maskave = afni.Maskave()
>>> maskave.inputs.in_file = 'functional.nii'
>>> maskave.inputs.mask= 'seed_mask.nii'
>>> maskave.inputs.quiet= True
>>> maskave.cmdline
'3dmaskave -mask seed_mask.nii -quiet functional.nii > functional_maskave.1D'
>>> res = maskave.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dmaskave
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        matrix to align input file
        flag: -mask %s, position: 1
out_file: (a file name)
        output image file name
        flag: > %s, position: -1
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
quiet: (a boolean)
        matrix to align input file
        flag: -quiet, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.24 Means

Link to code
Wraps command **3dMean**
Takes the voxel-by-voxel mean of all input datasets using 3dMean
see AFNI Documentation: <http://afni.nimh.nih.gov/pub/dist/doc/program_help/3dMean.html>

38.24.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> means = afni.Means()
>>> means.inputs.in_file_a = 'im1.nii'
>>> means.inputs.in_file_b = 'im2.nii'
>>> means.inputs.out_file =  'output.nii'
>>> means.cmdline
'3dMean im1.nii im2.nii -prefix output.nii'
```

Inputs:

```
[Mandatory]
in_file_a: (an existing file name)
        input file to 3dMean
        flag: %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
count: (a boolean)
        compute count of non-zero voxels
        flag: -count
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_file_b: (an existing file name)
        another input file to 3dMean
        flag: %s, position: 1
mask_inter: (a boolean)
        create intersection mask
        flag: -mask_inter
mask_union: (a boolean)
        create union mask
        flag: -mask_union
non_zero: (a boolean)
        use only non-zero values
        flag: -non_zero
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
scale: (a string)
        scaling of output
        flag: -%sscale
sqr: (a boolean)
        mean square instead of value
        flag: -sqr
std_dev: (a boolean)
        calculate std dev
        flag: -stdev
summ: (a boolean)
        take sum, (not average)
```

```
        flag: -sum
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.25 Merge

Link to code
Wraps command **3dmerge**
Merge or edit volumes using AFNI 3dmerge command
For complete details, see the 3dmerge Documentation.

38.25.1 Examples

```
>>> from nipype.interfaces import afni as 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'
>>> res = merge.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
blurfwhm: (an integer (int or long))
        FWHM blur value (mm)
        flag: -1blur_fwhm %d
doall: (a boolean)
        apply options to all sub-bricks in dataset
        flag: -doall
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
```

```
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.26 OutlierCount

Link to code
Wraps command **3dToutcount**
Create a 3D dataset from 2D image files using AFNI to3d command
For complete details, see the to3d Documentation

38.26.1 Examples

```
>>> from nipype.interfaces import afni
>>> toutcount = afni.OutlierCount()
>>> toutcount.inputs.in_file = 'functional.nii'
>>> toutcount.cmdline
'3dToutcount functional.nii > functional_outliers'
>>> res = toutcount.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input dataset
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
autoclip: (a boolean, nipype default value: False)
        clip off small voxels
        flag: -autoclip
        mutually_exclusive: in_file
automask: (a boolean, nipype default value: False)
        clip off small voxels
        flag: -automask
        mutually_exclusive: in_file
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fraction: (a boolean, nipype default value: False)
        write out the fraction of masked voxels which are outliers at each
        timepoint
        flag: -fraction
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interval: (a boolean, nipype default value: False)
        write out the median + 3.5 MAD of outlier count with each timepoint
```

```
        flag: -range
legendre: (a boolean, nipype default value: False)
        use Legendre polynomials
        flag: -legendre
mask: (an existing file name)
        only count voxels within the given mask
        flag: -mask %s
        mutually_exclusive: autoclip, automask
out_file: (a file name)
        capture standard output
        flag: > %s, position: -1
outliers_file: (a file name)
        output image file name
        flag: -save %s
polort: (an integer (int or long))
        detrend each voxel timeseries with polynomials
        flag: -polort %d
qthr: (0.0 <= a floating point number <= 1.0)
        indicate a value for q to compute alpha
        flag: -qthr %.5f
save_outliers: (a boolean, nipype default value: False)
        enables out_file option
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        capture standard output
        flag: > %s, position: -1
out_outliers: (an existing file name)
        output image file name
```

38.27 QualityIndex

Link to code

Wraps command **3dTqual**

Create a 3D dataset from 2D image files using AFNI to3d command

For complete details, see the to3d Documentation

38.27.1 Examples

```
>>> from nipype.interfaces import afni
>>> tqual = afni.QualityIndex()
>>> tqual.inputs.in_file = 'functional.nii'
>>> tqual.cmdline
'3dTqual functional.nii > functional_tqual'
>>> res = tqual.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input dataset
        flag: %s, position: -2
```

```
    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    autoclip: (a boolean, nipype default value: False)
            clip off small voxels
            flag: -autoclip
            mutually_exclusive: mask
    automask: (a boolean, nipype default value: False)
            clip off small voxels
            flag: -automask
            mutually_exclusive: mask
    clip: (a float)
            clip off values below
            flag: -clip %f
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    interval: (a boolean, nipype default value: False)
            write out the median + 3.5 MAD of outlier count with each timepoint
            flag: -range
    mask: (an existing file name)
            compute correlation only across masked voxels
            flag: -mask %s
            mutually_exclusive: autoclip, automask
    out_file: (a file name)
            capture standard output
            flag: > %s, position: -1
    quadrant: (a boolean, nipype default value: False)
            Similar to -spearman, but using 1 minus the quadrant correlation
            coefficient as the quality index.
            flag: -quadrant
    spearman: (a boolean, nipype default value: False)
            Quality index is 1 minus the Spearman (rank) correlation coefficient
            of each sub-brick with the median sub-brick. (default)
            flag: -spearman
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (a file name)
            file containing the caputured standard output
```

38.28 ROIStats

Link to code
Wraps command **3dROIstats**
Display statistics over masked regions
For complete details, see the 3dROIstats Documentation.

38.28.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> roistats = afni.ROIStats()
>>> roistats.inputs.in_file = 'functional.nii'
>>> roistats.inputs.mask = 'skeleton_mask.nii.gz'
>>> roistats.inputs.quiet=True
>>> res = roistats.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dROIstats
        flag: %s, position: -1
terminal_output: ('allatonce', nipype default value: allatonce)
        Control terminal output:`allatonce` - waits till command is finished
        to display output

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        input mask
        flag: -mask %s, position: 3
mask_f2short: (a boolean)
        Tells the program to convert a float mask to short integers, by
        simple rounding.
        flag: -mask_f2short, position: 2
quiet: (a boolean)
        execute quietly
        flag: -quiet, position: 1
```

Outputs:

```
stats: (an existing file name)
        output tab separated values file
```

38.29 Refit

Link to code
Wraps command **3drefit**
Changes some of the information inside a 3D dataset's header
For complete details, see the '3drefit Documentation. <http://afni.nimh.nih.gov/pub/dist/doc/program_help/3drefit.html>

38.29.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> refit = afni.Refit()
```

```
>>> refit.inputs.in_file = 'structural.nii'
>>> refit.inputs.deoblique = True
>>> refit.cmdline
'3drefit -deoblique structural.nii'
>>> res = refit.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3drefit
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
deoblique: (a boolean)
        replace current transformation matrix with cardinal matrix
        flag: -deoblique
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
space: ('TLRC' or 'MNI' or 'ORIG')
        Associates the dataset with a specific template type, e.g. TLRC,
        MNI, ORIG
        flag: -space %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
xdel: (a float)
        new x voxel dimension in mm
        flag: -xdel %f
xorigin: (a string)
        x distance for edge voxel offset
        flag: -xorigin %s
ydel: (a float)
        new y voxel dimension in mm
        flag: -ydel %f
yorigin: (a string)
        y distance for edge voxel offset
        flag: -yorigin %s
zdel: (a float)
        new z voxel dimension in mm
        flag: -zdel %f
zorigin: (a string)
        z distance for edge voxel offset
        flag: -zorigin %s
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.30 Resample

Link to code
Wraps command **3dresample**
Resample or reorient an image using AFNI 3dresample command
For complete details, see the 3dresample Documentation.

38.30.1 Examples

```
>>> from nipype.interfaces import afni as 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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dresample
        flag: -inset %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
master: (a file name)
        align dataset grid to a reference file
        flag: -master %s
orientation: (a string)
        new orientation code
        flag: -orient %s
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
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.
        flag: -rmode %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
voxel_size: (a tuple of the form: (a float, a float, a float))
        resample to new dx, dy and dz
```

```
        flag: -dxyz %f %f %f
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.31 Retroicor

Link to code

Wraps 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 Documentation.

38.31.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> ret = afni.Retroicor()
>>> ret.inputs.in_file = 'functional.nii'
>>> ret.inputs.card = 'mask.1D'
>>> ret.inputs.resp = 'resp.1D'
>>> res = ret.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dretroicor
        flag: %s, position: -1
out_file: (a file name)
        output image file name
        flag: -prefix %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
card: (an existing file name)
        1D cardiac data file for cardiac correction
        flag: -card %s, position: -2
cardphase: (a file name)
        Filename for 1D cardiac phase output
        flag: -cardphase %s, position: -6
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

```
    order: (an integer (int or long))
            The order of the correction (2 is typical)
            flag: -order %s, position: -5
    outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
            AFNI output filetype
    resp: (an existing file name)
            1D respiratory waveform data for correction
            flag: -resp %s, position: -3
    respphase: (a file name)
            Filename for 1D resp phase output
            flag: -respphase %s, position: -7
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    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)
            flag: -threshold %d, position: -4
```

Outputs:

```
    out_file: (an existing file name)
            output file
```

38.32 Seg

Link to code

Wraps 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. <https://afni.nimh.nih.gov/pub/dist/doc/program_help/3dSeg.html>

38.32.1 Examples

```
    >>> from nipype.interfaces.afni import preprocess
    >>> seg = preprocess.Seg()
    >>> seg.inputs.in_file = 'structural.nii'
    >>> seg.inputs.mask = 'AUTO'
    >>> res = seg.run()
```

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            ANAT is the volume to segment
            flag: -anat %s, position: -1
    mask: ('AUTO' or an existing file name)
            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.
            flag: -mask %s, position: -2

    [Optional]
    args: (a string)
            Additional parameters to the command
```

```
        flag: %s
bias_classes: (a string)
        A semcolon demlimited string of classes that contribute to the
        estimation of the bias field
        flag: -bias_classes %s
bias_fwhm: (a float)
        The amount of blurring used when estimating the field bias with the
        Wells method
        flag: -bias_fwhm %f
blur_meth: ('BFT' or 'BIM')
        set the blurring method for bias field estimation
        flag: -blur_meth %s
bmrf: (a float)
        Weighting factor controlling spatial homogeneity of the
        classifications
        flag: -bmrf %f
classes: (a string)
        CLASS_STRING is a semicolon delimited string of class labels
        flag: -classes %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
main_N: (an integer (int or long))
        Number of iterations to perform.
        flag: -main_N %d
mixfloor: (a float)
        Set the minimum value for any class's mixing fraction
        flag: -mixfloor %f
mixfrac: (a string)
        MIXFRAC sets up the volume-wide (within mask) tissue fractions while
        initializing the segmentation (see IGNORE for exception)
        flag: -mixfrac %s
prefix: (a string)
        the prefix for the output folder containing all output volumes
        flag: -prefix %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.33 SkullStrip

Link to code

Wraps command **3dSkullStrip**

A program to extract the brain from surrounding tissue from MRI T1-weighted images

For complete details, see the 3dSkullStrip Documentation.

38.33.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> skullstrip = afni.SkullStrip()
>>> skullstrip.inputs.in_file = 'functional.nii'
>>> skullstrip.inputs.args = '-o_ply'
>>> res = skullstrip.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dSkullStrip
        flag: -input %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.34 TCat

Link to code
Wraps command **3dTcat**
Concatenate sub-bricks from input datasets into one big 3D+time dataset
For complete details, see the 3dTcat Documentation.

38.34.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> tcat = afni.TCat()
>>> tcat.inputs.in_files = ['functional.nii', 'functional2.nii']
>>> tcat.inputs.out_file= 'functional_tcat.nii'
>>> tcat.inputs.rlt = '+'
>>> res = tcat.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        input file to 3dTcat
        flag:  %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
rlt: (a string)
        options
        flag: -rlt%s, position: 1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.35 TCorr1D

Link to code

Wraps 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 nipype.interfaces import afni as afni
>>> tcorr1D = afni.TCorr1D()
>>> tcorr1D.inputs.xset= 'u_rc1s1_Template.nii'
>>> tcorr1D.inputs.y_1d = 'seed.1D'
>>> tcorr1D.cmdline
'3dTcorr1D -prefix u_rc1s1_Template_correlation.nii.gz  u_rc1s1_Template.nii  seed.1D'
>>> res = tcorr1D.run()
```

Inputs:

```
[Mandatory]
xset: (an existing file name)
        3d+time dataset input
        flag:  %s, position: -2
y_1d: (an existing file name)
        1D time series file input
        flag:  %s, position: -1
```

```
    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    ktaub: (a boolean)
            Correlation is the Kendall's tau_b correlation coefficient
            flag:  -ktaub, position: 1
            mutually_exclusive: pearson, spearman, quadrant
    out_file: (a file name)
            output filename prefix
            flag: -prefix %s
    outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
            AFNI output filetype
    pearson: (a boolean)
            Correlation is the normal Pearson correlation coefficient
            flag:  -pearson, position: 1
            mutually_exclusive: spearman, quadrant, ktaub
    quadrant: (a boolean)
            Correlation is the quadrant correlation coefficient
            flag:  -quadrant, position: 1
            mutually_exclusive: pearson, spearman, ktaub
    spearman: (a boolean)
            Correlation is the Spearman (rank) correlation coefficient
            flag:  -spearman, position: 1
            mutually_exclusive: pearson, quadrant, ktaub
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
            output file containing correlations
```

38.36 TCorrMap

Link to code

Wraps 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. <http://afni.nimh.nih.gov/pub/dist/doc/program_help/3dTcorrMap.htm

38.36.1 Examples

```
    >>> from nipype.interfaces import afni as afni
    >>> tcm = afni.TCorrMap()
    >>> tcm.inputs.in_file = 'functional.nii'
    >>> tcm.inputs.mask = 'mask.nii'
```

```
>>> tcm.mean_file = '%s_meancorr.nii'
>>> res = tcm.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        flag: -input %s

[Optional]
absolute_threshold: (a file name)
        flag: -Thresh %f %s
        mutually_exclusive: absolute_threshold, var_absolute_threshold,
         var_absolute_threshold_normalize
args: (a string)
        Additional parameters to the command
        flag: %s
automask: (a boolean)
        flag: -automask
average_expr: (a file name)
        flag: -Aexpr %s %s
        mutually_exclusive: average_expr, average_expr_nonzero, sum_expr
average_expr_nonzero: (a file name)
        flag: -Cexpr %s %s
        mutually_exclusive: average_expr, average_expr_nonzero, sum_expr
bandpass: (a tuple of the form: (a float, a float))
        flag: -bpass %f %f
blur_fwhm: (a float)
        flag: -Gblur %f
correlation_maps: (a file name)
        flag: -CorrMap %s
correlation_maps_masked: (a file name)
        flag: -CorrMask %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
expr: (a string)
histogram: (a file name)
        flag: -Hist %d %s
histogram_bin_numbers: (an integer (int or long))
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        flag: -mask %s
mean_file: (a file name)
        flag: -Mean %s
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
pmean: (a file name)
        flag: -Pmean %s
polort: (an integer (int or long))
        flag: -polort %d
qmean: (a file name)
        flag: -Qmean %s
```

```
    regress_out_timeseries: (a file name)
            flag: -ort %s
    seeds: (an existing file name)
            flag: -seed %s
            mutually_exclusive: s, e, e, d, s, _, w, i, d, t, h
    seeds_width: (a float)
            flag: -Mseed %f
            mutually_exclusive: s, e, e, d, s
    sum_expr: (a file name)
            flag: -Sexpr %s %s
            mutually_exclusive: average_expr, average_expr_nonzero, sum_expr
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    thresholds: (a list of items which are an integer (int or long))
    var_absolute_threshold: (a file name)
            flag: -VarThresh %f %f %f %s
            mutually_exclusive: absolute_threshold, var_absolute_threshold,
             var_absolute_threshold_normalize
    var_absolute_threshold_normalize: (a file name)
            flag: -VarThreshN %f %f %f %s
            mutually_exclusive: absolute_threshold, var_absolute_threshold,
             var_absolute_threshold_normalize
    zmean: (a file name)
            flag: -Zmean %s
```

Outputs:

```
    absolute_threshold: (a file name)
    average_expr: (a file name)
    average_expr_nonzero: (a file name)
    correlation_maps: (a file name)
    correlation_maps_masked: (a file name)
    histogram: (a file name)
    mean_file: (a file name)
    pmean: (a file name)
    qmean: (a file name)
    sum_expr: (a file name)
    var_absolute_threshold: (a file name)
    var_absolute_threshold_normalize: (a file name)
    zmean: (a file name)
```

38.37 TCorrelate

Link to code

Wraps 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.

38.37.1 Examples

```
    >>> from nipype.interfaces import afni as afni
    >>> tcorrelate = afni.TCorrelate()
    >>> tcorrelate.inputs.xset= 'u_rc1s1_Template.nii'
```

```
>>> tcorrelate.inputs.yset = 'u_rc1s2_Template.nii'
>>> tcorrelate.inputs.out_file = 'functional_tcorrelate.nii.gz'
>>> tcorrelate.inputs.polort = -1
>>> tcorrelate.inputs.pearson = True
>>> res = tcarrelate.run()
```

Inputs:

```
[Mandatory]
xset: (an existing file name)
        input xset
        flag:  %s, position: -2
yset: (an existing file name)
        input yset
        flag:  %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
pearson: (a boolean)
        Correlation is the normal Pearson correlation coefficient
        flag: -pearson, position: 1
polort: (an integer (int or long))
        Remove polynomical trend of order m
        flag: -polort %d, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.38 TShift

Link to code

Wraps command **3dTshift**

Shifts voxel time series from input so that seperate slices are aligned to the same temporal origin

For complete details, see the ‘3dTshift Documentation. <http://afni.nimh.nih.gov/pub/dist/doc/program_help/3dTshift.html>

38.38.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> tshift = afni.TShift()
>>> tshift.inputs.in_file = 'functional.nii'
>>> tshift.inputs.tpattern = 'alt+z'
>>> tshift.inputs.tzero = 0.0
>>> tshift.cmdline #doctest:
'3dTshift -prefix functional_tshift -tpattern alt+z -tzero 0.0 functional.nii'
>>> res = tshift.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dTShift
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore: (an integer (int or long))
        ignore the first set of points specified
        flag: -ignore %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interp: ('Fourier' or 'linear' or 'cubic' or 'quintic' or 'heptic')
        different interpolation methods (see 3dTShift for details) default =
        Fourier
        flag: -%s
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
rlt: (a boolean)
        Before shifting, remove the mean and linear trend
        flag: -rlt
rltplus: (a boolean)
        Before shifting, remove the mean and linear trend and later put back
        the mean
        flag: -rlt+
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tpattern: (a string)
        use specified slice time pattern rather than one in header
        flag: -tpattern %s
tr: (a string)
        manually set the TRYou can attach suffix "s" for seconds or "ms" for
        milliseconds.
        flag: -TR %s
```

```
tslice: (an integer (int or long))
        align each slice to time offset of given slice
        flag: -slice %s
        mutually_exclusive: tzero
tzero: (a float)
        align each slice to given time offset
        flag: -tzero %s
        mutually_exclusive: tslice
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.39 TStat

Link to code
Wraps command **3dTstat**
Compute voxel-wise statistics using AFNI 3dTstat command
For complete details, see the 3dTstat Documentation.

38.39.1 Examples

```
>>> from nipype.interfaces import afni as 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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dTstat
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        mask file
        flag: -mask %s
options: (a string)
        selected statistical output
        flag: %s
out_file: (a file name)
```

```
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.40 To3D

Link to code
Wraps command **to3d**
Create a 3D dataset from 2D image files using AFNI to3d command
For complete details, see the to3d Documentation

38.40.1 Examples

```
>>> from nipype.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
'to3d -datum float -anat -prefix dicomdir.nii ./*.dcm'
>>> res = To3D.run()
```

Inputs:

```
[Mandatory]
in_folder: (an existing directory name)
        folder with DICOM images to convert
        flag: %s/*.dcm, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
assumemosaic: (a boolean)
        assume that Siemens image is mosaic
        flag: -assume_dicom_mosaic
datatype: ('short' or 'float' or 'byte' or 'complex')
        set output file datatype
        flag: -datum %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
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
        flag: -%s
funcparams: (a string)
        parameters for functional data
        flag: -time:zt %s alt+z2
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
skipoutliers: (a boolean)
        skip the outliers check
        flag: -skip_outliers
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.41 Volreg

Link to code

Wraps command **3dvolreg**

Register input volumes to a base volume using AFNI 3dvolreg command

For complete details, see the 3dvolreg Documentation.

38.41.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> volreg = afni.Volreg()
>>> volreg.inputs.in_file = 'functional.nii'
>>> volreg.inputs.args = '-Fourier -twopass'
>>> volreg.inputs.zpad = 4
>>> volreg.inputs.outputtype = "NIFTI"
>>> volreg.cmdline
'3dvolreg -Fourier -twopass -1Dfile functional.1D -1Dmatrix_save functional.aff12.1D -prefix fun
>>> res = volreg.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dvolreg
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
```

```
    basefile: (an existing file name)
            base file for registration
            flag: -base %s, position: -6
    copyorigin: (a boolean)
            copy base file origin coords to output
            flag: -twodup
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    md1d_file: (a file name)
            max displacement output file
            flag: -maxdisp1D %s, position: -4
    oned_file: (a file name)
            1D movement parameters output file
            flag: -1Dfile %s
    oned_matrix_save: (a file name)
            Save the matrix transformation
            flag: -1Dmatrix_save %s
    out_file: (a file name)
            output image file name
            flag: -prefix %s
    outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
            AFNI output filetype
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    timeshift: (a boolean)
            time shift to mean slice time offset
            flag: -tshift 0
    verbose: (a boolean)
            more detailed description of the process
            flag: -verbose
    zpad: (an integer (int or long))
            Zeropad around the edges by 'n' voxels during rotations
            flag: -zpad %d, position: -5
```

Outputs:

```
    md1d_file: (an existing file name)
            max displacement info file
    oned_file: (an existing file name)
            movement parameters info file
    oned_matrix_save: (an existing file name)
            matrix transformation from base to input
    out_file: (an existing file name)
            registered file
```

38.42 Warp

Link to code

Wraps command **3dWarp**

Use 3dWarp for spatially transforming a dataset

For complete details, see the 3dWarp Documentation.

38.42.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> warp = afni.Warp()
>>> warp.inputs.in_file = 'structural.nii'
>>> warp.inputs.deoblique = True
>>> warp.inputs.out_file = "trans.nii.gz"
>>> warp.cmdline
'3dWarp -deoblique -prefix trans.nii.gz structural.nii'
```

```
>>> 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'
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dWarp
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
deoblique: (a boolean)
        transform dataset from oblique to cardinal
        flag: -deoblique
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
gridset: (an existing file name)
        copy grid of specified dataset
        flag: -gridset %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interp: ('linear' or 'cubic' or 'NN' or 'quintic')
        spatial interpolation methods [default = linear]
        flag: -%s
matparent: (an existing file name)
        apply transformation from 3dWarpDrive
        flag: -matparent %s
mni2tta: (a boolean)
        transform dataset from MNI152 to Talaraich
        flag: -mni2tta
newgrid: (a float)
        specify grid of this size (mm)
        flag: -newgrid %f
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
```

```
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tta2mni: (a boolean)
        transform dataset from Talairach to MNI152
        flag: -tta2mni
zpad: (an integer (int or long))
        pad input dataset with N planes of zero on all sides.
        flag: -zpad %d
```

Outputs:

```
out_file: (an existing file name)
        output file
```

38.43 ZCutUp

Link to code
Wraps command **3dZcutup**
Cut z-slices from a volume using AFNI 3dZcutup command
For complete details, see the 3dZcutup Documentation.

38.43.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> zcutup = afni.ZCutUp()
>>> zcutup.inputs.in_file = 'functional.nii'
>>> zcutup.inputs.out_file = 'functional_zcutup.nii'
>>> zcutup.inputs.keep= '0 10'
>>> res = zcutup.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to 3dZcutup
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
keep: (a string)
        slice range to keep in output
        flag: -keep %s
out_file: (a file name)
        output image file name
        flag: -prefix %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
```

```
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file
```

CHAPTER 39

interfaces.afni.svm

39.1 SVMTest

Link to code
Wraps command **3dsvm**
Temporally predictive modeling with the support vector machine SVM Test Only For complete details, see the 3dsvm Documentation.

39.1.1 Examples

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        A 3D or 3D+t AFNI brik dataset to be used for testing.
        flag: -testvol %s
model: (a string)
        modname is the basename for the brik containing the SVM model
        flag: -model %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
classout: (a boolean)
        Flag to specify that pname files should be integer-valued,
        corresponding to class category decisions.
        flag: -classout
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
multiclass: (a boolean)
        Specifies multiclass algorithm for classification
```

```
        flag: -multiclass %s
nodetrend: (a boolean)
        Flag to specify that pname files should not be linearly detrended
        flag: -nodetrend
nopredcensord: (a boolean)
        Flag to prevent writing predicted values for censored time-points
        flag: -nopredcensord
options: (a string)
        additional options for SVM-light
        flag: %s
out_file: (a file name)
        filename for .1D prediction file(s).
        flag: -predictions %s
outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
        AFNI output filetype
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
testlabels: (an existing file name)
        *true* class category .1D labels for the test dataset. It is used to
        calculate the prediction accuracy performance
        flag: -testlabels %s
```

Outputs:

```
out_file: (an existing file name)
        output file
```

39.2 SVMTrain

Link to code

Wraps command **3dsvm**

Temporally predictive modeling with the support vector machine SVM Train Only For complete details, see the 3dsvm Documentation.

39.2.1 Examples

```
>>> from nipype.interfaces import afni as afni
>>> svmTrain = afni.SVMTrain()
>>> 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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        A 3D+t AFNI brik dataset to be used for training.
        flag: -trainvol %s
ttype: (a string)
        tname: classification or regression
        flag: -type %s
```

```
    [Optional]
    alphas: (a file name)
            output alphas file name
            flag: -alpha %s
    args: (a string)
            Additional parameters to the command
            flag: %s
    censor: (an existing file name)
            .1D censor file that allows the user to ignore certain samples in
            the training data.
            flag: -censor %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    kernel: (a string)
            string specifying type of kernel function:linear, polynomial, rbf,
            sigmoid
            flag: -kernel %s
    mask: (an existing file name)
            byte-format brik file used to mask voxels in the analysis
            flag: -mask %s, position: -1
    max_iterations: (an integer (int or long))
            Specify the maximum number of iterations for the optimization.
            flag: -max_iterations %d
    model: (a file name)
            basename for the brik containing the SVM model
            flag: -model %s
    nomodelmask: (a boolean)
            Flag to enable the omission of a mask file
            flag: -nomodelmask
    options: (a string)
            additional options for SVM-light
            flag: %s
    out_file: (a file name)
            output sum of weighted linear support vectors file name
            flag: -bucket %s
    outputtype: ('NIFTI_GZ' or 'AFNI' or 'NIFTI')
            AFNI output filetype
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    trainlabels: (an existing file name)
            .1D labels corresponding to the stimulus paradigm for the training
            data.
            flag: -trainlabels %s
    w_out: (a boolean)
            output sum of weighted linear support vectors
            flag: -wout
```

Outputs:

```
    alphas: (a file name)
            output alphas file name
    model: (a file name)
```

```
            brik containing the SVM model file name
    out_file: (a file name)
            sum of weighted linear support vectors file name
```

CHAPTER 40

interfaces.ants.legacy

40.1 GenWarpFields

Link to code
Wraps command **antsIntroduction.sh**
Inputs:

```
    [Mandatory]
    input_image: (an existing file name)
            input image to warp to template
            flag: -i %s
    reference_image: (an existing file name)
            template file to warp to
            flag: -r %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    bias_field_correction: (a boolean)
            Applies bias field correction to moving image
            flag: -n 1
    dimension: (3 or 2, nipype default value: 3)
            image dimension (2 or 3)
            flag: -d %d, position: 1
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    force_proceed: (a boolean)
            force script to proceed even if headers may be incompatible
            flag: -f 1
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    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)
            flag: -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 interations, L = fine resolution iterations
            flag: -m %s
    num_threads: (an integer (int or long), nipype default value: 1)
```

```
        Number of ITK threads to use
out_prefix: (a string, nipype default value: ants_)
        Prefix that is prepended to all output files (default = ants_)
        flag: -o %s
quality_check: (a boolean)
        Perform a quality check of the result
        flag: -q 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)
        flag: -s %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transformation_model: ('GR' or 'EL' or 'SY' or 'S2' or 'EX' or 'DD'
         or 'RI' or 'RA', nipype default value: GR)
        Type of transofmration 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
        flag: -t %s
```

Outputs:

```
affine_transformation: (an existing file name)
        affine (prefix_Affine.txt)
input_file: (an existing file name)
        input image (prefix_repaired.nii)
inverse_warp_field: (an existing file name)
        inverse warp field (prefix_InverseWarp.nii)
output_file: (an existing file name)
        output image (prefix_deformed.nii)
warp_field: (an existing file name)
        warp field (prefix_Warp.nii)
```

40.2 antsIntroduction

Link to code

Wraps command **antsIntroduction.sh**

Uses ANTS to generate matrices to warp data from one space to another.

40.2.1 Examples

```
>>> from nipype.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]
    input_image: (an existing file name)
            input image to warp to template
            flag: -i %s
    reference_image: (an existing file name)
            template file to warp to
            flag: -r %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    bias_field_correction: (a boolean)
            Applies bias field correction to moving image
            flag: -n 1
    dimension: (3 or 2, nipype default value: 3)
            image dimension (2 or 3)
            flag: -d %d, position: 1
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    force_proceed: (a boolean)
            force script to proceed even if headers may be incompatible
            flag: -f 1
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    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)
            flag: -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 interations, L = fine resolution iterations
            flag: -m %s
    num_threads: (an integer (int or long), nipype default value: 1)
            Number of ITK threads to use
    out_prefix: (a string, nipype default value: ants_)
            Prefix that is prepended to all output files (default = ants_)
            flag: -o %s
    quality_check: (a boolean)
            Perform a quality check of the result
            flag: -q 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)
            flag: -s %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    transformation_model: ('GR' or 'EL' or 'SY' or 'S2' or 'EX' or 'DD'
             or 'RI' or 'RA', nipype default value: GR)
            Type of transofmration 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
            flag: -t %s
```

Outputs:

```
affine_transformation: (an existing file name)
        affine (prefix_Affine.txt)
input_file: (an existing file name)
        input image (prefix_repaired.nii)
inverse_warp_field: (an existing file name)
        inverse warp field (prefix_InverseWarp.nii)
output_file: (an existing file name)
        output image (prefix_deformed.nii)
warp_field: (an existing file name)
        warp field (prefix_Warp.nii)
```

40.3 buildtemplateparallel

Link to code

Wraps command **buildtemplateparallel.sh**

Generate a optimal average template

> **Warning:** This can take a VERY long time to complete

40.3.1 Examples

```
>>> from nipype.interfaces.ants.legacy import buildtemplateparallel
>>> tmpl = buildtemplateparallel()
>>> tmpl.inputs.in_files = ['T1.nii', 'structural.nii']
>>> tmpl.inputs.max_iterations = [30, 90, 20]
>>> tmpl.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 an existing file name)
        list of images to generate template from
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
bias_field_correction: (a boolean)
        Applies bias field correction to moving image
        flag: -n 1
dimension: (3 or 2, nipype default value: 3)
        image dimension (2 or 3)
        flag: -d %d, position: 1
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
gradient_step_size: (a float)
```

```
        smaller magnitude results in more cautious steps (default = .25)
        flag: -g %f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
iteration_limit: (an integer (int or long), nipype default value: 4)
        iterations of template construction
        flag: -i %d
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 interations, L = fine resolution iterations
        flag: -m %s
num_cores: (an integer (int or long))
        Requires parallelization = 2 (PEXEC). Sets number of cpu cores to
        use
        flag: -j %d
        requires: parallelization
num_threads: (an integer (int or long), nipype default value: 1)
        Number of ITK threads to use
out_prefix: (a string, nipype default value: antsTMPL_)
        Prefix that is prepended to all output files (default = antsTMPL_)
        flag: -o %s
parallelization: (0 or 1 or 2, nipype default value: 0)
        control for parallel processing (0 = serial, 1 = use PBS, 2 = use
        PEXEC, 3 = use Apple XGrid
        flag: -c %d
rigid_body_registration: (a boolean)
        registers inputs before creating template (useful if no initial
        template available)
        flag: -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)
        flag: -s %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transformation_model: ('GR' or 'EL' or 'SY' or 'S2' or 'EX' or 'DD',
         nipype default value: GR)
        Type of transofmration 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
        flag: -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.
```

Outputs:

```
final_template_file: (an existing file name)
        final ANTS template
subject_outfiles: (a list of items which are an existing file name)
        Outputs for each input image. Includes warp field, inverse warp,
        Affine, original image (repaired) and warped image (deformed)
```

```
    template_files: (a list of items which are an existing file name)
            Templates from different stages of iteration
```

CHAPTER 41

interfaces.ants.registration

41.1 Registration

Link to code
Wraps command **antsRegistration**

41.1.1 Examples

```
>>> import copy, pprint
>>> from nipype.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.invert_initial_moving_transform = True
>>> 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]
>>> 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'
```

```
>>> reg1 = copy.deepcopy(reg)
>>> reg1.inputs.winsorize_lower_quantile = 0.025
>>> reg1.cmdline
'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-moving-transform [
>>> reg1.run()
```

```
    >>> reg2 = copy.deepcopy(reg)
    >>> reg2.inputs.winsorize_upper_quantile = 0.975
    >>> reg2.cmdline
    'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-moving-transform [
```

```
    >>> 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 [
```

```
    >>> reg3a = copy.deepcopy(reg)
    >>> reg3a.inputs.float = True
    >>> reg3a.cmdline
    'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --float 1 --initial-moving-t
```

```
    >>> reg3b = copy.deepcopy(reg)
    >>> reg3b.inputs.float = False
    >>> reg3b.cmdline
    'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --float 0 --initial-moving-t
```

```
    >>> # 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)
    {'composite_transform': '.../nipype/testing/data/output_Composite.h5',
     'forward_invert_flags': [],
     'forward_transforms': [],
     'inverse_composite_transform': '.../nipype/testing/data/output_InverseComposite.h5',
     'inverse_warped_image': <undefined>,
     'reverse_invert_flags': [],
     'reverse_transforms': [],
     'save_state': '.../nipype/testing/data/trans.mat',
     'warped_image': '.../nipype/testing/data/output_warped_image.nii.gz'}
    >>> reg4.cmdline
    'antsRegistration --collapse-output-transforms 1 --dimensionality 3 --initial-moving-transform [
```

```
    >>> # Test collapse transforms flag
    >>> reg4b = copy.deepcopy(reg4)
    >>> reg4b.inputs.write_composite_transform = False
    >>> outputs = reg4b._list_outputs()
    >>> pprint.pprint(outputs)
    {'composite_transform': <undefined>,
     'forward_invert_flags': [False, False],
     'forward_transforms': ['.../nipype/testing/data/output_0GenericAffine.mat',
     '.../nipype/testing/data/output_1Warp.nii.gz'],
     'inverse_composite_transform': <undefined>,
     'inverse_warped_image': <undefined>,
     'reverse_invert_flags': [True, False],
     'reverse_transforms': ['.../nipype/testing/data/output_0GenericAffine.mat', '.../nipype/testing
     'save_state': '.../nipype/testing/data/trans.mat',
     'warped_image': '.../nipype/testing/data/output_warped_image.nii.gz'}
    >>> reg4b.aggregate_outputs()
    >>> reg4b.cmdline
```

```
    'antsRegistration --collapse-output-transforms 1 --dimensionality 3 --initial-moving-transform [
```

```
    >>> # 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 [
```

```
    >>> # 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 [
```

```
    >>> # Test Interpolation Parameters (BSpline)
    >>> reg7a = copy.deepcopy(reg)
    >>> reg7a.inputs.interpolation = 'BSpline'
    >>> reg7a.inputs.interpolation_parameters = (3,)
    >>> reg7a.cmdline
    'antsRegistration --collapse-output-transforms 0 --dimensionality 3 --initial-moving-transform [
```

```
    >>> # 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 [
```

```
    >>> # 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 [
```

Inputs:

```
    [Mandatory]
    fixed_image: (a list of items which are an existing file name)
            image to apply transformation to (generally a coregistered
            functional)
    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, nipype default value: [1.0])
            the metric weight(s) for each stage. The weights must sum to 1 per
            stage.
            requires: metric
    moving_image: (a list of items which are an existing file name)
```

```
        image to apply transformation to (generally a coregistered
        functional)
shrink_factors: (a list of items which are a list of items which are
         an integer (int or long))
smoothing_sigmas: (a list of items which are a list of items which
         are a float)
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')
        flag: %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
collapse_output_transforms: (a boolean, nipype default value: False)
        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.
        flag: --collapse-output-transforms %d
convergence_threshold: (a list of at least 1 items which are a float,
         nipype 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), nipype default value: [10])
        requires: convergence_threshold
dimension: (3 or 2, nipype default value: 3)
        image dimension (2 or 3)
        flag: --dimensionality %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fixed_image_mask: (an existing file name)
        mask used to limit metric sampling region of the fixed image
        flag: %s
float: (a boolean)
        Use float instead of double for computations.
        flag: --float %d
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
initial_moving_transform: (an existing file name)
        flag: %s
        mutually_exclusive: initial_moving_transform_com
initial_moving_transform_com: (0 or 1 or 2)
        Use center of mass for moving transform
        flag: %s
        mutually_exclusive: initial_moving_transform
initialize_transforms_per_stage: (a boolean, nipype default value:
         False)
        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).
        flag: --initialize-transforms-per-stage %d
interpolation: ('Linear' or 'NearestNeighbor' or 'CosineWindowedSinc'
         or 'WelchWindowedSinc' or 'HammingWindowedSinc' or
         'LanczosWindowedSinc' or 'BSpline' or 'MultiLabel' or 'Gaussian',
         nipype default value: Linear)
        flag: %s
interpolation_parameters: (a tuple of the form: (an integer (int or
         long)) or a tuple of the form: (a float, a float))
invert_initial_moving_transform: (a boolean)
        mutually_exclusive: initial_moving_transform_com
        requires: initial_moving_transform
metric_item_trait: ('CC' or 'MeanSquares' or 'Demons' or 'GC' or 'MI'
         or 'Mattes')
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)
metric_weight_stage_trait: (a float or a list of items which are a
         float)
moving_image_mask: (an existing file name)
        mask used to limit metric sampling region of the moving image
        requires: fixed_image_mask
num_threads: (an integer (int or long), nipype default value: 1)
        Number of ITK threads to use
number_of_iterations: (a list of items which are a list of items
         which are an integer (int or long))
output_inverse_warped_image: (a boolean or a file name)
        requires: output_warped_image
output_transform_prefix: (a string, nipype default value: transform)
        flag: %s
output_warped_image: (a boolean or a file name)
radius_bins_item_trait: (an integer (int or long))
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),
         nipype default value: [5])
        the number of bins in each stage for the MI and Mattes metric, the
        radius for other metrics
        requires: metric_weight
restore_state: (an existing file name)
        Filename for restoring the internal restorable state of the
        registration
        flag: --restore-state %s
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
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_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_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)
save_state: (a file name)
        Filename for saving the internal restorable state of the
        registration
        flag: --save-state %s
sigma_units: (a list of items which are 'mm' or 'vox')
        units for smoothing sigmas
        requires: smoothing_sigmas
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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)))
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, nipype default value: True)
winsorize_lower_quantile: (0.0 <= a floating point number <= 1.0,
         nipype default value: 0.0)
        The Lower quantile to clip image ranges
        flag: %s
winsorize_upper_quantile: (0.0 <= a floating point number <= 1.0,
         nipype default value: 1.0)
        The Upper quantile to clip image ranges
        flag: %s
write_composite_transform: (a boolean, nipype default value: False)
        flag: --write-composite-transform %d
```

Outputs:

```
composite_transform: (an existing file name)
        Composite transform file
forward_invert_flags: (a list of items which are a boolean)
        List of flags corresponding to the forward transforms
forward_transforms: (a list of items which are an existing file name)
        List of output transforms for forward registration
inverse_composite_transform: (a file name)
        Inverse composite transform file
inverse_warped_image: (a file name)
        Outputs the inverse of the warped image
reverse_invert_flags: (a list of items which are a boolean)
        List of flags corresponding to the reverse transforms
reverse_transforms: (a list of items which are an existing file name)
        List of output transforms for reverse registration
save_state: (a file name)
```

```
            The saved registration state to be restored
    warped_image: (a file name)
            Outputs warped image
```

CHAPTER 42

interfaces.ants.resampling

42.1 ApplyTransforms

Link to code
Wraps command **antsApplyTransforms**
ApplyTransforms, applied to an input image, transforms it according to a reference image and a transform (or a set of transforms).

42.1.1 Examples

```
>>> from nipype.interfaces.ants import ApplyTransforms
>>> at = ApplyTransforms()
>>> at.inputs.dimension = 3
>>> at.inputs.input_image = 'moving1.nii'
>>> at.inputs.reference_image = 'fixed1.nii'
>>> 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 --input moving1.nii --interpolation Li
```

```
>>> 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 --input moving1.nii --interpolation BS
```

Inputs:

```
[Mandatory]
input_image: (an existing file name)
        image to apply transformation to (generally a coregistered
        functional)
        flag: --input %s
reference_image: (an existing file name)
        reference image space that you wish to warp INTO
```

```
        flag: --reference-image %s
transforms: (a list of items which are an existing file name)
        transform files: will be applied in reverse order. For example, the
        last specified transform will be applied first
        flag: %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
default_value: (a float, nipype default value: 0.0)
        flag: --default-value %g
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.
        flag: --dimensionality %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
float: (a boolean)
        Use float instead of double for computations.
        flag: --float %d
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
input_image_type: (0 or 1 or 2 or 3)
        Option specifying the input image type of scalar (default), vector,
        tensor, or time series.
        flag: --input-image-type %d
interpolation: ('Linear' or 'NearestNeighbor' or 'CosineWindowedSinc'
         or 'WelchWindowedSinc' or 'HammingWindowedSinc' or
         'LanczosWindowedSinc' or 'MultiLabel' or 'Gaussian' or 'BSpline',
         nipype default value: Linear)
        flag: %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)
num_threads: (an integer (int or long), nipype default value: 1)
        Number of ITK threads to use
out_postfix: (a string, nipype default value: _trans)
        Postfix that is appended to all output files (default = _trans)
output_image: (a string)
        output file name
        flag: --output %s
print_out_composite_warp_file: (a boolean)
        output a composite warp file instead of a transformed image
        requires: output_image
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
output_image: (an existing file name)
        Warped image
```

42.2 ApplyTransformsToPoints

Link to code
Wraps command **antsApplyTransformsToPoints**
ApplyTransformsToPoints, applied to an CSV file, transforms coordinates using provided transform (or a set of transforms).

42.2.1 Examples

```
>>> from nipype.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.c
```

Inputs:

```
[Mandatory]
input_file: (an existing file name)
        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 spacerequired by
        antsApplyTransformsToPoints try creating/drawing a simplelabel
        volume with only one voxel set to 1 and all others set to 0.Write
        down the voxel coordinates. Then use ImageMaths LabelStats to
        findout what coordinates for this voxel antsApplyTransformsToPoints
        isexpecting.
        flag: --input %s
transforms: (a list of items which are an existing file name)
        transforms that will be applied to the points
        flag: %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
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.
        flag: --dimensionality %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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), nipype default value: 1)
        Number of ITK threads to use
output_file: (a string)
        Name of the output CSV file
```

```
        flag: --output %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
output_file: (an existing file name)
        csv file with transformed coordinates
```

42.3 WarpImageMultiTransform

Link to code
Wraps command **WarpImageMultiTransform**
Warps an image from one space to another

42.3.1 Examples

```
>>> from nipype.interfaces.ants import WarpImageMultiTransform
>>> wimt = WarpImageMultiTransform()
>>> wimt.inputs.input_image = 'structural.nii'
>>> 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.
```

```
>>> 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
>>> wimt.inputs.invert_affine = [1]
>>> wimt.cmdline
'WarpImageMultiTransform 3 diffusion_weighted.nii diffusion_weighted_wimt.nii -R functional.nii
```

Inputs:

```
[Mandatory]
input_image: (a file name)
        image to apply transformation to (generally a coregistered
        functional)
        flag: %s, position: 2
transformation_series: (a list of items which are an existing file
         name)
        transformation file(s) to be applied
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
dimension: (3 or 2, nipype default value: 3)
        image dimension (2 or 3)
        flag: %d, position: 1
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
```

```
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    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), nipype default value: 1)
            Number of ITK threads to use
    out_postfix: (a file name, nipype default value: _wimt)
            Postfix that is prepended to all output files (default = _wimt)
            mutually_exclusive: output_image
    output_image: (a file name)
            name of the output warped image
            flag: %s, position: 3
            mutually_exclusive: out_postfix
    reference_image: (a file name)
            reference image space that you wish to warp INTO
            flag: -R %s
            mutually_exclusive: tightest_box
    reslice_by_header: (a boolean)
            Uses orientation matrix and origin encoded in reference image file
            header. Not typically used with additional transforms
            flag: --reslice-by-header
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    tightest_box: (a boolean)
            computes tightest bounding box (overrided by reference_image if
            given)
            flag: --tightest-bounding-box
            mutually_exclusive: reference_image
    use_bspline: (a boolean)
            Use 3rd order B-Spline interpolation
            flag: --use-BSpline
    use_nearest: (a boolean)
            Use nearest neighbor interpolation
            flag: --use-NN
```

Outputs:

```
    output_image: (an existing file name)
            Warped image
```

42.4 WarpTimeSeriesImageMultiTransform

Link to code

Wraps command **WarpTimeSeriesImageMultiTransform**

Warps a time-series from one space to another

42.4.1 Examples

```
>>> from nipype.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
```

Inputs:

```
[Mandatory]
input_image: (a file name)
        image to apply transformation to (generally a coregistered
        functional)
        flag: %s
transformation_series: (a list of items which are an existing file
         name)
        transformation file(s) to be applied
        flag: %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
dimension: (4 or 3, nipype default value: 4)
        image dimension (3 or 4)
        flag: %d, position: 1
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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
num_threads: (an integer (int or long), nipype default value: 1)
        Number of ITK threads to use
out_postfix: (a string, nipype default value: _wtsimt)
        Postfix that is prepended to all output files (default = _wtsimt)
        flag: %s
reference_image: (a file name)
        reference image space that you wish to warp INTO
        flag: -R %s
        mutually_exclusive: tightest_box
reslice_by_header: (a boolean)
        Uses orientation matrix and origin encoded in reference image file
        header. Not typically used with additional transforms
        flag: --reslice-by-header
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tightest_box: (a boolean)
        computes tightest bounding box (overrided by reference_image if
        given)
```

```
        flag: --tightest-bounding-box
        mutually_exclusive: reference_image
use_bspline: (a boolean)
        Use 3rd order B-Spline interpolation
        flag: --use-Bspline
use_nearest: (a boolean)
        Use nearest neighbor interpolation
        flag: --use-NN
```

Outputs:

```
output_image: (an existing file name)
        Warped image
```

CHAPTER 43

interfaces.ants.segmentation

43.1 AntsJointFusion

Link to code
Wraps command **antsJointFusion**

43.1.1 Examples

```
>>> from nipype.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_fus
```

```
>>> 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_fus
```

```
>>> 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 segmentat
```

```
>>> 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 segmentat
```

```
>>> 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 segmentat
```

```
>>> antsjointfusion.inputs.out_label_fusion = 'ants_fusion_label_output.nii'
>>> antsjointfusion.inputs.out_intensity_fusion_name_format = 'ants_joint_fusion_intensity_%d.ni
>>> antsjointfusion.inputs.out_label_post_prob_name_format = 'ants_joint_fusion_posterior_%d.nii
>>> antsjointfusion.inputs.out_atlas_voting_weight_name_format = 'ants_joint_fusion_voting_weigh
>>> antsjointfusion.cmdline
"antsJointFusion -a 0.5 -g ['rc1s1.nii', 'rc1s2.nii'] -g ['rc2s1.nii', 'rc2s2.nii'] -l segmentat
```

Inputs:

```
[Mandatory]
atlas_image: (a list of items which are a list of items which are an
         existing file name)
        The atlas image (or multimodal atlas images) assumed to be aligned
        to a common image domain.
        flag: -g %s...
atlas_segmentation_image: (a list of items which are an existing file
         name)
        The atlas segmentation images. For performing label fusion the
        number of specified segmentations should be identical to the number
        of atlas image sets.
        flag: -l %s...
target_image: (a list of items which are a list of items which are an
         existing file name)
        The target image (or multimodal target images) assumed to be aligned
        to a common image domain.
        flag: -t %s

[Optional]
alpha: (a float, nipype default value: 0.1)
        Regularization term added to matrix Mx for calculating the inverse.
        Default = 0.1
        flag: -a %s
args: (a string)
        Additional parameters to the command
        flag: %s
beta: (a float, nipype default value: 2.0)
        Exponent for mapping intensity difference to the joint error.
        Default = 2.0
        flag: -b %s
constrain_nonnegative: (a boolean, nipype default value: False)
        Constrain solution to non-negative weights.
        flag: -c
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.
        flag: -d %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
exclusion_image: (a list of items which are an existing file name)
        Specify an exclusion region for the given label.
exclusion_image_label: (a list of items which are a string)
        Specify a label for the exclusion region.
        flag: -e %s
        requires: exclusion_image
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
```

```
        interface fails to run
mask_image: (an existing file name)
        If a mask image is specified, fusion is only performed in the mask
        region.
        flag: -x %s
num_threads: (an integer (int or long), nipype default value: 1)
        Number of ITK threads to use
out_atlas_voting_weight_name_format: (a string)
        Optional atlas voting weight image file name format.
        requires: out_label_fusion, out_intensity_fusion_name_format,
         out_label_post_prob_name_format
out_intensity_fusion_name_format: (a string)
        Optional intensity fusion image file name format.
out_label_fusion: (a file name)
        The output label fusion image.
        flag: %s
out_label_post_prob_name_format: (a string)
        Optional label posterior probability image file name format.
        requires: out_label_fusion, out_intensity_fusion_name_format
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).
        flag: -m %s
patch_radius: (a list of items which are a value of type 'int')
        Patch radius for similarity measures.Default: 2x2x2
        flag: -p %s
retain_atlas_voting_images: (a boolean, nipype default value: False)
        Retain atlas voting images. Default = false
        flag: -f
retain_label_posterior_images: (a boolean, nipype default value:
         False)
        Retain label posterior probability images. Requires atlas
        segmentations to be specified. Default = false
        flag: -r
        requires: atlas_segmentation_image
search_radius: (a list of from 1 to 3 items which are any value,
         nipype 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.
        flag: -s %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        Verbose output.
        flag: -v
```

Outputs:

```
out_atlas_voting_weight_name_format: (a string)
out_intensity_fusion_name_format: (a string)
out_label_fusion: (an existing file name)
out_label_post_prob_name_format: (a string)
```

43.2 Atropos

Link to code

Wraps 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.

43.2.1 Examples

```
>>> from nipype.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_terations = 1
>>> at.inputs.n_iterations = 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/p
```

Inputs:

```
[Mandatory]
initialization: ('Random' or 'Otsu' or 'KMeans' or
         'PriorProbabilityImages' or 'PriorLabelImage')
        flag: %s
        requires: number_of_tissue_classes
intensity_images: (a list of items which are an existing file name)
        flag: --intensity-image %s...
mask_image: (an existing file name)
        flag: --mask-image %s
number_of_tissue_classes: (an integer (int or long))

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
convergence_threshold: (a float)
        requires: n_iterations
dimension: (3 or 2 or 4, nipype default value: 3)
        image dimension (2, 3, or 4)
        flag: --image-dimensionality %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
```

```
          {})
        Environment variables
icm_use_synchronous_update: (a boolean)
        flag: %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
likelihood_model: (a string)
        flag: --likelihood-model %s
maximum_number_of_icm_terations: (an integer (int or long))
        requires: icm_use_synchronous_update
mrf_radius: (a list of items which are an integer (int or long))
        requires: mrf_smoothing_factor
mrf_smoothing_factor: (a float)
        flag: %s
n_iterations: (an integer (int or long))
        flag: %s
num_threads: (an integer (int or long), nipype default value: 1)
        Number of ITK threads to use
out_classified_image_name: (a file name)
        flag: %s
output_posteriors_name_template: (a string, nipype default value:
         POSTERIOR_%02d.nii.gz)
posterior_formulation: (a string)
        flag: %s
prior_probability_images: (a list of items which are an existing file
         name)
prior_probability_threshold: (a float)
        requires: prior_weighting
prior_weighting: (a float)
save_posteriors: (a boolean)
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
use_mixture_model_proportions: (a boolean)
        requires: posterior_formulation
use_random_seed: (a boolean, nipype default value: True)
        use random seed value over constant
        flag: --use-random-seed %d
```

Outputs:

```
classified_image: (an existing file name)
posteriors: (a list of items which are a file name)
```

43.3 BrainExtraction

Link to code

Wraps command **antsBrainExtraction.sh**

43.3.1 Examples

```
>>> from nipype.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.
```

Inputs:

```
[Mandatory]
anatomical_image: (an existing file name)
        Structural image, typically T1. If more than oneanatomical image is
        specified, subsequently specifiedimages 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 withbuildtemplateparallel.sh in ANTs.
        flag: -a %s
brain_probability_mask: (an existing file name)
        Brain probability mask created using e.g. LPBA40 data set whichhave
        brain masks defined, and warped to anatomical template andaveraged
        resulting in a probability image.
        flag: -m %s
brain_template: (an existing file name)
        Anatomical template created using e.g. LPBA40 data set
        withbuildtemplateparallel.sh in ANTs.
        flag: -e %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
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.
        flag: -z 1
dimension: (3 or 2, nipype default value: 3)
        image dimension (2 or 3)
        flag: -d %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
extraction_registration_mask: (an existing file name)
        Mask (defined in the template space) used during registration for
        brain extraction.To limit the metric computation to a specific
        region.
        flag: -f %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
image_suffix: (a string, nipype default value: nii.gz)
        any of standard ITK formats, nii.gz is default
        flag: -s %s
keep_temporary_files: (an integer (int or long))
        Keep brain extraction/segmentation warps, etc (default = 0).
        flag: -k %d
num_threads: (an integer (int or long), nipype default value: 1)
        Number of ITK threads to use
out_prefix: (a string, nipype default value: highres001_)
```

```
        Prefix that is prepended to all output files (default =
        highress001_)
        flag: -o %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
use_floatingpoint_precision: (0 or 1)
        Use floating point precision in registrations (default = 0)
        flag: -q %d
use_random_seeding: (0 or 1)
        Use random number generated from system clock in Atropos(default =
        1)
        flag: -u %d
```

Outputs:

```
BrainExtractionBrain: (an existing file name)
        brain extraction image
BrainExtractionMask: (an existing file name)
        brain extraction mask
```

43.4 CorticalThickness

Link to code
Wraps command **antsCorticalThickness.sh**

43.4.1 Examples

```
>>> from nipype.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',     'Brai
>>> corticalthickness.inputs.t1_registration_template = 'brain_study_template.nii.gz'
>>> corticalthickness.cmdline
'antsCorticalThickness.sh -a T1.nii.gz -m ProbabilityMaskOfStudyTemplate.nii.gz -e study_templat
```

Inputs:

```
[Mandatory]
anatomical_image: (an existing file name)
        Structural *intensity* image, typically T1.If more than one
        anatomical image is specified,subsequently specified images are used
        during thesegmentation process. However, only the firstimage is used
        in the registration of priors.Our suggestion would be to specify the
        T1as the first image.
        flag: -a %s
brain_probability_mask: (an existing file name)
        brain probability mask in template space
        flag: -m %s
brain_template: (an existing file name)
        Anatomical *intensity* template (possibly created using apopulation
        data set with buildtemplateparallel.sh in ANTs).This template is
        *not* skull-stripped.
        flag: -e %s
```

```
    segmentation_priors: (a list of items which are an existing file
             name)
            flag: -p %s
    t1_registration_template: (an existing file name)
            Anatomical *intensity* template(assumed to be skull-stripped). A
            commoncase would be where this would be the sametemplate as
            specified in the -e option whichis not skull stripped.
            flag: -t %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    b_spline_smoothing: (a boolean)
            Use B-spline SyN for registrations and B-splineexponential mapping
            in DiReCT.
            flag: -v
    cortical_label_image: (an existing file name)
            Cortical ROI labels to use as a prior for ATITH.
    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.
            flag: -z 1
    dimension: (3 or 2, nipype default value: 3)
            image dimension (2 or 3)
            flag: -d %d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    extraction_registration_mask: (an existing file name)
            Mask (defined in the template space) used during registration for
            brain extraction.
            flag: -f %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    image_suffix: (a string, nipype default value: nii.gz)
            any of standard ITK formats, nii.gz is default
            flag: -s %s
    keep_temporary_files: (an integer (int or long))
            Keep brain extraction/segmentation warps, etc (default = 0).
            flag: -k %d
    label_propagation: (a string)
            Incorporate a distance prior one the posterior formulation. Should
            beof the form 'label[lambda,boundaryProbability]' where labelis a
            value of 1,2,3,... denoting label ID. The labelprobability for
            anything outside the current label = boundaryProbability * exp(
            -lambda * distanceFromBoundary )Intuitively, smaller lambda values
            will increase the spatial capturerange of the distance prior. To
            apply to all label values, simply omitspecifying the label, i.e. -l
            [lambda,boundaryProbability].
            flag: -l %s
    max_iterations: (an integer (int or long))
            ANTS registration max iterations(default = 100x100x70x20)
            flag: -i %d
    num_threads: (an integer (int or long), nipype default value: 1)
```

```
        Number of ITK threads to use
out_prefix: (a string, nipype default value: antsCT_)
        Prefix that is prepended to all output files (default = antsCT_)
        flag: -o %s
posterior_formulation: (a string)
        Atropos posterior formulation and whether or notto use mixture model
        proportions.e.g 'Socrates[1]' (default) or 'Aristotle[1]'.Choose the
        latter if youwant use the distance priors (see also the -l optionfor
        label propagation control).
        flag: -b %s
prior_segmentation_weight: (a float)
        Atropos spatial prior *probability* weight forthe segmentation
        flag: -w %f
quick_registration: (a boolean)
        If = 1, use antsRegistrationSyNQuick.sh as the basis for
        registrationduring brain extraction, brain segmentation,
        and(optional) normalization to a template.Otherwise use
        antsRegistrationSyN.sh (default = 0).
        flag: -q 1
segmentation_iterations: (an integer (int or long))
        N4 -> Atropos -> N4 iterations during segmentation(default = 3)
        flag: -n %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
use_floatingpoint_precision: (0 or 1)
        Use floating point precision in registrations (default = 0)
        flag: -j %d
use_random_seeding: (0 or 1)
        Use random number generated from system clock in Atropos(default =
        1)
        flag: -u %d
```

Outputs:

```
BrainExtractionMask: (an existing file name)
        brain extraction mask
BrainSegmentation: (an existing file name)
        brain segmentaion image
BrainSegmentationN4: (an existing file name)
        N4 corrected image
BrainSegmentationPosteriors: (a list of items which are an existing
         file name)
        Posterior probability images
BrainVolumes: (an existing file name)
        Brain volumes as text
CorticalThickness: (an existing file name)
        cortical thickness file
CorticalThicknessNormedToTemplate: (an existing file name)
        Normalized cortical thickness
SubjectToTemplate0GenericAffine: (an existing file name)
        Template to subject inverse affine
SubjectToTemplate1Warp: (an existing file name)
        Template to subject inverse warp
SubjectToTemplateLogJacobian: (an existing file name)
        Template to subject log jacobian
TemplateToSubject0Warp: (an existing file name)
        Template to subject warp
```

```
    TemplateToSubject1GenericAffine: (an existing file name)
            Template to subject affine
```

43.5 DenoiseImage

Link to code
Wraps command **DenoiseImage**

43.5.1 Examples

```
>>> import copy
>>> from nipype.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: (an existing file name)
        A scalar image is expected as input for noise correction.
        flag: -i %s
save_noise: (a boolean, nipype default value: False)
        True if the estimated noise should be saved to file.
        mutually_exclusive: noise_image

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
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.
        flag: -d %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

```
    noise_image: (a file name)
            Filename for the estimated noise.
    noise_model: ('Gaussian' or 'Rician', nipype default value: Gaussian)
            Employ a Rician or Gaussian noise model.
            flag: -n %s
    num_threads: (an integer (int or long), nipype default value: 1)
            Number of ITK threads to use
    output_image: (a file name)
            The output consists of the noise corrected version of the input
            image.
            flag: -o %s
    shrink_factor: (an integer (int or long), nipype 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.
            flag: -s %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    verbose: (a boolean)
            Verbose output.
            flag: -v
```

Outputs:

```
    noise_image: (a file name)
    output_image: (an existing file name)
```

43.6 JointFusion

Link to code

Wraps command **jointfusion**

43.6.1 Examples

```
    >>> from nipype.interfaces.ants import JointFusion
    >>> at = JointFusion()
    >>> 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.ni
```

```
    >>> 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
```

Inputs:

```
[Mandatory]
dimension: (3 or 2 or 4, nipype default value: 3)
        image dimension (2, 3, or 4)
        flag: %d, position: 0
modalities: (an integer (int or long))
        Number of modalities or features
        flag: %d, position: 1
output_label_image: (a file name)
        Output fusion label map image
        flag: %s, position: -1
target_image: (a list of items which are an existing file name)
        Target image(s)
        flag: -tg %s...
warped_intensity_images: (a list of items which are an existing file
         name)
        Warped atlas images
        flag: -g %s...
warped_label_images: (a list of items which are an existing file
         name)
        Warped atlas segmentations
        flag: -l %s...

[Optional]
alpha: (a float, nipype default value: 0.0)
        Regularization term added to matrix Mx for inverse
        requires: method
args: (a string)
        Additional parameters to the command
        flag: %s
atlas_group_id: (a list of items which are a value of type 'int')
        Assign a group ID for each atlas
        flag: -gp %d...
atlas_group_weights: (a list of items which are a value of type
         'int')
        Assign the voting weights to each atlas group
        flag: -gpw %d...
beta: (an integer (int or long), nipype default value: 0)
        Exponent for mapping intensity difference to joint error
        requires: method
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
exclusion_region: (an existing file name)
        Specify an exclusion region for the given label.
        flag: -x %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
method: (a string, nipype 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]
        flag: -m %s
```

```
num_threads: (an integer (int or long), nipype default value: 1)
        Number of ITK threads to use
patch_radius: (a list of items which are a value of type 'int')
        Patch radius for similarity measures, scalar or vector. Default:
        2x2x2
        flag: -rp %s
search_radius: (a list of items which are a value of type 'int')
        Local search radius. Default: 3x3x3
        flag: -rs %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
output_label_image: (an existing file name)
```

43.7 LaplacianThickness

Link to code

Wraps command **LaplacianThickness**

Calculates the cortical thickness from an anatomical image

43.7.1 Examples

```
>>> from nipype.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.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_gm: (a file name)
        gray matter segmentation image
        flag: %s, position: 2
input_wm: (a file name)
        white matter segmentation image
        flag: %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
dT: (a float)
        flag: dT=%d, position: 6
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

```
    num_threads: (an integer (int or long), nipype default value: 1)
            Number of ITK threads to use
    opt_tolerance: (a float)
            flag: optional-laplacian-tolerance=%d, position: 8
    output_image: (a file name)
            name of output file
            flag: %s, position: 3
    prior_thickness: (a float)
            flag: priorthickval=%d, position: 5
    smooth_param: (a float)
            flag: smoothparam=%d, position: 4
    sulcus_prior: (a boolean)
            flag: use-sulcus-prior, position: 7
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    output_image: (an existing file name)
            Cortical thickness
```

43.8 N4BiasFieldCorrection

Link to code

Wraps command **N4BiasFieldCorrection**

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]*.

43.8.1 Examples

```
    >>> import copy
    >>> from nipype.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
```

```
    >>> 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
```

```
    >>> 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 --converge
```

```
>>> 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, st
```

Inputs:

```
[Mandatory]
input_image: (a file name)
        image to apply transformation to (generally a coregistered
        functional)
        flag: --input-image %s
save_bias: (a boolean, nipype default value: False)
        True if the estimated bias should be saved to file.
        mutually_exclusive: bias_image

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
bias_image: (a file name)
        Filename for the estimated bias.
bspline_fitting_distance: (a float)
        flag: --bspline-fitting %s
bspline_order: (an integer (int or long))
        requires: bspline_fitting_distance
convergence_threshold: (a float)
        requires: n_iterations
dimension: (3 or 2, nipype default value: 3)
        image dimension (2 or 3)
        flag: -d %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask_image: (a file name)
        flag: --mask-image %s
n_iterations: (a list of items which are an integer (int or long))
        flag: --convergence %s
num_threads: (an integer (int or long), nipype default value: 1)
        Number of ITK threads to use
output_image: (a string)
        output file name
        flag: --output %s
shrink_factor: (an integer (int or long))
        flag: --shrink-factor %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
weight_image: (a file name)
        flag: --weight-image %s
```

Outputs:

```
    bias_image: (an existing file name)
            Estimated bias
    output_image: (an existing file name)
            Warped image
```

43.9 antsBrainExtraction

Link to code
Wraps command **antsBrainExtraction.sh**
Inputs:

```
    [Mandatory]
    anatomical_image: (an existing file name)
            Structural image, typically T1. If more than oneanatomical image is
            specified, subsequently specifiedimages 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 withbuildtemplateparallel.sh in ANTs.
            flag: -a %s
    brain_probability_mask: (an existing file name)
            Brain probability mask created using e.g. LPBA40 data set whichhave
            brain masks defined, and warped to anatomical template andaveraged
            resulting in a probability image.
            flag: -m %s
    brain_template: (an existing file name)
            Anatomical template created using e.g. LPBA40 data set
            withbuildtemplateparallel.sh in ANTs.
            flag: -e %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    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.
            flag: -z 1
    dimension: (3 or 2, nipype default value: 3)
            image dimension (2 or 3)
            flag: -d %d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    extraction_registration_mask: (an existing file name)
            Mask (defined in the template space) used during registration for
            brain extraction.To limit the metric computation to a specific
            region.
            flag: -f %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    image_suffix: (a string, nipype default value: nii.gz)
            any of standard ITK formats, nii.gz is default
            flag: -s %s
```

```
keep_temporary_files: (an integer (int or long))
        Keep brain extraction/segmentation warps, etc (default = 0).
        flag: -k %d
num_threads: (an integer (int or long), nipype default value: 1)
        Number of ITK threads to use
out_prefix: (a string, nipype default value: highres001_)
        Prefix that is prepended to all output files (default =
        highress001_)
        flag: -o %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
use_floatingpoint_precision: (0 or 1)
        Use floating point precision in registrations (default = 0)
        flag: -q %d
use_random_seeding: (0 or 1)
        Use random number generated from system clock in Atropos(default =
        1)
        flag: -u %d
```

Outputs:

```
BrainExtractionBrain: (an existing file name)
        brain extraction image
BrainExtractionMask: (an existing file name)
        brain extraction mask
```

43.10 antsCorticalThickness

Link to code

Wraps command **antsCorticalThickness.sh**

Inputs:

```
[Mandatory]
anatomical_image: (an existing file name)
        Structural *intensity* image, typically T1.If more than one
        anatomical image is specified,subsequently specified images are used
        during thesegmentation process. However, only the firstimage is used
        in the registration of priors.Our suggestion would be to specify the
        T1as the first image.
        flag: -a %s
brain_probability_mask: (an existing file name)
        brain probability mask in template space
        flag: -m %s
brain_template: (an existing file name)
        Anatomical *intensity* template (possibly created using apopulation
        data set with buildtemplateparallel.sh in ANTs).This template is
        *not* skull-stripped.
        flag: -e %s
segmentation_priors: (a list of items which are an existing file
         name)
        flag: -p %s
t1_registration_template: (an existing file name)
        Anatomical *intensity* template(assumed to be skull-stripped). A
        commoncase would be where this would be the sametemplate as
        specified in the -e option whichis not skull stripped.
        flag: -t %s
```

```
    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    b_spline_smoothing: (a boolean)
            Use B-spline SyN for registrations and B-splineexponential mapping
            in DiReCT.
            flag: -v
    cortical_label_image: (an existing file name)
            Cortical ROI labels to use as a prior for ATITH.
    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.
            flag: -z 1
    dimension: (3 or 2, nipype default value: 3)
            image dimension (2 or 3)
            flag: -d %d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    extraction_registration_mask: (an existing file name)
            Mask (defined in the template space) used during registration for
            brain extraction.
            flag: -f %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    image_suffix: (a string, nipype default value: nii.gz)
            any of standard ITK formats, nii.gz is default
            flag: -s %s
    keep_temporary_files: (an integer (int or long))
            Keep brain extraction/segmentation warps, etc (default = 0).
            flag: -k %d
    label_propagation: (a string)
            Incorporate a distance prior one the posterior formulation. Should
            beof the form 'label[lambda,boundaryProbability]' where labelis a
            value of 1,2,3,... denoting label ID. The labelprobability for
            anything outside the current label = boundaryProbability * exp(
            -lambda * distanceFromBoundary )Intuitively, smaller lambda values
            will increase the spatial capturerange of the distance prior. To
            apply to all label values, simply omitspecifying the label, i.e. -l
            [lambda,boundaryProbability].
            flag: -l %s
    max_iterations: (an integer (int or long))
            ANTS registration max iterations(default = 100x100x70x20)
            flag: -i %d
    num_threads: (an integer (int or long), nipype default value: 1)
            Number of ITK threads to use
    out_prefix: (a string, nipype default value: antsCT_)
            Prefix that is prepended to all output files (default = antsCT_)
            flag: -o %s
    posterior_formulation: (a string)
            Atropos posterior formulation and whether or notto use mixture model
            proportions.e.g 'Socrates[1]' (default) or 'Aristotle[1]'.Choose the
            latter if youwant use the distance priors (see also the -l optionfor
            label propagation control).
```

```
        flag: -b %s
prior_segmentation_weight: (a float)
        Atropos spatial prior *probability* weight forthe segmentation
        flag: -w %f
quick_registration: (a boolean)
        If = 1, use antsRegistrationSyNQuick.sh as the basis for
        registrationduring brain extraction, brain segmentation,
        and(optional) normalization to a template.Otherwise use
        antsRegistrationSyN.sh (default = 0).
        flag: -q 1
segmentation_iterations: (an integer (int or long))
        N4 -> Atropos -> N4 iterations during segmentation(default = 3)
        flag: -n %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
use_floatingpoint_precision: (0 or 1)
        Use floating point precision in registrations (default = 0)
        flag: -j %d
use_random_seeding: (0 or 1)
        Use random number generated from system clock in Atropos(default =
        1)
        flag: -u %d
```

Outputs:

```
BrainExtractionMask: (an existing file name)
        brain extraction mask
BrainSegmentation: (an existing file name)
        brain segmentaion image
BrainSegmentationN4: (an existing file name)
        N4 corrected image
BrainSegmentationPosteriors: (a list of items which are an existing
         file name)
        Posterior probability images
BrainVolumes: (an existing file name)
        Brain volumes as text
CorticalThickness: (an existing file name)
        cortical thickness file
CorticalThicknessNormedToTemplate: (an existing file name)
        Normalized cortical thickness
SubjectToTemplate0GenericAffine: (an existing file name)
        Template to subject inverse affine
SubjectToTemplate1Warp: (an existing file name)
        Template to subject inverse warp
SubjectToTemplateLogJacobian: (an existing file name)
        Template to subject log jacobian
TemplateToSubject0Warp: (an existing file name)
        Template to subject warp
TemplateToSubject1GenericAffine: (an existing file name)
        Template to subject affine
```

CHAPTER 44

interfaces.ants.utils

44.1 AverageAffineTransform

Link to code
Wraps command **AverageAffineTransform**

44.1.1 Examples

```
>>> from nipype.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)
        flag: %d, position: 0
output_affine_transform: (a file name)
        Outputfname.txt: the name of the resulting transform.
        flag: %s, position: 1
transforms: (a list of items which are an existing file name)
        transforms to average
        flag: %s, position: 3

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
num_threads: (an integer (int or long), nipype default value: 1)
        Number of ITK threads to use
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
```

```
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
affine_transform: (an existing file name)
        average transform file
```

44.2 AverageImages

Link to code
Wraps command **AverageImages**

44.2.1 Examples

```
>>> from nipype.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 = ['rc1s1.nii', 'rc1s1.nii']
>>> avg.cmdline
'AverageImages 3 average.nii.gz 1 rc1s1.nii rc1s1.nii'
```

Inputs:

```
[Mandatory]
dimension: (3 or 2)
        image dimension (2 or 3)
        flag: %d, position: 0
images: (a list of items which are an existing file name)
        image to apply transformation to (generally a coregistered
        functional)
        flag: %s, position: 3
normalize: (a boolean)
        Normalize: if true, the 2nd imageis divided by its mean. This will
        select the largest image to average into.
        flag: %d, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
num_threads: (an integer (int or long), nipype default value: 1)
        Number of ITK threads to use
output_average_image: (a file name, nipype default value:
         average.nii)
        the name of the resulting image.
        flag: %s, position: 1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
```

```
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
output_average_image: (an existing file name)
        average image file
```

44.3 JacobianDeterminant

Link to code
Wraps command **ANTSJacobian**

44.3.1 Examples

```
>>> from nipype.interfaces.ants import JacobianDeterminant
>>> jacobian = JacobianDeterminant()
>>> jacobian.inputs.dimension = 3
>>> jacobian.inputs.warp_file = 'ants_Warp.nii.gz'
>>> jacobian.inputs.output_prefix = 'Sub001_'
>>> jacobian.inputs.use_log = 1
>>> jacobian.cmdline
'ANTSJacobian 3 ants_Warp.nii.gz Sub001_ 1'
```

Inputs:

```
[Mandatory]
dimension: (3 or 2)
        image dimension (2 or 3)
        flag: %d, position: 0
warp_file: (an existing file name)
        input warp file
        flag: %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
norm_by_total: (0 or 1)
        normalize jacobian by total in mask to adjust for head size
        flag: %d, position: 5
num_threads: (an integer (int or long), nipype default value: 1)
        Number of ITK threads to use
output_prefix: (a file name)
        prefix of the output image filename: PREFIX(log)jacobian.nii.gz
        flag: %s, position: 2
projection_vector: (a list of items which are a float)
        vector to project warp against
        flag: %s, position: 6
template_mask: (an existing file name)
        template mask to adjust for head size
```

```
        flag: %s, position: 4
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
use_log: (0 or 1)
        log transform the jacobian determinant
        flag: %d, position: 3
```

Outputs:

```
jacobian_image: (an existing file name)
        (log transformed) jacobian image
```

44.4 MultiplyImages

Link to code
Wraps command **MultiplyImages**

44.4.1 Examples

```
>>> from nipype.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)
        flag: %d, position: 0
first_input: (an existing file name)
        image 1
        flag: %s, position: 1
output_product_image: (a file name)
        Outputfname.nii.gz: the name of the resulting image.
        flag: %s, position: 3
second_input: (an existing file name or a float)
        image 2 or multiplication weight
        flag: %s, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
num_threads: (an integer (int or long), nipype default value: 1)
```

```
        Number of ITK threads to use
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
output_product_image: (an existing file name)
        average image file
```

CHAPTER 45

interfaces.ants.visualization

45.1 ConvertScalarImageToRGB

Link to code
Wraps command **ConvertScalarImageToRGB**

45.1.1 Examples

```
>>> from nipype.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]
colormap: (a string, nipype default value: )
        Possible colormaps: grey, red, green, blue, copper, jet, hsv,
        spring, summer, autumn, winter, hot, cool, overunder, custom
        flag: %s, position: 4
dimension: (3 or 2, nipype default value: 3)
        image dimension (2 or 3)
        flag: %d, position: 0
input_image: (an existing file name)
        Main input is a 3-D grayscale image.
        flag: %s, position: 1
maximum_input: (an integer (int or long))
        maximum input
        flag: %d, position: 7
minimum_input: (an integer (int or long))
        minimum input
        flag: %d, position: 6

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
custom_color_map_file: (a string, nipype default value: none)
        custom color map file
        flag: %s, position: 5
```

```
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    mask_image: (an existing file name, nipype default value: none)
            mask image
            flag: %s, position: 3
    maximum_RGB_output: (an integer (int or long), nipype default value:
             255)
            flag: %d, position: 9
    minimum_RGB_output: (an integer (int or long), nipype default value:
             0)
            flag: %d, position: 8
    num_threads: (an integer (int or long), nipype default value: 1)
            Number of ITK threads to use
    output_image: (a string, nipype default value: rgb.nii.gz)
            rgb output image
            flag: %s, position: 2
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    output_image: (an existing file name)
            converted RGB image
```

45.2 CreateTiledMosaic

Link to code

Wraps 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.

45.2.1 Examples

```
    >>> from nipype.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 -
```

Inputs:

```
    [Mandatory]
    input_image: (an existing file name)
            Main input is a 3-D grayscale image.
            flag: -i %s
    rgb_image: (an existing file name)
            An optional Rgb image can be added as an overlay.It must have the
            same imagegeometry as the input grayscale image.
            flag: -r %s

    [Optional]
    alpha_value: (a float)
            If an Rgb image is provided, render the overlay using the specified
            alpha parameter.
            flag: -a %.2f
    args: (a string)
            Additional parameters to the command
            flag: %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.
            flag: -d %d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    flip_slice: (a string)
            flipXxflipY
            flag: -f %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    mask_image: (an existing file name)
            Specifies the ROI of the RGB voxels used.
            flag: -x %s
    num_threads: (an integer (int or long), nipype default value: 1)
            Number of ITK threads to use
    output_image: (a string, nipype default value: output.png)
            The output consists of the tiled mosaic image.
            flag: -o %s
    pad_or_crop: (a 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".
            flag: -p %s
    permute_axes: (a boolean)
            doPermute
            flag: -g
    slices: (a string)
            Number of slices to increment Slice1xSlice2xSlice3[numberOfSlicesToI
            ncrement,<minSlice=0>,<maxSlice=lastSlice>]
            flag: -s %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
```

```
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tile_geometry: (a string)
        The tile geometry specifies the number of rows and columnsin 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 selectedbased on direction.
        flag: -t %s
```

Outputs:

```
output_image: (an existing file name)
        image file
```

CHAPTER 46

interfaces.brainsuite.brainsuite

46.1 Bfc

Link to code
Wraps command **bfc**
bias field corrector (BFC) This program corrects gain variation in T1-weighted MRI.
http://brainsuite.org/processing/surfaceextraction/bfc/

46.1.1 Examples

```
>>> from nipype.interfaces import brainsuite
>>> from nipype.testing import example_data
>>> bfc = brainsuite.Bfc()
>>> bfc.inputs.inputMRIFile = example_data('structural.nii')
>>> bfc.inputs.inputMaskFile = example_data('mask.nii')
>>> results = bfc.run()
```

Inputs:

```
[Mandatory]
inputMRIFile: (a file name)
        input skull-stripped MRI volume
        flag: -i %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
biasEstimateConvergenceThreshold: (a float)
        bias estimate convergence threshold (values > 0.1 disable)
        flag: --beps %f
biasEstimateSpacing: (an integer (int or long))
        bias sample spacing (voxels)
        flag: -s %d
biasFieldEstimatesOutputPrefix: (a string)
        save iterative biasfield estimates as<prefix>.n.field.nii.gz
        flag: --biasprefix %s
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]
        flag: %s
controlPointSpacing: (an integer (int or long))
        control point spacing (voxels)
```

```
        flag: -c %d
    convergenceThreshold: (a float)
        convergence threshold
        flag: --eps %f
    correctWholeVolume: (a boolean)
        apply correction field to entirevolume
        flag: --extrapolate
    correctedImagesOutputPrefix: (a string)
        save iterative correctedimages as<prefix>.n.bfc.nii.gz
        flag: --prefix %s
    correctionScheduleFile: (a file name)
        list of parameters
        flag: --schedule %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
        Environment variables
    histogramRadius: (an integer (int or long))
        histogram radius (voxels)
        flag: -r %d
    histogramType: ('ellipse' or 'block')
        Options for type of histogram
        ellipse:use ellipsoid for ROI histogram
        block:use block for ROI histogram
        flag: %s
    ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
    inputMaskFile: (a file name)
        mask file
        flag: -m %s
    intermediate_file_type: ('analyze' or 'nifti' or 'gzippedAnalyze' or
             'gzippedNifti')
        Options for the format inwhich intermediate files aregenerated
        flag: %s
    iterativeMode: (a boolean)
        iterative mode (overrides -r, -s, -c,-w settings)
        flag: --iterate
    maxBias: (a float, nipype default value: 1.5)
        maximum allowed biasvalue
        flag: -U %f
    minBias: (a float, nipype default value: 0.5)
        minimum allowed biasvalue
        flag: -L %f
    outputBiasField: (a file name)
        save bias field estimate
        flag: --bias %s
    outputMRIVolume: (a file name)
        output bias-corrected MRI volume.If unspecified, output file
        namewill be auto generated.
        flag: -o %s
    outputMaskedBiasField: (a file name)
        save bias field estimate (masked)
        flag: --maskedbias %s
    splineLambda: (a float)
        spline stiffness weighting parameter
        flag: -w %f
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
```

```
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
timer: (a boolean)
        display timing information
        flag: --timer
verbosityLevel: (an integer (int or long))
        verbosity level (0=silent)
        flag: -v %d
```

Outputs:

```
correctionScheduleFile: (a file name)
        path/name of schedule file
outputBiasField: (a file name)
        path/name of bias field output file
outputMRIVolume: (a file name)
        path/name of output file
outputMaskedBiasField: (a file name)
        path/name of masked bias field output
```

46.2 Bse

Link to code

Wraps 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/

46.2.1 Examples

```
>>> from nipype.interfaces import brainsuite
>>> from nipype.testing import example_data
>>> bse = brainsuite.Bse()
>>> bse.inputs.inputMRIFile = example_data('structural.nii')
>>> results = bse.run()
```

Inputs:

```
[Mandatory]
inputMRIFile: (a file name)
        input MRI volume
        flag: -i %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
diffusionConstant: (a float, nipype default value: 25)
        diffusion constant
        flag: -d %f
diffusionIterations: (an integer (int or long), nipype default value:
         3)
        diffusion iterations
        flag: -n %d
dilateFinalMask: (a boolean, nipype default value: True)
        dilate final mask
```

```
        flag: -p
edgeDetectionConstant: (a float, nipype default value: 0.64)
        edge detection constant
        flag: -s %f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
noRotate: (a boolean)
        retain original orientation(default behavior will auto-rotate input
        NII filesto LPI orientation)
        flag: --norotate
outputCortexFile: (a file name)
        cortex file
        flag: --cortex %s
outputDetailedBrainMask: (a file name)
        save detailed brain mask
        flag: --hires %s
outputDiffusionFilter: (a file name)
        diffusion filter output
        flag: --adf %s
outputEdgeMap: (a file name)
        edge map output
        flag: --edge %s
outputMRIVolume: (a file name)
        output brain-masked MRI volume. Ifunspecified, output file name will
        be autogenerated.
        flag: -o %s
outputMaskFile: (a file name)
        save smooth brain mask
        flag: --mask %s
radius: (a float, nipype default value: 1)
        radius of erosion/dilation filter
        flag: -r %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
timer: (a boolean)
        show timing
        flag: --timer
trim: (a boolean, nipype default value: True)
        trim brainstem
        flag: --trim
verbosityLevel: (a float, nipype default value: 1)
         verbosity level (0=silent)
        flag: -v %f
```

Outputs:

```
outputCortexFile: (a file name)
        path/name of cortex file
outputDetailedBrainMask: (a file name)
        path/name of detailed brain mask
outputDiffusionFilter: (a file name)
        path/name of diffusion filter output
```

```
outputEdgeMap: (a file name)
        path/name of edge map output
outputMRIVolume: (a file name)
        path/name of brain-masked MRI volume
outputMaskFile: (a file name)
        path/name of smooth brain mask
```

46.3 Cerebro

Link to code

Wraps 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/

46.3.1 Examples

```
>>> from nipype.interfaces import brainsuite
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
inputAtlasLabelFile: (a file name)
        atlas labeling
        flag: --atlaslabels %s
inputAtlasMRIFile: (a file name)
        atlas MRI volume
        flag: --atlas %s
inputMRIFile: (a file name)
        input 3D MRI volume
        flag: -i %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
costFunction: (an integer (int or long), nipype default value: 2)
        0,1,2
        flag: -c %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputBrainMaskFile: (a file name)
        brain mask file
        flag: -m %s
```

```
    keepTempFiles: (a boolean)
            don't remove temporary files
            flag: --keep
    linearConvergence: (a float)
            linear convergence
            flag: --linconv %f
    outputAffineTransformFile: (a file name)
            save affine transform to file.
            flag: --air %s
    outputCerebrumMaskFile: (a file name)
            output cerebrum mask volume. If unspecified, output file name will
            be auto generated.
            flag: -o %s
    outputLabelMaskFile: (a file name)
            output labeled hemisphere/cerebrum volume. If unspecified, output
            file name will be auto generated.
            flag: -l %s
    outputWarpTransformFile: (a file name)
            save warp transform to file.
            flag: --warp %s
    tempDirectory: (a string)
            specify directory to use for temporary files
            flag: --tempdir %s
    tempDirectoryBase: (a string)
            create a temporary directory within this directory
            flag: --tempdirbase %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    useCentroids: (a boolean)
            use centroids of data to initialize position
            flag: --centroids
    verbosity: (an integer (int or long))
            verbosity level (0=silent)
            flag: -v %d
    warpConvergence: (a float)
            warp convergence
            flag: --warpconv %f
    warpLabel: (an integer (int or long))
            warp order (2,3,4,5,6,7,8)
            flag: --warplevel %d
```

Outputs:

```
    outputAffineTransformFile: (a file name)
            path/name of affine transform file
    outputCerebrumMaskFile: (a file name)
            path/name of cerebrum mask file
    outputLabelMaskFile: (a file name)
            path/name of label mask file
    outputWarpTransformFile: (a file name)
            path/name of warp transform file
```

46.4 Cortex

Link to code
Wraps 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/

46.4.1 Examples

```
>>> from nipype.interfaces import brainsuite
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
inputHemisphereLabelFile: (a file name)
        hemisphere / lobe label volume
        flag: -h %s
inputTissueFractionFile: (a file name)
        tissue fraction file (32-bit float)
        flag: -f %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
computeGCBoundary: (a boolean)
        compute GM/CSF boundary
        flag: -g
computeWGBoundary: (a boolean, nipype default value: True)
        compute WM/GM boundary
        flag: -w
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
includeAllSubcorticalAreas: (a boolean, nipype default value: True)
        include all subcortical areas in WM mask
        flag: -a
outputCerebrumMask: (a file name)
        output structure mask. If unspecified, output file name will be auto
        generated.
        flag: -o %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
timer: (a boolean)
        timing function
        flag: --timer
tissueFractionThreshold: (a float, nipype default value: 50.0)
        tissue fraction threshold (percentage)
        flag: -p %f
verbosity: (an integer (int or long))
```

```
        verbosity level
        flag: -v %d
```

Outputs:

```
outputCerebrumMask: (a file name)
        path/name of cerebrum mask
```

46.5 Dewisp

Link to code

Wraps 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/

46.5.1 Examples

```
>>> from nipype.interfaces import brainsuite
>>> from nipype.testing import example_data
>>> dewisp = brainsuite.Dewisp()
>>> dewisp.inputs.inputMaskFile = example_data('mask.nii')
>>> results = dewisp.run()
```

Inputs:

```
[Mandatory]
inputMaskFile: (a file name)
        input file
        flag: -i %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
maximumIterations: (an integer (int or long))
        maximum number of iterations
        flag: -n %d
outputMaskFile: (a file name)
        output file. If unspecified, output file name will be auto
        generated.
        flag: -o %s
sizeThreshold: (an integer (int or long))
        size threshold
        flag: -t %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
```

```
        output, `file` - writes output to file, `none` - output is ignored
timer: (a boolean)
        time processing
        flag: --timer
verbosity: (an integer (int or long))
        verbosity
        flag: -v %d
```

Outputs:

```
outputMaskFile: (a file name)
        path/name of mask file
```

46.6 Dfs

Link to code
Wraps command **dfs**
Surface Generator Generates mesh surfaces using an isosurface algorithm.
http://brainsuite.org/processing/surfaceextraction/inner-cortical-surface/

46.6.1 Examples

```
>>> from nipype.interfaces import brainsuite
>>> from nipype.testing import example_data
>>> dfs = brainsuite.Dfs()
>>> dfs.inputs.inputVolumeFile = example_data('structural.nii')
>>> results = dfs.run()
```

Inputs:

```
[Mandatory]
inputVolumeFile: (a file name)
        input 3D volume
        flag: -i %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
curvatureWeighting: (a float, nipype default value: 5.0)
        curvature weighting
        flag: -w %f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputShadingVolume: (a file name)
        shade surface model with data from image volume
        flag: -c %s
noNormalsFlag: (a boolean)
        do not compute vertex normals
        flag: --nonormals
nonZeroTessellation: (a boolean)
        tessellate non-zero voxels
```

```
        flag: -nz
        mutually_exclusive: nonZeroTessellation, specialTessellation
outputSurfaceFile: (a file name)
        output surface mesh file. If unspecified, output file name will be
        auto generated.
        flag: -o %s
postSmoothFlag: (a boolean)
        smooth vertices after coloring
        flag: --postsmooth
scalingPercentile: (a float)
        scaling percentile
        flag: -f %f
smoothingConstant: (a float, nipype default value: 0.5)
        smoothing constant
        flag: -a %f
smoothingIterations: (an integer (int or long), nipype default value:
         10)
        number of smoothing iterations
        flag: -n %d
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>
        flag: %s, position: -1
        mutually_exclusive: nonZeroTessellation, specialTessellation
        requires: tessellationThreshold
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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>
        flag: %f
timer: (a boolean)
        timing function
        flag: --timer
verbosity: (an integer (int or long))
        verbosity (0 = quiet)
        flag: -v %d
zeroPadFlag: (a boolean)
        zero-pad volume (avoids clipping at edges)
        flag: -z
```

Outputs:

```
outputSurfaceFile: (a file name)
        path/name of surface file
```

46.7 Hemisplit

Link to code

Wraps 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.

46.7.1 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()
```

Inputs:

```
[Mandatory]
inputHemisphereLabelFile: (a file name)
        input hemisphere label volume
        flag: -l %s
inputSurfaceFile: (a file name)
        input surface
        flag: -i %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
outputLeftHemisphere: (a file name)
        output surface file, left hemisphere. If unspecified, output file
        name will be auto generated.
        flag: --left %s
outputLeftPialHemisphere: (a file name)
        output pial surface file, left hemisphere. If unspecified, output
        file name will be auto generated.
        flag: -pl %s
outputRightHemisphere: (a file name)
        output surface file, right hemisphere. If unspecified, output file
        name will be auto generated.
        flag: --right %s
outputRightPialHemisphere: (a file name)
        output pial surface file, right hemisphere. If unspecified, output
        file name will be auto generated.
        flag: -pr %s
pialSurfaceFile: (a file name)
        pial surface file -- must have same geometry as input surface
        flag: -p %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
timer: (a boolean)
        timing function
        flag: --timer
```

```
verbosity: (an integer (int or long))
        verbosity (0 = silent)
        flag: -v %d
```

Outputs:

```
outputLeftHemisphere: (a file name)
        path/name of left hemisphere
outputLeftPialHemisphere: (a file name)
        path/name of left pial hemisphere
outputRightHemisphere: (a file name)
        path/name of right hemisphere
outputRightPialHemisphere: (a file name)
        path/name of right pial hemisphere
```

46.8 Pialmesh

Link to code

Wraps 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/

46.8.1 Examples

```
>>> from nipype.interfaces import brainsuite
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
inputMaskFile: (a file name)
        restrict growth to mask file region
        flag: -m %s
inputSurfaceFile: (a file name)
        input file
        flag: -i %s
inputTissueFractionFile: (a file name)
        floating point (32) tissue fraction image
        flag: -f %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
exportPrefix: (a string)
        prefix for exporting surfaces if interval is set
        flag: --prefix %s
ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
laplacianSmoothing: (a float, nipype default value: 0.025)
        apply Laplacian smoothing
        flag: --smooth %f
maxThickness: (a float, nipype default value: 20)
        maximum allowed tissue thickness
        flag: --max %f
normalSmoother: (a float, nipype default value: 0.2)
        strength of normal smoother.
        flag: --nc %f
numIterations: (an integer (int or long), nipype default value: 100)
        number of iterations
        flag: -n %d
outputInterval: (an integer (int or long), nipype default value: 10)
        output interval
        flag: --interval %d
outputSurfaceFile: (a file name)
        output file. If unspecified, output file name will be auto
        generated.
        flag: -o %s
recomputeNormals: (a boolean)
        recompute normals at each iteration
        flag: --norm
searchRadius: (a float, nipype default value: 1)
        search radius
        flag: -r %f
stepSize: (a float, nipype default value: 0.4)
        step size
        flag: -s %f
tangentSmoother: (a float)
        strength of tangential smoother.
        flag: --tc %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
timer: (a boolean)
        show timing
        flag: --timer
tissueThreshold: (a float, nipype default value: 1.05)
        tissue threshold
        flag: -t %f
verbosity: (an integer (int or long))
        verbosity
        flag: -v %d
```

Outputs:

```
outputSurfaceFile: (a file name)
        path/name of surface file
```

46.9 Pvc

Link to code

Wraps 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/

46.9.1 Examples

```
>>> from nipype.interfaces import brainsuite
>>> from nipype.testing import example_data
>>> pvc = brainsuite.Pvc()
>>> pvc.inputs.inputMRIFile = example_data('structural.nii')
>>> pvc.inputs.inputMaskFile = example_data('mask.nii')
>>> results = pvc.run()
```

Inputs:

```
[Mandatory]
inputMRIFile: (a file name)
        MRI file
        flag: -i %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputMaskFile: (a file name)
        brain mask file
        flag: -m %s
outputLabelFile: (a file name)
        output label file. If unspecified, output file name will be auto
        generated.
        flag: -o %s
outputTissueFractionFile: (a file name)
        output tissue fraction file
        flag: -f %s
spatialPrior: (a float)
        spatial prior strength
        flag: -l %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
threeClassFlag: (a boolean)
        use a three-class (CSF=0,GM=1,WM=2) labeling
        flag: -3
timer: (a boolean)
        time processing
        flag: --timer
verbosity: (an integer (int or long))
        verbosity level (0 = silent)
        flag: -v %d
```

Outputs:

```
    outputLabelFile: (a file name)
            path/name of label file
    outputTissueFractionFile: (a file name)
            path/name of tissue fraction file
```

46.10 Scrubmask

Link to code
Wraps 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/

46.10.1 Examples

```
    >>> from nipype.interfaces import brainsuite
    >>> from nipype.testing import example_data
    >>> scrubmask = brainsuite.Scrubmask()
    >>> scrubmask.inputs.inputMaskFile = example_data('mask.nii')
    >>> results = scrubmask.run()
```

Inputs:

```
    [Mandatory]
    inputMaskFile: (a file name)
            input structure mask file
            flag: -i %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    backgroundFillThreshold: (an integer (int or long), nipype default
             value: 2)
            background fill threshold
            flag: -b %d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    foregroundTrimThreshold: (an integer (int or long), nipype default
             value: 0)
            foreground trim threshold
            flag: -f %d
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    numberIterations: (an integer (int or long))
            number of iterations
            flag: -n %d
    outputMaskFile: (a file name)
            output structure mask file. If unspecified, output file name will be
            auto generated.
            flag: -o %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
```

```
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
timer: (a boolean)
        timing function
        flag: --timer
verbosity: (an integer (int or long))
        verbosity (0=silent)
        flag: -v %d
```

Outputs:

```
outputMaskFile: (a file name)
        path/name of mask file
```

46.11 Skullfinder

Link to code

Wraps command **skullfinder**

Skull and scalp segmentation algorithm.

46.11.1 Examples

```
>>> from nipype.interfaces import brainsuite
>>> from nipype.testing import example_data
>>> skullfinder = brainsuite.Skullfinder()
>>> skullfinder.inputs.inputMRIFile = example_data('structural.nii')
>>> skullfinder.inputs.inputMaskFile = example_data('mask.nii')
>>> results = skullfinder.run()
```

Inputs:

```
[Mandatory]
inputMRIFile: (a file name)
        input file
        flag: -i %s
inputMaskFile: (a file name)
        A brain mask file, 8-bit image (0=non-brain, 255=brain)
        flag: -m %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
bgLabelValue: (an integer (int or long))
        background label value (0-255)
        flag: --bglabel %d
brainLabelValue: (an integer (int or long))
        brain label value (0-255)
        flag: --brainlabel %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
lowerThreshold: (an integer (int or long))
```

```
        Lower threshold for segmentation
        flag: -l %d
outputLabelFile: (a file name)
        output file. If unspecified, output file name will be auto
        generated.
        flag: -o %s
performFinalOpening: (a boolean)
        perform a final opening operation on the scalp mask
        flag: --finalOpening
scalpLabelValue: (an integer (int or long))
        scalp label value (0-255)
        flag: --scalplabel %d
skullLabelValue: (an integer (int or long))
        skull label value (0-255)
        flag: --skulllabel %d
spaceLabelValue: (an integer (int or long))
        space label value (0-255)
        flag: --spacelabel %d
surfaceFilePrefix: (a string)
        if specified, generate surface files for brain, skull, and scalp
        flag: -s %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
upperThreshold: (an integer (int or long))
        Upper threshold for segmentation
        flag: -u %d
verbosity: (an integer (int or long))
        verbosity
        flag: -v %d
```

Outputs:

```
outputLabelFile: (a file name)
        path/name of label file
```

46.12 Tca

Link to code

Wraps command **tca**

topological correction algorithm (TCA) This program removes topological handles from a binary object.

http://brainsuite.org/processing/surfaceextraction/tca/

46.12.1 Examples

```
>>> from nipype.interfaces import brainsuite
>>> from nipype.testing import example_data
>>> tca = brainsuite.Tca()
>>> tca.inputs.inputMaskFile = example_data('mask.nii')
>>> results = tca.run()
```

Inputs:

```
[Mandatory]
inputMaskFile: (a file name)
        input mask volume
```

```
        flag: -i %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
foregroundDelta: (an integer (int or long), nipype default value: 20)
        foreground delta
        flag: --delta %d
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
maxCorrectionSize: (an integer (int or long))
        minimum correction size
        flag: -n %d
minCorrectionSize: (an integer (int or long), nipype default value:
         2500)
        maximum correction size
        flag: -m %d
outputMaskFile: (a file name)
        output mask volume. If unspecified, output file name will be auto
        generated.
        flag: -o %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
timer: (a boolean)
        timing function
        flag: --timer
verbosity: (an integer (int or long))
        verbosity (0 = quiet)
        flag: -v %d
```

Outputs:

```
outputMaskFile: (a file name)
        path/name of mask file
```

46.13 getFileName()

Link to code

46.14 l_outputs()

Link to code

CHAPTER 47

interfaces.bru2nii

47.1 Bru2

Link to code
Wraps command **Bru2**
Uses bru2nii's Bru2 to convert Bruker files

47.1.1 Examples

```
>>> from nipype.interfaces.bru2nii import Bru2
>>> converter = Bru2()
>>> converter.inputs.input_dir = "brukerdir"
>>> converter.cmdline
'Bru2 -o .../nipype/nipype/testing/data/brukerdir brukerdir'
```

Inputs:

```
[Mandatory]
input_dir: (an existing directory name)
        Input Directory
        flag: %s, position: -1

[Optional]
actual_size: (a boolean)
        Keep actual size - otherwise x10 scale so animals match human.
        flag: -a
append_protocol_name: (a boolean)
        Append protocol name to output filename.
        flag: -p
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
force_conversion: (a boolean)
        Force conversion of localizers images (multiple slice orientations).
        flag: -f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_filename: (a string)
        Output filename ('.nii' will be appended)
        flag: -o %s
```

```
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
nii_file: (an existing file name)
```

CHAPTER 48

interfaces.c3

48.1 C3dAffineTool

Link to code
Wraps command **c3d_affine_tool**
Converts fsl-style Affine registration into ANTS compatible itk format

48.1.1 Example

```
>>> from nipype.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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fsl2ras: (a boolean)
        flag: -fsl2ras, position: 4
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
itk_transform: (a boolean or a file name)
        Export ITK transform.
        flag: -oitk %s, position: 5
reference_file: (an existing file name)
        flag: -ref %s, position: 1
source_file: (an existing file name)
        flag: -src %s, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

```
    transform_file: (an existing file name)
            flag: %s, position: 3
```

Outputs:

```
    itk_transform: (an existing file name)
```

CHAPTER 49

interfaces.camino.calib

49.1 SFLUTGen

Link to code

Wraps 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
```

49.1.1 Example

To create a calibration dataset using the default settings

```
>>> import nipype.interfaces.camino as cam
>>> lutgen = cam.SFLUTGen()
>>> lutgen.inputs.in_file = 'QSH_peaks.Bdouble'
>>> lutgen.inputs.info_file = 'PICO_calib.info'
>>> lutgen.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Voxel-order data of the spherical functions peaks.
        flag: -inputfile %s
```

```
    info_file: (a file name)
            The Info file that corresponds to the calibration datafile used in
            the reconstruction.
            flag: -infofile %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %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.
            flag: -binincsize %d
    directmap: (a boolean)
            Use direct mapping between the eigenvalues and the distribution
            parameters instead of the log of the eigenvalues.
            flag: -directmap
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    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.
            flag: -minvectsperbin %d
    order: (an integer (int or long))
            The order of the polynomial fitting the surface. Order 1 is linear.
            Order 2 (default) is quadratic.
            flag: -order %d
    out_file: (a file name)
            flag: > %s, position: -1
    outputstem: (a string, nipype default value: LUT)
            Define the name of the generated luts. The form of the filenames
            will be [outputstem]_oneFibreSurfaceCoeffs.Bdouble and
            [outputstem]_twoFibreSurfaceCoeffs.Bdouble
            flag: -outputstem %s
    pdf: ('bingham' or 'watson', nipype 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.
            flag: -pdf %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
lut_one_fibre: (an existing file name)
        PICo lut for one-fibre model
lut_two_fibres: (an existing file name)
        PICo lut for two-fibre model
```

49.2 SFPICOCalibData

Link to code
Wraps 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.

49.2.1 Example 1

To create a calibration dataset using the default settings

```
>>> import nipype.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()
```

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.

49.2.2 Example 2

To create a custom calibration dataset

```
>>> import nipype.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()
```

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]
info_file: (a file name)
        The name to be given to the information output filename.
```

```
        flag: -infooutputfile %s
scheme_file: (an existing file name)
        Specifies the scheme file for the diffusion MRI data
        flag: -schemefile %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
onedtfarange: (a list of from 2 to 2 items which are a float)
        Minimum and maximum FA for the single tensor synthetic data.
        flag: -onedtfarange %s
onedtfastep: (a float)
        FA step size controlling how many steps there are between the
        minimum and maximum FA settings.
        flag: -onedtfastep %f
out_file: (a file name)
        flag: > %s, position: -1
seed: (a float)
        Specifies the random seed to use for noise generation in simulation
        trials.
        flag: -seed %f
snr: (a float)
        Specifies the signal-to-noise ratio of the non-diffusion-weighted
        measurements to use in simulations.
        flag: -snr %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
trace: (a float)
        Trace of the diffusion tensor(s) used in the test function.
        flag: -trace %f
twodtanglerange: (a list of from 2 to 2 items which are a float)
        Minimum and maximum crossing angles between the two fibres.
        flag: -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.
        flag: -twodtanglestep %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.
        flag: -twodtfarange %s
twodtfastep: (a float)
        FA step size controlling how many steps there are between the
        minimum and maximum FA settings for the two tensor cases.
        flag: -twodtfastep %f
twodtmixmax: (a float)
        Mixing parameter controlling the proportion of one fibre population
        to the other. The minimum mixing parameter is (1 - twodtmixmax).
```

```
        flag: -twodtmixmax %f
twodtmixstep: (a float)
        Mixing parameter step size for the two tensor cases. Specify how
        many mixing parameter increments to use.
        flag: -twodtmixstep %f
```

Outputs:

```
PICOCalib: (an existing file name)
        Calibration dataset
calib_info: (an existing file name)
        Calibration dataset
```

CHAPTER 50

interfaces.camino.connectivity

50.1 Conmat

Link to code

Wraps 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 labled 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.

50.1.1 Example 1

To create a standard connectivity matrix based on streamline counts.

```
>>> import nipype.interfaces.camino as cam
>>> conmat = cam.Conmat()
>>> conmat.inputs.in_file = 'tracts.Bdouble'
>>> conmat.inputs.target_file = 'atlas.nii.gz'
>>> conmat.run()
```

50.1.2 Example 1

To create a standard connectivity matrix and mean tractwise FA statistics.

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Streamlines as generated by the Track interface
        flag: -inputfile %s
target_file: (an existing file name)
        An image containing targets, as used in ProcStreamlines interface.
        flag: -targetfile %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_root: (a file name)
        filename root prepended onto the names of the output files. The
        extension will be determined from the input.
        flag: -outputroot %s
scalar_file: (an existing file name)
        Optional scalar file for computing tract-based statistics. Must be
        in the same space as the target file.
        flag: -scalarfile %s
        requires: tract_stat
targetname_file: (an existing file name)
        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.
        flag: -targetnamefile %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
```

```
        output, `file` - writes output to file, `none` - output is ignored
tract_prop: ('length' or 'endpointsep')
        Tract property average to compute in the connectivity matrix. See
        TractStats for details.
        flag: -tractstat %s
        mutually_exclusive: tract_stat
tract_stat: ('mean' or 'min' or 'max' or 'sum' or 'median' or 'var')
        Tract statistic to use. See TractStats for other options.
        flag: -tractstat %s
        mutually_exclusive: tract_prop
        requires: scalar_file
```

Outputs:

```
conmat_sc: (an existing file name)
        Connectivity matrix in CSV file.
conmat_ts: (a file name)
        Tract statistics in CSV file.
```

CHAPTER 51

interfaces.camino.convert

51.1 AnalyzeHeader

Link to code
Wraps 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 commisure) 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.

51.1.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
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.
        flag: -datatype %s
in_file: (an existing file name)
        Tensor-fitted data filename
        flag: < %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %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].
```

```
        flag: -centre %s
data_dims: (a list of from 3 to 3 items which are an integer (int or
         long))
        data dimensions in voxels
        flag: -datadims %s
description: (a string)
        Short description - No spaces, max length 79 bytes. Will be null
        terminated automatically.
        flag: -description %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
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.
        flag: -gl %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
initfromheader: (an existing file name)
        Reads header information from file and intializes 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.
        flag: -initfromheader %s, position: 3
intelbyteorder: (a boolean)
        Write header in intel byte order (little-endian).
        flag: -intelbyteorder
networkbyteorder: (a boolean)
        Write header in network byte order (big-endian). This is the default
        for new headers.
        flag: -networkbyteorder
nimages: (an integer (int or long))
        Number of images in the img file. Default 1.
        flag: -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.
        flag: -offset %d
out_file: (a file name)
        flag: > %s, position: -1
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].
        flag: -picoseed %s
printbigendian: (an existing file name)
        Prints 1 if the header is big-endian, 0 otherwise.
        flag: -printbigendian %s, position: 3
printimagedims: (an existing file name)
        Prints image data and voxel dimensions as Camino arguments and
        exits.
        flag: -printimagedims %s, position: 3
printintelbyteorder: (an existing file name)
        Prints 1 if the header is little-endian, 0 otherwise.
        flag: -printintelbyteorder %s, position: 3
printprogargs: (an existing file name)
```

```
        Prints data dimension (and type, if relevant) arguments for a
        specific Camino program, where prog is one of shredder,
        scanner2voxel, vcthreshselect, pdview, track.
        flag: -printprogargs %s, position: 3
readheader: (an existing file name)
        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.
        flag: -readheader %s, position: 3
scaleinter: (a float)
        Constant to add to the image intensities. Used by SPM and MRIcro.
        flag: -scaleinter %d
scaleslope: (a float)
        Intensities in the image are scaled by this factor by SPM and
        MRICro. Default is 1.0.
        flag: -scaleslope %d
scheme_file: (an existing file name)
        Camino scheme file (b values / vectors, see camino.fsl2scheme)
        flag: %s, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
voxel_dims: (a list of from 3 to 3 items which are a float)
        voxel dimensions in mm
        flag: -voxeldims %s
```

Outputs:

```
header: (an existing file name)
        Analyze header
```

51.2 DT2NIfTI

Link to code

Wraps 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]
header_file: (an existing file name)
         A Nifti .nii or .hdr file containing the header information
        flag: -header %s, position: 3
in_file: (an existing file name)
        tract file
        flag: -inputfile %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
```

```
        interface fails to run
output_root: (a file name)
        filename root prepended onto the names of three output files.
        flag: -outputroot %s, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
dt: (an existing file name)
        diffusion tensors in NIfTI format
exitcode: (an existing file name)
        exit codes from Camino reconstruction in NIfTI format
lns0: (an existing file name)
        estimated lns0 from Camino reconstruction in NIfTI format
```

51.3 Image2Voxel

Link to code

Wraps 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.

51.3.1 Examples

```
>>> import nipype.interfaces.camino as cmon
>>> img2vox = cmon.Image2Voxel()
>>> img2vox.inputs.in_file = '4d_dwi.nii'
>>> img2vox.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        4d image file
        flag: -4dimage %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        flag: > %s, position: -1
out_type: ('float' or 'char' or 'short' or 'int' or 'long' or
         'double', nipype default value: float)
        "i.e. Bfloat". Can be "char", "short", "int", "long", "float" or
        "double"
```

```
        flag: -outputdatatype %s, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
voxel_order: (an existing file name)
        path/name of 4D volume in voxel order
```

51.4 NIfTIDT2Camino

Link to code

Wraps 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 dtifit 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: (an existing file name)
        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.
        flag: -inputfile %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
bgmask: (an existing file name)
        Binary valued brain / background segmentation, may be a raw binary
        file (specify type with -maskdatatype) or a supported image file.
        flag: -bgmask %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
lns0_file: (an existing file name)
        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.
        flag: -lns0 %s
out_file: (a file name)
        flag: > %s, position: -1
s0_file: (an existing file name)
```

```
        File containing the unweighted signal for each voxel, may be a raw
        binary file (specify type with -inputdatatype) or a supported image
        file.
        flag: -s0 %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.
        flag: -scaleinter %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.
        flag: -scaleslope %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
uppertriangular: (a boolean)
        Specifies input in upper-triangular (VTK style) order.
        flag: -uppertriangular %s
```

Outputs:

```
out_file: (a file name)
        diffusion tensors data in Camino format
```

51.5 ProcStreamlines

Link to code

Wraps command **procstreamlines**

Process streamline data

This program does post-processing of streamline output from track. It can either output streamlines or connection probal

http://web4.cs.ucl.ac.uk/research/medic/camino/pmwiki/pmwiki.php?n=Man.procstreamlines

51.5.1 Examples

```
>>> import nipype.interfaces.camino as cmon
>>> proc = cmon.ProcStreamlines()
>>> proc.inputs.in_file = 'tract_data.Bfloat'
>>> proc.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        data file
        flag: -inputfile %s, position: 1

[Optional]
allowmultitargets: (a boolean)
        Allows streamlines to connect to multiple target volumes.
        flag: -allowmultitargets
args: (a string)
        Additional parameters to the command
        flag: %s
```

```
    datadims: (a list of from 3 to 3 items which are an integer (int or
             long))
            data dimensions in voxels
            flag: -datadims %s
    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).
            flag: -directional %s
    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.
            flag: -discardloops
    endpointfile: (a file name)
            Image containing endpoint ROIs. This should be an Analyze 7.5 header
            / image file.hdr and file.img.
            flag: -endpointfile %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    exclusionfile: (a file name)
            Image containing exclusion ROIs. This should be an Analyze 7.5
            header / image file.hdr and file.img.
            flag: -exclusionfile %s
    gzip: (a boolean)
            save the output image in gzip format
            flag: -gzip
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputmodel: ('raw' or 'voxels', nipype default value: raw)
            input model type (raw or voxels)
            flag: -inputmodel %s
    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.
            flag: -iterations %d
    maxtractlength: (an integer (int or long))
            maximum length of tracts
            flag: -maxtractlength %d
    maxtractpoints: (an integer (int or long))
            maximum number of tract points
            flag: -maxtractpoints %d
    mintractlength: (an integer (int or long))
            minimum length of tracts
            flag: -mintractlength %d
    mintractpoints: (an integer (int or long))
            minimum number of tract points
            flag: -mintractpoints %d
```

```
    noresample: (a boolean)
            Disables resampling of input streamlines. Resampling is
            automatically disabled if the input model is voxels.
            flag: -noresample
    out_file: (a file name)
            flag: > %s, position: -1
    outputacm: (a boolean)
            output all tracts in a single connection probability map (Analyze
            image)
            flag: -outputacm
            requires: outputroot, seedfile
    outputcbs: (a boolean)
            outputs connectivity-based segmentation maps; requires target
            outputfile
            flag: -outputcbs
            requires: outputroot, targetfile, seedfile
    outputcp: (a boolean)
            output the connection probability map (Analyze image, float)
            flag: -outputcp
            requires: outputroot, seedfile
    outputroot: (a file name)
            Prepended onto all output file names.
            flag: -outputroot %s
    outputsc: (a boolean)
            output the connection probability map (raw streamlines, int)
            flag: -outputsc
            requires: outputroot, seedfile
    outputtracts: (a boolean)
            Output streamlines in raw binary format.
            flag: -outputtracts
    regionindex: (an integer (int or long))
            index of specific region to process
            flag: -regionindex %d
    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.
            flag: -resamplestepsize %d
    seedfile: (a file name)
            Image Containing Seed Points
            flag: -seedfile %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
            flag: -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
            flag: -seedpointvox %s
    targetfile: (a file name)
            Image containing target volumes.
```

```
        flag: -targetfile %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
truncateinexclusion: (a boolean)
        Retain segments of a streamline before entry to an exclusion ROI.
        flag: -truncateinexclusion
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.
        flag: -truncateloops
voxeldims: (a list of from 3 to 3 items which are an integer (int or
         long))
        voxel dimensions in mm
        flag: -voxeldims %s
waypointfile: (a file name)
        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.
        flag: -waypointfile %s
```

Outputs:

```
outputroot_files: (a list of items which are an existing file name)
proc: (an existing file name)
        Processed Streamlines
```

51.6 Shredder

Link to code

Wraps 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.

51.6.1 Examples

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        raw binary data file
        flag: < %s, position: -2
```

```
[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
chunksize: (an integer (int or long))
        reads and outputs a chunk of chunksize bytes
        flag: %d, position: 2
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
offset: (an integer (int or long))
        initial offset of offset bytes
        flag: %d, position: 1
out_file: (a file name)
        flag: > %s, position: -1
space: (an integer (int or long))
        skips space bytes
        flag: %d, position: 3
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
shredded: (an existing file name)
        Shredded binary data file
```

51.7 TractShredder

Link to code

Wraps 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.

51.7.1 Examples

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        tract file
```

```
        flag: < %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
bunchsize: (an integer (int or long))
        reads and outputs a group of bunchsize tracts
        flag: %d, position: 2
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
offset: (an integer (int or long))
        initial offset of offset tracts
        flag: %d, position: 1
out_file: (a file name)
        flag: > %s, position: -1
space: (an integer (int or long))
        skips space tracts
        flag: %d, position: 3
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
shredded: (an existing file name)
        Shredded tract file
```

51.8 VtkStreamlines

Link to code

Wraps command **vtkstreamlines**

Use vtkstreamlines to convert raw or voxel format streamlines to VTK polydata

51.8.1 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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        data file
        flag:  < %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
```

```
        flag: %s
colourorient: (a boolean)
        Each point on the streamline is coloured by the local orientation.
        flag: -colourorient
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputmodel: ('raw' or 'voxels', nipype default value: raw)
        input model type (raw or voxels)
        flag: -inputmodel %s
interpolate: (a boolean)
        the scalar value at each point on the streamline is calculated by
        trilinear interpolation
        flag: -interpolate
interpolatescalars: (a boolean)
        the scalar value at each point on the streamline is calculated by
        trilinear interpolation
        flag: -interpolatescalars
out_file: (a file name)
        flag: > %s, position: -1
scalar_file: (a file name)
        image that is in the same physical space as the tracts
        flag: -scalarfile %s, position: 3
seed_file: (a file name)
        image containing seed points
        flag: -seedfile %s, position: 1
target_file: (a file name)
        image containing integer-valued target regions
        flag: -targetfile %s, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
voxeldims: (a list of from 3 to 3 items which are an integer (int or
         long))
        voxel dimensions in mm
        flag: -voxeldims %s, position: 4
```

Outputs:

```
vtk: (an existing file name)
        Streamlines in VTK format
```

CHAPTER 52

interfaces.camino.dti

52.1 ComputeEigensystem

Link to code
Wraps 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_33, l_3, e_31, e_32, e_33}, where l_1 >= l_2 >= 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.

52.1.1 Example

```
>>> import nipype.interfaces.camino as cmon
>>> dteig = cmon.ComputeEigensystem()
>>> dteig.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> dteig.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Tensor-fitted data filename
        flag: < %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputdatatype: ('double' or 'float' or 'long' or 'int' or 'short' or
         'char', nipype 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
        flag: -inputdatatype %s
inputmodel: ('dt' or 'multitensor')
```

```
        Specifies the model that the input data contains parameters for.
        Possible model types are: "dt" (diffusion-tensor data) and
        "multitensor"
        flag: -inputmodel %s
maxcomponents: (an integer (int or long))
        The maximum number of tensor components in a voxel of the input
        data.
        flag: -maxcomponents %d
out_file: (a file name)
        flag: > %s, position: -1
outputdatatype: ('double' or 'float' or 'long' or 'int' or 'short' or
         'char', nipype 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
        flag: -outputdatatype %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
eigen: (an existing file name)
        Trace of the diffusion tensor
```

52.2 ComputeFractionalAnisotropy

Link to code

Wraps 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.

52.2.1 Example

```
>>> import nipype.interfaces.camino as cmon
>>> fa = cmon.ComputeFractionalAnisotropy()
>>> fa.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> fa.inputs.scheme_file = 'A.scheme'
>>> fa.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Tensor-fitted data filename
        flag: < %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
```

```
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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 thefollowing strings: "char", "short", "int", "long", "float" or
        "double".
        flag: -inputdatatype %s
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.
        flag: -inputmodel %s
out_file: (a file name)
        flag: > %s, position: -1
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 thefollowing strings: "char", "short", "int", "long", "float" or
        "double".
        flag: -outputdatatype %s
scheme_file: (an existing file name)
        Camino scheme file (b values / vectors, see camino.fsl2scheme)
        flag: %s, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
fa: (an existing file name)
        Fractional Anisotropy Map
```

52.3 ComputeMeanDiffusivity

Link to code

Wraps command **md**

Computes the mean diffusivity (trace/3) from diffusion tensors.

52.3.1 Example

```
>>> import nipype.interfaces.camino as cmon
>>> md = cmon.ComputeMeanDiffusivity()
>>> md.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> md.inputs.scheme_file = 'A.scheme'
>>> md.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Tensor-fitted data filename
```

```
        flag: < %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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 thefollowing strings: "char", "short", "int", "long", "float" or
        "double".
        flag: -inputdatatype %s
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.
        flag: -inputmodel %s
out_file: (a file name)
        flag: > %s, position: -1
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 thefollowing strings: "char", "short", "int", "long", "float" or
        "double".
        flag: -outputdatatype %s
scheme_file: (an existing file name)
        Camino scheme file (b values / vectors, see camino.fsl2scheme)
        flag: %s, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
md: (an existing file name)
        Mean Diffusivity Map
```

52.4 ComputeTensorTrace

Link to code

Wraps 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.

52.4.1 Example

```
>>> import nipype.interfaces.camino as cmon
>>> trace = cmon.ComputeTensorTrace()
>>> trace.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> trace.inputs.scheme_file = 'A.scheme'
>>> trace.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Tensor-fitted data filename
        flag: < %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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 thefollowing strings: "char", "short", "int", "long", "float" or
        "double".
        flag: -inputdatatype %s
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.
        flag: -inputmodel %s
out_file: (a file name)
        flag: > %s, position: -1
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 thefollowing strings: "char", "short", "int", "long", "float" or
        "double".
        flag: -outputdatatype %s
scheme_file: (an existing file name)
        Camino scheme file (b values / vectors, see camino.fsl2scheme)
        flag: %s, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
trace: (an existing file name)
        Trace of the diffusion tensor
```

52.5 DTIFit

Link to code
Wraps 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.

52.5.1 Example

```
>>> import nipype.interfaces.camino as cmon
>>> fit = cmon.DTIFit()
>>> fit.inputs.scheme_file = 'A.scheme'
>>> fit.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> fit.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        voxel-order data filename
        flag: %s, position: 1
scheme_file: (an existing file name)
        Camino scheme file (b values / vectors, see camino.fsl2scheme)
        flag: %s, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
bgmask: (an existing file name)
        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.
        flag: -bgmask %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
non_linear: (a boolean)
        Use non-linear fitting instead of the default linear regression to
        the log measurements.
        flag: -nonlinear, position: 3
out_file: (a file name)
        flag: > %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
```

```
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
tensor_fitted: (an existing file name)
        path/name of 4D volume in voxel order
```

52.6 DTLUTGen

Link to code

Wraps 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.

52.6.1 Example

```
>>> import nipype.interfaces.camino as cmon
>>> dtl = cmon.DTLUTGen()
>>> dtl.inputs.snr = 16
>>> dtl.inputs.scheme_file = 'A.scheme'
>>> dtl.run()
```

Inputs:

```
[Mandatory]
scheme_file: (a file name)
        The scheme file of the images to be processed using this LUT.
        flag: -schemefile %s, position: 2

[Optional]
acg: (a boolean)
        Compute a LUT for the ACG PDF.
        flag: -acg
args: (a string)
        Additional parameters to the command
        flag: %s
bingham: (a boolean)
        Compute a LUT for the Bingham PDF. This is the default.
        flag: -bingham
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
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
        flag: -frange %s, position: 1
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inversion: (an integer (int or long))
        Index of the inversion to use. The default is 1 (linear single
```

```
        tensor inversion).
        flag: -inversion %d
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 >= 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.
        flag: -lrange %s, position: 1
out_file: (a file name)
        flag: > %s, position: -1
samples: (an integer (int or long))
        The number of synthetic measurements to generate at each point in
        the LUT. The default is 2000.
        flag: -samples %d
snr: (a float)
        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.
        flag: -snr %f
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.
        flag: -step %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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.
        flag: -trace %G
watson: (a boolean)
        Compute a LUT for the Watson PDF.
        flag: -watson
```

Outputs:

```
dtLUT: (an existing file name)
        Lookup Table
```

52.7 DTMetric

Link to code

Wraps command **dtshape**

Computes tensor metric statistics based on the eigenvalues l1 >= l2 >= l3 typically obtained from ComputeEigensystem.

The full list of statistics is:

- <cl> = (l1 - l2) / l1 , a measure of linearity
- <cp> = (l2 - l3) / l1 , a measure of planarity
- <cs> = l3 / l1 , a measure of isotropy with: cl + cp + cs = 1
- <l1> = first eigenvalue
- <l2> = second eigenvalue

- <l3> = third eigenvalue
- <tr> = l1 + l2 + l3
- <md> = tr / 3
- <rd> = (l2 + l3) / 2
- <fa> = fractional anisotropy. (Basser et al, J Magn Reson B 1996)
- <ra> = relative anisotropy (Basser et al, J Magn Reson B 1996)
- <2dfa> = 2D FA of the two minor eigenvalues l2 and l3 i.e. sqrt(2 * [(l2 - <l>)^2 + (l3 - <l>)^2] / (l2^2 + l3^2)) with: <l> = (l2 + l3) / 2

52.7.1 Example

Compute the CP planar metric as float data type.

```
>>> import nipype.interfaces.camino as cam
>>> dtmetric = cam.DTMetric()
>>> dtmetric.inputs.eigen_data = 'dteig.Bdouble'
>>> dtmetric.inputs.metric = 'cp'
>>> dtmetric.inputs.outputdatatype = 'float'
>>> dtmetric.run()
```

Inputs:

```
[Mandatory]
eigen_data: (an existing file name)
        voxel-order data filename
        flag: -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".
        flag: -stat %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
data_header: (an existing file name)
        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.
        flag: -header %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputdatatype: ('double' or 'float' or 'long' or 'int' or 'short' or
         'char', nipype 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
        flag: -inputdatatype %s
outputdatatype: ('double' or 'float' or 'long' or 'int' or 'short' or
         'char', nipype 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
```

```
        flag: -outputdatatype %s
outputfile: (a file name)
        Output name. Output will be a .nii.gz file if data_header is
        provided andin voxel order with outputdatatype datatype (default:
        double) otherwise.
        flag: -outputfile %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
metric_stats: (an existing file name)
        Diffusion Tensor statistics of the chosen metric
```

52.8 ModelFit

Link to code

Wraps 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.

52.8.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        voxel-order data filename
        flag: -inputfile %s
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 'posposcyl nldt' or
            'posposcyl ldt_wtd' or 'posposcyl adc' or 'posposcyl ball_stick' or
            'posposcyl_eq dt' or 'posposcyl_eq restore' or 'posposcyl_eq algdt'
            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 algdt' 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 algdt' 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.
        flag: -model %s
scheme_file: (an existing file name)
        Camino scheme file (b values / vectors, see camino.fsl2scheme)
        flag: -schemefile %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
bgmask: (an existing file name)
        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.
        flag: -bgmask %s
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
        from the exit code which is -1.
        flag: -bgthresh %G
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.
        flag: -csfthresh %G
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
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.
```

```
        flag: -fixedbvalue %s
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.
        flag: -fixedmod %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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".
        flag: -inputdatatype %s
noisemap: (an existing file name)
        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.
        flag: -noisemap %s
out_file: (a file name)
        flag: > %s, position: -1
outlier: (an existing file name)
        Specifies the name of the file to contain the outlier map generated
        by the RESTORE algorithm.
        flag: -outliermap %s
outputfile: (a file name)
        Filename of the output file.
        flag: -outputfile %s
residualmap: (an existing file name)
        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.
        flag: -residualmap %s
sigma: (a float)
        Specifies the standard deviation of the noise in the data. Required
        by the RESTORE algorithm.
        flag: -sigma %G
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.
        flag: -tau %G
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
fitted_data: (an existing file name)
        output file of 4D volume in voxel order
```

52.9 PicoPDFs

Link to code
Wraps command **picopdfs**
Constructs a spherical PDF in each voxel for probabilistic tractography.

52.9.1 Example

```
>>> import nipype.interfaces.camino as cmon
>>> pdf = cmon.PicoPDFs()
>>> pdf.inputs.inputmodel = 'dt'
>>> pdf.inputs.luts = ['lut_file']
>>> pdf.inputs.in_file = 'voxel-order_data.Bfloat'
>>> pdf.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        voxel-order data filename
        flag: < %s, position: 1
luts: (a list of items which are an existing file name)
        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.
        flag: -luts %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
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.
        flag: -directmap
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputmodel: ('dt' or 'multitensor' or 'pds', nipype default value:
         dt)
        input model type
        flag: -inputmodel %s, position: 2
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.
        flag: -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.
        flag: -numpds %d
out_file: (a file name)
        flag: > %s, position: -1
pdf: ('bingham' or 'watson' or 'acg', nipype default value: bingham)
         Specifies the PDF to use. There are three choices:watson - The
        Watson distribution. This distribution is rotationally
        symmetric.bingham - The Bingham distributionn, which allows
        elliptical probability density contours.acg - The Angular Central
        Gaussian distribution, which also allows elliptical probability
        density contours
        flag: -pdf %s, position: 4
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
pdfs: (an existing file name)
        path/name of 4D volume in voxel order
```

52.10 Track

Link to code

Wraps command **track**

Performs tractography using one of the following models: dt', 'multitensor', 'pds', 'pico', 'bootstrap', 'ball-stick', 'bayesdirac'

52.10.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]

[Optional]
anisfile: (an existing file name)
        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.
        flag: -anisfile %s
anisthresh: (a float)
        Terminate fibres that enter a voxel with lower anisotropy than the
        threshold.
        flag: -anisthresh %f
args: (a string)
        Additional parameters to the command
        flag: %s
```

```
    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.
            flag: -curveinterval %f
            requires: curvethresh
    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.
            flag: -curvethresh %f
    data_dims: (a list of from 3 to 3 items which are an integer (int or
             long))
            data dimensions in voxels
            flag: -datadims %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    gzip: (a boolean)
            save the output image in gzip format
            flag: -gzip
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    in_file: (an existing file name)
            input data file
            flag: -inputfile %s, position: 1
    inputdatatype: ('float' or 'double')
            input file type
            flag: -inputdatatype %s
    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',
             nipype default value: dt)
            input model type
            flag: -inputmodel %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.
            flag: -interpolator %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.
        flag: -ipthresh %f
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.
        flag: -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.
        flag: -numpds %d
out_file: (a file name)
        output data file
        flag: -outputfile %s, position: -1
output_root: (a file name)
        root directory for output
        flag: -outputroot %s, position: -1
outputtracts: ('float' or 'double' or 'oogl')
        output tract file type
        flag: -outputtracts %s
seed_file: (an existing file name)
        seed file
        flag: -seedfile %s, position: 2
stepsize: (a float)
        Step size for EULER and RK4 tracking. The default is 1mm.
        flag: -stepsize %f
        requires: tracker
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tracker: ('fact' or 'euler' or 'rk4', nipype 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.
        flag: -tracker %s
voxel_dims: (a list of from 3 to 3 items which are a float)
        voxel dimensions in mm
        flag: -voxeldims %s
```

Outputs:

```
tracked: (an existing file name)
        output file containing reconstructed tracts
```

52.11 TrackBallStick

Link to code
Wraps command **track**
Performs streamline tractography using ball-stick fitted data

52.11.1 Example

```
>>> import nipype.interfaces.camino as cmon
>>> track = cmon.TrackBallStick()
>>> track.inputs.in_file = 'ballstickfit_data.Bfloat'
>>> track.inputs.seed_file = 'seed_mask.nii'
>>> track.run()
```

Inputs:

```
[Mandatory]

[Optional]
anisfile: (an existing file name)
        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.
        flag: -anisfile %s
anisthresh: (a float)
        Terminate fibres that enter a voxel with lower anisotropy than the
        threshold.
        flag: -anisthresh %f
args: (a string)
        Additional parameters to the command
        flag: %s
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.
        flag: -curveinterval %f
        requires: curvethresh
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.
        flag: -curvethresh %f
data_dims: (a list of from 3 to 3 items which are an integer (int or
         long))
        data dimensions in voxels
        flag: -datadims %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
gzip: (a boolean)
        save the output image in gzip format
        flag: -gzip
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

```
    in_file: (an existing file name)
            input data file
            flag: -inputfile %s, position: 1
    inputdatatype: ('float' or 'double')
            input file type
            flag: -inputdatatype %s
    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',
             nipype default value: dt)
            input model type
            flag: -inputmodel %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.
            flag: -interpolator %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.
            flag: -ipthresh %f
    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.
            flag: -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.
            flag: -numpds %d
    out_file: (a file name)
            output data file
            flag: -outputfile %s, position: -1
    output_root: (a file name)
            root directory for output
            flag: -outputroot %s, position: -1
    outputtracts: ('float' or 'double' or 'oogl')
            output tract file type
            flag: -outputtracts %s
    seed_file: (an existing file name)
```

```
        seed file
        flag: -seedfile %s, position: 2
stepsize: (a float)
        Step size for EULER and RK4 tracking. The default is 1mm.
        flag: -stepsize %f
        requires: tracker
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tracker: ('fact' or 'euler' or 'rk4', nipype 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.
        flag: -tracker %s
voxel_dims: (a list of from 3 to 3 items which are a float)
        voxel dimensions in mm
        flag: -voxeldims %s
```

Outputs:

```
tracked: (an existing file name)
        output file containing reconstructed tracts
```

52.12 TrackBayesDirac

Link to code

Wraps command **track**

Performs streamline tractography using a Bayesian tracking with Dirac priors

52.12.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
scheme_file: (an existing file name)
        The scheme file corresponding to the data being processed.
        flag: -schemefile %s

[Optional]
anisfile: (an existing file name)
        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.
        flag: -anisfile %s
anisthresh: (a float)
        Terminate fibres that enter a voxel with lower anisotropy than the
        threshold.
        flag: -anisthresh %f
args: (a string)
        Additional parameters to the command
        flag: %s
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.
        flag: -curveinterval %f
        requires: curvethresh
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.
        flag: -curvepriorg %G
curvepriork: (a float)
        Concentration parameter for the prior distribution on fibre
        orientations given the fibre orientation at the previous step.
        Larger values of k make curvature less likely.
        flag: -curvepriork %G
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.
        flag: -curvethresh %f
data_dims: (a list of from 3 to 3 items which are an integer (int or
         long))
        data dimensions in voxels
        flag: -datadims %s
datamodel: ('cylsymmdt' or 'ballstick')
        Model of the data for Bayesian tracking. The default model is
        "cylsymmdt", a diffusion tensor with cylindrical symmetry about e_1,
        ie L1 >= L_2 = L_3. The other model is "ballstick", the partial
        volume model (see ballstickfit).
        flag: -datamodel %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
extpriordatatype: ('float' or 'double')
        Datatype of the prior image. The default is "double".
        flag: -extpriordatatype %s
extpriorfile: (an existing file name)
        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.
        flag: -extpriorfile %s
gzip: (a boolean)
        save the output image in gzip format
        flag: -gzip
ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_file: (an existing file name)
        input data file
        flag: -inputfile %s, position: 1
inputdatatype: ('float' or 'double')
        input file type
        flag: -inputdatatype %s
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',
         nipype default value: dt)
        input model type
        flag: -inputmodel %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.
        flag: -interpolator %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.
        flag: -ipthresh %f
iterations: (an integer (int or long))
        Number of streamlines to generate at each seed point. The default is
        5000.
        flag: -iterations %d
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.
        flag: -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.
        flag: -numpds %d
out_file: (a file name)
        output data file
        flag: -outputfile %s, position: -1
output_root: (a file name)
```

```
        root directory for output
        flag: -outputroot %s, position: -1
outputtracts: ('float' or 'double' or 'oogl')
        output tract file type
        flag: -outputtracts %s
pdf: ('bingham' or 'watson' or 'acg')
        Specifies the model for PICo priors (not the curvature priors). The
        default is "bingham".
        flag: -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.
        flag: -pointset %s
seed_file: (an existing file name)
        seed file
        flag: -seedfile %s, position: 2
stepsize: (a float)
        Step size for EULER and RK4 tracking. The default is 1mm.
        flag: -stepsize %f
        requires: tracker
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tracker: ('fact' or 'euler' or 'rk4', nipype 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.
        flag: -tracker %s
voxel_dims: (a list of from 3 to 3 items which are a float)
        voxel dimensions in mm
        flag: -voxeldims %s
```

Outputs:

```
tracked: (an existing file name)
        output file containing reconstructed tracts
```

52.13 TrackBedpostxDeter

Link to code

Wraps 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.

52.13.1 Example

```
>>> import nipype.interfaces.camino as cam
>>> track = cam.TrackBedpostxDeter()
>>> track.inputs.bedpostxdir = 'bedpostxout'
>>> track.inputs.seed_file = 'seed_mask.nii'
>>> track.run()
```

Inputs:

```
[Mandatory]
bedpostxdir: (an existing directory name)
        Directory containing bedpostx output
        flag: -bedpostxdir %s

[Optional]
anisfile: (an existing file name)
        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.
        flag: -anisfile %s
anisthresh: (a float)
        Terminate fibres that enter a voxel with lower anisotropy than the
        threshold.
        flag: -anisthresh %f
args: (a string)
        Additional parameters to the command
        flag: %s
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.
        flag: -curveinterval %f
        requires: curvethresh
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.
        flag: -curvethresh %f
data_dims: (a list of from 3 to 3 items which are an integer (int or
         long))
        data dimensions in voxels
        flag: -datadims %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
gzip: (a boolean)
        save the output image in gzip format
        flag: -gzip
ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_file: (an existing file name)
        input data file
        flag: -inputfile %s, position: 1
inputdatatype: ('float' or 'double')
        input file type
        flag: -inputdatatype %s
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',
         nipype default value: dt)
        input model type
        flag: -inputmodel %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.
        flag: -interpolator %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.
        flag: -ipthresh %f
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.
        flag: -maxcomponents %d
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.
        flag: -bedpostxminf %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.
        flag: -numpds %d
out_file: (a file name)
        output data file
        flag: -outputfile %s, position: -1
output_root: (a file name)
```

```
        root directory for output
        flag: -outputroot %s, position: -1
outputtracts: ('float' or 'double' or 'oogl')
        output tract file type
        flag: -outputtracts %s
seed_file: (an existing file name)
        seed file
        flag: -seedfile %s, position: 2
stepsize: (a float)
        Step size for EULER and RK4 tracking. The default is 1mm.
        flag: -stepsize %f
        requires: tracker
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tracker: ('fact' or 'euler' or 'rk4', nipype 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.
        flag: -tracker %s
voxel_dims: (a list of from 3 to 3 items which are a float)
        voxel dimensions in mm
        flag: -voxeldims %s
```

Outputs:

```
tracked: (an existing file name)
        output file containing reconstructed tracts
```

52.14 TrackBedpostxProba

Link to code

Wraps 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 Xth 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.

52.14.1 Example

```
>>> import nipype.interfaces.camino as cam
>>> track = cam.TrackBedpostxProba()
>>> track.inputs.bedpostxdir = 'bedpostxout'
>>> track.inputs.seed_file = 'seed_mask.nii'
>>> track.inputs.iterations = 100
>>> track.run()
```

Inputs:

```
[Mandatory]
bedpostxdir: (an existing directory name)
        Directory containing bedpostx output
        flag: -bedpostxdir %s

[Optional]
anisfile: (an existing file name)
        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.
        flag: -anisfile %s
anisthresh: (a float)
        Terminate fibres that enter a voxel with lower anisotropy than the
        threshold.
        flag: -anisthresh %f
args: (a string)
        Additional parameters to the command
        flag: %s
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.
        flag: -curveinterval %f
        requires: curvethresh
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.
        flag: -curvethresh %f
data_dims: (a list of from 3 to 3 items which are an integer (int or
         long))
        data dimensions in voxels
        flag: -datadims %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
gzip: (a boolean)
        save the output image in gzip format
        flag: -gzip
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_file: (an existing file name)
        input data file
        flag: -inputfile %s, position: 1
```

```
    inputdatatype: ('float' or 'double')
            input file type
            flag: -inputdatatype %s
    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',
             nipype default value: dt)
            input model type
            flag: -inputmodel %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.
            flag: -interpolator %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.
            flag: -ipthresh %f
    iterations: (an integer (int or long))
            Number of streamlines to generate at each seed point. The default is
            1.
            flag: -iterations %d
    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.
            flag: -maxcomponents %d
    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.
            flag: -bedpostxminf %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.
            flag: -numpds %d
    out_file: (a file name)
            output data file
            flag: -outputfile %s, position: -1
    output_root: (a file name)
            root directory for output
```

```
        flag: -outputroot %s, position: -1
outputtracts: ('float' or 'double' or 'oogl')
        output tract file type
        flag: -outputtracts %s
seed_file: (an existing file name)
        seed file
        flag: -seedfile %s, position: 2
stepsize: (a float)
        Step size for EULER and RK4 tracking. The default is 1mm.
        flag: -stepsize %f
        requires: tracker
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tracker: ('fact' or 'euler' or 'rk4', nipype 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.
        flag: -tracker %s
voxel_dims: (a list of from 3 to 3 items which are a float)
        voxel dimensions in mm
        flag: -voxeldims %s
```

Outputs:

```
tracked: (an existing file name)
        output file containing reconstructed tracts
```

52.15 TrackBootstrap

Link to code

Wraps command **track**

Performs bootstrap streamline tractography using mulitple scans of the same subject

52.15.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
bsdatafiles: (a list of items which are an existing file name)
        Specifies files containing raw data for repetition bootstrapping.
```

```
        Use -inputfile for wild bootstrap data.
        flag: -bsdatafile %s
scheme_file: (an existing file name)
        The scheme file corresponding to the data being processed.
        flag: -schemefile %s

[Optional]
anisfile: (an existing file name)
        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.
        flag: -anisfile %s
anisthresh: (a float)
        Terminate fibres that enter a voxel with lower anisotropy than the
        threshold.
        flag: -anisthresh %f
args: (a string)
        Additional parameters to the command
        flag: %s
bgmask: (an existing file name)
        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.
        flag: -bgmask %s
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.
        flag: -curveinterval %f
        requires: curvethresh
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.
        flag: -curvethresh %f
data_dims: (a list of from 3 to 3 items which are an integer (int or
         long))
        data dimensions in voxels
        flag: -datadims %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
gzip: (a boolean)
        save the output image in gzip format
        flag: -gzip
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_file: (an existing file name)
        input data file
        flag: -inputfile %s, position: 1
inputdatatype: ('float' or 'double')
        input file type
        flag: -inputdatatype %s
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',
            nipype default value: dt)
        input model type
        flag: -inputmodel %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.
        flag: -interpolator %s
inversion: (an integer (int or long))
        Tensor reconstruction algorithm for repetition bootstrapping.
        Default is 1 (linear reconstruction, single tensor).
        flag: -inversion %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.
        flag: -ipthresh %f
iterations: (an integer (int or long))
        Number of streamlines to generate at each seed point.
        flag: -iterations %d
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.
        flag: -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.
        flag: -numpds %d
out_file: (a file name)
        output data file
        flag: -outputfile %s, position: -1
output_root: (a file name)
        root directory for output
        flag: -outputroot %s, position: -1
outputtracts: ('float' or 'double' or 'oogl')
        output tract file type
        flag: -outputtracts %s
seed_file: (an existing file name)
```

```
        seed file
        flag: -seedfile %s, position: 2
stepsize: (a float)
        Step size for EULER and RK4 tracking. The default is 1mm.
        flag: -stepsize %f
        requires: tracker
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tracker: ('fact' or 'euler' or 'rk4', nipype 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.
        flag: -tracker %s
voxel_dims: (a list of from 3 to 3 items which are a float)
        voxel dimensions in mm
        flag: -voxeldims %s
```

Outputs:

```
tracked: (an existing file name)
        output file containing reconstructed tracts
```

52.16 TrackDT

Link to code

Wraps command **track**

Performs streamline tractography using tensor data

52.16.1 Example

```
>>> import nipype.interfaces.camino as cmon
>>> track = cmon.TrackDT()
>>> track.inputs.in_file = 'tensor_fitted_data.Bdouble'
>>> track.inputs.seed_file = 'seed_mask.nii'
>>> track.run()
```

Inputs:

```
[Mandatory]

[Optional]
anisfile: (an existing file name)
        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.
        flag: -anisfile %s
anisthresh: (a float)
        Terminate fibres that enter a voxel with lower anisotropy than the
```

```
        threshold.
        flag: -anisthresh %f
args: (a string)
        Additional parameters to the command
        flag: %s
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.
        flag: -curveinterval %f
        requires: curvethresh
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.
        flag: -curvethresh %f
data_dims: (a list of from 3 to 3 items which are an integer (int or
         long))
        data dimensions in voxels
        flag: -datadims %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
gzip: (a boolean)
        save the output image in gzip format
        flag: -gzip
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_file: (an existing file name)
        input data file
        flag: -inputfile %s, position: 1
inputdatatype: ('float' or 'double')
        input file type
        flag: -inputdatatype %s
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',
         nipype default value: dt)
        input model type
        flag: -inputmodel %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.
        flag: -interpolator %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.
            flag: -ipthresh %f
    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.
            flag: -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.
            flag: -numpds %d
    out_file: (a file name)
            output data file
            flag: -outputfile %s, position: -1
    output_root: (a file name)
            root directory for output
            flag: -outputroot %s, position: -1
    outputtracts: ('float' or 'double' or 'oogl')
            output tract file type
            flag: -outputtracts %s
    seed_file: (an existing file name)
            seed file
            flag: -seedfile %s, position: 2
    stepsize: (a float)
            Step size for EULER and RK4 tracking. The default is 1mm.
            flag: -stepsize %f
            requires: tracker
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    tracker: ('fact' or 'euler' or 'rk4', nipype 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.
            flag: -tracker %s
    voxel_dims: (a list of from 3 to 3 items which are a float)
            voxel dimensions in mm
            flag: -voxeldims %s
```

Outputs:

```
tracked: (an existing file name)
        output file containing reconstructed tracts
```

52.17 TrackPICo

Link to code
Wraps command **track**
Performs streamline tractography using the Probabilistic Index of Connectivity (PICo) algorithm

52.17.1 Example

```
>>> import nipype.interfaces.camino as cmon
>>> track = cmon.TrackPICo()
>>> track.inputs.in_file = 'pdfs.Bfloat'
>>> track.inputs.seed_file = 'seed_mask.nii'
>>> track.run()
```

Inputs:

```
[Mandatory]

[Optional]
anisfile: (an existing file name)
        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.
        flag: -anisfile %s
anisthresh: (a float)
        Terminate fibres that enter a voxel with lower anisotropy than the
        threshold.
        flag: -anisthresh %f
args: (a string)
        Additional parameters to the command
        flag: %s
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.
        flag: -curveinterval %f
        requires: curvethresh
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.
        flag: -curvethresh %f
data_dims: (a list of from 3 to 3 items which are an integer (int or
         long))
        data dimensions in voxels
        flag: -datadims %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
```

```
    gzip: (a boolean)
            save the output image in gzip format
            flag: -gzip
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    in_file: (an existing file name)
            input data file
            flag: -inputfile %s, position: 1
    inputdatatype: ('float' or 'double')
            input file type
            flag: -inputdatatype %s
    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',
             nipype default value: dt)
            input model type
            flag: -inputmodel %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.
            flag: -interpolator %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.
            flag: -ipthresh %f
    iterations: (an integer (int or long))
            Number of streamlines to generate at each seed point. The default is
            5000.
            flag: -iterations %d
    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.
            flag: -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.
            flag: -numpds %d
```

```
    out_file: (a file name)
            output data file
            flag: -outputfile %s, position: -1
    output_root: (a file name)
            root directory for output
            flag: -outputroot %s, position: -1
    outputtracts: ('float' or 'double' or 'oogl')
            output tract file type
            flag: -outputtracts %s
    pdf: ('bingham' or 'watson' or 'acg')
            Specifies the model for PICo parameters. The default is "bingham.
            flag: -pdf %s
    seed_file: (an existing file name)
            seed file
            flag: -seedfile %s, position: 2
    stepsize: (a float)
            Step size for EULER and RK4 tracking. The default is 1mm.
            flag: -stepsize %f
            requires: tracker
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    tracker: ('fact' or 'euler' or 'rk4', nipype 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.
            flag: -tracker %s
    voxel_dims: (a list of from 3 to 3 items which are a float)
            voxel dimensions in mm
            flag: -voxeldims %s
```

Outputs:

```
    tracked: (an existing file name)
            output file containing reconstructed tracts
```

CHAPTER 53

interfaces.camino.odf

53.1 LinRecon

Link to code

Wraps 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 ouput in every voxel is actually:

```
[exit code, ln(S(0)), p1, ..., pR]
```

where p1, ..., pR 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.

53.1.1 Example

First run QBallMX and create a linear transform matrix using Spherical Harmonics (sh).

```
>>> import nipype.interfaces.camino as cam
>>> qballmx = cam.QBallMX()
>>> qballmx.inputs.scheme_file = 'A.scheme'
>>> qballmx.inputs.basistype = 'sh'
>>> qballmx.inputs.order = 4
>>> qballmx.run()
```

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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        voxel-order data filename
        flag: %s, position: 1
qball_mat: (an existing file name)
        Linear transformation matrix.
```

```
        flag: %s, position: 3
scheme_file: (an existing file name)
        Specifies the scheme file for the diffusion MRI data
        flag: %s, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
bgmask: (an existing file name)
        background mask
        flag: -bgmask %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
log: (a boolean)
        Transform the log measurements rather than the measurements
        themselves
        flag: -log
normalize: (a boolean)
        Normalize the measurements and discard the zero measurements before
        the linear transform.
        flag: -normalize
out_file: (a file name)
        flag: > %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
recon_data: (an existing file name)
        Transformed data
```

53.2 MESD

Link to code

Wraps 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)), lambda_0, lambda_1, ..., lambda_N }

The exitcode contains the results of three tests. The first test thresholds the maximum relative error between the numerical integrals computed at con- vergence 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 <X> = 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 <X> here specifies the number of lambda parameters. To obtain speed-up, set <X> < N; complexity become O(<X>^2) rather than O(N^2). Note that <X> 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 <X> is low -fastmesd is worth using to get even more speed-up.
  The choice of <X> is a parameter of the technique. Too low and you lose angular resoloution; too high and you see no computational benefit and may even suffer from overfitting. Empirically, we have found that <X>=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.

53.2.1 Example

Run MESD on every voxel of the data file SubjectA.Bfloat using the PASMRI kernel.

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        voxel-order data filename
        flag: -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
        flag: -filter %s, position: 2
inverter_param: (a float)
        Parameter associated with the inverter. Cf. inverter description
        formore information.
        flag: %f, position: 3
scheme_file: (an existing file name)
        Specifies the scheme file for the diffusion MRI data
```

```
        flag: -schemefile %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
bgmask: (an existing file name)
        background mask
        flag: -bgmask %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fastmesd: (a boolean)
        Turns off numerical integration checks and fixes the integration
        point set size at that ofthe index specified by -basepointset..
        flag: -fastmesd
        requires: mepointset
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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".
        flag: -inputdatatype %s
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".
        flag: -mepointset %d
out_file: (a file name)
        flag: > %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
mesd_data: (an existing file name)
        MESD data
```

53.3 QBallMX

Link to code

Wraps command **qballmx**

Generates a reconstruction matrix for Q-Ball. Used in LinRecon with the same scheme file to reconstruct data.

53.3.1 Example 1

To create a linear transform matrix using Spherical Harmonics (sh).

```
>>> import nipype.interfaces.camino as cam
>>> qballmx = cam.QBallMX()
>>> qballmx.inputs.scheme_file = 'A.scheme'
```

```
>>> qballmx.inputs.basistype = 'sh'
>>> qballmx.inputs.order = 6
>>> qballmx.run()
```

53.3.2 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 nipype.interfaces.camino as cam
>>> qballmx = cam.QBallMX()
>>> qballmx.inputs.scheme_file = 'A.scheme'
>>> qballmx.run()
```

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()
```

Inputs:

```
[Mandatory]
scheme_file: (an existing file name)
        Specifies the scheme file for the diffusion MRI data
        flag: -schemefile %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
basistype: ('rbf' or 'sh', nipype default value: rbf)
        Basis function type. "rbf" to use radial basis functions "sh" to use
        spherical harmonics
        flag: -basistype %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
order: (an integer (int or long))
        Specific to sh. Maximum order of the spherical harmonic series.
        Default is 4.
        flag: -order %d
out_file: (a file name)
        flag: > %s, position: -1
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.
        flag: -rbfpointset %d
rbfsigma: (a float)
        Specific to rbf. Sets the width of the interpolating basis
        functions. The default value is 0.2618 (15 degrees).
```

```
        flag: -rbfsigma %f
smoothingsigma: (a float)
        Specific to rbf. Sets the width of the smoothing basis functions.
        The default value is 0.1309 (7.5 degrees).
        flag: -smoothingsigma %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
qmat: (an existing file name)
        Q-Ball reconstruction matrix
```

53.4 SFPeaks

Link to code

Wraps 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 con- sistency with a second set of starting points, but skips the optimization step. To speed up execution, you can turn off the con- sistency 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.

53.4.1 Example

First run QBallMX and create a linear transform matrix using Spherical Harmonics (sh).

```
>>> import nipype.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
>>> sf_peaks.inputs.searchradius = 1.0
>>> sf_peaks.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Voxel-order data of spherical functions
        flag: -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.
        flag: -inputmodel %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
density: (an integer (int or long))
        The number of randomly rotated icosahedra to use in constructing the
        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.
        flag: -density %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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.
        flag: -mepointset %d
noconsistencycheck: (a boolean)
        Turns off the consistency check. The output shows all consistencies
        as true.
        flag: -noconsistencycheck
numpds: (an integer (int or long))
        The largest number of peak directions to output in each voxel.
        flag: -numpds %d
order: (an integer (int or long))
        Specific to sh. Maximum order of the spherical harmonic series.
        flag: -order %d
out_file: (a file name)
        flag: > %s, position: -1
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).
        flag: -pdthresh %f
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.
        flag: -pointset %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.
        flag: -rbfpointset %d
scheme_file: (an existing file name)
        Specific to maxent. Specifies the scheme file.
        flag: %s
searchradius: (a float)
        The search radius in the peak finding algorithm. The default is 0.4
        (cf. "density")
        flag: -searchradius %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.
        flag: -stdsfrommean %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
peaks: (an existing file name)
        Peaks of the spherical functions.
```

CHAPTER 54

interfaces.camino.utils

54.1 ImageStats

Link to code
Wraps 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.

54.1.1 Examples

```
>>> import nipype.interfaces.camino as cam
>>> imstats = cam.ImageStats()
>>> imstats.inputs.in_files = ['im1.nii','im2.nii','im3.nii']
>>> imstats.inputs.stat = 'max'
>>> imstats.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        List of images to process. They must be in the same space and have
        the same dimensions.
        flag: -images %s, position: -1
output_root: (a file name)
        Filename root prepended onto the names of the output files. The
        extension will be determined from the input.
        flag: -outputroot %s
stat: ('min' or 'max' or 'mean' or 'median' or 'sum' or 'std' or
         'var')
        The statistic to compute.
        flag: -stat %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_type: ('float' or 'char' or 'short' or 'int' or 'long' or
         'double', nipype default value: float)
```

```
        A Camino data type string, default is "float". Type must be signed.
        flag: -outputdatatype %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        Path of the file computed with the statistic chosen
```

CHAPTER 55

interfaces.camino2trackvis.convert

55.1 Camino2Trackvis

Link to code
Wraps command **camino_to_trackvis**
Wraps camino_to_trackvis from Camino-Trackvis
Convert files from camino .Bfloat format to trackvis .trk format.

55.1.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
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.
        flag: -d %s, position: 4
in_file: (an existing file name)
        The input .Bfloat (camino) file.
        flag: -i %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.
        flag: -x %s, position: 5
voxel_order: (a file name)
        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.
        flag: --voxel-order %s, position: 6

[Optional]
args: (a string)
```

```
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
min_length: (a float)
        The minimum length of tracts to output
        flag: -l %d, position: 3
nifti_file: (an existing file name)
        Read coordinate system from a NIfTI file.
        flag: --nifti %s, position: 7
out_file: (a file name)
        The filename to which to write the .trk (trackvis) file.
        flag: -o %s, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
trackvis: (an existing file name)
        The filename to which to write the .trk (trackvis) file.
```

55.2 Trackvis2Camino

Link to code

Wraps command **trackvis_to_camino**

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        The input .trk (trackvis) file.
        flag: -i %s, position: 1

[Optional]
append_file: (an existing file name)
        A file to which the append the .Bfloat data.
        flag: -a %s, position: 2
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        The filename to which to write the .Bfloat (camino).
        flag: -o %s, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
```

```
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    camino: (an existing file name)
            The filename to which to write the .Bfloat (camino).
```

CHAPTER 56

interfaces.cmtk.cmtk

56.1 CreateMatrix

Link to code
Performs connectivity mapping and outputs the result as a NetworkX graph and a Matlab matrix

56.1.1 Example

```
>>> import nipype.interfaces.cmtk as cmtk
>>> conmap = cmtk.CreateMatrix()
>>> conmap.roi_file = 'fsLUT_aparc+aseg.nii'
>>> conmap.tract_file = 'fibers.trk'
>>> conmap.run()
```

Inputs:

```
[Mandatory]
resolution_network_file: (an existing file name)
        Parcellation files from Connectome Mapping Toolkit
roi_file: (an existing file name)
        Freesurfer aparc+aseg file
tract_file: (an existing file name)
        Trackvis tract file

[Optional]
count_region_intersections: (a boolean, nipype default value: False)
        Counts all of the fiber-region traversals in the connectivity matrix
        (requires significantly more computational time)
out_endpoint_array_name: (a file name)
        Name for the generated endpoint arrays
out_fiber_length_std_matrix_mat_file: (a file name)
        Matlab matrix describing the deviation in fiber lengths connecting
        each node.
out_intersection_matrix_mat_file: (a file name)
        Matlab connectivity matrix if all region/fiber intersections are
        counted.
out_matrix_file: (a file name)
        NetworkX graph describing the connectivity
out_matrix_mat_file: (a file name, nipype default value: cmatrix.mat)
        Matlab matrix describing the connectivity
out_mean_fiber_length_matrix_mat_file: (a file name)
        Matlab matrix describing the mean fiber lengths between each node.
out_median_fiber_length_matrix_mat_file: (a file name)
        Matlab matrix describing the mean fiber lengths between each node.
```

Outputs:

```
    endpoint_file: (an existing file name)
            Saved Numpy array with the endpoints of each fiber
    endpoint_file_mm: (an existing file name)
            Saved Numpy array with the endpoints of each fiber (in millimeters)
    fiber_label_file: (an existing file name)
            Saved Numpy array with the labels for each fiber
    fiber_labels_noorphans: (an existing file name)
            Saved Numpy array with the labels for each non-orphan fiber
    fiber_length_file: (an existing file name)
            Saved Numpy array with the lengths of each fiber
    fiber_length_std_matrix_mat_file: (an existing file name)
            Matlab matrix describing the deviation in fiber lengths connecting
            each node.
    filtered_tractographies: (a list of items which are an existing file
             name)
    filtered_tractography: (an existing file name)
            TrackVis file containing only those fibers originate in one and
            terminate in another region
    filtered_tractography_by_intersections: (an existing file name)
            TrackVis file containing all fibers which connect two regions
    intersection_matrix_file: (an existing file name)
            NetworkX graph describing the connectivity
    intersection_matrix_mat_file: (an existing file name)
            Matlab matrix describing the mean fiber lengths between each node.
    matlab_matrix_files: (a list of items which are an existing file
             name)
    matrix_file: (an existing file name)
            NetworkX graph describing the connectivity
    matrix_files: (a list of items which are an existing file name)
    matrix_mat_file: (an existing file name)
            Matlab matrix describing the connectivity
    mean_fiber_length_matrix_mat_file: (an existing file name)
            Matlab matrix describing the mean fiber lengths between each node.
    median_fiber_length_matrix_mat_file: (an existing file name)
            Matlab matrix describing the median fiber lengths between each node.
    stats_file: (an existing file name)
            Saved Matlab .mat file with the number of fibers saved at each stage
```

56.2 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.

56.2.1 Example

```
    >>> import nipype.interfaces.cmtk as cmtk
    >>> mknode = cmtk.CreateNodes()
    >>> mknode.inputs.roi_file = 'ROI_scale500.nii.gz'
    >>> mknode.run()
```

Inputs:

```
    [Mandatory]
    resolution_network_file: (an existing file name)
            Parcellation file from Connectome Mapping Toolkit
    roi_file: (an existing file name)
```

```
        Region of interest file

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_filename: (a file name, nipype default value: nodenetwork.pck)
        Output gpickled network with the nodes defined.
```

Outputs:

```
node_network: (a file name)
        Output gpickled network with the nodes defined.
```

56.3 ROIGen

Link to code

Generates a ROI file for connectivity mapping and a dictionary file containing relevant node information

56.3.1 Example

```
>>> import nipype.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()
```

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)
>>> labelDict
```

Inputs:

```
[Mandatory]
aparc_aseg_file: (an existing file name)
        Freesurfer aparc+aseg file

[Optional]
LUT_file: (an existing file name)
        Custom lookup table (cf. FreeSurferColorLUT.txt)
        mutually_exclusive: use_freesurfer_LUT
freesurfer_dir: (a directory name)
        Freesurfer main directory
        requires: use_freesurfer_LUT
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_dict_file: (a file name)
        Label dictionary saved in Pickle format
out_roi_file: (a file name)
        Region of Interest file for connectivity mapping
use_freesurfer_LUT: (a boolean)
        Boolean value; Set to True to use default Freesurfer LUT, False for
        custom LUT
        mutually_exclusive: LUT_file
```

Outputs:

```
dict_file: (a file name)
        Label dictionary saved in Pickle format
roi_file: (a file name)
        Region of Interest file for connectivity mapping
```

56.4 cmat()

Link to code
Create the connection matrix for each resolution using fibers and ROIs.

56.5 create_allpoints_cmat()

Link to code
Create the intersection arrays for each fiber

56.6 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

56.7 create_nodes()

Link to code

56.8 get_connectivity_matrix()

Link to code

56.9 get_rois_crossed()

Link to code

56.10 length()

Link to code
Euclidean length of track line

56.10.1 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.

56.10.2 Returns

L [scalar or array shape (N-1,)] scalar in case of *along* == False, giving total length, array if *along* == True, giving cumulative lengths.

56.10.3 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])
```

56.11 save_fibers()

Link to code

Stores a new trackvis file fname using only given indices

CHAPTER 57

interfaces.cmtk.convert

57.1 CFFConverter

Link to code
Creates a Connectome File Format (CFF) file from input networks, surfaces, volumes, tracts, etcetera....

57.1.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]

[Optional]
creator: (a string)
        Creator
data_files: (a list of items which are an existing file name)
        list of external data files (i.e. Numpy, HD5, XML)
description: (a string, nipype default value: Created with the Nipype
         CFF converter)
        Description
email: (a string)
        Email address
gifti_labels: (a list of items which are an existing file name)
        list of GIFTI labels
gifti_surfaces: (a list of items which are an existing file name)
        list of GIFTI surfaces
gpickled_networks: (a list of items which are an existing file name)
        list of gpickled Networkx graphs
graphml_networks: (a list of items which are an existing file name)
        list of graphML networks
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
license: (a string)
        License
nifti_volumes: (a list of items which are an existing file name)
        list of NIFTI volumes
```

```
out_file: (a file name, nipype default value: connectome.cff)
        Output connectome file
publisher: (a string)
        Publisher
references: (a string)
        References
relation: (a string)
        Relation
rights: (a string)
        Rights
script_files: (a list of items which are an existing file name)
        list of script files to include
species: (a string, nipype default value: Homo sapiens)
        Species
timeseries_files: (a list of items which are an existing file name)
        list of HDF5 timeseries files
title: (a string)
        Connectome Title
tract_files: (a list of items which are an existing file name)
        list of Trackvis fiber files
```

Outputs:

```
connectome_file: (an existing file name)
        Output connectome file
```

57.2 MergeCNetworks

Link to code

Merges networks from multiple CFF files into one new CFF file.

57.2.1 Example

```
>>> import nipype.interfaces.cmtk as cmtk
>>> mrg = cmtk.MergeCNetworks()
>>> mrg.inputs.in_files = ['subj1.cff','subj2.cff']
>>> mrg.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        List of CFF files to extract networks from

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name, nipype default value:
         merged_network_connectome.cff)
        Output CFF file with all the networks added
```

Outputs:

```
connectome_file: (an existing file name)
        Output CFF file with all the networks added
```

CHAPTER 58

interfaces.cmtk.nbs

58.1 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

58.1.1 Example

```
>>> import nipype.interfaces.cmtk as cmtk
>>> nbs = cmtk.NetworkBasedStatistic()
>>> nbs.inputs.in_group1 = ['subj1.pck', 'subj2.pck']
>>> nbs.inputs.in_group2 = ['pat1.pck', 'pat2.pck']
>>> nbs.run()
```

Inputs:

```
[Mandatory]
in_group1: (a list of items which are an existing file name)
        Networks for the first group of subjects
in_group2: (a list of items which are an existing file name)
        Networks for the second group of subjects

[Optional]
edge_key: (a string, nipype 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.
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
node_position_network: (a file name)
        An optional network used to position the nodes for the output
        networks
number_of_permutations: (an integer (int or long), nipype default
         value: 1000)
        Number of permutations to perform
out_nbs_network: (a file name)
        Output network with edges identified by the NBS
out_nbs_pval_network: (a file name)
        Output network with p-values to weight the edges identified by the
        NBS
t_tail: ('left' or 'right' or 'both', nipype default value: left)
        Can be one of "left", "right", or "both"
```

```
    threshold: (a float, nipype default value: 3)
            T-statistic threshold
```

Outputs:

```
    nbs_network: (an existing file name)
            Output network with edges identified by the NBS
    nbs_pval_network: (an existing file name)
            Output network with p-values to weight the edges identified by the
            NBS
    network_files: (a list of items which are an existing file name)
            Output network with edges identified by the NBS
```

58.2 ntwks_to_matrices()

Link to code

CHAPTER 59

interfaces.cmtk.nx

59.1 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.

59.1.1 Example

```
>>> import nipype.interfaces.cmtk as cmtk
>>> avg = cmtk.AverageNetworks()
>>> avg.inputs.in_files = ['subj1.pck', 'subj2.pck']
>>> avg.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        Networks for a group of subjects

[Optional]
group_id: (a string, nipype default value: group1)
        ID for group
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_gexf_groupavg: (a file name)
        Average network saved as a .gexf file
out_gpickled_groupavg: (a file name)
        Average network saved as a NetworkX .pck
resolution_network_file: (an existing file name)
        Parcellation files from Connectome Mapping Toolkit. This is not
        necessary, but if included, the interface will output the
        statistical maps as networkx graphs.
```

Outputs:

```
gexf_groupavg: (a file name)
        Average network saved as a .gexf file
gpickled_groupavg: (a file name)
        Average network saved as a NetworkX .pck
matlab_groupavgs: (a list of items which are a file name)
```

59.2 NetworkXMetrics

Link to code
Calculates and outputs NetworkX-based measures for an input network

59.2.1 Example

```
>>> import nipype.interfaces.cmtk as cmtk
>>> nxmetrics = cmtk.NetworkXMetrics()
>>> nxmetrics.inputs.in_file = 'subj1.pck'
>>> nxmetrics.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Input network

[Optional]
compute_clique_related_measures: (a boolean, nipype default value:
         False)
        Computing clique-related measures (e.g. node clique number) can be
        very time consuming
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_edge_metrics_matlab: (a file name)
        Output edge metrics in MATLAB .mat format
out_global_metrics_matlab: (a file name)
        Output node metrics in MATLAB .mat format
out_k_core: (a file name, nipype default value: k_core)
        Computed k-core network stored as a NetworkX pickle.
out_k_crust: (a file name, nipype default value: k_crust)
        Computed k-crust network stored as a NetworkX pickle.
out_k_shell: (a file name, nipype default value: k_shell)
        Computed k-shell network stored as a NetworkX pickle.
out_node_metrics_matlab: (a file name)
        Output node metrics in MATLAB .mat format
out_pickled_extra_measures: (a file name, nipype default value:
         extra_measures)
        Network measures for group 1 that return dictionaries stored as a
        Pickle.
treat_as_weighted_graph: (a boolean, nipype default value: True)
        Some network metrics can be calculated while considering only a
        binarized version of the graph
```

Outputs:

```
edge_measure_networks: (a list of items which are a file name)
edge_measures_matlab: (a file name)
        Output edge metrics in MATLAB .mat format
global_measures_matlab: (a file name)
        Output global metrics in MATLAB .mat format
gpickled_network_files: (a list of items which are a file name)
k_core: (a file name)
        Computed k-core network stored as a NetworkX pickle.
k_crust: (a file name)
        Computed k-crust network stored as a NetworkX pickle.
k_networks: (a list of items which are a file name)
```

```
    k_shell: (a file name)
            Computed k-shell network stored as a NetworkX pickle.
    matlab_dict_measures: (a list of items which are a file name)
    matlab_matrix_files: (a list of items which are a file name)
    node_measure_networks: (a list of items which are a file name)
    node_measures_matlab: (a file name)
            Output node metrics in MATLAB .mat format
    pickled_extra_measures: (a file name)
            Network measures for the group that return dictionaries, stored as a
            Pickle.
```

59.3 add_dicts_by_key()

Link to code
Combines two dictionaries and adds the values for those keys that are shared

59.4 add_edge_data()

Link to code

59.5 add_node_data()

Link to code

59.6 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

59.7 compute_dict_measures()

Link to code
Returns a dictionary

59.8 compute_edge_measures()

Link to code
These return edge-based measures

59.9 compute_network_measures()

Link to code

59.10 compute_node_measures()

Link to code
These return node-based measures

59.11 compute_singlevalued_measures()

Link to code
Returns a single value per network

59.12 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

59.13 read_unknown_ntwk()

Link to code

59.14 remove_all_edges()

Link to code

CHAPTER 60

interfaces.cmtk.parcellation

60.1 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').

60.1.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
subject_id: (a string)
        Subject ID

[Optional]
dilation: (a boolean, nipype default value: False)
        Dilate cortical parcels? Useful for fMRI connectivity
freesurfer_dir: (an existing directory name)
        Freesurfer main directory
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_roi_file: (a file name)
        Region of Interest file for connectivity mapping
parcellation_name: ('scale33' or 'scale60' or 'scale125' or
         'scale250' or 'scale500', nipype default value: scale500)
subjects_dir: (an existing directory name)
        Freesurfer subjects directory
```

Outputs:

```
aseg_file: (an existing file name)
        Automated segmentation file converted from Freesurfer "subjects"
        directory
cc_unknown_file: (an existing file name)
```

```
        Image file with regions labelled as unknown cortical structures
dilated_roi_file_in_structural_space: (a file name)
        dilated ROI image resliced to the dimensions of the original
        structural image
ribbon_file: (an existing file name)
        Image file detailing the cortical ribbon
roi_file: (an existing file name)
        Region of Interest file for connectivity mapping
roi_file_in_structural_space: (an existing file name)
        ROI image resliced to the dimensions of the original structural
        image
roiv_file: (a file name)
        Region of Interest file for fMRI connectivity mapping
white_matter_mask_file: (an existing file name)
        White matter mask file
```

60.2 create_annot_label()

Link to code

60.3 create_roi()

Link to code
Creates the ROI_%s.nii.gz files using the given parcellation information from networks. Iteratively create volume.

60.4 create_wm_mask()

Link to code

60.5 crop_and_move_datasets()

Link to code

60.6 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

CHAPTER 61

interfaces.dcm2nii

61.1 Dcm2nii

Link to code
Wraps command **dcm2nii**
Uses MRIcron's dcm2nii to convert dicom files

61.1.1 Examples

```
>>> from nipype.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
'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.
```

Inputs:

```
[Mandatory]
source_dir: (an existing directory name)
        flag: %s, position: -1
        mutually_exclusive: source_names
source_names: (a list of items which are an existing file name)
        flag: %s, position: -1
        mutually_exclusive: source_dir

[Optional]
anonymize: (a boolean, nipype default value: True)
        Remove identifying information
        flag: -a
args: (a string)
        Additional parameters to the command
        flag: %s
collapse_folders: (a boolean, nipype default value: True)
        Collapse input folders
        flag: -c
config_file: (an existing file name)
        Load settings from specified inifile
        flag: -b %s
convert_all_pars: (a boolean, nipype default value: True)
        Convert every image in directory
        flag: -v
date_in_filename: (a boolean, nipype default value: True)
        Date in filename
```

```
        flag: -d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
events_in_filename: (a boolean, nipype default value: True)
        Events (series/acq) in filename
        flag: -e
gzip_output: (a boolean, nipype default value: False)
        Gzip output (.gz)
        flag: -g
id_in_filename: (a boolean, nipype default value: False)
        ID in filename
        flag: -i
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
nii_output: (a boolean, nipype default value: True)
        Save as .nii - if no, create .hdr/.img pair
        flag: -n
output_dir: (an existing directory name)
        Output dir - if unspecified, source directory is used
        flag: -o %s
protocol_in_filename: (a boolean, nipype default value: True)
        Protocol in filename
        flag: -p
reorient: (a boolean)
        Reorient image to nearest orthogonal
        flag: -r
reorient_and_crop: (a boolean, nipype default value: False)
        Reorient and crop 3D images
        flag: -x
source_in_filename: (a boolean, nipype default value: False)
        Source filename
        flag: -f
spm_analyze: (a boolean)
        SPM2/Analyze not SPM5/NIfTI
        flag: -s
        mutually_exclusive: nii_output
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
bvals: (a list of items which are an existing file name)
bvecs: (a list of items which are an existing file name)
converted_files: (a list of items which are an existing file name)
reoriented_and_cropped_files: (a list of items which are an existing
         file name)
reoriented_files: (a list of items which are an existing file name)
```

61.2 Dcm2niix

Link to code

Wraps command **dcm2niix**

Uses Chris Rorden's dcm2niix to convert dicom files

61.2.1 Examples

```
>>> from nipype.interfaces.dcm2nii import Dcm2niix
>>> converter = Dcm2niix()
>>> converter.inputs.source_names = ['functional_1.dcm', 'functional_2.dcm']
>>> converter.inputs.compress = 'i'
>>> converter.inputs.single_file = True
>>> converter.inputs.output_dir = '.'
>>> converter.cmdline
'dcm2niix -b y -z i -x n -t n -m n -f %t%p -o . -s y -v n functional_1.dcm'
```

```
>>> flags = '-'.join([val.strip() + ' ' for val in sorted(' '.join(converter.cmdline.split()[1:-
>>> flags
' -b y -f %t%p -m n -o . -s y -t n -v n -x n -z i '
```

Inputs:

```
[Mandatory]
source_dir: (an existing directory name)
        flag: %s, position: -1
        mutually_exclusive: source_names
source_names: (a list of items which are an existing file name)
        flag: %s, position: -1
        mutually_exclusive: source_dir

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
bids_format: (a boolean, nipype default value: True)
        Create a BIDS sidecar file
        flag: -b
compress: ('y' or 'i' or 'n', nipype default value: i)
        Gzip compress images - [y=pigz, i=internal, n=no]
        flag: -z %s
crop: (a boolean, nipype default value: False)
        Crop 3D T1 acquisitions
        flag: -x
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
has_private: (a boolean, nipype default value: False)
        Flag if text notes includes private patient details
        flag: -t
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
merge_imgs: (a boolean, nipype default value: False)
        merge 2D slices from same series
        flag: -m
out_filename: (a string, nipype default value: %t%p)
        Output filename
        flag: -f %s
output_dir: (an existing directory name)
        Output directory
        flag: -o %s
single_file: (a boolean, nipype default value: False)
        Convert only one image (filename as last input
```

```
        flag: -s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean, nipype default value: False)
        Verbose output
        flag: -v
```

Outputs:

```
bids: (a list of items which are an existing file name)
bvals: (a list of items which are an existing file name)
bvecs: (a list of items which are an existing file name)
converted_files: (a list of items which are an existing file name)
```

CHAPTER 62

interfaces.dcmstack

62.1 CopyMeta

Link to code

Copy meta data from one Nifti file to another. Useful for preserving meta data after some processing steps.

Inputs:

```
[Mandatory]
dest_file: (an existing file name)
src_file: (an existing file name)

[Optional]
exclude_classes: (a list of items which are any value)
        List of meta data classifications to exclude
include_classes: (a list of items which are any value)
        List of specific meta data classifications to include. If not
        specified include everything.
```

Outputs:

```
dest_file: (an existing file name)
```

62.2 DcmStack

Link to code

Create one Nifti file from a set of DICOM files. Can optionally embed meta data.

62.2.1 Example

```
>>> from nipype.interfaces.dcmstack import DcmStack
>>> stacker = DcmStack()
>>> stacker.inputs.dicom_files = 'path/to/series/'
>>> stacker.run()
>>> result.outputs.out_file
'/path/to/cwd/sequence.nii.gz'
```

Inputs:

```
[Mandatory]
dicom_files: (a list of items which are an existing file name or an
         existing directory name or a 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, suplementing any default exclude filters
    force_read: (a boolean, nipype default value: True)
            Force reading files without DICM marker
    include_regexes: (a list of items which are any value)
            Meta data to include, overriding any exclude filters
    out_ext: (a string, nipype default value: .nii.gz)
            Determines output file type
    out_format: (a string)
            String which can be formatted with meta data to create the output
            filename(s)
    out_path: (a directory name)
            output path, current working directory if not set
```

Outputs:

```
    out_file: (an existing file name)
```

62.3 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 an existing file name or an
             existing directory name or a 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, suplementing any default exclude filters
    force_read: (a boolean, nipype default value: True)
            Force reading files without DICM marker
    include_regexes: (a list of items which are any value)
            Meta data to include, overriding any exclude filters
    out_ext: (a string, nipype default value: .nii.gz)
            Determines output file type
    out_format: (a string)
            String which can be formatted with meta data to create the output
            filename(s)
    out_path: (a directory name)
            output path, current working directory if not set
```

Outputs:

```
    out_list: (a list of items which are any value)
            List of output nifti files
```

62.4 LookupMeta

Link to code

Lookup meta data values from a Nifti with embedded meta data.

62.4.1 Example

```
>>> from nipype.interfaces import dcmstack
>>> lookup = dcmstack.LookupMeta()
>>> lookup.inputs.in_file = 'functional.nii'
>>> lookup.inputs.meta_keys = {'RepetitionTime' : 'TR',                                    'Echo
>>> result = lookup.run()
>>> result.outputs.TR
9500.0
>>> result.outputs.TE
95.0
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        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

[Optional]
```

Outputs:

```
None
```

62.5 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]
merge_dim: (an integer (int or long))
        Dimension to merge along. If not specified, the last singular or
        non-existant dimension is used.
out_ext: (a string, nipype default value: .nii.gz)
        Determines output file type
out_format: (a string)
        String which can be formatted with meta data to create the output
        filename(s)
out_path: (a directory name)
        output path, current working directory if not set
sort_order: (a string or a list of items which are any value)
        One or more meta data keys to sort files by.
```

Outputs:

```
out_file: (an existing file name)
        Merged Nifti file
```

62.6 NiftiGeneratorBase

Link to code

Base class for interfaces that produce Nifti files, potentially with embedded meta data.
Inputs:

```
[Mandatory]

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
None
```

62.7 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: (an existing file name)
        Nifti file to split

[Optional]
out_ext: (a string, nipype default value: .nii.gz)
        Determines output file type
out_format: (a string)
        String which can be formatted with meta data to create the output
        filename(s)
out_path: (a directory name)
        output path, current working directory if not set
split_dim: (an integer (int or long))
        Dimension to split along. If not specified, the last dimension is
        used.
```

Outputs:

```
out_list: (a list of items which are an existing file name)
        Split Nifti files
```

62.8 make_key_func()

Link to code

62.9 sanitize_path_comp()

Link to code

interfaces.diffusion_toolkit.dti

63.1 DTIRecon

Link to code
Wraps command **dti_recon**
Use dti_recon to generate tensors and other maps
Inputs:

```
    [Mandatory]
    DWI: (an existing file name)
            Input diffusion volume
            flag: %s, position: 1
    bvals: (an existing file name)
            b values file
    bvecs: (an existing file name)
            b vectors file
            flag: -gm %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    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.
            flag: -b0_th
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    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
            flag: -iop %f
    n_averages: (an integer (int or long))
```

```
        Number of averages
        flag: -nex %s
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
        flag: -oc
out_prefix: (a string, nipype default value: dti)
        Output file prefix
        flag: %s, position: 2
output_type: ('nii' or 'analyze' or 'ni1' or 'nii.gz', nipype default
         value: nii)
        output file type
        flag: -ot %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
ADC: (an existing file name)
B0: (an existing file name)
FA: (an existing file name)
FA_color: (an existing file name)
L1: (an existing file name)
L2: (an existing file name)
L3: (an existing file name)
V1: (an existing file name)
V2: (an existing file name)
V3: (an existing file name)
exp: (an existing file name)
tensor: (an existing file name)
```

63.2 DTITracker

Link to code

Wraps command **dti_tracker**

Inputs:

```
[Mandatory]
mask1_file: (a file name)
        first mask image
        flag: -m %s, position: 2

[Optional]
angle_threshold: (a float)
        set angle threshold. default value is 35 degree
        flag: -at %f
angle_threshold_weight: (a float)
        set angle threshold weighting factor. weighting will be be applied
        on top of the angle_threshold
        flag: -atw %f
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
```

```
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
input_data_prefix: (a string, nipype default value: dti)
        for internal naming use only
        flag: %s, position: 0
input_type: ('nii' or 'analyze' or 'ni1' or 'nii.gz')
        input and output file type. accepted values are:
         analyze -> analyze format 7.5
         ni1 -> 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'
        flag: -it %s
invert_x: (a boolean)
        invert x component of the vector
        flag: -ix
invert_y: (a boolean)
        invert y component of the vector
        flag: -iy
invert_z: (a boolean)
        invert z component of the vector
        flag: -iz
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 file name)
        second mask image
        flag: -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
output_file: (a file name, nipype default value: tracks.trk)
        flag: %s, position: 1
output_mask: (a file name)
        output a binary mask file in analyze format
        flag: -om %s
primary_vector: ('v2' or 'v3')
        which vector to use for fibre tracking: v2 or v3. If not set use v1
        flag: -%s
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
        flag: -rseed
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
        flag: -l %f
swap_xy: (a boolean)
        swap x & y vectors while tracking
        flag: -sxy
swap_yz: (a boolean)
        swap y & z vectors while tracking
        flag: -syz
```

```
    swap_zx: (a boolean)
            swap x & z vectors while tracking
            flag: -szx
    tensor_file: (an existing file name)
            reconstructed tensor file
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    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
            flag: -%s
```

Outputs:

```
    mask_file: (an existing file name)
    track_file: (an existing file name)
```

CHAPTER 64

interfaces.diffusion_toolkit.odf

64.1 HARDIMat

Link to code
Wraps command **hardi_mat**
Use hardi_mat to calculate a reconstruction matrix from a gradient table
Inputs:

```
    [Mandatory]
    bvals: (an existing file name)
            b values file
    bvecs: (an existing file name)
            b vectors file
            flag: %s, position: 1

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    image_info: (an existing file name)
            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
            flag: -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
            flag: -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
        flag: -oc
odf_file: (an existing file name)
        filename that contains the reconstruction points on a HEMI-sphere.
         use the pre-set 181 points by default
        flag: -odf %s
order: (an integer (int or long))
        maximum order of spherical harmonics. must be even number. default
         is 4
        flag: -order %s
out_file: (a file name, nipype default value: recon_mat.dat)
        output matrix file
        flag: %s, position: 2
reference_file: (an existing file name)
        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
        flag: -ref %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output matrix file
```

64.2 ODFRecon

Link to code

Wraps command **odf_recon**

Use odf_recon to generate tensors and other maps

Inputs:

```
[Mandatory]
DWI: (an existing file name)
        Input raw data
        flag: %s, position: 1
matrix: (an existing file name)
        use given file as reconstruction matrix.
        flag: -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
        flag: -b0 %s
n_directions: (an integer (int or long))
        Number of directions
        flag: %s, position: 2
n_output_directions: (an integer (int or long))
        Number of output directions
        flag: %s, position: 3
```

```
    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    dsi: (a boolean)
            indicates that the data is dsi
            flag: -dsi
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    filter: (a boolean)
            apply a filter (e.g. high pass) to the raw image
            flag: -f
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    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
            flag: -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
            flag: -oc
    out_prefix: (a string, nipype default value: odf)
            Output file prefix
            flag: %s, position: 4
    output_entropy: (a boolean)
            output entropy map
            flag: -oe
    output_type: ('nii' or 'analyze' or 'ni1' or 'nii.gz', nipype default
             value: nii)
            output file type
            flag: -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
            flag: -s %f
    subtract_background: (a boolean)
            subtract the background value before reconstruction
            flag: -bg
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
B0: (an existing file name)
DWI: (an existing file name)
ODF: (an existing file name)
entropy: (a file name)
max: (an existing file name)
```

64.3 ODFTracker

Link to code
Wraps command **odf_tracker**
Use odf_tracker to generate track file
Inputs:

```
[Mandatory]
ODF: (an existing file name)
mask1_file: (a file name)
        first mask image
        flag: -m %s, position: 2
max: (an existing file name)

[Optional]
angle_threshold: (a float)
        set angle threshold. default value is 35 degree for
         default tracking method and 25 for rk2
        flag: -at %f
args: (a string)
        Additional parameters to the command
        flag: %s
disc: (a boolean)
        use disc tracking
        flag: -disc
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.
        flag: -dsi
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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
        flag: -iop %f
input_data_prefix: (a string, nipype default value: odf)
        recon data prefix
        flag: %s, position: 0
input_output_type: ('nii' or 'analyze' or 'ni1' or 'nii.gz', nipype
```

```
         default value: nii)
        input and output file type
        flag: -it %s
invert_x: (a boolean)
        invert x component of the vector
        flag: -ix
invert_y: (a boolean)
        invert y component of the vector
        flag: -iy
invert_z: (a boolean)
        invert z component of the vector
        flag: -iz
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)
        flag: -limit %d
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 file name)
        second mask image
        flag: -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
out_file: (a file name, nipype default value: tracks.trk)
        output track file
        flag: %s, position: 1
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
        flag: -rseed %s
runge_kutta2: (a boolean)
        use 2nd order runge-kutta method for tracking.
         default tracking method is non-interpolate streamline
        flag: -rk2
slice_order: (an integer (int or long))
        set the slice order. 1 means normal, -1 means reversed. default
        value is 1
        flag: -sorder %d
step_length: (a float)
        set step length, in the unit of minimum voxel size.
         default value is 0.1.
        flag: -l %f
swap_xy: (a boolean)
        swap x and y vectors while tracking
        flag: -sxy
swap_yz: (a boolean)
        swap y and z vectors while tracking
        flag: -syz
swap_zx: (a boolean)
        swap x and z vectors while tracking
        flag: -szx
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

```
    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
             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
            flag: -vorder %s
```

Outputs:

```
    track_file: (an existing file name)
            output track file
```

interfaces.diffusion_toolkit.postproc

65.1 SplineFilter

Link to code
Wraps command **spline_filter**
Smoothes 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.

65.1.1 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()
```

Inputs:

```
[Mandatory]
step_length: (a float)
        in the unit of minimum voxel size
        flag: %f, position: 1
track_file: (an existing file name)
        file containing tracks to be filtered
        flag: %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_file: (a file name, nipype default value: spline_tracks.trk)
        target file for smoothed tracks
        flag: %s, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
smoothed_track_file: (an existing file name)
```

65.2 TrackMerge

Link to code

Wraps 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).

65.2.1 Example

```
>>> import nipype.interfaces.diffusion_toolkit as dtk
>>> mrg = dtk.TrackMerge()
>>> mrg.inputs.track_files = ['track1.trk','track2.trk']
>>> mrg.run()
```

Inputs:

```
[Mandatory]
track_files: (a list of items which are an existing file name)
        file containing tracks to be filtered
        flag: %s..., position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_file: (a file name, nipype default value: merged_tracks.trk)
        target file for merged tracks
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
track_file: (an existing file name)
```

CHAPTER 66

interfaces.dipy.base

66.1 DipyBaseInterface

Link to code
A base interface for py:mod:*dipy* computations
Inputs:

```
[Mandatory]

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
None
```

66.2 DipyDiffusionInterface

Link to code
A base interface for py:mod:*dipy* computations
Inputs:

```
[Mandatory]
in_bval: (an existing file name)
        input b-values table
in_bvec: (an existing file name)
        input b-vectors table
in_file: (an existing file name)
        input diffusion data

[Optional]
b0_thres: (an integer (int or long), nipype default value: 700)
        b0 threshold
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_prefix: (a string)
        output prefix for file names
```

Outputs:

```
None
```

CHAPTER 67

interfaces.dipy.preprocess

67.1 Denoise

Link to code
An interface to denoising diffusion datasets *[Coupe2008]*. See http://nipy.org/dipy/examples_built/denoise_nlmeans.html#example-denoise-nlmeans.

67.1.1 Example

```
>>> import nipype.interfaces.dipy as dipy
>>> denoise = dipy.Denoise()
>>> denoise.inputs.in_file = 'diffusion.nii'
>>> denoise.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        The input 4D diffusion-weighted image file
noise_model: ('rician' or 'gaussian', nipype default value: rician)
        noise distribution model

[Optional]
block_radius: (an integer (int or long))
        block_radius
in_mask: (an existing file name)
        brain mask
noise_mask: (an existing file name)
        mask in which the standard deviation of noise will be computed
patch_radius: (an integer (int or long))
        patch radius
signal_mask: (an existing file name)
        mask in which the mean signal will be computed
snr: (a float)
        manually set an SNR
```

Outputs:

```
out_file: (an existing file name)
```

67.2 Resample

Link to code
An interface to reslicing diffusion datasets. See http://nipy.org/dipy/examples_built/reslice_datasets.html#example-reslice-datasets.

67.2.1 Example

```
>>> import nipype.interfaces.dipy as dipy
>>> reslice = dipy.Resample()
>>> reslice.inputs.in_file = 'diffusion.nii'
>>> reslice.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        The input 4D diffusion-weighted image file
interp: (an integer (int or long), nipype 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: (an existing file name)
```

67.3 nlmeans_proxy()

Link to code

Uses non-local means to denoise 4D datasets

67.4 resample_proxy()

Link to code

Performs regridding of an image to set isotropic voxel sizes using dipy.

interfaces.dipy.reconstruction

68.1 CSD

Link to code
Uses CSD *[Tournier2007]* to generate the fODF of DWIs. The interface uses `dipy`, as explained in dipy's CSD example.

68.1.1 Example

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
in_bval: (an existing file name)
        input b-values table
in_bvec: (an existing file name)
        input b-vectors table
in_file: (an existing file name)
        input diffusion data

[Optional]
b0_thres: (an integer (int or long), nipype default value: 700)
        b0 threshold
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_mask: (an existing file name)
        input mask in which compute tensors
out_fods: (a file name)
        fODFs output file name
out_prefix: (a string)
        output prefix for file names
response: (an existing file name)
        single fiber estimated response
save_fods: (a boolean, nipype default value: True)
        save fODFs in file
sh_order: (an integer (int or long), nipype default value: 8)
        maximal shperical harmonics order
```

Outputs:

```
    model: (a file name)
            Python pickled object of the CSD model fitted.
    out_fods: (a file name)
            fODFs output file name
```

68.2 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`.

68.2.1 Example

```
>>> from nipype.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()
```

Inputs:

```
    [Mandatory]
    in_bval: (an existing file name)
            input b-values table
    in_bvec: (an existing file name)
            input b-vectors table
    in_evals: (an existing file name)
            input eigenvalues file
    in_file: (an existing file name)
            input diffusion data

    [Optional]
    auto: (a boolean, nipype default value: True)
            use the auto_response estimator from dipy
            mutually_exclusive: recursive
    b0_thres: (an integer (int or long), nipype default value: 700)
            b0 threshold
    fa_thresh: (a float, nipype default value: 0.7)
            FA threshold
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    in_mask: (an existing file name)
            input mask in which we find single fibers
    out_mask: (a file name, nipype default value: wm_mask.nii.gz)
            computed wm mask
    out_prefix: (a string)
            output prefix for file names
    recursive: (a boolean, nipype default value: False)
            use the recursive response estimator from dipy
            mutually_exclusive: auto
    response: (a file name, nipype default value: response.txt)
            the output response file
    roi_radius: (an integer (int or long), nipype default value: 10)
            ROI radius to be used in auto_response
```

Outputs:

```
out_mask: (an existing file name)
        output wm mask
response: (an existing file name)
        the response file
```

68.3 RESTORE

Link to code
Uses RESTORE *[Chang2005]* to perform DTI fitting with outlier detection. The interface uses `dipy`, as explained in dipy's documentation.

68.3.1 Example

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
in_bval: (an existing file name)
        input b-values table
in_bvec: (an existing file name)
        input b-vectors table
in_file: (an existing file name)
        input diffusion data

[Optional]
b0_thres: (an integer (int or long), nipype default value: 700)
        b0 threshold
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_mask: (an existing file name)
        input mask in which compute tensors
noise_mask: (an existing file name)
        input mask in which compute noise variance
out_prefix: (a string)
        output prefix for file names
```

Outputs:

```
evals: (a file name)
        output the eigenvalues of the fitted DTI
evecs: (a file name)
        output the eigenvectors of the fitted DTI
fa: (a file name)
        output fractional anisotropy (FA) map computed from the fitted DTI
md: (a file name)
        output mean diffusivity (MD) map computed from the fitted DTI
mode: (a file name)
        output mode (MO) map computed from the fitted DTI
rd: (a file name)
```

```
            output radial diffusivity (RD) map computed from the fitted DTI
    trace: (a file name)
            output the tensor trace map computed from the fitted DTI
```

CHAPTER 69

interfaces.dipy.simulate

69.1 SimulateMultiTensor

Link to code
Interface to MultiTensor model simulator in dipy http://nipy.org/dipy/examples_built/simulate_multi_tensor.html

69.1.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
baseline: (an existing file name)
        baseline T2 signal
in_dirs: (a list of items which are an existing file name)
        list of fibers (principal directions)
in_frac: (a list of items which are an existing file name)
        volume fraction of each fiber
in_vfms: (a list of items which are an existing file name)
        volume fractions of isotropic compartiments

[Optional]
bvalues: (a list of items which are an integer (int or long), nipype
         default value: [1000, 3000])
        list of b-values (when table is automatically generated)
diff_iso: (a list of items which are a float, nipype 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), nipype
         default value: (0.0017, 0.0002, 0.0002))
        Single fiber tensor
gradients: (an existing file name)
        gradients file
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
```

```
        interface fails to run
in_bval: (an existing file name)
        input bvals file
in_bvec: (an existing file name)
        input bvecs file
in_mask: (an existing file name)
        mask to simulate data
n_proc: (an integer (int or long), nipype default value: 0)
        number of processes
num_dirs: (an integer (int or long), nipype default value: 32)
        number of gradient directions (when table is automatically
        generated)
out_bval: (a file name, nipype default value: bval.sim)
        simulated b values
out_bvec: (a file name, nipype default value: bvec.sim)
        simulated b vectors
out_file: (a file name, nipype default value: sim_dwi.nii.gz)
        output file with fractions to be simluated
out_mask: (a file name, nipype default value: sim_msk.nii.gz)
        file with the mask simulated
snr: (an integer (int or long), nipype default value: 0)
        signal-to-noise ratio (dB)
```

Outputs:

```
out_bval: (an existing file name)
        simulated b values
out_bvec: (an existing file name)
        simulated b vectors
out_file: (an existing file name)
        simulated DWIs
out_mask: (an existing file name)
        mask file
```

CHAPTER 70

interfaces.dipy.tensors

70.1 DTI

Link to code
Calculates the diffusion tensor model parameters

70.1.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_bval: (an existing file name)
        input b-values table
in_bvec: (an existing file name)
        input b-vectors table
in_file: (an existing file name)
        input diffusion data

[Optional]
b0_thres: (an integer (int or long), nipype default value: 700)
        b0 threshold
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask_file: (an existing file name)
        An optional white matter mask
out_prefix: (a string)
        output prefix for file names
```

Outputs:

```
ad_file: (an existing file name)
fa_file: (an existing file name)
md_file: (an existing file name)
out_file: (an existing file name)
rd_file: (an existing file name)
```

70.2 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.

70.2.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_bval: (an existing file name)
        input b-values table
in_bvec: (an existing file name)
        input b-vectors table
in_file: (an existing file name)
        input diffusion data

[Optional]
b0_thres: (an integer (int or long), nipype default value: 700)
        b0 threshold
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask_file: (an existing file name)
        An optional white matter mask
out_prefix: (a string)
        output prefix for file names
```

Outputs:

```
out_file: (an existing file name)
```

CHAPTER 71

interfaces.dipy.tracks

71.1 StreamlineTractography

Link to code
Streamline tractography using EuDX *[Garyfallidis12]*.

71.1.1 Example

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
gfa_thresh: (a float, nipype default value: 0.2)
        GFA threshold to compute tracking mask
in_file: (an existing file name)
        input diffusion data
min_angle: (a float, nipype default value: 25.0)
        minimum separation angle
multiprocess: (a boolean, nipype default value: True)
        use multiprocessing
num_seeds: (an integer (int or long), nipype default value: 10000)
        desired number of tracks in tractography
peak_threshold: (a float, nipype default value: 0.5)
        threshold to consider peaks from model
save_seeds: (a boolean, nipype default value: False)
        save seeding voxels coordinates

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_model: (an existing file name)
        input f/d-ODF model extracted from.
in_peaks: (an existing file name)
        peaks computed from the odf
out_prefix: (a string)
        output prefix for file names
seed_coord: (an existing file name)
        file containing the list of seed voxel coordinates (N,3)
```

```
seed_mask: (an existing file name)
        input mask within which perform seeding
tracking_mask: (an existing file name)
        input mask within which perform tracking
```

Outputs:

```
gfa: (a file name)
        The resulting GFA (generalized FA) computed using the peaks of the
        ODF
odf_peaks: (a file name)
        peaks computed from the odf
out_seeds: (a file name)
        file containing the (N,3) *voxel* coordinates used in seeding.
tracks: (a file name)
        TrackVis file containing extracted streamlines
```

71.2 TrackDensityMap

Link to code

Creates a tract density image from a TrackVis track file using functions from dipy

71.2.1 Example

```
>>> import nipype.interfaces.dipy as dipy
>>> trk2tdi = dipy.TrackDensityMap()
>>> trk2tdi.inputs.in_file = 'converted.trk'
>>> trk2tdi.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        The input TrackVis track file

[Optional]
data_dims: (a list of from 3 to 3 items which are an integer (int or
         long))
        The size of the image in voxels.
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_filename: (a file name, nipype default value: tdi.nii)
        The output filename for the tracks in TrackVis (.trk) format
points_space: ('rasmm' or 'voxel' or None, nipype default value:
         rasmm)
        coordinates of trk file
reference: (an existing file name)
        A reference file to define RAS coordinates space
voxel_dims: (a list of from 3 to 3 items which are a float)
        The size of each voxel in mm.
```

Outputs:

```
out_file: (an existing file name)
```

CHAPTER 72

interfaces.dynamic_slicer

72.1 SlicerCommandLine

Link to code
Wraps command **Slicer3**
Experimental Slicer wrapper. Work in progress.
Inputs:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
module: (a string)
        name of the Slicer command line module you want to use
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
None
```

interfaces.elastix.registration

73.1 AnalyzeWarp

Link to code
Wraps command **transformix -def all -jac all -jacmat all**
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)

73.1.1 Example

```
>>> from nipype.interfaces.elastix import AnalyzeWarp
>>> reg = AnalyzeWarp()
>>> reg.inputs.transform_file = 'TransformParameters.0.txt'
>>> reg.cmdline
'transformix -def all -jac all -jacmat all -out ./ -tp TransformParameters.0.txt'
```

Inputs:

```
[Mandatory]
output_path: (an existing directory name, nipype default value: ./)
        output directory
        flag: -out %s
transform_file: (an existing file name)
        transform-parameter file, only 1
        flag: -tp %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
num_threads: (an integer (int or long))
        set the maximum number of threads of elastix
        flag: -threads %01d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
disp_field: (a file name)
        displacements field
jacdet_map: (a file name)
        det(Jacobian) map
jacmat_map: (a file name)
        Jacobian matrix map
```

73.2 ApplyWarp

Link to code

Wraps command **transformix**

Use `transformix` to apply a transform on an input image. The transform is specified in the transform-parameter file.

73.2.1 Example

```
>>> from nipype.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 -out ./ -tp TransformParameters.0.txt'
```

Inputs:

```
[Mandatory]
moving_image: (an existing file name)
        input image to deform
        flag: -in %s
output_path: (an existing directory name, nipype default value: ./)
        output directory
        flag: -out %s
transform_file: (an existing file name)
        transform-parameter file, only 1
        flag: -tp %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
num_threads: (an integer (int or long))
        set the maximum number of threads of elastix
        flag: -threads %01d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    warped_file: (a file name)
            input moving image warped to fixed image
```

73.3 PointsWarp

Link to code

Wraps command **transformix**

Use `transformix` to apply a transform on an input point set. The transform is specified in the transform-parameter file.

73.3.1 Example

```
>>> from nipype.interfaces.elastix import PointsWarp
>>> reg = PointsWarp()
>>> reg.inputs.points_file = 'surf1.vtk'
>>> reg.inputs.transform_file = 'TransformParameters.0.txt'
>>> reg.cmdline
'transformix -out ./ -def surf1.vtk -tp TransformParameters.0.txt'
```

Inputs:

```
    [Mandatory]
    output_path: (an existing directory name, nipype default value: ./)
            output directory
            flag: -out %s
    points_file: (an existing file name)
            input points (accepts .vtk triangular meshes).
            flag: -def %s
    transform_file: (an existing file name)
            transform-parameter file, only 1
            flag: -tp %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    num_threads: (an integer (int or long))
            set the maximum number of threads of elastix
            flag: -threads %01d
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    warped_file: (a file name)
            input points displaced in fixed image domain
```

73.4 Registration

Link to code
Wraps command **elastix**
Elastix nonlinear registration interface

73.4.1 Example

```
>>> from nipype.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 -out ./ -p elastix.txt'
```

Inputs:

```
[Mandatory]
fixed_image: (an existing file name)
        fixed image
        flag: -f %s
moving_image: (an existing file name)
        moving image
        flag: -m %s
output_path: (an existing directory name, nipype default value: ./)
        output directory
        flag: -out %s
parameters: (a list of items which are an existing file name)
        parameter file, elastix handles 1 or more -p
        flag: -p %s...

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fixed_mask: (an existing file name)
        mask for fixed image
        flag: -fMask %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
initial_transform: (an existing file name)
        parameter file for initial transform
        flag: -t0 %s
moving_mask: (an existing file name)
        mask for moving image
        flag: -mMask %s
num_threads: (an integer (int or long))
        set the maximum number of threads of elastix
        flag: -threads %01d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
```

```
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
transform: (a list of items which are an existing file name)
        output transform
warped_file: (a file name)
        input moving image warped to fixed image
warped_files: (a list of items which are a file name)
        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
```

interfaces.elastix.utils

74.1 EditTransform

Link to code
Manipulates an existing transform file generated with elastix

74.1.1 Example

```
>>> from nipype.interfaces.elastix import EditTransform
>>> tfm = EditTransform()
>>> tfm.inputs.transform_file = 'TransformParameters.0.txt'
>>> tfm.inputs.reference_image = 'fixed1.nii'
>>> tfm.inputs.output_type = 'unsigned char'
>>> tfm.run()
```

Inputs:

```
[Mandatory]
transform_file: (an existing file name)
        transform-parameter file, only 1

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interpolation: ('cubic' or 'linear' or 'nearest', nipype default
         value: cubic)
        set a new interpolator for transformation
        flag: FinalBSplineInterpolationOrder
output_file: (a file name)
        the filename for the resulting transform file
output_format: ('nii.gz' or 'nii' or 'mhd' or 'hdr' or 'vtk')
        set a new image format for resampled images
        flag: ResultImageFormat
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
        flag: ResultImagePixelType
reference_image: (an existing file name)
        set a new reference image to change the target coordinate system.
```

Outputs:

```
output_file: (an existing file name)
        output transform file
```

CHAPTER 75

interfaces.freesurfer.longitudinal

75.1 FuseSegmentations

Link to code
Wraps command **mri_fuse_segmentations**
fuse segmentations together from multiple timepoints

75.1.1 Examples

```
>>> from nipype.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]
in_norms: (a list of items which are an existing file name)
        -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
        flag: -n %s
in_segmentations: (a list of items which are an existing file name)
        name of aseg file to use (default: aseg.mgz) must include the aseg
        files for all the given timepoints
        flag: -a %s
in_segmentations_noCC: (a list of items which are an existing file
         name)
        name of aseg file w/o CC labels (default: aseg.auto_noCCseg.mgz)
        must include the corresponding file for all the given timepoints
        flag: -c %s
out_file: (a file name)
        output fused segmentation file
timepoints: (a list of items which are a string)
        subject_ids or timepoints to be processed
        flag: %s, position: -2

[Optional]
args: (a string)
```

```
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
subject_id: (a string)
        subject_id being processed
        flag: %s, position: -3
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        output fused segmentation file
```

75.2 RobustTemplate

Link to code

Wraps command **mri_robust_template**

construct an unbiased robust template for longitudinal volumes

75.2.1 Examples

```
>>> from nipype.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
'mri_robust_template --satit --average 0 --fixtp --mov structural.nii functional.nii --inittp 1
>>> template.inputs.out_file = 'T1.nii'
>>> template.cmdline
'mri_robust_template --satit --average 0 --fixtp --mov structural.nii functional.nii --inittp 1
```

```
>>> template.inputs.transform_outputs = ['structural.lta', 'functional.lta']
>>> template.inputs.scaled_intensity_outputs = ['structural-iscale.txt', 'functional-iscale.txt'
>>> template.cmdline
'mri_robust_template --satit --average 0 --fixtp --mov structural.nii functional.nii --inittp 1
```

```
>>> template.run()
```

75.2.2 References

[https://surfer.nmr.mgh.harvard.edu/fswiki/mri_robust_template]

Inputs:

```
[Mandatory]
auto_detect_sensitivity: (a boolean)
        auto-detect good sensitivity (recommended for head or full brain
        scans)
        flag: --satit
        mutually_exclusive: outlier_sensitivity
in_files: (a list of items which are an existing file name)
        input movable volumes to be aligned to common mean/median template
        flag: --mov %s
out_file: (a file name, nipype default value:
         mri_robust_template_out.mgz)
        output template volume (final mean/median image)
        flag: --template %s
outlier_sensitivity: (a float)
        set outlier sensitivity manually (e.g. "--sat 4.685" ). Higher
        values mean less sensitivity.
        flag: --sat %.4f
        mutually_exclusive: auto_detect_sensitivity

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
average_metric: ('median' or 'mean')
        construct template from: 0 Mean, 1 Median (default)
        flag: --average %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fixed_timepoint: (a boolean)
        map everthing to init TP# (init TP is not resampled)
        flag: --fixtp
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_intensity_scales: (a list of items which are an existing file
         name)
        use initial intensity scales
        flag: --iscalein %s
initial_timepoint: (an integer (int or long))
        use TP# for spacial init (default random), 0: no init
        flag: --inittp %d
initial_transforms: (a list of items which are an existing file name)
        use initial transforms (lta) on source
        flag: --ixforms %s
intensity_scaling: (a boolean)
        allow also intensity scaling (default off)
        flag: --iscale
no_iteration: (a boolean)
        do not iterate, just create first template
        flag: --noit
scaled_intensity_outputs: (a list of items which are a file name)
        final intensity scales (will activate --iscale)
        flag: --iscaleout %s
subjects_dir: (an existing directory name)
        subjects directory
```

```
    subsample_threshold: (an integer (int or long))
            subsample if dim > # on all axes (default no subs.)
            flag: --subsample %d
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    transform_outputs: (a list of items which are a file name)
            output xforms to template (for each input)
            flag: --lta %s
```

Outputs:

```
    out_file: (an existing file name)
            output template volume (final mean/median image)
    scaled_intensity_outputs: (a list of items which are an existing file
             name)
            output final intensity scales
    transform_outputs: (a list of items which are an existing file name)
            output xform files from moving to template
```

CHAPTER 76

interfaces.freesurfer.model

76.1 Binarize

Link to code
Wraps command **mri_binarize**
Use FreeSurfer mri_binarize to threshold an input volume

76.1.1 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: (an existing file name)
        input volume
        flag: --i %s

[Optional]
abs: (a boolean)
        take abs of invol first (ie, make unsigned)
        flag: --abs
args: (a string)
        Additional parameters to the command
        flag: %s
bin_col_num: (a boolean)
        set binarized voxel value to its column number
        flag: --bincol
bin_val: (an integer (int or long))
        set vox within thresh to val (default is 1)
        flag: --binval %d
bin_val_not: (an integer (int or long))
        set vox outside range to val (default is 0)
        flag: --binvalnot %d
binary_file: (a file name)
        binary output volume
        flag: --o %s
count_file: (a boolean or a file name)
        save number of hits in ascii file (hits, ntotvox, pct)
        flag: --count %s
dilate: (an integer (int or long))
        niters: dilate binarization in 3D
        flag: --dilate %d
```

```
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    erode: (an integer (int or long))
            nerode: erode binarization in 3D (after any dilation)
            flag: --erode  %d
    erode2d: (an integer (int or long))
            nerode2d: erode binarization in 2D (after any 3D erosion)
            flag: --erode2d %d
    frame_no: (an integer (int or long))
            use 0-based frame of input (default is 0)
            flag: --frame %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    invert: (a boolean)
            set binval=0, binvalnot=1
            flag: --inv
    mask_file: (an existing file name)
            must be within mask
            flag: --mask maskvol
    mask_thresh: (a float)
            set thresh for mask
            flag: --mask-thresh %f
    match: (a list of items which are an integer (int or long))
            match instead of threshold
            flag: --match %d...
    max: (a float)
            max thresh
            flag: --max %f
            mutually_exclusive: wm_ven_csf
    merge_file: (an existing file name)
            merge with mergevol
            flag: --merge %s
    min: (a float)
            min thresh
            flag: --min %f
            mutually_exclusive: wm_ven_csf
    out_type: ('nii' or 'nii.gz' or 'mgz')
            output file type
    rmax: (a float)
            compute max based on rmax*globalmean
            flag: --rmax %f
    rmin: (a float)
            compute min based on rmin*globalmean
            flag: --rmin %f
    subjects_dir: (an existing directory name)
            subjects directory
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    ventricles: (a boolean)
            set match vals those for aseg ventricles+choroid (not 4th)
            flag: --ventricles
    wm: (a boolean)
            set match vals to 2 and 41 (aseg for cerebral WM)
```

```
        flag: --wm
wm_ven_csf: (a boolean)
        WM and ventricular CSF, including choroid (not 4th)
        flag: --wm+vcsf
        mutually_exclusive: min, max
zero_edges: (a boolean)
        zero the edge voxels
        flag: --zero-edges
zero_slice_edge: (a boolean)
        zero the edge slice voxels
        flag: --zero-slice-edges
```

Outputs:

```
binary_file: (an existing file name)
        binarized output volume
count_file: (a file name)
        ascii file containing number of hits
```

76.2 Concatenate

Link to code

Wraps 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.

76.2.1 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 an existing file name)
        Individual volumes to be concatenated
        flag: --i %s...

[Optional]
add_val: (a float)
        Add some amount to the input volume
        flag: --add %f
args: (a string)
        Additional parameters to the command
        flag: %s
combine: (a boolean)
        Combine non-zero values into single frame volume
        flag: --combine
concatenated_file: (a file name)
        Output volume
        flag: --o %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
```

```
         {})
        Environment variables
gmean: (an integer (int or long))
        create matrix to average Ng groups, Nper=Ntot/Ng
        flag: --gmean %d
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
keep_dtype: (a boolean)
        Keep voxelwise precision type (default is float
        flag: --keep-datatype
mask_file: (an existing file name)
        Mask input with a volume
        flag: --mask %s
max_bonfcor: (a boolean)
        Compute max and bonferroni correct (assumes -log10(ps))
        flag: --max-bonfcor
max_index: (a boolean)
        Compute the index of max voxel in concatenated volumes
        flag: --max-index
mean_div_n: (a boolean)
        compute mean/nframes (good for var)
        flag: --mean-div-n
multiply_by: (a float)
        Multiply input volume by some amount
        flag: --mul %f
multiply_matrix_file: (an existing file name)
        Multiply input by an ascii matrix in file
        flag: --mtx %s
paired_stats: ('sum' or 'avg' or 'diff' or 'diff-norm' or 'diff-
         norm1' or 'diff-norm2')
        Compute paired sum, avg, or diff
        flag: --paired-%s
sign: ('abs' or 'pos' or 'neg')
        Take only pos or neg voxles from input, or take abs
        flag: --%s
sort: (a boolean)
        Sort each voxel by ascending frame value
        flag: --sort
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
        flag: --%s
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
vote: (a boolean)
        Most frequent value at each voxel and fraction of occurances
        flag: --vote
```

Outputs:

```
concatenated_file: (an existing file name)
        Path/name of the output volume
```

76.3 GLMFit

Link to code
Wraps command **mri_glmfit**
Use FreeSurfer's mri_glmfit to specify and estimate a general linear model.

76.3.1 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 file name)
        input 4D file
        flag: --y %s

[Optional]
allow_ill_cond: (a boolean)
        allow ill-conditioned design matrices
        flag: --illcond
allow_repeated_subjects: (a boolean)
        allow subject names to repeat in the fsgd file (must appear before
        --fsgd
        flag: --allowsubjrep
args: (a string)
        Additional parameters to the command
        flag: %s
calc_AR1: (a boolean)
        compute and save temporal AR1 of residual
        flag: --tar1
check_opts: (a boolean)
        don't run anything, just check options and exit
        flag: --checkopts
compute_log_y: (a boolean)
        compute natural log of y prior to analysis
        flag: --logy
contrast: (a list of items which are an existing file name)
        contrast file
        flag: --C %s...
cortex: (a boolean)
        use subjects ?h.cortex.label as label
        flag: --cortex
        mutually_exclusive: label_file
debug: (a boolean)
        turn on debugging
        flag: --debug
design: (an existing file name)
        design matrix file
        flag: --X %s
        mutually_exclusive: fsgd, design, one_sample
diag: (an integer (int or long))
        Gdiag_no : set diagnositc level
diag_cluster: (a boolean)
```

```
        save sig volume and exit from first sim loop
        flag: --diag-cluster
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fixed_fx_dof: (an integer (int or long))
        dof for fixed effects analysis
        flag: --ffxdof %d
        mutually_exclusive: fixed_fx_dof_file
fixed_fx_dof_file: (a file name)
        text file with dof for fixed effects analysis
        flag: --ffxdofdat %d
        mutually_exclusive: fixed_fx_dof
fixed_fx_var: (an existing file name)
        for fixed effects analysis
        flag: --yffxvar %s
force_perm: (a boolean)
        force perumtation test, even when design matrix is not orthog
        flag: --perm-force
fsgd: (a tuple of the form: (an existing file name, 'doss' or
         'dods'))
        freesurfer descriptor file
        flag: --fsgd %s %s
        mutually_exclusive: fsgd, design, one_sample
fwhm: (a floating point number >= 0.0)
        smooth input by fwhm
        flag: --fwhm %f
glm_dir: (a string)
        save outputs to dir
        flag: --glmdir %s
hemi: ('lh' or 'rh')
        surface hemisphere
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
invert_mask: (a boolean)
        invert mask
        flag: --mask-inv
label_file: (an existing file name)
        use label as mask, surfaces only
        flag: --label %s
        mutually_exclusive: cortex
mask_file: (an existing file name)
        binary mask
        flag: --mask %s
no_contrast_ok: (a boolean)
        do not fail if no contrasts specified
        flag: --no-contrasts-ok
no_est_fwhm: (a boolean)
        turn off FWHM output estimation
        flag: --no-est-fwhm
no_mask_smooth: (a boolean)
        do not mask when smoothing
        flag: --no-mask-smooth
no_prune: (a boolean)
        do not prune
        flag: --no-prune
```

```
        mutually_exclusive: prunethresh
one_sample: (a boolean)
        construct X and C as a one-sample group mean
        flag: --osgm
        mutually_exclusive: one_sample, fsgd, design, contrast
pca: (a boolean)
        perform pca/svd analysis on residual
        flag: --pca
per_voxel_reg: (a list of items which are an existing file name)
        per-voxel regressors
        flag: --pvr %s...
profile: (an integer (int or long))
        niters : test speed
        flag: --profile %d
prune: (a boolean)
        remove voxels that do not have a non-zero value at each frame (def)
        flag: --prune
prune_thresh: (a float)
        prune threshold. Default is FLT_MIN
        flag: --prune_thr %f
        mutually_exclusive: noprune
resynth_test: (an integer (int or long))
        test GLM by resynthsis
        flag: --resynthtest %d
save_cond: (a boolean)
        flag to save design matrix condition at each voxel
        flag: --save-cond
save_estimate: (a boolean)
        save signal estimate (yhat)
        flag: --yhat-save
save_res_corr_mtx: (a boolean)
        save residual error spatial correlation matrix (eres.scm). Big!
        flag: --eres-scm
save_residual: (a boolean)
        save residual error (eres)
        flag: --eres-save
seed: (an integer (int or long))
        used for synthesizing noise
        flag: --seed %d
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
        flag: --selfreg %d %d %d
sim_done_file: (a file name)
        create file when simulation finished
        flag: --sim-done %s
sim_sign: ('abs' or 'pos' or 'neg')
        abs, pos, or neg
        flag: --sim-sign %s
simulation: (a tuple of the form: ('perm' or 'mc-full' or 'mc-z', an
         integer (int or long), a float, a string))
        nulltype nsim thresh csdbasename
        flag: --sim %s %d %f %s
subject_id: (a string)
        subject id for surface geometry
subjects_dir: (an existing directory name)
        subjects directory
surf: (a boolean)
```

```
        analysis is on a surface mesh
        flag: --surf %s %s %s
        requires: subject_id, hemi
surf_geo: (a string, nipype default value: white)
        surface geometry name (e.g. white, pial)
synth: (a boolean)
        replace input with gaussian
        flag: --synth
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
uniform: (a tuple of the form: (a float, a float))
        use uniform distribution instead of gaussian
        flag: --uniform %f %f
var_fwhm: (a floating point number >= 0.0)
        smooth variance by fwhm
        flag: --var-fwhm %f
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
        flag: --voxdump %d %d %d
weight_file: (an existing file name)
        weight for each input at each voxel
        mutually_exclusive: weighted_ls
weight_inv: (a boolean)
        invert weights
        flag: --w-inv
        mutually_exclusive: weighted_ls
weight_sqrt: (a boolean)
        sqrt of weights
        flag: --w-sqrt
        mutually_exclusive: weighted_ls
weighted_ls: (an existing file name)
        weighted least squares
        flag: --wls %s
        mutually_exclusive: weight_file, weight_inv, weight_sqrt
```

Outputs:

```
beta_file: (an existing file name)
        map of regression coefficients
dof_file: (a file name)
        text file with effective degrees-of-freedom for the analysis
error_file: (a file name)
        map of residual error
error_stddev_file: (a file name)
        map of residual error standard deviation
error_var_file: (a file name)
        map of residual error variance
estimate_file: (a file name)
        map of the estimated Y values
frame_eigenvectors: (a file name)
        matrix of frame eigenvectors from residual PCA
ftest_file: (a list of items which are any value)
        map of test statistic values
fwhm_file: (a file name)
        text file with estimated smoothness
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
glm_dir: (an existing directory name)
        output directory
mask_file: (a file name)
        map of the mask used in the analysis
sig_file: (a list of items which are any value)
        map of F-test significance (in -log10p)
singular_values: (a file name)
        matrix singular values from residual PCA
spatial_eigenvectors: (a file name)
        map of spatial eigenvectors from residual PCA
svd_stats_file: (a file name)
        text file summarizing the residual PCA
```

76.4 Label2Annot

Link to code
Wraps command **mris_label2annot**
Converts a set of surface labels to an annotation file

76.4.1 Examples

```
>>> from nipype.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
        flag: --hemi %s
in_labels: (a list of items which are any value)
        List of input label files
        flag: --l %s...
orig: (an existing file name)
        implicit {hemisphere}.orig
out_annot: (a string)
        Name of the annotation to create
        flag: --a %s
subject_id: (a string, nipype default value: subject_id)
        Subject name/ID
        flag: --s %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
color_table: (an existing file name)
```

```
        File that defines the structure names, their indices, and their
        color
        flag: --ctab %s
copy_inputs: (a boolean)
        copy implicit inputs and create a temp subjects_dir
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
keep_max: (a boolean)
        Keep label with highest 'stat' value
        flag: --maxstatwinner
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose_off: (a boolean)
        Turn off overlap and stat override messages
        flag: --noverbose
```

Outputs:

```
out_file: (an existing file name)
        Output annotation file
```

76.5 Label2Label

Link to code

Wraps 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.

76.5.1 Examples

```
>>> from nipype.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-pi
```

Inputs:

```
[Mandatory]
hemisphere: ('lh' or 'rh')
        Input hemisphere
        flag: --hemi %s
source_label: (an existing file name)
        Source label
        flag: --srclabel %s
source_sphere_reg: (an existing file name)
        Implicit input <hemisphere>.sphere.reg
source_subject: (a string)
        Source subject name
        flag: --srcsubject %s
source_white: (an existing file name)
        Implicit input <hemisphere>.white
sphere_reg: (an existing file name)
        Implicit input <hemisphere>.sphere.reg
subject_id: (a string, nipype default value: subject_id)
        Target subject
        flag: --trgsubject %s
white: (an existing file name)
        Implicit input <hemisphere>.white

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
copy_inputs: (a boolean)
        If running as a node, set this to True.This will copy the input
        files to the node directory.
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        Target label
        flag: --trglabel %s
registration_method: ('surface' or 'volume', nipype default value:
         surface)
        Registration method
        flag: --regmethod %s
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        Output label
```

76.6 Label2Vol

Link to code

Wraps command **mri_label2vol**
Make a binary volume from a Freesurfer label

76.6.1 Examples

```
>>> binvol = Label2Vol(label_file='cortex.label', template_file='structural.nii', reg_file='regi
>>> binvol.cmdline
'mri_label2vol --fillthresh 0 --label cortex.label --reg register.dat --temp structural.nii --o
```

Inputs:

```
[Mandatory]
annot_file: (an existing file name)
        surface annotation file
        flag: --annot %s
        mutually_exclusive: label_file, annot_file, seg_file, aparc_aseg
        requires: subject_id, hemi
aparc_aseg: (a boolean)
        use aparc+aseg.mgz in subjectdir as seg
        flag: --aparc+aseg
        mutually_exclusive: label_file, annot_file, seg_file, aparc_aseg
label_file: (a list of items which are an existing file name)
        list of label files
        flag: --label %s...
        mutually_exclusive: label_file, annot_file, seg_file, aparc_aseg
seg_file: (an existing file name)
        segmentation file
        flag: --seg %s
        mutually_exclusive: label_file, annot_file, seg_file, aparc_aseg
template_file: (an existing file name)
        output template volume
        flag: --temp %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fill_thresh: (0.0 <= a floating point number <= 1.0)
        thresh : between 0 and 1
        flag: --fillthresh %.f
hemi: ('lh' or 'rh')
        hemisphere to use lh or rh
        flag: --hemi %s
identity: (a boolean)
        set R=I
        flag: --identity
        mutually_exclusive: reg_file, reg_header, identity
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
invert_mtx: (a boolean)
        Invert the registration matrix
        flag: --invertmtx
label_hit_file: (a file name)
        file with each frame is nhits for a label
```

```
        flag: --hits %s
label_voxel_volume: (a float)
        volume of each label point (def 1mm3)
        flag: --labvoxvol %f
map_label_stat: (a file name)
        map the label stats field into the vol
        flag: --label-stat %s
native_vox2ras: (a boolean)
        use native vox2ras xform instead of tkregister-style
        flag: --native-vox2ras
proj: (a tuple of the form: ('abs' or 'frac', a float, a float, a
         float))
        project along surface normal
        flag: --proj %s %f %f %f
        requires: subject_id, hemi
reg_file: (an existing file name)
        tkregister style matrix VolXYZ = R*LabelXYZ
        flag: --reg %s
        mutually_exclusive: reg_file, reg_header, identity
reg_header: (an existing file name)
        label template volume
        flag: --regheader %s
        mutually_exclusive: reg_file, reg_header, identity
subject_id: (a string)
        subject id
        flag: --subject %s
subjects_dir: (an existing directory name)
        subjects directory
surface: (a string)
        use surface instead of white
        flag: --surf %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
vol_label_file: (a file name)
        output volume
        flag: --o %s
```

Outputs:

```
vol_label_file: (an existing file name)
        output volume
```

76.7 MRISPreproc

Link to code

Wraps command **mris_preproc**

Use FreeSurfer mris_preproc to prepare a group of contrasts for a second level analysis

76.7.1 Examples

```
>>> preproc = MRISPreproc()
>>> preproc.inputs.target = 'fsaverage'
>>> preproc.inputs.hemi = 'lh'
>>> preproc.inputs.vol_measure_file = [('cont1.nii', 'register.dat'),
>>> preproc.inputs.out_file = 'concatenated_file.mgz'
```

```
>>> preproc.cmdline
'mris_preproc --hemi lh --out concatenated_file.mgz --target fsaverage --iv cont1.nii register.d
```

Inputs:

```
[Mandatory]
hemi: ('lh' or 'rh')
        hemisphere for source and target
        flag: --hemi %s
target: (a string)
        target subject name
        flag: --target %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fsgd_file: (an existing file name)
        specify subjects using fsgd file
        flag: --fsgd %s
        mutually_exclusive: subjects, fsgd_file, subject_file
fwhm: (a float)
        smooth by fwhm mm on the target surface
        flag: --fwhm %f
        mutually_exclusive: num_iters
fwhm_source: (a float)
        smooth by fwhm mm on the source surface
        flag: --fwhm-src %f
        mutually_exclusive: num_iters_source
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
num_iters: (an integer (int or long))
        niters : smooth by niters on the target surface
        flag: --niters %d
        mutually_exclusive: fwhm
num_iters_source: (an integer (int or long))
        niters : smooth by niters on the source surface
        flag: --niterssrc %d
        mutually_exclusive: fwhm_source
out_file: (a file name)
        output filename
        flag: --out %s
proj_frac: (a float)
        projection fraction for vol2surf
        flag: --projfrac %s
smooth_cortex_only: (a boolean)
        only smooth cortex (ie, exclude medial wall)
        flag: --smooth-cortex-only
source_format: (a string)
        source format
        flag: --srcfmt %s
subject_file: (an existing file name)
        file specifying subjects separated by white space
        flag: --f %s
```

```
        mutually_exclusive: subjects, fsgd_file, subject_file
subjects: (a list of items which are any value)
        subjects from who measures are calculated
        flag: --s %s...
        mutually_exclusive: subjects, fsgd_file, subject_file
subjects_dir: (an existing directory name)
        subjects directory
surf_area: (a string)
        Extract vertex area from subject/surf/hemi.surfname to use as input.
        flag: --area %s
        mutually_exclusive: surf_measure, surf_measure_file, surf_area
surf_dir: (a string)
        alternative directory (instead of surf)
        flag: --surfdir %s
surf_measure: (a string)
        Use subject/surf/hemi.surf_measure as input
        flag: --meas %s
        mutually_exclusive: surf_measure, surf_measure_file, surf_area
surf_measure_file: (a list of items which are an existing file name)
        file alternative to surfmeas, still requires list of subjects
        flag: --is %s...
        mutually_exclusive: surf_measure, surf_measure_file, surf_area
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
vol_measure_file: (a list of items which are a tuple of the form: (an
         existing file name, an existing file name))
        list of volume measure and reg file tuples
        flag: --iv %s %s...
```

Outputs:

```
out_file: (a file name)
        preprocessed output file
```

76.8 MRISPreprocReconAll

Link to code

Wraps command **mris_preproc**

Extends MRISPreproc to allow it to be used in a recon-all workflow

76.8.1 Examples

```
>>> preproc = MRISPreprocReconAll()
>>> preproc.inputs.target = 'fsaverage'
>>> preproc.inputs.hemi = 'lh'
>>> preproc.inputs.vol_measure_file = [('cont1.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
```

Inputs:

```
[Mandatory]
hemi: ('lh' or 'rh')
        hemisphere for source and target
```

```
        flag: --hemi %s
target: (a string)
        target subject name
        flag: --target %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
copy_inputs: (a boolean)
        If running as a node, set this to True this will copy some implicit
        inputs to the node directory.
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fsgd_file: (an existing file name)
        specify subjects using fsgd file
        flag: --fsgd %s
        mutually_exclusive: subjects, fsgd_file, subject_file
fwhm: (a float)
        smooth by fwhm mm on the target surface
        flag: --fwhm %f
        mutually_exclusive: num_iters
fwhm_source: (a float)
        smooth by fwhm mm on the source surface
        flag: --fwhm-src %f
        mutually_exclusive: num_iters_source
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
lh_surfreg_target: (a file name)
        Implicit target surface registration file
        requires: surfreg_files
num_iters: (an integer (int or long))
        niters : smooth by niters on the target surface
        flag: --niters %d
        mutually_exclusive: fwhm
num_iters_source: (an integer (int or long))
        niters : smooth by niters on the source surface
        flag: --niterssrc %d
        mutually_exclusive: fwhm_source
out_file: (a file name)
        output filename
        flag: --out %s
proj_frac: (a float)
        projection fraction for vol2surf
        flag: --projfrac %s
rh_surfreg_target: (a file name)
        Implicit target surface registration file
        requires: surfreg_files
smooth_cortex_only: (a boolean)
        only smooth cortex (ie, exclude medial wall)
        flag: --smooth-cortex-only
source_format: (a string)
        source format
        flag: --srcfmt %s
subject_file: (an existing file name)
```

```
            file specifying subjects separated by white space
            flag: --f %s
            mutually_exclusive: subjects, fsgd_file, subject_file
    subject_id: (a string, nipype default value: subject_id)
            subject from whom measures are calculated
            flag: --s %s
            mutually_exclusive: subjects, fsgd_file, subject_file, subject_id
    subjects: (a list of items which are any value)
            subjects from who measures are calculated
            flag: --s %s...
            mutually_exclusive: subjects, fsgd_file, subject_file
    subjects_dir: (an existing directory name)
            subjects directory
    surf_area: (a string)
            Extract vertex area from subject/surf/hemi.surfname to use as input.
            flag: --area %s
            mutually_exclusive: surf_measure, surf_measure_file, surf_area
    surf_dir: (a string)
            alternative directory (instead of surf)
            flag: --surfdir %s
    surf_measure: (a string)
            Use subject/surf/hemi.surf_measure as input
            flag: --meas %s
            mutually_exclusive: surf_measure, surf_measure_file, surf_area
    surf_measure_file: (an existing file name)
            file necessary for surfmeas
            flag: --meas %s
            mutually_exclusive: surf_measure, surf_measure_file, surf_area
    surfreg_files: (a list of items which are an existing file name)
            lh and rh input surface registration files
            flag: --surfreg %s
            requires: lh_surfreg_target, rh_surfreg_target
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    vol_measure_file: (a list of items which are a tuple of the form: (an
             existing file name, an existing file name))
            list of volume measure and reg file tuples
            flag: --iv %s %s...
```

Outputs:

```
    out_file: (a file name)
            preprocessed output file
```

76.9 MS_LDA

Link to code

Wraps command **mri_ms_LDA**

Perform LDA reduction on the intensity space of an arbitrary # of FLASH images

76.9.1 Examples

```
>>> grey_label = 2
>>> white_label = 3
>>> zero_value = 1
```

```
>>> optimalWeights = MS_LDA(lda_labels=[grey_label, white_label],
>>> optimalWeights.cmdline
'mri_ms_LDA -conform -label label.mgz -lda 2 3 -shift 1 -W -synth synth_out.mgz -weight weights.
```

Inputs:

```
[Mandatory]
images: (a list of items which are an existing file name)
        list of input FLASH images
        flag: %s, position: -1
lda_labels: (a list of from 2 to 2 items which are an integer (int or
         long))
        pair of class labels to optimize
        flag: -lda %s
vol_synth_file: (a file name)
        filename for the synthesized output volume
        flag: -synth %s
weight_file: (a file name)
        filename for the LDA weights (input or output)
        flag: -weight %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
conform: (a boolean)
        Conform the input volumes (brain mask typically already conformed)
        flag: -conform
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
label_file: (a file name)
        filename of the label volume
        flag: -label %s
mask_file: (a file name)
        filename of the brain mask volume
        flag: -mask %s
shift: (an integer (int or long))
        shift all values equal to the given value to zero
        flag: -shift %d
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
use_weights: (a boolean)
        Use the weights from a previously generated weight file
        flag: -W
```

Outputs:

```
vol_synth_file: (an existing file name)
weight_file: (an existing file name)
```

76.10 OneSampleTTest

Link to code
Wraps command **mri_glmfit**
Inputs:

```
[Mandatory]
in_file: (a file name)
        input 4D file
        flag: --y %s

[Optional]
allow_ill_cond: (a boolean)
        allow ill-conditioned design matrices
        flag: --illcond
allow_repeated_subjects: (a boolean)
        allow subject names to repeat in the fsgd file (must appear before
        --fsgd
        flag: --allowsubjrep
args: (a string)
        Additional parameters to the command
        flag: %s
calc_AR1: (a boolean)
        compute and save temporal AR1 of residual
        flag: --tar1
check_opts: (a boolean)
        don't run anything, just check options and exit
        flag: --checkopts
compute_log_y: (a boolean)
        compute natural log of y prior to analysis
        flag: --logy
contrast: (a list of items which are an existing file name)
        contrast file
        flag: --C %s...
cortex: (a boolean)
        use subjects ?h.cortex.label as label
        flag: --cortex
        mutually_exclusive: label_file
debug: (a boolean)
        turn on debugging
        flag: --debug
design: (an existing file name)
        design matrix file
        flag: --X %s
        mutually_exclusive: fsgd, design, one_sample
diag: (an integer (int or long))
        Gdiag_no : set diagnositc level
diag_cluster: (a boolean)
        save sig volume and exit from first sim loop
        flag: --diag-cluster
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fixed_fx_dof: (an integer (int or long))
        dof for fixed effects analysis
        flag: --ffxdof %d
        mutually_exclusive: fixed_fx_dof_file
```

```
    fixed_fx_dof_file: (a file name)
            text file with dof for fixed effects analysis
            flag: --ffxdofdat %d
            mutually_exclusive: fixed_fx_dof
    fixed_fx_var: (an existing file name)
            for fixed effects analysis
            flag: --yffxvar %s
    force_perm: (a boolean)
            force perumtation test, even when design matrix is not orthog
            flag: --perm-force
    fsgd: (a tuple of the form: (an existing file name, 'doss' or
             'dods'))
            freesurfer descriptor file
            flag: --fsgd %s %s
            mutually_exclusive: fsgd, design, one_sample
    fwhm: (a floating point number >= 0.0)
            smooth input by fwhm
            flag: --fwhm %f
    glm_dir: (a string)
            save outputs to dir
            flag: --glmdir %s
    hemi: ('lh' or 'rh')
            surface hemisphere
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    invert_mask: (a boolean)
            invert mask
            flag: --mask-inv
    label_file: (an existing file name)
            use label as mask, surfaces only
            flag: --label %s
            mutually_exclusive: cortex
    mask_file: (an existing file name)
            binary mask
            flag: --mask %s
    no_contrast_ok: (a boolean)
            do not fail if no contrasts specified
            flag: --no-contrasts-ok
    no_est_fwhm: (a boolean)
            turn off FWHM output estimation
            flag: --no-est-fwhm
    no_mask_smooth: (a boolean)
            do not mask when smoothing
            flag: --no-mask-smooth
    no_prune: (a boolean)
            do not prune
            flag: --no-prune
            mutually_exclusive: prunethresh
    one_sample: (a boolean)
            construct X and C as a one-sample group mean
            flag: --osgm
            mutually_exclusive: one_sample, fsgd, design, contrast
    pca: (a boolean)
            perform pca/svd analysis on residual
            flag: --pca
    per_voxel_reg: (a list of items which are an existing file name)
            per-voxel regressors
```

```
        flag: --pvr %s...
profile: (an integer (int or long))
        niters : test speed
        flag: --profile %d
prune: (a boolean)
        remove voxels that do not have a non-zero value at each frame (def)
        flag: --prune
prune_thresh: (a float)
        prune threshold. Default is FLT_MIN
        flag: --prune_thr %f
        mutually_exclusive: noprune
resynth_test: (an integer (int or long))
        test GLM by resynthsis
        flag: --resynthtest %d
save_cond: (a boolean)
        flag to save design matrix condition at each voxel
        flag: --save-cond
save_estimate: (a boolean)
        save signal estimate (yhat)
        flag: --yhat-save
save_res_corr_mtx: (a boolean)
        save residual error spatial correlation matrix (eres.scm). Big!
        flag: --eres-scm
save_residual: (a boolean)
        save residual error (eres)
        flag: --eres-save
seed: (an integer (int or long))
        used for synthesizing noise
        flag: --seed %d
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
        flag: --selfreg %d %d %d
sim_done_file: (a file name)
        create file when simulation finished
        flag: --sim-done %s
sim_sign: ('abs' or 'pos' or 'neg')
        abs, pos, or neg
        flag: --sim-sign %s
simulation: (a tuple of the form: ('perm' or 'mc-full' or 'mc-z', an
         integer (int or long), a float, a string))
        nulltype nsim thresh csdbasename
        flag: --sim %s %d %f %s
subject_id: (a string)
        subject id for surface geometry
subjects_dir: (an existing directory name)
        subjects directory
surf: (a boolean)
        analysis is on a surface mesh
        flag: --surf %s %s %s
        requires: subject_id, hemi
surf_geo: (a string, nipype default value: white)
        surface geometry name (e.g. white, pial)
synth: (a boolean)
        replace input with gaussian
        flag: --synth
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
```

```
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
uniform: (a tuple of the form: (a float, a float))
        use uniform distribution instead of gaussian
        flag: --uniform %f %f
var_fwhm: (a floating point number >= 0.0)
        smooth variance by fwhm
        flag: --var-fwhm %f
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
        flag: --voxdump %d %d %d
weight_file: (an existing file name)
        weight for each input at each voxel
        mutually_exclusive: weighted_ls
weight_inv: (a boolean)
        invert weights
        flag: --w-inv
        mutually_exclusive: weighted_ls
weight_sqrt: (a boolean)
        sqrt of weights
        flag: --w-sqrt
        mutually_exclusive: weighted_ls
weighted_ls: (an existing file name)
        weighted least squares
        flag: --wls %s
        mutually_exclusive: weight_file, weight_inv, weight_sqrt
```

Outputs:

```
beta_file: (an existing file name)
        map of regression coefficients
dof_file: (a file name)
        text file with effective degrees-of-freedom for the analysis
error_file: (a file name)
        map of residual error
error_stddev_file: (a file name)
        map of residual error standard deviation
error_var_file: (a file name)
        map of residual error variance
estimate_file: (a file name)
        map of the estimated Y values
frame_eigenvectors: (a file name)
        matrix of frame eigenvectors from residual PCA
ftest_file: (a list of items which are any value)
        map of test statistic values
fwhm_file: (a file name)
        text file with estimated smoothness
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
glm_dir: (an existing directory name)
        output directory
mask_file: (a file name)
        map of the mask used in the analysis
sig_file: (a list of items which are any value)
        map of F-test significance (in -log10p)
singular_values: (a file name)
```

```
        matrix singular values from residual PCA
spatial_eigenvectors: (a file name)
        map of spatial eigenvectors from residual PCA
svd_stats_file: (a file name)
        text file summarizing the residual PCA
```

76.11 SegStats

Link to code
Wraps command **mri_segstats**
Use FreeSurfer mri_segstats for ROI analysis

76.11.1 Examples

```
>>> import nipype.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.stat
```

Inputs:

```
[Mandatory]
annot: (a tuple of the form: (a string, 'lh' or 'rh', a string))
        subject hemi parc : use surface parcellation
        flag: --annot %s %s %s
        mutually_exclusive: segmentation_file, annot, surf_label
segmentation_file: (an existing file name)
        segmentation volume path
        flag: --seg %s
        mutually_exclusive: segmentation_file, annot, surf_label
surf_label: (a tuple of the form: (a string, 'lh' or 'rh', a string))
        subject hemi label : use surface label
        flag: --slabel %s %s %s
        mutually_exclusive: segmentation_file, annot, surf_label

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
avgwf_file: (a boolean or a file name)
        Save as binary volume (bool or filename)
        flag: --avgwfvol %s
avgwf_txt_file: (a boolean or a file name)
        Save average waveform into file (bool or filename)
        flag: --avgwf %s
brain_vol: ('brain-vol-from-seg' or 'brainmask')
        Compute brain volume either with ``brainmask`` or ``brain-vol-from-
        seg``
        flag: --%s
brainmask_file: (an existing file name)
        Load brain mask and compute the volume of the brain as the non-zero
        voxels in this volume
```

```
        flag: --brainmask %s
calc_power: ('sqr' or 'sqrt')
        Compute either the sqr or the sqrt of the input
        flag: --%s
calc_snr: (a boolean)
        save mean/std as extra column in output table
        flag: --snr
color_table_file: (an existing file name)
        color table file with seg id names
        flag: --ctab %s
        mutually_exclusive: color_table_file, default_color_table,
         gca_color_table
cortex_vol_from_surf: (a boolean)
        Compute cortex volume from surf
        flag: --surf-ctx-vol
default_color_table: (a boolean)
        use $FREESURFER_HOME/FreeSurferColorLUT.txt
        flag: --ctab-default
        mutually_exclusive: color_table_file, default_color_table,
         gca_color_table
empty: (a boolean)
        Report on segmentations listed in the color table
        flag: --empty
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
etiv: (a boolean)
        Compute ICV from talairach transform
        flag: --etiv
etiv_only: ('etiv' or 'old-etiv' or '--%s-only')
        Compute etiv and exit. Use ``etiv`` or ``old-etiv``
euler: (a boolean)
        Write out number of defect holes in orig.nofix based on the euler
        number
        flag: --euler
exclude_ctx_gm_wm: (a boolean)
        exclude cortical gray and white matter
        flag: --excl-ctxgmwm
exclude_id: (an integer (int or long))
        Exclude seg id from report
        flag: --excludeid %d
frame: (an integer (int or long))
        Report stats on nth frame of input volume
        flag: --frame %d
gca_color_table: (an existing file name)
        get color table from GCA (CMA)
        flag: --ctab-gca %s
        mutually_exclusive: color_table_file, default_color_table,
         gca_color_table
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_file: (an existing file name)
        Use the segmentation to report stats on this volume
        flag: --i %s
in_intensity: (a file name)
        Undocumented input norm.mgz file
```

```
        flag: --in %s --in-intensity-name %s
intensity_units: ('MR')
        Intensity units
        flag: --in-intensity-units %s
        requires: in_intensity
mask_erode: (an integer (int or long))
        Erode mask by some amount
        flag: --maskerode %d
mask_file: (an existing file name)
        Mask volume (same size as seg
        flag: --mask %s
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
        flag: --maskinvert
mask_sign: ('abs' or 'pos' or 'neg' or '--masksign %s')
        Sign for mask threshold: pos, neg, or abs
mask_thresh: (a float)
        binarize mask with this threshold <0.5>
        flag: --maskthresh %f
multiply: (a float)
        multiply input by val
        flag: --mul %f
non_empty_only: (a boolean)
        Only report nonempty segmentations
        flag: --nonempty
partial_volume_file: (an existing file name)
        Compensate for partial voluming
        flag: --pv %s
segment_id: (a list of items which are any value)
        Manually specify segmentation ids
        flag: --id %s...
sf_avg_file: (a boolean or a file name)
        Save mean across space and time
        flag: --sfavg %s
subcort_gm: (a boolean)
        Compute volume of subcortical gray matter
        flag: --subcortgray
subjects_dir: (an existing directory name)
        subjects directory
summary_file: (a file name)
        Segmentation stats summary table file
        flag: --sum %s, position: -1
supratent: (a boolean)
        Undocumented input flag
        flag: --supratent
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
total_gray: (a boolean)
        Compute volume of total gray matter
        flag: --totalgray
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)
        flag: --vox %s
```

```
wm_vol_from_surf: (a boolean)
        Compute wm volume from surf
        flag: --surf-wm-vol
```

Outputs:

```
avgwf_file: (a file name)
        Volume with functional statistics averaged over segs
avgwf_txt_file: (a file name)
        Text file with functional statistics averaged over segs
sf_avg_file: (a file name)
        Text file with func statistics averaged over segs and framss
summary_file: (an existing file name)
        Segmentation summary statistics table
```

76.12 SegStatsReconAll

Link to code

Wraps 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.

76.12.1 Examples

```
>>> from nipype.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'
>>> 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 --e
```

Inputs:

```
[Mandatory]
annot: (a tuple of the form: (a string, 'lh' or 'rh', a string))
```

```
        subject hemi parc : use surface parcellation
        flag: --annot %s %s %s
        mutually_exclusive: segmentation_file, annot, surf_label
lh_orig_nofix: (an existing file name)
        Input lh.orig.nofix
lh_pial: (an existing file name)
        Input file must be <subject_id>/surf/lh.pial
lh_white: (an existing file name)
        Input file must be <subject_id>/surf/lh.white
rh_orig_nofix: (an existing file name)
        Input rh.orig.nofix
rh_pial: (an existing file name)
        Input file must be <subject_id>/surf/rh.pial
rh_white: (an existing file name)
        Input file must be <subject_id>/surf/rh.white
ribbon: (a file name)
        Input file mri/ribbon.mgz
segmentation_file: (an existing file name)
        segmentation volume path
        flag: --seg %s
        mutually_exclusive: segmentation_file, annot, surf_label
subject_id: (a string, nipype default value: subject_id)
        Subject id being processed
        flag: --subject %s
surf_label: (a tuple of the form: (a string, 'lh' or 'rh', a string))
        subject hemi label : use surface label
        flag: --slabel %s %s %s
        mutually_exclusive: segmentation_file, annot, surf_label
transform: (an existing file name)
        Input transform file

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
aseg: (an existing file name)
        Mandatory implicit input in 5.3
avgwf_file: (a boolean or a file name)
        Save as binary volume (bool or filename)
        flag: --avgwfvol %s
avgwf_txt_file: (a boolean or a file name)
        Save average waveform into file (bool or filename)
        flag: --avgwf %s
brain_vol: ('brain-vol-from-seg' or 'brainmask')
        Compute brain volume either with ``brainmask`` or ``brain-vol-from-
        seg``
        flag: --%s
brainmask_file: (an existing file name)
        Load brain mask and compute the volume of the brain as the non-zero
        voxels in this volume
        flag: --brainmask %s
calc_power: ('sqr' or 'sqrt')
        Compute either the sqr or the sqrt of the input
        flag: --%s
calc_snr: (a boolean)
        save mean/std as extra column in output table
        flag: --snr
color_table_file: (an existing file name)
```

```
        color table file with seg id names
        flag: --ctab %s
        mutually_exclusive: color_table_file, default_color_table,
         gca_color_table
copy_inputs: (a boolean)
        If running as a node, set this to True otherwise, this will copy the
        implicit inputs to the node directory.
cortex_vol_from_surf: (a boolean)
        Compute cortex volume from surf
        flag: --surf-ctx-vol
default_color_table: (a boolean)
        use $FREESURFER_HOME/FreeSurferColorLUT.txt
        flag: --ctab-default
        mutually_exclusive: color_table_file, default_color_table,
         gca_color_table
empty: (a boolean)
        Report on segmentations listed in the color table
        flag: --empty
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
etiv: (a boolean)
        Compute ICV from talairach transform
        flag: --etiv
etiv_only: ('etiv' or 'old-etiv' or '--%s-only')
        Compute etiv and exit. Use ``etiv`` or ``old-etiv``
euler: (a boolean)
        Write out number of defect holes in orig.nofix based on the euler
        number
        flag: --euler
exclude_ctx_gm_wm: (a boolean)
        exclude cortical gray and white matter
        flag: --excl-ctxgmwm
exclude_id: (an integer (int or long))
        Exclude seg id from report
        flag: --excludeid %d
frame: (an integer (int or long))
        Report stats on nth frame of input volume
        flag: --frame %d
gca_color_table: (an existing file name)
        get color table from GCA (CMA)
        flag: --ctab-gca %s
        mutually_exclusive: color_table_file, default_color_table,
         gca_color_table
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_file: (an existing file name)
        Use the segmentation to report stats on this volume
        flag: --i %s
in_intensity: (a file name)
        Undocumented input norm.mgz file
        flag: --in %s --in-intensity-name %s
intensity_units: ('MR')
        Intensity units
        flag: --in-intensity-units %s
        requires: in_intensity
```

```
    mask_erode: (an integer (int or long))
            Erode mask by some amount
            flag: --maskerode %d
    mask_file: (an existing file name)
            Mask volume (same size as seg
            flag: --mask %s
    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
            flag: --maskinvert
    mask_sign: ('abs' or 'pos' or 'neg' or '--masksign %s')
            Sign for mask threshold: pos, neg, or abs
    mask_thresh: (a float)
            binarize mask with this threshold <0.5>
            flag: --maskthresh %f
    multiply: (a float)
            multiply input by val
            flag: --mul %f
    non_empty_only: (a boolean)
            Only report nonempty segmentations
            flag: --nonempty
    partial_volume_file: (an existing file name)
            Compensate for partial voluming
            flag: --pv %s
    presurf_seg: (an existing file name)
            Input segmentation volume
    segment_id: (a list of items which are any value)
            Manually specify segmentation ids
            flag: --id %s...
    sf_avg_file: (a boolean or a file name)
            Save mean across space and time
            flag: --sfavg %s
    subcort_gm: (a boolean)
            Compute volume of subcortical gray matter
            flag: --subcortgray
    subjects_dir: (an existing directory name)
            subjects directory
    summary_file: (a file name)
            Segmentation stats summary table file
            flag: --sum %s, position: -1
    supratent: (a boolean)
            Undocumented input flag
            flag: --supratent
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    total_gray: (a boolean)
            Compute volume of total gray matter
            flag: --totalgray
    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)
            flag: --vox %s
    wm_vol_from_surf: (a boolean)
            Compute wm volume from surf
            flag: --surf-wm-vol
```

Outputs:

```
avgwf_file: (a file name)
        Volume with functional statistics averaged over segs
avgwf_txt_file: (a file name)
        Text file with functional statistics averaged over segs
sf_avg_file: (a file name)
        Text file with func statistics averaged over segs and framss
summary_file: (an existing file name)
        Segmentation summary statistics table
```

76.13 SphericalAverage

Link to code
Wraps command **mris_spherical_average**
This program will add a template into an average surface.

76.13.1 Examples

```
>>> from nipype.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]
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'
        flag: %s, position: -5
hemisphere: ('lh' or 'rh')
        Input hemisphere
        flag: %s, position: -4
in_surf: (an existing file name)
        Input surface file
        flag: %s, position: -3
subject_id: (a string)
        Output subject id
        flag: -o %s
which: ('coords' or 'label' or 'vals' or 'curv' or 'area')
        No documentation
        flag: %s, position: -6

[Optional]
```

```
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    erode: (an integer (int or long))
            Undocumented
            flag: -erode %d
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    in_average: (a directory name)
            Average subject
            flag: %s, position: -2
    in_orig: (an existing file name)
            Original surface filename
            flag: -orig %s
    out_file: (a file name)
            Output filename
            flag: %s, position: -1
    subjects_dir: (an existing directory name)
            subjects directory
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    threshold: (a float)
            Undocumented
            flag: -t %.1f
```

Outputs:

```
    out_file: (a file name)
            Output label
```

CHAPTER 77

interfaces.freesurfer.preprocess

77.1 ApplyVolTransform

Link to code
Wraps command **mri_vol2vol**
Use FreeSurfer mri_vol2vol to apply a transform.

77.1.1 Examples

```
>>> from nipype.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]
fs_target: (a boolean)
        use orig.mgz from subject in regfile as target
        flag: --fstarg
        mutually_exclusive: target_file, tal, fs_target
        requires: reg_file
fsl_reg_file: (an existing file name)
        fslRAS-to-fslRAS matrix (FSL format)
        flag: --fsl %s
        mutually_exclusive: reg_file, fsl_reg_file, xfm_reg_file,
         reg_header, subject
reg_file: (an existing file name)
        tkRAS-to-tkRAS matrix (tkregister2 format)
        flag: --reg %s
        mutually_exclusive: reg_file, fsl_reg_file, xfm_reg_file,
         reg_header, subject
reg_header: (a boolean)
        ScannerRAS-to-ScannerRAS matrix = identity
        flag: --regheader
        mutually_exclusive: reg_file, fsl_reg_file, xfm_reg_file,
         reg_header, subject
source_file: (an existing file name)
        Input volume you wish to transform
        flag: --mov %s
subject: (a string)
```

```
        set matrix = identity and use subject for any templates
        flag: --s %s
        mutually_exclusive: reg_file, fsl_reg_file, xfm_reg_file,
         reg_header, subject
tal: (a boolean)
        map to a sub FOV of MNI305 (with --reg only)
        flag: --tal
        mutually_exclusive: target_file, tal, fs_target
target_file: (an existing file name)
        Output template volume
        flag: --targ %s
        mutually_exclusive: target_file, tal, fs_target
xfm_reg_file: (an existing file name)
        ScannerRAS-to-ScannerRAS matrix (MNI format)
        flag: --xfm %s
        mutually_exclusive: reg_file, fsl_reg_file, xfm_reg_file,
         reg_header, subject

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interp: ('trilin' or 'nearest' or 'cubic')
        Interpolation method (<trilin> or nearest)
        flag: --interp %s
inverse: (a boolean)
        sample from target to source
        flag: --inv
invert_morph: (a boolean)
        Compute and use the inverse of the non-linear morph to resample the
        input volume. To be used by --m3z.
        flag: --inv-morph
        requires: m3z_file
m3z_file: (a file name)
        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.
        flag: --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.
        flag: --noDefM3zPath
        requires: m3z_file
no_resample: (a boolean)
        Do not resample; just change vox2ras matrix
        flag: --no-resample
subjects_dir: (an existing directory name)
        subjects directory
```

```
    tal_resolution: (a float)
            Resolution to sample when using tal
            flag: --talres %.10f
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    transformed_file: (a file name)
            Output volume
            flag: --o %s
```

Outputs:

```
    transformed_file: (an existing file name)
            Path to output file if used normally
```

77.2 BBRegister

Link to code

Wraps command **bbregister**

Use FreeSurfer bbregister to register a volume to the Freesurfer anatomical.

This program performs within-subject, cross-modal registration using a boundary-based cost function. The registration is constrained to be 6 DOF (rigid). It is required that you have an anatomical scan of the subject that has already been recon-all-ed using freesurfer.

77.2.1 Examples

```
    >>> from nipype.interfaces.freesurfer import BBRegister
    >>> bbreg = BBRegister(subject_id='me', source_file='structural.nii', init='header', contrast_ty
    >>> bbreg.cmdline
    'bbregister --t2 --init-header --reg structural_bbreg_me.dat --mov structural.nii --s me'
```

Inputs:

```
    [Mandatory]
    contrast_type: ('t1' or 't2')
            contrast type of image
            flag: --%s
    init: ('spm' or 'fsl' or 'header')
            initialize registration spm, fsl, header
            flag: --init-%s
            mutually_exclusive: init_reg_file
    init_reg_file: (an existing file name)
            existing registration file
            flag: --init-reg %s
            mutually_exclusive: init
    source_file: (a file name)
            source file to be registered
            flag: --mov %s
    subject_id: (a string)
            freesurfer subject id
            flag: --s %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
```

```
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    epi_mask: (a boolean)
            mask out B0 regions in stages 1 and 2
            flag: --epi-mask
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    intermediate_file: (an existing file name)
            Intermediate image, e.g. in case of partial FOV
            flag: --int %s
    out_fsl_file: (a boolean or a file name)
            write the transformation matrix in FSL FLIRT format
            flag: --fslmat %s
    out_reg_file: (a file name)
            output registration file
            flag: --reg %s
    reg_frame: (an integer (int or long))
            0-based frame index for 4D source file
            flag: --frame %d
            mutually_exclusive: reg_middle_frame
    reg_middle_frame: (a boolean)
            Register middle frame of 4D source file
            flag: --mid-frame
            mutually_exclusive: reg_frame
    registered_file: (a boolean or a file name)
            output warped sourcefile either True or filename
            flag: --o %s
    spm_nifti: (a boolean)
            force use of nifti rather than analyze with SPM
            flag: --spm-nii
    subjects_dir: (an existing directory name)
            subjects directory
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    min_cost_file: (an existing file name)
            Output registration minimum cost file
    out_fsl_file: (a file name)
            Output FLIRT-style registration file
    out_reg_file: (an existing file name)
            Output registration file
    registered_file: (a file name)
            Registered and resampled source file
```

77.3 CALabel

Link to code
Wraps command **mri_ca_label**
For complete details, see the FS Documentation

77.3.1 Examples

```
>>> from nipype.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: (an existing file name)
        Input volume for CALabel
        flag: %s, position: -4
out_file: (a file name)
        Output file for CALabel
        flag: %s, position: -1
template: (an existing file name)
        Input template for CALabel
        flag: %s, position: -2
transform: (an existing file name)
        Input transform for CALabel
        flag: %s, position: -3

[Optional]
align: (a boolean)
        Align CALabel
        flag: -align
args: (a string)
        Additional parameters to the command
        flag: %s
aseg: (a file name)
        Undocumented flag. Autorecon3 uses ../mri/aseg.presurf.mgz as input
        file
        flag: -aseg %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_vol: (an existing file name)
        set input volume
        flag: -r %s
intensities: (an existing file name)
        input label intensities file(used in longitudinal processing)
        flag: -r %s
label: (a file name)
        Undocumented flag. Autorecon3 uses
        ../label/{hemisphere}.cortex.label as input file
        flag: -l %s
no_big_ventricles: (a boolean)
        No big ventricles
        flag: -nobigventricles
num_threads: (an integer (int or long))
```

```
        allows for specifying more threads
prior: (a float)
        Prior for CALabel
        flag: -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
        flag: -relabel_unlikely %d %.1f
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output volume from CALabel
```

77.4 CANormalize

Link to code

Wraps 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

77.4.1 Examples

```
>>> from nipype.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]
atlas: (an existing file name)
        The atlas file in gca format
        flag: %s, position: -3
in_file: (an existing file name)
        The input file for CANormalize
        flag: %s, position: -4
transform: (an existing file name)
        The tranform file in lta format
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
control_points: (a file name)
        File name for the output control points
```

```
        flag: -c %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
long_file: (a file name)
        undocumented flag used in longitudinal processing
        flag: -long %s
mask: (an existing file name)
        Specifies volume to use as mask
        flag: -mask %s
out_file: (a file name)
        The output file for CANormalize
        flag: %s, position: -1
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
control_points: (a file name)
        The output control points for Normalize
out_file: (a file name)
        The output file for Normalize
```

77.5 CARegister

Link to code

Wraps 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

77.5.1 Examples

```
>>> from nipype.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: (an existing file name)
        The input volume for CARegister
        flag: %s, position: -3

[Optional]
A: (an integer (int or long))
        undocumented flag used in longitudinal processing
```

```
        flag: -A %d
align: (a string)
        Specifies when to perform alignment
        flag: -align-%s
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
invert_and_save: (a boolean)
        Invert and save the .m3z multi-dimensional talaraich transform to x,
        y, and z .mgz files
        flag: -invert-and-save, position: -4
l_files: (a list of items which are a file name)
        undocumented flag used in longitudinal processing
        flag: -l %s
levels: (an integer (int or long))
        defines how many surrounding voxels will be used in interpolations,
        default is 6
        flag: -levels %d
mask: (an existing file name)
        Specifies volume to use as mask
        flag: -mask %s
no_big_ventricles: (a boolean)
        No big ventricles
        flag: -nobigventricles
num_threads: (an integer (int or long))
        allows for specifying more threads
out_file: (a file name)
        The output volume for CARegister
        flag: %s, position: -1
subjects_dir: (an existing directory name)
        subjects directory
template: (an existing file name)
        The template file in gca format
        flag: %s, position: -2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transform: (an existing file name)
        Specifies transform in lta format
        flag: -T %s
```

Outputs:

```
out_file: (a file name)
        The output file for CARegister
```

77.6 ConcatenateLTA

Link to code

Wraps command **mri_concatenate_lta**

concatenates two consecutive LTA transformations into one overall transformation, Out = LTA2*LTA1

77.6.1 Examples

```
>>> from nipype.interfaces.freesurfer import ConcatenateLTA
>>> conc_lta = ConcatenateLTA()
>>> conc_lta.inputs.in_lta1 = 'trans.mat'
>>> conc_lta.inputs.in_lta2 = 'trans.mat'
>>> conc_lta.cmdline
'mri_concatenate_lta trans.mat trans.mat trans-long.mat'
```

Inputs:

```
[Mandatory]
in_lta1: (an existing file name)
        maps some src1 to dst1
        flag: %s, position: -3
in_lta2: (an existing file name)
        maps dst1(src2) to dst2
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        the combined LTA maps: src1 to dst2 = LTA2*LTA1
        flag: %s, position: -1
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        the combined LTA maps: src1 to dst2 = LTA2*LTA1
```

77.7 DICOMConvert

Link to code
Wraps command **mri_convert**
use fs mri_convert to convert dicom files

77.7.1 Examples

```
>>> from nipype.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]
base_output_dir: (a directory name)
        directory in which subject directories are created
dicom_dir: (an existing directory name)
        dicom directory from which to convert dicom files

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
dicom_info: (an existing file name)
        File containing summary information from mri_parse_sdcmdir
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
file_mapping: (a list of items which are a tuple of the form: (a
         string, a string))
        defines the output fields of interface
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
ignore_single_slice: (a boolean)
        ignore volumes containing a single slice
        requires: dicom_info
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', nipype default value: niigz)
        defines the type of output file produced
seq_list: (a list of items which are a string)
        list of pulse sequence names to be converted.
        requires: dicom_info
subject_dir_template: (a string, nipype default value: S.%04d)
        template for subject directory name
subject_id: (any value)
        subject identifier to insert into template
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
None
```

77.8 EditWMwithAseg

Link to code

Wraps command **mri_edit_wm_with_aseg**

Edits a wm file using a segmentation

77.8.1 Examples

```
>>> from nipype.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]
brain_file: (an existing file name)
        Input brain/T1 file
        flag: %s, position: -3
in_file: (an existing file name)
        Input white matter segmentation file
        flag: %s, position: -4
out_file: (a file name)
        File to be written as output
        flag: %s, position: -1
seg_file: (an existing file name)
        Input presurf segmentation file
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
keep_in: (a boolean)
        Keep edits as found in input volume
        flag: -keep-in
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output edited WM file
```

77.9 FitMSParams

Link to code

Wraps command **mri_ms_fitparms**

Estimate tissue paramaters from a set of FLASH images.

77.9.1 Examples

```
>>> from nipype.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 an existing file name)
        list of FLASH images (must be in mgh format)
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
flip_list: (a list of items which are an integer (int or long))
        list of flip angles of the input files
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_dir: (a directory name)
        directory to store output in
        flag: %s, position: -1
subjects_dir: (an existing directory name)
        subjects directory
te_list: (a list of items which are a float)
        list of TEs of the input files (in msec)
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tr_list: (a list of items which are an integer (int or long))
        list of TRs of the input files (in msec)
xfm_list: (a list of items which are an existing file name)
        list of transform files to apply to each FLASH image
```

Outputs:

```
pd_image: (an existing file name)
        image of estimated proton density values
t1_image: (an existing file name)
        image of estimated T1 relaxation values
t2star_image: (an existing file name)
        image of estimated T2* values
```

77.10 MNIBiasCorrection

Link to code

Wraps 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] 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

77.10.1 Examples

```
>>> from nipype.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'
```

77.10.2 References:

[http://freesurfer.net/fswiki/mri_nu_correct.mni] [http://www.bic.mni.mcgill.ca/software/N3] [https://github.com/BIC-MNI/N3]
Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input volume. Input can be any format accepted by mri_convert.
        flag: --i %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
distance: (an integer (int or long))
        N3 -distance option
        flag: --distance %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
iterations: (an integer (int or long))
        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.
        flag: --n %d
mask: (an existing file name)
        brainmask volume. Input can be any format accepted by mri_convert.
        flag: --mask %s
no_rescale: (a boolean)
        do not rescale so that global mean of output == input global mean
        flag: --no-rescale
out_file: (a file name)
        output volume. Output can be any format accepted by mri_convert. If
        the output format is COR, then the directory must exist.
        flag: --o %s
```

```
    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.
            flag: --proto-iters %d
    shrink: (an integer (int or long))
            Shrink parameter for finer sampling (default is 4)
            flag: --shrink %d
    stop: (a float)
            Convergence threshold below which iteration stops (suggest 0.01 to
            0.0001)
            flag: --stop %f
    subjects_dir: (an existing directory name)
            subjects directory
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    transform: (an existing file name)
            tal.xfm. Use mri_make_uchar instead of conforming
            flag: --uchar %s
```

Outputs:

```
    out_file: (a file name)
            output volume
```

77.11 MRIConvert

Link to code

Wraps command **mri_convert**

use fs mri_convert to manipulate files

Note: Adds niigz as an output type option

77.11.1 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: (an existing file name)
            File to read/convert
            flag: --input_volume %s, position: -2

    [Optional]
    apply_inv_transform: (an existing file name)
            apply inverse transformation xfm file
            flag: --apply_inverse_transform %s
    apply_transform: (an existing file name)
```

```
        apply xfm file
        flag: --apply_transform %s
args: (a string)
        Additional parameters to the command
        flag: %s
ascii: (a boolean)
        save output as ascii col>row>slice>frame
        flag: --ascii
autoalign_matrix: (an existing file name)
        text file with autoalign matrix
        flag: --autoalign %s
color_file: (an existing file name)
        color file
        flag: --color_file %s
conform: (a boolean)
        conform to 1mm voxel size in coronal slice direction with 256^3 or
        more
        flag: --conform
conform_min: (a boolean)
        conform to smallest size
        flag: --conform_min
conform_size: (a float)
        conform to size_in_mm
        flag: --conform_size %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)
        flag: --crop %d %d %d
crop_gdf: (a boolean)
        apply GDF cropping
        flag: --crop_gdf
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>
        flag: --cropsize %d %d %d
cut_ends: (an integer (int or long))
        remove ncut slices from the ends
        flag: --cutends %d
cw256: (a boolean)
        confrom to dimensions of 256^3
        flag: --cw256
devolve_transform: (a string)
        subject id
        flag: --devolvexfm %s
drop_n: (an integer (int or long))
        drop the last n frames
        flag: --ndrop %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fill_parcellation: (a boolean)
        fill parcellation
        flag: --fill_parcellation
force_ras: (a boolean)
        use default when orientation info absent
        flag: --force_ras_good
frame: (an integer (int or long))
```

```
        keep only 0-based frame number
        flag: --frame %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)
        flag: --fsubsample %d %d %d
fwhm: (a float)
        smooth input volume by fwhm mm
        flag: --fwhm %f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_center: (a list of at most 3 items which are a float)
        <R coordinate> <A coordinate> <S coordinate>
        flag: --in_center %s
in_i_dir: (a tuple of the form: (a float, a float, a float))
        <R direction> <A direction> <S direction>
        flag: --in_i_direction %f %f %f
in_i_size: (an integer (int or long))
        input i size
        flag: --in_i_size %d
in_info: (a boolean)
        display input info
        flag: --in_info
in_j_dir: (a tuple of the form: (a float, a float, a float))
        <R direction> <A direction> <S direction>
        flag: --in_j_direction %f %f %f
in_j_size: (an integer (int or long))
        input j size
        flag: --in_j_size %d
in_k_dir: (a tuple of the form: (a float, a float, a float))
        <R direction> <A direction> <S direction>
        flag: --in_k_direction %f %f %f
in_k_size: (an integer (int or long))
        input k size
        flag: --in_k_size %d
in_like: (an existing file name)
        input looks like
        flag: --in_like %s
in_matrix: (a boolean)
        display input matrix
        flag: --in_matrix
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
        flag: --in_orientation %s
in_scale: (a float)
        input intensity scale factor
        flag: --scale %f
in_stats: (a boolean)
        display input stats
        flag: --in_stats
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
        flag: --in_type %s
invert_contrast: (a float)
        threshold for inversting contrast
        flag: --invert_contrast %f
midframe: (a boolean)
        keep only the middle frame
        flag: --mid-frame
no_change: (a boolean)
        don't change type of input to that of template
        flag: --nochange
no_scale: (a boolean)
        dont rescale values for COR
        flag: --no_scale 1
no_translate: (a boolean)
        ~~~
        flag: --no_translate
no_write: (a boolean)
        do not write output
        flag: --no_write
out_center: (a tuple of the form: (a float, a float, a float))
        <R coordinate> <A coordinate> <S coordinate>
        flag: --out_center %f %f %f
out_datatype: ('uchar' or 'short' or 'int' or 'float')
        output data type <uchar|short|int|float>
        flag: --out_data_type %s
out_file: (a file name)
        output filename or True to generate one
        flag: --output_volume %s, position: -1
out_i_count: (an integer (int or long))
        some count ?? in i direction
        flag: --out_i_count %d
out_i_dir: (a tuple of the form: (a float, a float, a float))
        <R direction> <A direction> <S direction>
        flag: --out_i_direction %f %f %f
out_i_size: (an integer (int or long))
        output i size
        flag: --out_i_size %d
out_info: (a boolean)
        display output info
        flag: --out_info
out_j_count: (an integer (int or long))
        some count ?? in j direction
        flag: --out_j_count %d
out_j_dir: (a tuple of the form: (a float, a float, a float))
        <R direction> <A direction> <S direction>
        flag: --out_j_direction %f %f %f
out_j_size: (an integer (int or long))
        output j size
        flag: --out_j_size %d
out_k_count: (an integer (int or long))
        some count ?? in k direction
        flag: --out_k_count %d
out_k_dir: (a tuple of the form: (a float, a float, a float))
```

```
        <R direction> <A direction> <S direction>
        flag: --out_k_direction %f %f %f
out_k_size: (an integer (int or long))
        output k size
        flag: --out_k_size %d
out_matrix: (a boolean)
        display output matrix
        flag: --out_matrix
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
        flag: --out_orientation %s
out_scale: (a float)
        output intensity scale factor
        flag: --out-scale %d
out_stats: (a boolean)
        display output stats
        flag: --out_stats
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')
        output file type
        flag: --out_type %s
parse_only: (a boolean)
        parse input only
        flag: --parse_only
read_only: (a boolean)
        read the input volume
        flag: --read_only
reorder: (a tuple of the form: (an integer (int or long), an integer
         (int or long), an integer (int or long)))
        olddim1 olddim2 olddim3
        flag: --reorder %d %d %d
resample_type: ('interpolate' or 'weighted' or 'nearest' or 'sinc' or
         'cubic')
        <interpolate|weighted|nearest|sinc|cubic> (default is interpolate)
        flag: --resample_type %s
reslice_like: (an existing file name)
        reslice output to match file
        flag: --reslice_like %s
sdcm_list: (an existing file name)
        list of DICOM files for conversion
        flag: --sdcmlist %s
skip_n: (an integer (int or long))
        skip the first n frames
        flag: --nskip %d
slice_bias: (a float)
        apply half-cosine bias field
        flag: --slice-bias %f
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
```

```
        flag: --slice-crop %d %d
slice_reverse: (a boolean)
        reverse order of slices, update vox2ras
        flag: --slice-reverse
smooth_parcellation: (a boolean)
        smooth parcellation
        flag: --smooth_parcellation
sphinx: (a boolean)
        change orientation info to sphinx
        flag: --sphinx
split: (a boolean)
        split output frames into separate output files.
        flag: --split
status_file: (a file name)
        status file for DICOM conversion
        flag: --status %s
subject_name: (a string)
        subject name ???
        flag: --subject_name %s
subjects_dir: (an existing directory name)
        subjects directory
te: (an integer (int or long))
        TE in msec
        flag: -te %d
template_info: (a boolean)
        dump info about template
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
        flag: --template_type %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
ti: (an integer (int or long))
        TI in msec (note upper case flag)
        flag: -ti %d
tr: (an integer (int or long))
        TR in msec
        flag: -tr %d
unwarp_gradient: (a boolean)
        unwarp gradient nonlinearity
        flag: --unwarp_gradient_nonlinearity
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
        flag: -voxsize %f %f %f
zero_ge_z_offset: (a boolean)
        zero ge z offset ???
        flag: --zero_ge_z_offset
zero_outlines: (a boolean)
        zero outlines
        flag: --zero_outlines
```

Outputs:

```
    out_file: (a list of items which are an existing file name)
            converted output file
```

77.12 MRIsCALabel

Link to code

Wraps command **mris_ca_label**

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 mris_ca_train).

77.12.1 Examples

```
    >>> from nipype.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 = "im1.nii" # in pracice, use .gcs extension
    >>> ca_label.inputs.smoothwm = "lh.pial"
    >>> ca_label.cmdline
    'mris_ca_label test lh lh.pial im1.nii lh.aparc.annot'
```

Inputs:

```
    [Mandatory]
    canonsurf: (an existing file name)
            Input canonical surface file
            flag: %s, position: -3
    classifier: (an existing file name)
            Classifier array input file
            flag: %s, position: -2
    curv: (an existing file name)
            implicit input {hemisphere}.curv
    hemisphere: ('lh' or 'rh')
            Hemisphere ('lh' or 'rh')
            flag: %s, position: -4
    smoothwm: (an existing file name)
            implicit input {hemisphere}.smoothwm
    subject_id: (a string, nipype default value: subject_id)
            Subject name or ID
            flag: %s, position: -5
    sulc: (an existing file name)
            implicit input {hemisphere}.sulc

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    aseg: (a file name)
            Undocumented flag. Autorecon3 uses ../mri/aseg.presurf.mgz as input
            file
```

```
        flag: -aseg %s
copy_inputs: (a boolean)
        Copies implicit inputs to node directory and creates a temp
        subjects_directory. Use this when running as a node
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
label: (a file name)
        Undocumented flag. Autorecon3 uses
        ../label/{hemisphere}.cortex.label as input file
        flag: -l %s
num_threads: (an integer (int or long))
        allows for specifying more threads
out_file: (a file name)
        Annotated surface output file
        flag: %s, position: -1
seed: (an integer (int or long))
        flag: -seed %d
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output volume from MRIsCALabel
```

77.13 Normalize

Link to code

Wraps 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.

77.13.1 Examples

```
>>> from nipype.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: (an existing file name)
        The input file for Normalize
        flag: %s, position: -2
```

```
    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    gradient: (an integer (int or long))
            use max intensity/mm gradient g (default=1)
            flag: -g %d
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    mask: (an existing file name)
            The input mask file for Normalize
            flag: -mask %s
    out_file: (a file name)
            The output file for Normalize
            flag: %s, position: -1
    segmentation: (an existing file name)
            The input segmentation for Normalize
            flag: -aseg %s
    subjects_dir: (an existing directory name)
            subjects directory
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    transform: (an existing file name)
            Tranform file from the header of the input file
```

Outputs:

```
    out_file: (a file name)
            The output file for Normalize
```

77.14 ParseDICOMDir

Link to code

Wraps command **mri_parse_sdcmdir**

Uses mri_parse_sdcmdir to get information from dicom directories

77.14.1 Examples

```
    >>> from nipype.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: (an existing directory name)
```

```
        path to siemens dicom directory
        flag: --d %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
dicom_info_file: (a file name, nipype default value: dicominfo.txt)
        file to which results are written
        flag: --o %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
sortbyrun: (a boolean)
        assign run numbers
        flag: --sortbyrun
subjects_dir: (an existing directory name)
        subjects directory
summarize: (a boolean)
        only print out info for run leaders
        flag: --summarize
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
dicom_info_file: (an existing file name)
        text file containing dicom information
```

77.15 ReconAll

Link to code

Wraps command **recon-all**

Uses recon-all to generate surfaces and parcellations of structural data from anatomical images of a subject.

77.15.1 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 .'
```

Inputs:

```
[Mandatory]

[Optional]
```

```
    T1_files: (a list of items which are an existing file name)
            name of T1 file to process
            flag: -i %s...
    T2_file: (an existing file name)
            Convert T2 image to orig directory
            flag: -T2 %s
    args: (a string)
            Additional parameters to the command
            flag: %s
    directive: ('all' or 'autorecon1' or 'autorecon2' or 'autorecon2-cp'
             or 'autorecon2-wm' or 'autorecon2-inflate1' or 'autorecon2-perhemi'
             or 'autorecon3' or 'localGI' or 'qcache', nipype default value:
             all)
            process directive
            flag: -%s, position: 0
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    flags: (a string)
            additional parameters
            flag: %s
    hemi: ('lh' or 'rh')
            hemisphere to process
            flag: -hemi %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    openmp: (an integer (int or long))
            Number of processors to use in parallel
            flag: -openmp %d
    subject_id: (a string, nipype default value: recon_all)
            subject name
            flag: -subjid %s
    subjects_dir: (an existing directory name)
            path to subjects directory
            flag: -sd %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    use_T2: (a boolean)
            Use converted T2 to refine the cortical surface
            flag: -T2pial
```

Outputs:

```
    BA_stats: (a list of items which are an existing file name)
            Brodmann Area statistics files
    T1: (an existing file name)
            Intensity normalized whole-head volume
    annot: (a list of items which are an existing file name)
            Surface annotation files
    aparc_a2009s_stats: (a list of items which are an existing file name)
            Aparc a2009s parcellation statistics files
    aparc_aseg: (a list of items which are an existing file name)
            Aparc parcellation projected into aseg volume
    aparc_stats: (a list of items which are an existing file name)
            Aparc parcellation statistics files
```

```
    aseg: (an existing file name)
            Volumetric map of regions from automatic segmentation
    aseg_stats: (a list of items which are an existing file name)
            Automated segmentation statistics file
    brain: (an existing file name)
            Intensity normalized brain-only volume
    brainmask: (an existing file name)
            Skull-stripped (brain-only) volume
    curv: (a list of items which are an existing file name)
            Maps of surface curvature
    curv_stats: (a list of items which are an existing file name)
            Curvature statistics files
    entorhinal_exvivo_stats: (a list of items which are an existing file
             name)
            Entorhinal exvivo statistics files
    filled: (an existing file name)
            Subcortical mass volume
    inflated: (a list of items which are an existing file name)
            Inflated surface meshes
    label: (a list of items which are an existing file name)
            Volume and surface label files
    norm: (an existing file name)
            Normalized skull-stripped volume
    nu: (an existing file name)
            Non-uniformity corrected whole-head volume
    orig: (an existing file name)
            Base image conformed to Freesurfer space
    pial: (a list of items which are an existing file name)
            Gray matter/pia mater surface meshes
    rawavg: (an existing file name)
            Volume formed by averaging input images
    ribbon: (a list of items which are an existing file name)
            Volumetric maps of cortical ribbons
    smoothwm: (a list of items which are an existing file name)
            Smoothed original surface meshes
    sphere: (a list of items which are an existing file name)
            Spherical surface meshes
    sphere_reg: (a list of items which are an existing file name)
            Spherical registration file
    subject_id: (a string)
            Subject name for whom to retrieve data
    subjects_dir: (an existing directory name)
            Freesurfer subjects directory.
    sulc: (a list of items which are an existing file name)
            Surface maps of sulcal depth
    thickness: (a list of items which are an existing file name)
            Surface maps of cortical thickness
    volume: (a list of items which are an existing file name)
            Surface maps of cortical volume
    white: (a list of items which are an existing file name)
            White/gray matter surface meshes
    wm: (an existing file name)
            Segmented white-matter volume
    wmparc: (an existing file name)
            Aparc parcellation projected into subcortical white matter
    wmparc_stats: (a list of items which are an existing file name)
            White matter parcellation statistics file
```

77.16 Resample

Link to code
Wraps command **mri_convert**
Use FreeSurfer mri_convert to up or down-sample image files

77.16.1 Examples

```
>>> from nipype.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: (an existing file name)
        file to resample
        flag: -i %s, position: -2
voxel_size: (a tuple of the form: (a float, a float, a float))
        triplet of output voxel sizes
        flag: -vs %.2f %.2f %.2f

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
resampled_file: (a file name)
        output filename
        flag: -o %s, position: -1
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
resampled_file: (an existing file name)
        output filename
```

77.17 RobustRegister

Link to code
Wraps command **mri_robust_register**
Perform intramodal linear registration (translation and rotation) using robust statistics.

77.17.1 Examples

```
>>> from nipype.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
'mri_robust_register --satit --initorient --lta structural_robustreg.lta --mov structural.nii --
```

77.17.2 References

Reuter, M, Rosas, HD, and Fischl, B, (2010). Highly Accurate Inverse Consistent Registration: A Robust Approach. Neuroimage 53(4) 1181-96.
Inputs:

```
[Mandatory]
auto_sens: (a boolean)
        auto-detect good sensitivity
        flag: --satit
        mutually_exclusive: outlier_sens
outlier_sens: (a float)
        set outlier sensitivity explicitly
        flag: --sat %.4f
        mutually_exclusive: auto_sens
source_file: (a file name)
        volume to be registered
        flag: --mov %s
target_file: (a file name)
        target volume for the registration
        flag: --dst %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
est_int_scale: (a boolean)
        estimate intensity scale (recommended for unnormalized images)
        flag: --iscale
force_double: (a boolean)
        use double-precision intensities
        flag: --doubleprec
force_float: (a boolean)
        use float intensities
        flag: --floattype
half_source: (a boolean or a file name)
        write source volume mapped to halfway space
        flag: --halfmov %s
half_source_xfm: (a boolean or a file name)
        write transform from source to halfway space
        flag: --halfmovlta %s
half_targ: (a boolean or a file name)
        write target volume mapped to halfway space
```

```
        flag: --halfdst %s
half_targ_xfm: (a boolean or a file name)
        write transform from target to halfway space
        flag: --halfdstlta %s
half_weights: (a boolean or a file name)
        write weights volume mapped to halfway space
        flag: --halfweights %s
high_iterations: (an integer (int or long))
        max # of times on highest resolution
        flag: --highit %d
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_xfm_file: (an existing file name)
        use initial transform on source
        flag: --transform
init_orient: (a boolean)
        use moments for initial orient (recommended for stripped brains)
        flag: --initorient
iteration_thresh: (a float)
        stop iterations when below threshold
        flag: --epsit %.3f
least_squares: (a boolean)
        use least squares instead of robust estimator
        flag: --leastsquares
mask_source: (an existing file name)
        image to mask source volume with
        flag: --maskmov %s
mask_target: (an existing file name)
        image to mask target volume with
        flag: --maskdst %s
max_iterations: (an integer (int or long))
        maximum # of times on each resolution
        flag: --maxit %d
no_init: (a boolean)
        skip transform init
        flag: --noinit
no_multi: (a boolean)
        work on highest resolution
        flag: --nomulti
out_reg_file: (a file name)
        registration file to write
        flag: --lta %s
outlier_limit: (a float)
        set maximal outlier limit in satit
        flag: --wlimit %.3f
registered_file: (a boolean or a file name)
        registered image; either True or filename
        flag: --warp %s
subjects_dir: (an existing directory name)
        subjects directory
subsample_thresh: (an integer (int or long))
        subsample if dimension is above threshold size
        flag: --subsample %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

```
trans_only: (a boolean)
        find 3 parameter translation only
        flag: --transonly
weights_file: (a boolean or a file name)
        weights image to write; either True or filename
        flag: --weights %s
write_vo2vox: (a boolean)
        output vox2vox matrix (default is RAS2RAS)
        flag: --vox2vox
```

Outputs:

```
half_source: (a file name)
        source image mapped to halfway space
half_source_xfm: (a file name)
        transform file to map source image to halfway space
half_targ: (a file name)
        target image mapped to halfway space
half_targ_xfm: (a file name)
        transform file to map target image to halfway space
half_weights: (a file name)
        weights image mapped to halfway space
out_reg_file: (an existing file name)
        output registration file
registered_file: (a file name)
        output image with registration applied
weights_file: (a file name)
        image of weights used
```

77.18 SegmentCC

Link to code

Wraps 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.

77.18.1 Examples

```
>>> from nipype.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: (an existing file name)
        Input aseg file to read from subjects directory
        flag: -aseg %s
in_norm: (an existing file name)
```

```
        Required undocumented input {subject}/mri/norm.mgz
out_rotation: (a file name)
        Global filepath for writing rotation lta
        flag: -lta %s
subject_id: (a string, nipype default value: subject_id)
        Subject name
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
copy_inputs: (a boolean)
        If running as a node, set this to True.This will copy the input
        files to the node directory.
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        Filename to write aseg including CC
        flag: -o %s
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output segmentation uncluding corpus collosum
out_rotation: (a file name)
        Output lta rotation file
```

77.19 SegmentWM

Link to code

Wraps 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.

77.19.1 Examples

```
>>> from nipype.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: (an existing file name)
        Input file for SegmentWM
        flag: %s, position: -2
out_file: (a file name)
        File to be written as output for SegmentWM
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output white matter segmentation
```

77.20 Smooth

Link to code

Wraps command **mris_volsmooth**

Use FreeSurfer mris_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.

77.20.1 Examples

```
>>> from nipype.interfaces.freesurfer import Smooth
>>> smoothvol = Smooth(in_file='functional.nii', smoothed_file = 'foo_out.nii', reg_file='regist
>>> smoothvol.cmdline
'mris_volsmooth --i functional.nii --reg register.dat --o foo_out.nii --fwhm 10.000000 --vol-fwh
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        source volume
        flag: --i %s
num_iters: (an integer >= 1)
```

```
        number of iterations instead of fwhm
        flag: --niters %d
        mutually_exclusive: surface_fwhm
reg_file: (an existing file name)
        registers volume to surface anatomical
        flag: --reg %s
surface_fwhm: (a floating point number >= 0.0)
        surface FWHM in mm
        flag: --fwhm %f
        mutually_exclusive: num_iters
        requires: reg_file

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
proj_frac: (a float)
        project frac of thickness a long surface normal
        flag: --projfrac %s
        mutually_exclusive: proj_frac_avg
proj_frac_avg: (a tuple of the form: (a float, a float, a float))
        average a long normal min max delta
        flag: --projfrac-avg %.2f %.2f %.2f
        mutually_exclusive: proj_frac
smoothed_file: (a file name)
        output volume
        flag: --o %s
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
vol_fwhm: (a floating point number >= 0.0)
        volume smoothing outside of surface
        flag: --vol-fwhm %f
```

Outputs:

```
smoothed_file: (an existing file name)
        smoothed input volume
```

77.21 SynthesizeFLASH

Link to code

Wraps command **mri_synthesize**

Synthesize a FLASH acquisition from T1 and proton density maps.

77.21.1 Examples

```
>>> from nipype.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]
flip_angle: (a float)
        flip angle (in degrees)
        flag: %.2f, position: 3
pd_image: (an existing file name)
        image of proton density values
        flag: %s, position: 6
t1_image: (an existing file name)
        image of T1 values
        flag: %s, position: 5
te: (a float)
        echo time (in msec)
        flag: %.3f, position: 4
tr: (a float)
        repetition time (in msec)
        flag: %.2f, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fixed_weighting: (a boolean)
        use a fixed weighting to generate optimal gray/white contrast
        flag: -w, position: 1
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        image to write
        flag: %s
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        synthesized FLASH acquisition
```

77.22 UnpackSDICOMDir

Link to code
Wraps command **unpacksdcmdir**
Use unpacksdcmdir to convert dicom files
Call unpacksdcmdir -help from the command line to see more information on using this command.

77.22.1 Examples

```
>>> from nipype.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]
config: (an existing file name)
        specify unpacking rules in file
        flag: -cfg %s
        mutually_exclusive: run_info, config, seq_config
run_info: (a tuple of the form: (an integer (int or long), a string,
         a string, a string))
        runno subdir format name : spec unpacking rules on cmdline
        flag: -run %d %s %s %s
        mutually_exclusive: run_info, config, seq_config
seq_config: (an existing file name)
        specify unpacking rules based on sequence
        flag: -seqcfg %s
        mutually_exclusive: run_info, config, seq_config
source_dir: (an existing directory name)
        directory with the DICOM files
        flag: -src %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
dir_structure: ('fsfast' or 'generic')
        unpack to specified directory structures
        flag: -%s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
log_file: (an existing file name)
        explicilty set log file
        flag: -log %s
no_info_dump: (a boolean)
        do not create infodump file
        flag: -noinfodump
```

```
no_unpack_err: (a boolean)
        do not try to unpack runs with errors
        flag: -no-unpackerr
output_dir: (a directory name)
        top directory into which the files will be unpacked
        flag: -targ %s
scan_only: (an existing file name)
        only scan the directory and put result in file
        flag: -scanonly %s
spm_zeropad: (an integer (int or long))
        set frame number zero padding width for SPM
        flag: -nspmzeropad %d
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
None
```

77.23 WatershedSkullStrip

Link to code

Wraps 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)

77.23.1 Examples

```
>>> from nipype.interfaces.freesurfer import WatershedSkullStrip
>>> skullstrip = WatershedSkullStrip()
>>> 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: (an existing file name)
        input volume
        flag: %s, position: -2
out_file: (a file name, nipype default value: brainmask.auto.mgz)
        output volume
        flag: %s, position: -1

[Optional]
```

```
    args: (a string)
            Additional parameters to the command
            flag: %s
    brain_atlas: (an existing file name)
            flag: -brain_atlas %s, position: -4
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    subjects_dir: (an existing directory name)
            subjects directory
    t1: (a boolean)
            specify T1 input volume (T1 grey value = 110)
            flag: -T1
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    transform: (a file name)
            undocumented
            flag: %s, position: -3
```

Outputs:

```
    out_file: (a file name)
            skull stripped brain volume
```

CHAPTER 78

interfaces.freesurfer.registration

78.1 EMRegister

Link to code
Wraps command **mri_em_register**
This program creates a tranform in lta format

78.1.1 Examples

```
>>> from nipype.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: (an existing file name)
        in brain volume
        flag: %s, position: -3
template: (an existing file name)
        template gca
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        use volume as a mask
        flag: -mask %s
nbrspacing: (an integer (int or long))
        align to atlas containing skull setting unknown_nbr_spacing =
```

```
        nbrspacing
        flag: -uns %d
num_threads: (an integer (int or long))
        allows for specifying more threads
out_file: (a file name)
        output transform
        flag: %s, position: -1
skull: (a boolean)
        align to atlas containing skull (uns=5)
        flag: -skull
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transform: (an existing file name)
        Previously computed transform
        flag: -t %s
```

Outputs:

```
out_file: (a file name)
        output transform
```

78.2 MPRtoMNI305

Link to code
Wraps command **mpr2mni305**
For complete details, see FreeSurfer documentation

78.2.1 Examples

```
>>> from nipype.interfaces.freesurfer import MPRtoMNI305, Info
>>> mprtomni305 = MPRtoMNI305()
>>> mprtomni305.inputs.target = 'structural.nii'
>>> mprtomni305.inputs.reference_dir = '.'
>>> mprtomni305.cmdline
'mpr2mni305 output'
>>> mprtomni305.inputs.out_file = 'struct_out'
>>> mprtomni305.cmdline
'mpr2mni305 struct_out'
>>> mprtomni305.inputs.environ['REFDIR'] == os.path.join(Info.home(), 'average')
True
>>> mprtomni305.inputs.environ['MPR2MNI305_TARGET']
'structural'
>>> mprtomni305.run()
```

Inputs:

```
[Mandatory]
reference_dir: (an existing directory name, nipype default value: )
        TODO
target: (a string, nipype default value: )
        input atlas file

[Optional]
```

```
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    in_file: (a file name, nipype default value: )
            the input file prefix for MPRtoMNI305
            flag: %s
    subjects_dir: (an existing directory name)
            subjects directory
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    log_file: (an existing file name, nipype default value:
             stdout.nipype)
            The output log
    out_file: (a file name)
            The output file '<in_file>_to_<target>_t4_vox2vox.txt'
```

78.3 Paint

Link to code

Wraps command **mrisp_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".

78.3.1 Examples

```
    >>> from nipype.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: (an existing file name)
            Surface file with grid (vertices) onto which the template data is to
            be sampled or 'painted'
            flag: %s, position: -2
    template: (an existing file name)
            Template file
            flag: %s, position: -3
```

```
    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    averages: (an integer (int or long))
            Average curvature patterns
            flag: -a %d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    out_file: (a file name)
            File containing a surface-worth of per-vertex values, saved in
            'curvature' format.
            flag: %s, position: -1
    subjects_dir: (an existing directory name)
            subjects directory
    template_param: (an integer (int or long))
            Frame number of the input template
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (a file name)
            File containing a surface-worth of per-vertex values, saved in
            'curvature' format.
```

78.4 Register

Link to code

Wraps command **mris_register**

This program registers a surface to an average surface template.

78.4.1 Examples

```
    >>> from nipype.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_sulc: (an existing file name)
            Undocumented mandatory input file
```

```
        ${SUBJECTS_DIR}/surf/{hemisphere}.sulc
in_surf: (an existing file name)
        Surface to register, often {hemi}.sphere
        flag: %s, position: -3
target: (an existing file name)
        The data to register to. In normal recon-all usage, this is a
        template file for average surface.
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
curv: (a boolean)
        Use smoothwm curvature for final alignment
        flag: -curv
        requires: in_smoothwm
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_smoothwm: (an existing file name)
        Undocumented input file ${SUBJECTS_DIR}/surf/{hemisphere}.smoothwm
out_file: (a file name)
        Output surface file to capture registration
        flag: %s, position: -1
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output surface file to capture registration
```

78.5 RegisterAVItoTalairach

Link to code

Wraps command **avi2talxfm**

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 talsrcimg.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

78.5.1 Examples

```
>>> from nipype.interfaces.freesurfer import RegisterAVItoTalairach
>>> register = RegisterAVItoTalairach()
>>> register.inputs.in_file = 'structural.mgz'
>>> register.inputs.target = 'mni305.cor.mgz'
>>> register.inputs.vox2vox = 'talsrcimg_to_structural_t4_vox2vox.txt'
>>> register.cmdline
'avi2talxfm structural.mgz mni305.cor.mgz talsrcimg_to_structural_t4_vox2vox.txt talairach.auto.
```

```
>>> register.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        The input file
        flag: %s, position: 0
target: (an existing file name)
        The target file
        flag: %s, position: 1
vox2vox: (an existing file name)
        The vox2vox file
        flag: %s, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name, nipype default value: talairach.auto.xfm)
        The transform output
        flag: %s, position: 3
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
log_file: (an existing file name, nipype default value:
         stdout.nipype)
        The output log
out_file: (a file name)
        The output file for RegisterAVItoTalairach
```

CHAPTER 79

interfaces.freesurfer.utils

79.1 AddXFormToHeader

Link to code
Wraps 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()
```

79.1.1 References:

[https://surfer.nmr.mgh.harvard.edu/fswiki/mri_add_xform_to_header]
Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input volume
        flag: %s, position: -2
transform: (a file name)
        xfm file
        flag: %s, position: -3

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
copy_name: (a boolean)
        do not try to load the xfmfile, just copy name
        flag: -c
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
```

```
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name, nipype default value: output.mgz)
        output volume
        flag: %s, position: -1
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        be verbose
        flag: -v
```

Outputs:

```
out_file: (an existing file name)
        output volume
```

79.2 Aparc2Aseg

Link to code

Wraps 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.

79.2.1 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
'mri_aparc2aseg --labelwm  --o aparc+aseg.mgz --rip-unknown --s subject_id'
```

Inputs:

```
    [Mandatory]
    lh_annotation: (an existing file name)
            Input file must be <subject_id>/label/lh.aparc.annot
    lh_pial: (an existing file name)
            Input file must be <subject_id>/surf/lh.pial
    lh_ribbon: (an existing file name)
            Input file must be <subject_id>/mri/lh.ribbon.mgz
    lh_white: (an existing file name)
            Input file must be <subject_id>/surf/lh.white
    out_file: (a file name)
            Full path of file to save the output segmentation in
            flag: --o %s
    rh_annotation: (an existing file name)
            Input file must be <subject_id>/label/rh.aparc.annot
    rh_pial: (an existing file name)
            Input file must be <subject_id>/surf/rh.pial
    rh_ribbon: (an existing file name)
            Input file must be <subject_id>/mri/rh.ribbon.mgz
    rh_white: (an existing file name)
            Input file must be <subject_id>/surf/rh.white
    ribbon: (an existing file name)
            Input file must be <subject_id>/mri/ribbon.mgz
    subject_id: (a string, nipype default value: subject_id)
            Subject being processed
            flag: --s %s

    [Optional]
    a2009s: (a boolean)
            Using the a2009s atlas
            flag: --a2009s
    args: (a string)
            Additional parameters to the command
            flag: %s
    aseg: (an existing file name)
            Input aseg file
            flag: --aseg %s
    copy_inputs: (a boolean)
            If running as a node, set this to True.This will copy the input
            files to the node directory.
    ctxseg: (an existing file name)
            flag: --ctxseg %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    filled: (an existing file name)
            Implicit input filled file. Only required with FS v5.3.
    hypo_wm: (a boolean)
            Label hypointensities as WM
            flag: --hypo-as-wm
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    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
            flag: --labelwm
```

```
rip_unknown: (a boolean)
        Do not label WM based on 'unknown' corical label
        flag: --rip-unknown
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
volmask: (a boolean)
        Volume mask flag
        flag: --volmask
```

Outputs:

```
out_file: (a file name)
        Output aseg file
        flag: %s
```

79.3 Apas2Aseg

Link to code

Wraps 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).

79.3.1 Examples

```
>>> from nipype.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: (an existing file name)
        Input aparc+aseg.mgz
        flag: --i %s
out_file: (a file name)
        Output aseg file
        flag: --o %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

```
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output aseg file
        flag: %s
```

79.4 ApplyMask

Link to code

Wraps 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: (an existing file name)
        input image (will be masked)
        flag: %s, position: -3
mask_file: (an existing file name)
        image defining mask space
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
invert_xfm: (a boolean)
        invert transformation
        flag: -invert
keep_mask_deletion_edits: (a boolean)
        transfer voxel-deletion edits (voxels=1) from mask to out vol
        flag: -keep_mask_deletion_edits
mask_thresh: (a float)
        threshold mask before applying
        flag: -T %.4f
out_file: (a file name)
        final image to write
        flag: %s, position: -1
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
```

```
        output, `file` - writes output to file, `none` - output is ignored
transfer: (an integer (int or long))
        transfer only voxel value # from mask to out
        flag: -transfer %d
use_abs: (a boolean)
        take absolute value of mask before applying
        flag: -abs
xfm_file: (an existing file name)
        LTA-format transformation matrix to align mask with input
        flag: -xform %s
xfm_source: (an existing file name)
        image defining transform source space
        flag: -lta_src %s
xfm_target: (an existing file name)
        image defining transform target space
        flag: -lta_dst %s
```

Outputs:

```
out_file: (an existing file name)
        masked image
```

79.5 CheckTalairachAlignment

Link to code
Wraps command **talairach_afd**
This program detects Talairach alignment failures

79.5.1 Examples

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        specify the talairach.xfm file to check
        flag: -xfm %s, position: -1
        mutually_exclusive: subject
subject: (a string)
        specify subject's name
        flag: -subj %s, position: -1
        mutually_exclusive: in_file

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
```

```
          with values which are a value of type 'str', nipype default value:
          {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
threshold: (a float)
        Talairach transforms for subjects with p-values <= T are considered
        as very unlikely default=0.010
        flag: -T %.3f
```

Outputs:

```
out_file: (a file name)
        The input file for CheckTalairachAlignment
```

79.6 Contrast

Link to code
Wraps command **pctsurfcon**
Compute surface-wise gray/white contrast

79.6.1 Examples

```
>>> from nipype.interfaces.freesurfer import Contrast
>>> contrast = Contrast()
>>> contrast.inputs.subject_id = '10335'
>>> contrast.inputs.hemisphere = 'lh'
>>> contrast.inputs.white = 'lh.white'
>>> contrast.inputs.thickness = 'lh.thickness'
>>> contrast.inputs.annotation = '../label/lh.aparc.annot'
>>> contrast.inputs.cortex = '../label/lh.cortex.label'
>>> contrast.inputs.rawavg = '../mri/rawavg.mgz'
>>> contrast.inputs.orig = '../mri/orig.mgz'
>>> contrast.cmdline
'pctsurfcon --lh-only --s 10335'
```

Inputs:

```
[Mandatory]
annotation: (a file name)
        Input annotation file must be
        <subject_id>/label/<hemisphere>.aparc.annot
cortex: (a file name)
        Input cortex label must be
        <subject_id>/label/<hemisphere>.cortex.label
hemisphere: ('lh' or 'rh')
        Hemisphere being processed
        flag: --%s-only
orig: (an existing file name)
        Implicit input file mri/orig.mgz
```

```
    rawavg: (an existing file name)
            Implicit input file mri/rawavg.mgz
    subject_id: (a string, nipype default value: subject_id)
            Subject being processed
            flag: --s %s
    thickness: (an existing file name)
            Input file must be <subject_id>/surf/?h.thickness
    white: (an existing file name)
            Input file must be <subject_id>/surf/<hemisphere>.white

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    copy_inputs: (a boolean)
            If running as a node, set this to True.This will copy the input
            files to the node directory.
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    subjects_dir: (an existing directory name)
            subjects directory
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_contrast: (a file name)
            Output contrast file from Contrast
    out_log: (an existing file name)
            Output log from Contrast
    out_stats: (a file name)
            Output stats file from Contrast
```

79.7 Curvature

Link to code

Wraps 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.

79.7.1 Examples

```
>>> from nipype.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: (an existing file name)
            Input file for Curvature
            flag: %s, position: -2

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    averages: (an integer (int or long))
            Perform this number iterative averages of curvature measure before
            saving
            flag: -a %d
    copy_input: (a boolean)
            Copy input file to current directory
    distances: (a tuple of the form: (an integer (int or long), an
             integer (int or long)))
            Undocumented input integer distances
            flag: -distances %d %d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    n: (a boolean)
            Undocumented boolean flag
            flag: -n
    save: (a boolean)
            Save curvature files (will only generate screen output without this
            option)
            flag: -w
    subjects_dir: (an existing directory name)
            subjects directory
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    threshold: (a float)
            Undocumented input threshold
            flag: -thresh %.3f
```

Outputs:

```
    out_gauss: (a file name)
            Gaussian curvature output file
    out_mean: (a file name)
            Mean curvature output file
```

79.8 CurvatureStats

Link to code

Wraps 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.

79.8.1 Examples

```
>>> from nipype.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 pi
```

Inputs:

```
[Mandatory]
curvfile1: (an existing file name)
        Input file for CurvatureStats
        flag: %s, position: -2
curvfile2: (an existing file name)
        Input file for CurvatureStats
        flag: %s, position: -1
hemisphere: ('lh' or 'rh')
        Hemisphere being processed
        flag: %s, position: -3
subject_id: (a string, nipype default value: subject_id)
        Subject being processed
        flag: %s, position: -4

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
copy_inputs: (a boolean)
        If running as a node, set this to True.This will copy the input
        files to the node directory.
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
min_max: (a boolean)
        Output min / max information for the processed curvature.
        flag: -m
out_file: (a file name)
        Output curvature stats file
```

```
        flag: -o %s
subjects_dir: (an existing directory name)
        subjects directory
surface: (an existing file name)
        Specify surface file for CurvatureStats
        flag: -F %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
values: (a boolean)
        Triggers a series of derived curvature values
        flag: -G
write: (a boolean)
        Write curvature files
        flag: --writeCurvatureFiles
```

Outputs:

```
out_file: (a file name)
        Output curvature stats file
```

79.9 EulerNumber

Link to code

Wraps command **mris_euler_number**

This program computes EulerNumber for a cortical surface

79.9.1 Examples

```
>>> from nipype.interfaces.freesurfer import EulerNumber
>>> ft = EulerNumber()
>>> ft.inputs.in_file = 'lh.pial'
>>> ft.cmdline
'mris_euler_number lh.pial'
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Input file for EulerNumber
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
```

```
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output file for EulerNumber
```

79.10 ExtractMainComponent

Link to code
Wraps command **mris_extract_main_component**
Extract the main component of a tesselated surface

79.10.1 Examples

```
>>> from nipype.interfaces.freesurfer import ExtractMainComponent
>>> mcmp = ExtractMainComponent(in_file='lh.pial')
>>> mcmp.cmdline
'mris_extract_main_component lh.pial lh.maincmp'
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input surface file
        flag: %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        surface containing main component
        flag: %s, position: 2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        surface containing main component
```

79.11 FixTopology

Link to code
Wraps 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.

79.11.1 Examples

```
>>> from nipype.interfaces.freesurfer import FixTopology
>>> ft = FixTopology()
>>> ft.inputs.in_orig = 'lh.orig'
>>> ft.inputs.in_inflated = 'lh.inflated'
>>> ft.inputs.sphere = 'lh.qsphere.nofix'
>>> ft.inputs.hemisphere = 'lh'
>>> ft.inputs.subject_id = '10335'
>>> ft.inputs.mgz = True
>>> ft.inputs.ga = True
>>> ft.cmdline
'mris_fix_topology -ga -mgz -sphere qsphere.nofix 10335 lh'
```

Inputs:

```
[Mandatory]
copy_inputs: (a boolean)
        If running as a node, set this to True otherwise, the topology
        fixing will be done in place.
hemisphere: (a string)
        Hemisphere being processed
        flag: %s, position: -1
in_brain: (an existing file name)
        Implicit input brain.mgz
in_inflated: (an existing file name)
        Undocumented input file <hemisphere>.inflated
in_orig: (an existing file name)
        Undocumented input file <hemisphere>.orig
in_wm: (an existing file name)
        Implicit input wm.mgz
subject_id: (a string, nipype default value: subject_id)
        Subject being processed
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ga: (a boolean)
        No documentation. Direct questions to analysis-
        bugs@nmr.mgh.harvard.edu
        flag: -ga
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mgz: (a boolean)
        No documentation. Direct questions to analysis-
        bugs@nmr.mgh.harvard.edu
        flag: -mgz
seed: (an integer (int or long))
        Seed for setting random number generator
```

```
        flag: -seed %d
sphere: (a file name)
        Sphere input file
        flag: -sphere %s
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output file for FixTopology
```

79.12 Jacobian

Link to code

Wraps command **mris_jacobian**

This program computes the Jacobian of a surface mapping.

79.12.1 Examples

```
>>> from nipype.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_mappedsurf: (an existing file name)
        Mapped surface
        flag: %s, position: -2
in_origsurf: (an existing file name)
        Original surface
        flag: %s, position: -3

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        Output Jacobian of the surface mapping
        flag: %s, position: -1
subjects_dir: (an existing directory name)
        subjects directory
```

```
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output Jacobian of the surface mapping
```

79.13 MRIFill

Link to code

Wraps command **mri_fill**

This program creates hemispheric cutting planes and fills white matter with specific values for subsequent surface tesselation.

79.13.1 Examples

```
>>> from nipype.interfaces.freesurfer import MRIFill
>>> fill = MRIFill()
>>> fill.inputs.in_file = 'wm.mgz'
>>> fill.inputs.out_file = 'filled.mgz'
>>> fill.cmdline
'mri_fill wm.mgz filled.mgz'
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Input white matter file
        flag: %s, position: -2
out_file: (a file name)
        Output filled volume file name for MRIFill
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
log_file: (a file name)
        Output log file for MRIFill
        flag: -a %s
segmentation: (an existing file name)
        Input segmentation file for MRIFill
        flag: -segmentation %s
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
```

```
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transform: (an existing file name)
        Input transform file for MRIFill
        flag: -xform %s
```

Outputs:

```
log_file: (a file name)
        Output log file from MRIFill
out_file: (a file name)
        Output file from MRIFill
```

79.14 MRIMarchingCubes

Link to code

Wraps command **mri_mc**

Uses Freesurfer's mri_mc to create surfaces by tessellating a given input volume

79.14.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Input volume to tesselate voxels from.
        flag: %s, position: 1
label_value: (an integer (int or long))
        Label value which to tesselate from the input volume. (integer, if
        input is "filled.mgz" volume, 127 is rh, 255 is lh)
        flag: %d, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
connectivity_value: (an integer (int or long), nipype default value:
         1)
        Alter the marching cubes connectivity: 1=6+,2=18,3=6,4=26
        (default=1)
        flag: %d, position: -1
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output filename or True to generate one
```

```
        flag: ./%s, position: -2
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
surface: (an existing file name)
        binary surface of the tessellation
```

79.15 MRIPretess

Link to code
Wraps command **mri_pretess**
Uses Freesurfer's mri_pretess to prepare volumes to be tessellated.

79.15.1 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.

79.15.2 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_filled: (an existing file name)
        filled volume, usually wm.mgz
        flag: %s, position: -4
in_norm: (an existing file name)
        the normalized, brain-extracted T1w image. Usually norm.mgz
        flag: %s, position: -2
label: (a string or an integer (int or long), nipype 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)
        flag: %s, position: -3

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
```

```
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
keep: (a boolean)
        keep WM edits
        flag: -keep
nocorners: (a boolean)
        do not remove corner configurations in addition to edge ones.
        flag: -nocorners
out_file: (a file name)
        the output file after mri_pretess.
        flag: %s, position: -1
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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.
        flag: -test
```

Outputs:

```
out_file: (an existing file name)
        output file after mri_pretess
```

79.16 MRITessellate

Link to code

Wraps command **mri_tessellate**

Uses Freesurfer's mri_tessellate to create surfaces by tessellating a given input volume

79.16.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Input volume to tesselate voxels from.
        flag: %s, position: -3
label_value: (an integer (int or long))
        Label value which to tesselate from the input volume. (integer, if
        input is "filled.mgz" volume, 127 is rh, 255 is lh)
        flag: %d, position: -2

[Optional]
args: (a string)
```

```
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output filename or True to generate one
        flag: %s, position: -1
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tesselate_all_voxels: (a boolean)
        Tessellate the surface of all voxels with different labels
        flag: -a
use_real_RAS_coordinates: (a boolean)
        Saves surface with real RAS coordinates where c_(r,a,s) != 0
        flag: -n
```

Outputs:

```
surface: (an existing file name)
        binary surface of the tessellation
```

79.17 MRIsCalc

Link to code

Wraps 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.

79.17.1 Examples

```
>>> from nipype.interfaces.freesurfer import MRIsCalc
>>> example = MRIsCalc()
>>> example.inputs.in_file1 = 'lh.area'
>>> example.inputs.in_file2 = 'lh.area.pial'
>>> example.inputs.action = 'add'
>>> example.inputs.out_file = 'area.mid'
>>> example.cmdline
'mris_calc -o lh.area.mid lh.area add lh.area.pial'
```

Inputs:

```
[Mandatory]
action: (a string)
```

```
        Action to perform on input file(s)
        flag: %s, position: -2
in_file1: (an existing file name)
        Input file 1
        flag: %s, position: -3
out_file: (a file name)
        Output file after calculation
        flag: -o %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_file2: (an existing file name)
        Input file 2
        flag: %s, position: -1
        mutually_exclusive: in_float, in_int
in_float: (a float)
        Input float
        flag: %f, position: -1
        mutually_exclusive: in_file2, in_int
in_int: (an integer (int or long))
        Input integer
        flag: %d, position: -1
        mutually_exclusive: in_file2, in_float
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output file after calculation
```

79.18 MRIsConvert

Link to code

Wraps command **mris_convert**

Uses Freesurfer's mris_convert to convert surface files to various formats

79.18.1 Example

```
>>> import nipype.interfaces.freesurfer as fs
>>> mris = fs.MRIsConvert()
>>> mris.inputs.in_file = 'lh.pial'
>>> mris.inputs.out_datatype = 'gii'
>>> mris.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        File to read/convert
        flag: %s, position: -2
out_datatype: ('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
out_file: (a file name)
        output filename or True to generate one
        flag: %s, position: -1
        mutually_exclusive: out_datatype

[Optional]
annot_file: (an existing file name)
        input is annotation or gifti label data
        flag: --annot %s
args: (a string)
        Additional parameters to the command
        flag: %s
dataarray_num: (an integer (int or long))
        if input is gifti, 'num' specifies which data array to use
        flag: --da_num %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
functional_file: (an existing file name)
        input is functional time-series or other multi-frame data (must
        specify surface)
        flag: -f %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
label_file: (an existing file name)
        infile is .label file, label is name of this label
        flag: --label %s
labelstats_outfile: (a file name)
        outfile is name of gifti file to which label stats will be written
        flag: --labelstats %s
normal: (a boolean)
        output is an ascii file where vertex data
        flag: -n
origname: (a string)
        read orig positions
        flag: -o %s
parcstats_file: (an existing file name)
        infile is name of text file containing label/val pairs
        flag: --parcstats %s
patch: (a boolean)
        input is a patch, not a full surface
        flag: -p
rescale: (a boolean)
        rescale vertex xyz so total area is same as group average
        flag: -r
```

```
    scalarcurv_file: (an existing file name)
            input is scalar curv overlay file (must still specify surface)
            flag: -c %s
    scale: (a float)
            scale vertex xyz by scale
            flag: -s %.3f
    subjects_dir: (an existing directory name)
            subjects directory
    talairachxfm_subjid: (a string)
            apply talairach xfm of subject to vertex xyz
            flag: -t %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    to_scanner: (a boolean)
            convert coordinates from native FS (tkr) coords to scanner coords
            flag: --to-scanner
    to_tkr: (a boolean)
            convert coordinates from scanner coords to native FS (tkr) coords
            flag: --to-tkr
    vertex: (a boolean)
            Writes out neighbors of a vertex in each row
            flag: -v
    xyz_ascii: (a boolean)
            Print only surface xyz to ascii file
            flag: -a
```

Outputs:

```
    converted: (an existing file name)
            converted output surface
```

79.19 MRIsInflate

Link to code

Wraps command **mris_inflate**

This program will inflate a cortical surface.

79.19.1 Examples

```
    >>> from nipype.interfaces.freesurfer import MRIsInflate
    >>> inflate = MRIsInflate()
    >>> inflate.inputs.in_file = 'lh.pial'
    >>> inflate.inputs.no_save_sulc = True
    >>> inflate.cmdline
    'mris_inflate -no-save-sulc lh.pial lh.inflated'
```

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            Input file for MRIsInflate
            flag: %s, position: -2

    [Optional]
    args: (a string)
```

```
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
no_save_sulc: (a boolean)
        Do not save sulc file as output
        flag: -no-save-sulc
        mutually_exclusive: out_sulc
out_file: (a file name)
        Output file for MRIsInflate
        flag: %s, position: -1
out_sulc: (a file name)
        Output sulc file
        mutually_exclusive: no_save_sulc
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output file for MRIsInflate
out_sulc: (a file name)
        Output sulc file
```

79.20 MakeAverageSubject

Link to code

Wraps command **make_average_subject**

Make an average freesurfer subject

79.20.1 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 string)
        freesurfer subjects ids to average
        flag: --subjects %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
```

```
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    out_name: (a file name, nipype default value: average)
            name for the average subject
            flag: --out %s
    subjects_dir: (an existing directory name)
            subjects directory
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    average_subject_name: (a string)
            Output registration file
```

79.21 MakeSurfaces

Link to code

Wraps 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.

79.21.1 Examples

```
    >>> from nipype.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
            flag: %s, position: -1
    in_filled: (an existing file name)
            Implicit input file filled.mgz
    in_orig: (an existing file name)
            Implicit input file <hemisphere>.orig
            flag: -orig %s
    in_wm: (an existing file name)
```

```
        Implicit input file wm.mgz
subject_id: (a string, nipype default value: subject_id)
        Subject being processed
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
copy_inputs: (a boolean)
        If running as a node, set this to True.This will copy the input
        files to the node directory.
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fix_mtl: (a boolean)
        Undocumented flag
        flag: -fix_mtl
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_T1: (an existing file name)
        Input brain or T1 file
        flag: -T1 %s
in_aseg: (an existing file name)
        Input segmentation file
        flag: -aseg %s
in_label: (an existing file name)
        Implicit input label/<hemisphere>.aparc.annot
        mutually_exclusive: noaparc
in_white: (an existing file name)
        Implicit input that is sometimes used
longitudinal: (a boolean)
        No documentation (used for longitudinal processing)
        flag: -long
maximum: (a float)
        No documentation (used for longitudinal processing)
        flag: -max %.1f
mgz: (a boolean)
        No documentation. Direct questions to analysis-
        bugs@nmr.mgh.harvard.edu
        flag: -mgz
no_white: (a boolean)
        Undocumented flag
        flag: -nowhite
noaparc: (a boolean)
        No documentation. Direct questions to analysis-
        bugs@nmr.mgh.harvard.edu
        flag: -noaparc
        mutually_exclusive: in_label
orig_pial: (an existing file name)
        Specify a pial surface to start with
        flag: -orig_pial %s
        requires: in_label
orig_white: (an existing file name)
        Specify a white surface to start with
        flag: -orig_white %s
```

```
    subjects_dir: (an existing directory name)
            subjects directory
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    white: (a string)
            White surface name
            flag: -white %s
    white_only: (a boolean)
            Undocumented flage
            flag: -whiteonly
```

Outputs:

```
    out_area: (a file name)
            Output area file for MakeSurfaces
    out_cortex: (a file name)
            Output cortex file for MakeSurfaces
    out_curv: (a file name)
            Output curv file for MakeSurfaces
    out_pial: (a file name)
            Output pial surface for MakeSurfaces
    out_thickness: (a file name)
            Output thickness file for MakeSurfaces
    out_white: (a file name)
            Output white matter hemisphere surface
```

79.22 ParcellationStats

Link to code

Wraps command **mris_anatomical_stats**

This program computes a number of anatomical properties.

79.22.1 Examples

```
>>> from nipype.interfaces.freesurfer import ParcellationStats
>>> import os
>>> parcstats = ParcellationStats()
>>> parcstats.inputs.subject_id = '10335'
>>> parcstats.inputs.hemisphere = 'lh'
>>> parcstats.inputs.wm = './../mri/wm.mgz'
>>> parcstats.inputs.transform = './../mri/transforms/talairach.xfm'
>>> parcstats.inputs.brainmask = './../mri/brainmask.mgz'
>>> parcstats.inputs.aseg = './../mri/aseg.presurf.mgz'
>>> parcstats.inputs.ribbon = './../mri/ribbon.mgz'
>>> parcstats.inputs.lh_pial = 'lh.pial'
>>> parcstats.inputs.rh_pial = 'lh.pial'
>>> parcstats.inputs.lh_white = 'lh.white'
>>> parcstats.inputs.rh_white = 'rh.white'
>>> parcstats.inputs.thickness = 'lh.thickness'
>>> parcstats.inputs.surface = 'white'
>>> parcstats.inputs.out_table = 'lh.test.stats'
>>> parcstats.inputs.out_color = 'test.ctab'
>>> parcstats.cmdline
'mris_anatomical_stats -c test.ctab -f lh.test.stats 10335 lh white'
```

Inputs:

```
[Mandatory]
aseg: (an existing file name)
        Input file must be <subject_id>/mri/aseg.presurf.mgz
brainmask: (an existing file name)
        Input file must be <subject_id>/mri/brainmask.mgz
hemisphere: ('lh' or 'rh')
        Hemisphere being processed
        flag: %s, position: -2
lh_pial: (an existing file name)
        Input file must be <subject_id>/surf/lh.pial
lh_white: (an existing file name)
        Input file must be <subject_id>/surf/lh.white
rh_pial: (an existing file name)
        Input file must be <subject_id>/surf/rh.pial
rh_white: (an existing file name)
        Input file must be <subject_id>/surf/rh.white
ribbon: (an existing file name)
        Input file must be <subject_id>/mri/ribbon.mgz
subject_id: (a string, nipype default value: subject_id)
        Subject being processed
        flag: %s, position: -3
thickness: (an existing file name)
        Input file must be <subject_id>/surf/?h.thickness
transform: (an existing file name)
        Input file must be <subject_id>/mri/transforms/talairach.xfm
wm: (an existing file name)
        Input file must be <subject_id>/mri/wm.mgz

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
copy_inputs: (a boolean)
        If running as a node, set this to True.This will copy the input
        files to the node directory.
cortex_label: (an existing file name)
        implicit input file {hemi}.cortex.label
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_annotation: (a file name)
        compute properties for each label in the annotation file separately
        flag: -a %s
        mutually_exclusive: in_label
in_cortex: (a file name)
        Input cortex label
        flag: -cortex %s
in_label: (a file name)
        limit calculations to specified label
        flag: -l %s
        mutually_exclusive: in_annotatoin, out_color
mgz: (a boolean)
        Look for mgz files
```

```
        flag: -mgz
out_color: (a file name)
        Output annotation files's colortable to text file
        flag: -c %s
        mutually_exclusive: in_label
out_table: (a file name)
        Table output to tablefile
        flag: -f %s
        requires: tabular_output
subjects_dir: (an existing directory name)
        subjects directory
surface: (a string)
        Input surface (e.g. 'white')
        flag: %s, position: -1
tabular_output: (a boolean)
        Tabular output
        flag: -b
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
th3: (a boolean)
        turns on new vertex-wise volume calc for mris_anat_stats
        flag: -th3
        requires: cortex_label
```

Outputs:

```
out_color: (a file name)
        Output annotation files's colortable to text file
out_table: (a file name)
        Table output to tablefile
```

79.23 RelabelHypointensities

Link to code

Wraps command **mri_relabel_hypointensities**

Relabel Hypointensities

79.23.1 Examples

```
>>> from nipype.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]
aseg: (an existing file name)
        Input aseg file
        flag: %s, position: -3
lh_white: (an existing file name)
```

```
        Implicit input file must be lh.white
rh_white: (an existing file name)
        Implicit input file must be rh.white

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        Output aseg file
        flag: %s, position: -1
subjects_dir: (an existing directory name)
        subjects directory
surf_directory: (a directory name, nipype default value: .)
        Directory containing lh.white and rh.white
        flag: %s, position: -2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output aseg file
        flag: %s
```

79.24 RemoveIntersection

Link to code

Wraps command **mris_remove_intersection**

This program removes the intersection of the given MRI

79.24.1 Examples

```
>>> from nipype.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: (an existing file name)
        Input file for RemoveIntersection
        flag: %s, position: -2

[Optional]
args: (a string)
```

```
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        Output file for RemoveIntersection
        flag: %s, position: -1
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output file for RemoveIntersection
```

79.25 RemoveNeck

Link to code

Wraps command **mri_remove_neck**
Crops the neck out of the mri image

79.25.1 Examples

```
>>> from nipype.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: (an existing file name)
        Input file for RemoveNeck
        flag: %s, position: -4
template: (an existing file name)
        Input template file for RemoveNeck
        flag: %s, position: -2
transform: (an existing file name)
        Input transform file for RemoveNeck
        flag: %s, position: -3

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
```

```
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    out_file: (a file name)
            Output file for RemoveNeck
            flag: %s, position: -1
    radius: (an integer (int or long))
            Radius
            flag: -radius %d
    subjects_dir: (an existing directory name)
            subjects directory
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (a file name)
            Output file with neck removed
```

79.26 SampleToSurface

Link to code

Wraps 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.

79.26.1 Examples

```
    >>> import nipype.interfaces.freesurfer as fs
    >>> sampler = fs.SampleToSurface(hemi="lh")
    >>> sampler.inputs.source_file = "cope1.nii.gz"
    >>> sampler.inputs.reg_file = "register.dat"
    >>> sampler.inputs.sampling_method = "average"
    >>> sampler.inputs.sampling_range = 1
    >>> sampler.inputs.sampling_units = "frac"
    >>> res = sampler.run()
```

Inputs:

```
    [Mandatory]
    hemi: ('lh' or 'rh')
            target hemisphere
            flag: --hemi %s
    mni152reg: (a boolean)
```

```
        source volume is in MNI152 space
        flag: --mni152reg
        mutually_exclusive: reg_file, reg_header, mni152reg
projection_stem: (a string)
        stem for precomputed linear estimates and volume fractions
        mutually_exclusive: sampling_method
reg_file: (an existing file name)
        source-to-reference registration file
        flag: --reg %s
        mutually_exclusive: reg_file, reg_header, mni152reg
reg_header: (a boolean)
        register based on header geometry
        flag: --regheader %s
        mutually_exclusive: reg_file, reg_header, mni152reg
        requires: subject_id
sampling_method: ('point' or 'max' or 'average')
        how to sample -- at a point or at the max or average over a range
        flag: %s
        mutually_exclusive: projection_stem
        requires: sampling_range, sampling_units
source_file: (an existing file name)
        volume to sample values from
        flag: --mov %s

[Optional]
apply_rot: (a tuple of the form: (a float, a float, a float))
        rotation angles (in degrees) to apply to reg matrix
        flag: --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
        flag: --trans %.3f %.3f %.3f
args: (a string)
        Additional parameters to the command
        flag: %s
cortex_mask: (a boolean)
        mask the target surface with hemi.cortex.label
        flag: --cortex
        mutually_exclusive: mask_label
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fix_tk_reg: (a boolean)
        make reg matrix round-compatible
        flag: --fixtkreg
float2int_method: ('round' or 'tkregister')
        method to convert reg matrix values (default is round)
        flag: --float2int %s
frame: (an integer (int or long))
        save only one frame (0-based)
        flag: --frame %d
hits_file: (a boolean or an existing file name)
        save image with number of hits at each voxel
        flag: --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
        flag: --srchit_type
ico_order: (an integer (int or long))
        icosahedron order when target_subject is 'ico'
        flag: --icoorder %d
        requires: target_subject
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interp_method: ('nearest' or 'trilinear')
        interpolation method
        flag: --interp %s
mask_label: (an existing file name)
        label file to mask output with
        flag: --mask %s
        mutually_exclusive: cortex_mask
no_reshape: (a boolean)
        do not reshape surface vector (default)
        flag: --noreshape
        mutually_exclusive: reshape
out_file: (a file name)
        surface file to write
        flag: --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')
        output file type
        flag: --out_type %s
override_reg_subj: (a boolean)
        override the subject in the reg file header
        flag: --srcsubject %s
        requires: subject_id
reference_file: (an existing file name)
        reference volume (default is orig.mgz)
        flag: --ref %s
reshape: (a boolean)
        reshape surface vector to fit in non-mgh format
        flag: --reshape
        mutually_exclusive: no_reshape
reshape_slices: (an integer (int or long))
        number of 'slices' for reshaping
        flag: --rf %d
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'
scale_input: (a float)
        multiple all intensities by scale factor
        flag: --scale %.3f
smooth_surf: (a float)
        smooth output surface (mm fwhm)
        flag: --surf-fwhm %.3f
smooth_vol: (a float)
        smooth input volume (mm fwhm)
        flag: --fwhm %.3f
subject_id: (a string)
```

```
        subject id
subjects_dir: (an existing directory name)
        subjects directory
surf_reg: (a boolean)
        use surface registration to target subject
        flag: --surfreg
        requires: target_subject
surface: (a string)
        target surface (default is white)
        flag: --surf %s
target_subject: (a string)
        sample to surface of different subject than source
        flag: --trgsubject %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
vox_file: (a boolean or a file name)
        text file with the number of voxels intersecting the surface
        flag: --nvox %s
```

Outputs:

```
hits_file: (an existing file name)
        image with number of hits at each voxel
out_file: (an existing file name)
        surface file
vox_file: (an existing file name)
        text file with the number of voxels intersecting the surface
```

79.27 SmoothTessellation

Link to code

Wraps 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

79.27.1 Example

```
>>> import nipype.interfaces.freesurfer as fs
>>> smooth = fs.SmoothTessellation()
>>> smooth.inputs.in_file = 'lh.hippocampus.stl'
>>> smooth.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Input volume to tesselate voxels from.
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
curvature_averaging_iterations: (an integer (int or long))
```

```
        Number of curvature averaging iterations (default=10)
        flag: -a %d
disable_estimates: (a boolean)
        Disables the writing of curvature and area estimates
        flag: -nw
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
gaussian_curvature_norm_steps: (an integer (int or long))
        Use Gaussian curvature smoothing
        flag: %d
gaussian_curvature_smoothing_steps: (an integer (int or long))
        Use Gaussian curvature smoothing
        flag: %d
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
normalize_area: (a boolean)
        Normalizes the area after smoothing
        flag: -area
out_area_file: (a file name)
        Write area to ?h.areaname (default "area")
        flag: -b %s
out_curvature_file: (a file name)
        Write curvature to ?h.curvname (default "curv")
        flag: -c %s
out_file: (a file name)
        output filename or True to generate one
        flag: %s, position: -1
seed: (an integer (int or long))
        Seed for setting random number generator
        flag: -seed %d
smoothing_iterations: (an integer (int or long))
        Number of smoothing iterations (default=10)
        flag: -n %d
snapshot_writing_iterations: (an integer (int or long))
        Write snapshot every "n" iterations
        flag: -w %d
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
use_gaussian_curvature_smoothing: (a boolean)
        Use Gaussian curvature smoothing
        flag: -g
use_momentum: (a boolean)
        Uses momentum
        flag: -m
```

Outputs:

```
surface: (an existing file name)
        Smoothed surface file
```

79.28 Sphere

Link to code
Wraps command **mris_sphere**
This program will add a template into an average surface

79.28.1 Examples

```
>>> from nipype.interfaces.freesurfer import Sphere
>>> sphere = Sphere()
>>> sphere.inputs.in_file = 'lh.pial'
>>> sphere.cmdline
'mris_sphere lh.pial lh.sphere'
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Input file for Sphere
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_smoothwm: (an existing file name)
        Input surface required when -q flag is not selected
magic: (a boolean)
        No documentation. Direct questions to analysis-
        bugs@nmr.mgh.harvard.edu
        flag: -q
num_threads: (an integer (int or long))
        allows for specifying more threads
out_file: (a file name)
        Output file for Sphere
        flag: %s, position: -1
seed: (an integer (int or long))
        Seed for setting random number generator
        flag: -seed %d
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output file for Sphere
```

79.29 Surface2VolTransform

Link to code
Wraps command **mri_surf2vol**
Use FreeSurfer mri_surf2vol to apply a transform.

79.29.1 Examples

```
>>> from nipype.interfaces.freesurfer import Surface2VolTransform
>>> xfm2vol = Surface2VolTransform()
>>> xfm2vol.inputs.source_file = 'lh.cope1.mgz'
>>> xfm2vol.inputs.reg_file = 'register.mat'
>>> xfm2vol.inputs.hemi = 'lh'
>>> xfm2vol.inputs.template_file = 'cope1.nii.gz'
>>> xfm2vol.inputs.subjects_dir = '.'
>>> xfm2vol.cmdline
'mri_surf2vol --hemi lh --volreg register.mat --surfval lh.cope1.mgz --sd . --template cope1.nii
>>> res = xfm2vol.run()
```

Inputs:

```
[Mandatory]
hemi: (a string)
        hemisphere of data
        flag: --hemi %s
reg_file: (an existing file name)
        tkRAS-to-tkRAS matrix (tkregister2 format)
        flag: --volreg %s
        mutually_exclusive: subject_id
source_file: (an existing file name)
        This is the source of the surface values
        flag: --surfval %s
        mutually_exclusive: mkmask

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mkmask: (a boolean)
        make a mask instead of loading surface values
        flag: --mkmask
        mutually_exclusive: source_file
projfrac: (a float)
        thickness fraction
        flag: --projfrac %s
subject_id: (a string)
        subject id
        flag: --identity %s
        mutually_exclusive: reg_file
subjects_dir: (a string)
        freesurfer subjects directory defaults to $SUBJECTS_DIR
```

```
        flag: --sd %s
surf_name: (a string)
        surfname (default is white)
        flag: --surf %s
template_file: (an existing file name)
        Output template volume
        flag: --template %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transformed_file: (a file name)
        Output volume
        flag: --outvol %s
vertexvol_file: (a file name)
        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.
        flag: --vtxvol %s
```

Outputs:

```
transformed_file: (an existing file name)
        Path to output file if used normally
vertexvol_file: (a file name)
        vertex map volume path id. Optional
```

79.30 SurfaceSmooth

Link to code

Wraps command **mri_surf2surf**

Smooth a surface image with mri_surf2surf.

The surface is smoothed by an interative 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)

79.30.1 Examples

```
>>> import nipype.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.run()
```

Inputs:

```
[Mandatory]
hemi: ('lh' or 'rh')
        hemisphere to operate on
        flag: --hemi %s
in_file: (a file name)
        source surface file
        flag: --sval %s
```

```
    subject_id: (a string)
            subject id of surface file
            flag: --s %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    cortex: (a boolean, nipype default value: True)
            only smooth within $hemi.cortex.label
            flag: --cortex
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    fwhm: (a float)
            effective FWHM of the smoothing process
            flag: --fwhm %.4f
            mutually_exclusive: smooth_iters
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    out_file: (a file name)
            surface file to write
            flag: --tval %s
    reshape: (a boolean)
            reshape surface vector to fit in non-mgh format
            flag: --reshape
    smooth_iters: (an integer (int or long))
            iterations of the smoothing process
            flag: --smooth %d
            mutually_exclusive: fwhm
    subjects_dir: (an existing directory name)
            subjects directory
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
            smoothed surface file
```

79.31 SurfaceSnapshots

Link to code

Wraps 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.

Node that this interface will not run if you do not have graphics enabled on your system.

79.31.1 Examples

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
hemi: ('lh' or 'rh')
        hemisphere to visualize
        flag: %s, position: 2
subject_id: (a string)
        subject to visualize
        flag: %s, position: 1
surface: (a string)
        surface to visualize
        flag: %s, position: 3

[Optional]
annot_file: (an existing file name)
        path to annotation file to display
        flag: -annotation %s
        mutually_exclusive: annot_name
annot_name: (a string)
        name of annotation to display (must be in $subject/label directory
        flag: -annotation %s
        mutually_exclusive: annot_file
args: (a string)
        Additional parameters to the command
        flag: %s
colortable: (an existing file name)
        load colortable file
        flag: -colortable %s
demean_overlay: (a boolean)
        remove mean from overlay
        flag: -zm
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
identity_reg: (a boolean)
        use the identity matrix to register the overlay to the surface
        flag: -overlay-reg-identity
        mutually_exclusive: overlay_reg, identity_reg, mni152_reg
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
invert_overlay: (a boolean)
        invert the overlay display
        flag: -invphaseflag 1
label_file: (an existing file name)
        path to label file to display
        flag: -label %s
        mutually_exclusive: label_name
label_name: (a string)
```

```
        name of label to display (must be in $subject/label directory
        flag: -label %s
        mutually_exclusive: label_file
label_outline: (a boolean)
        draw label/annotation as outline
        flag: -label-outline
label_under: (a boolean)
        draw label/annotation under overlay
        flag: -labels-under
mni152_reg: (a boolean)
        use to display a volume in MNI152 space on the average subject
        flag: -mni152reg
        mutually_exclusive: overlay_reg, identity_reg, mni152_reg
orig_suffix: (a string)
        set the orig surface suffix string
        flag: -orig %s
overlay: (an existing file name)
        load an overlay volume/surface
        flag: -overlay %s
        requires: overlay_range
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)
        flag: %s
overlay_range_offset: (a float)
        overlay range will be symettric around offset value
        flag: -foffset %.3f
overlay_reg: (a file name)
        registration matrix file to register overlay to surface
        flag: -overlay-reg %s
        mutually_exclusive: overlay_reg, identity_reg, mni152_reg
patch_file: (an existing file name)
        load a patch
        flag: -patch %s
reverse_overlay: (a boolean)
        reverse the overlay display
        flag: -revphaseflag 1
screenshot_stem: (a string)
        stem to use for screenshot file names
show_color_scale: (a boolean)
        display the color scale bar
        flag: -colscalebarflag 1
show_color_text: (a boolean)
        display text in the color scale bar
        flag: -colscaletext 1
show_curv: (a boolean)
        show curvature
        flag: -curv
        mutually_exclusive: show_gray_curv
show_gray_curv: (a boolean)
        show curvature in gray
        flag: -gray
        mutually_exclusive: show_curv
six_images: (a boolean)
        also take anterior and posterior snapshots
sphere_suffix: (a string)
        set the sphere.reg suffix string
        flag: -sphere %s
```

```
    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
    subjects_dir: (an existing directory name)
            subjects directory
    tcl_script: (an existing file name)
            override default screenshot script
            flag: %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    truncate_overlay: (a boolean)
            truncate the overlay display
            flag: -truncphaseflag 1
```

Outputs:

```
    snapshots: (a list of items which are an existing file name)
            tiff images of the surface from different perspectives
```

79.32 SurfaceTransform

Link to code

Wraps 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.

79.32.1 Examples

```
>>> from nipype.interfaces.freesurfer import SurfaceTransform
>>> sxfm = SurfaceTransform()
>>> sxfm.inputs.source_file = "lh.cope1.nii.gz"
>>> sxfm.inputs.source_subject = "my_subject"
>>> sxfm.inputs.target_subject = "fsaverage"
>>> sxfm.inputs.hemi = "lh"
>>> sxfm.run()
```

Inputs:

```
    [Mandatory]
    hemi: ('lh' or 'rh')
            hemisphere to transform
            flag: --hemi %s
    source_annot_file: (an existing file name)
            surface annotation file
            flag: --sval-annot %s
            mutually_exclusive: source_file
    source_file: (an existing file name)
            surface file with source values
            flag: --sval %s
            mutually_exclusive: source_annot_file
    source_subject: (a string)
            subject id for source surface
            flag: --srcsubject %s
    target_subject: (a string)
```

```
        subject id of target surface
        flag: --trgsubject %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        surface file to write
        flag: --tval %s
reshape: (a boolean)
        reshape output surface to conform with Nifti
        flag: --reshape
reshape_factor: (an integer (int or long))
        number of slices in reshaped image
        flag: --reshape-factor
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
        flag: --sfmt %s
        requires: source_file
subjects_dir: (an existing directory name)
        subjects directory
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'
        flag: --trgicoorder %d
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')
        output format
        flag: --tfmt %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        transformed surface file
```

79.33 TalairachAVI

Link to code

Wraps 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.

79.33.1 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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input volume
        flag: --i %s
out_file: (a file name)
        output xfm file
        flag: --xfm %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
atlas: (a string)
        alternate target atlas (in freesurfer/average dir)
        flag: --atlas %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        The output transform for TalairachAVI
out_log: (a file name)
        The output log file for TalairachAVI
out_txt: (a file name)
        The output text file for TaliarachAVI
```

79.34 TalairachQC

Link to code
Wraps command **tal_QC_AZS**

79.34.1 Examples

```
>>> from nipype.interfaces.freesurfer import TalairachQC
>>> qc = TalairachQC()
>>> qc.inputs.log_file = 'dirs.txt'
>>> qc.cmdline
'tal_QC_AZS dirs.txt'
```

Inputs:

```
[Mandatory]
log_file: (an existing file name)
        The log file for TalairachQC
        flag: %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
log_file: (an existing file name, nipype default value:
         stdout.nipype)
        The output log
```

79.35 Tkregister2

Link to code
Wraps command **tkregister2**

79.35.1 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 nipype.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()
```

The example below uses tkregister2 without the manual editing stage to convert FSL-style registration matrix (.mat) to FreeSurfer-style registration matrix (.dat)

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
moving_image: (an existing file name)
        moving volume
        flag: --mov %s
reg_file: (a file name, nipype default value: register.dat)
        freesurfer-style registration file
        flag: --reg %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fsl_in_matrix: (an existing file name)
        fsl-style registration input matrix
        flag: --fsl %s
fsl_out: (a file name)
        compute an FSL-compatible resgitration matrix
        flag: --fslregout %s
fstal: (a boolean)
        set mov to be tal and reg to be tal xfm
        flag: --fstal
        mutually_exclusive: target_image, moving_image
fstarg: (a boolean)
        use subject's T1 as reference
        flag: --fstarg
        mutually_exclusive: target_image
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
movscale: (a float)
        adjust registration matrix to scale mov
        flag: --movscale %f
noedit: (a boolean, nipype default value: True)
        do not open edit window (exit)
        flag: --noedit
reg_header: (a boolean)
        compute regstration from headers
        flag: --regheader
subject_id: (a string)
        freesurfer subject ID
        flag: --s %s
subjects_dir: (an existing directory name)
        subjects directory
```

```
    target_image: (an existing file name)
            target volume
            flag: --targ %s
            mutually_exclusive: fstarg
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    xfm: (an existing file name)
            use a matrix in MNI coordinates as initial registration
            flag: --xfm %s
```

Outputs:

```
    fsl_file: (a file name)
            FSL-style registration file
    reg_file: (an existing file name)
            freesurfer-style registration file
```

79.36 VolumeMask

Link to code

Wraps command **mris_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].[white|pial] and labels voxels based on the signed-distance function from the surface.

79.36.1 Examples

```
    >>> from nipype.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_w
```

Inputs:

```
    [Mandatory]
    left_ribbonlabel: (an integer (int or long))
            Left cortical ribbon label
            flag: --label_left_ribbon %d
    left_whitelabel: (an integer (int or long))
            Left white matter label
            flag: --label_left_white %d
    lh_pial: (an existing file name)
            Implicit input left pial surface
    lh_white: (an existing file name)
```

```
        Implicit input left white matter surface
rh_pial: (an existing file name)
        Implicit input right pial surface
rh_white: (an existing file name)
        Implicit input right white matter surface
right_ribbonlabel: (an integer (int or long))
        Right cortical ribbon label
        flag: --label_right_ribbon %d
right_whitelabel: (an integer (int or long))
        Right white matter label
        flag: --label_right_white %d
subject_id: (a string, nipype default value: subject_id)
        Subject being processed
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
aseg: (an existing file name)
        Implicit aseg.mgz segmentation. Specify a different aseg by using
        the 'in_aseg' input.
        mutually_exclusive: in_aseg
copy_inputs: (a boolean)
        If running as a node, set this to True.This will copy the implicit
        input files to the node directory.
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_aseg: (an existing file name)
        Input aseg file for VolumeMask
        flag: --aseg_name %s
        mutually_exclusive: aseg
save_ribbon: (a boolean)
        option to save just the ribbon for the hemispheres in the format
        ?h.ribbon.mgz
        flag: --save_ribbon
subjects_dir: (an existing directory name)
        subjects directory
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
lh_ribbon: (a file name)
        Output left cortical ribbon mask
out_ribbon: (a file name)
        Output cortical ribbon mask
rh_ribbon: (a file name)
        Output right cortical ribbon mask
```

79.37 copy2subjdir()

Link to code
Method to copy an input to the subjects directory

79.38 createoutputdirs()

Link to code
create all output directories. If not created, some freesurfer interfaces fail

CHAPTER 80

interfaces.fsl.dti

80.1 BEDPOSTX5

Link to code
Wraps 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 `nipype.workflows.fsl.dmri.create_bedpostx_pipeline()` instead.

80.1.1 Example

```
>>> from nipype.interfaces import fsl
>>> bedp = fsl.BEDPOSTX5(bvecs='bvecs', bvals='bvals', dwi='diffusion.nii',
...                      mask='mask.nii', n_fibres=1)
>>> bedp.cmdline
'bedpostx bedpostx --forcedir -n 1'
```

Inputs:

```
[Mandatory]
bvals: (an existing file name)
        b values file
bvecs: (an existing file name)
        b vectors file
dwi: (an existing file name)
        diffusion weighted image data file
mask: (an existing file name)
        bet binary mask file
n_fibres: (an integer >= 1, nipype default value: 1)
        Maximum number of fibres to fit in each voxel
        flag: -n %d
out_dir: (a directory name, nipype default value: bedpostx)
        output directory
        flag: %s, position: 1

[Optional]
all_ard: (a boolean)
        Turn ARD on on all fibres
        flag: --allard
        mutually_exclusive: no_ard, all_ard
args: (a string)
```

```
        Additional parameters to the command
        flag: %s
burn_in: (an integer >= 0)
        Total num of jumps at start of MCMC to be discarded
        flag: -b %d
burn_in_no_ard: (an integer >= 0)
        num of burnin jumps before the ard is imposed
        flag: --burninnoard=%d
cnlinear: (a boolean)
        Initialise with constrained nonlinear fitting
        flag: --cnonlinear
        mutually_exclusive: no_spat, non_linear, cnlinear
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
f0_ard: (a boolean)
        Noise floor model: add to the model an unattenuated signal
        compartment f0
        flag: --f0 --ardf0
        mutually_exclusive: f0_noard, f0_ard, all_ard
f0_noard: (a boolean)
        Noise floor model: add to the model an unattenuated signal
        compartment f0
        flag: --f0
        mutually_exclusive: f0_noard, f0_ard
force_dir: (a boolean, nipype default value: True)
        use the actual directory name given (do not add + to make a new
        directory)
        flag: --forcedir
fudge: (an integer (int or long))
        ARD fudge factor
        flag: -w %d
grad_dev: (an existing file name)
        grad_dev file, if gradnonlin, -g is True
gradnonlin: (a boolean)
        consider gradient nonlinearities, default off
        flag: -g
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
logdir: (a directory name)
        flag: --logdir=%s
model: (1 or 2 or 3)
        use monoexponential (1, default, required for single-shell) or
        multiexponential (2, multi-shell) model
        flag: -model %d
n_jumps: (an integer (int or long))
        Num of jumps to be made by MCMC
        flag: -j %d
no_ard: (a boolean)
        Turn ARD off on all fibres
        flag: --noard
        mutually_exclusive: no_ard, all_ard
no_spat: (a boolean)
        Initialise with tensor, not spatially
        flag: --nospat
        mutually_exclusive: no_spat, non_linear, cnlinear
```

```
    non_linear: (a boolean)
            Initialise with nonlinear fitting
            flag: --nonlinear
            mutually_exclusive: no_spat, non_linear, cnlinear
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    rician: (a boolean)
            use Rician noise modeling
            flag: --rician
    sample_every: (an integer >= 0)
            Num of jumps for each sample (MCMC)
            flag: -s %d
    seed: (an integer (int or long))
            seed for pseudo random number generator
            flag: --seed=%d
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    update_proposal_every: (an integer >= 1)
            Num of jumps for each update to the proposal density std (MCMC)
            flag: --updateproposalevery=%d
    use_gpu: (a boolean)
            Use the GPU version of bedpostx
```

Outputs:

```
    dyads: (a list of items which are an existing file name)
            Mean of PDD distribution in vector form.
    dyads_dispersion: (a list of items which are an existing file name)
            Dispersion
    mean_S0samples: (an existing file name)
            Mean of distribution on T2wbaseline signal intensity S0
    mean_dsamples: (an existing file name)
            Mean of distribution on diffusivity d
    mean_fsamples: (a list of items which are an existing file name)
            Mean of distribution on f anisotropy
    mean_phsamples: (a list of items which are an existing file name)
            Mean of distribution on phi
    mean_thsamples: (a list of items which are an existing file name)
            Mean of distribution on theta
    merged_fsamples: (a list of items which are an existing file name)
            Samples from the distribution on anisotropic volume fraction
    merged_phsamples: (a list of items which are an existing file name)
            Samples from the distribution on phi
    merged_thsamples: (a list of items which are an existing file name)
            Samples from the distribution on theta
```

80.2 DTIFit

Link to code

Wraps command **dtifit**

Use FSL dtifit command for fitting a diffusion tensor model at each voxel

80.2.1 Example

```
>>> from nipype.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]
bvals: (an existing file name)
        b values file
        flag: -b %s, position: 4
bvecs: (an existing file name)
        b vectors file
        flag: -r %s, position: 3
dwi: (an existing file name)
        diffusion weighted image data file
        flag: -k %s, position: 0
mask: (an existing file name)
        bet binary mask file
        flag: -m %s, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
base_name: (a string, nipype default value: dtifit_)
        base_name that all output files will start with
        flag: -o %s, position: 1
cni: (an existing file name)
        input counfound regressors
        flag: --cni=%s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
gradnonlin: (an existing file name)
        gradient non linearities
        flag: --gradnonlin=%s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
little_bit: (a boolean)
        only process small area of brain
        flag: --littlebit
max_x: (an integer (int or long))
        max x
        flag: -X %d
max_y: (an integer (int or long))
        max y
        flag: -Y %d
max_z: (an integer (int or long))
        max z
```

```
        flag: -Z %d
min_x: (an integer (int or long))
        min x
        flag: -x %d
min_y: (an integer (int or long))
        min y
        flag: -y %d
min_z: (an integer (int or long))
        min z
        flag: -z %d
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
save_tensor: (a boolean)
        save the elements of the tensor
        flag: --save_tensor
sse: (a boolean)
        output sum of squared errors
        flag: --sse
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
FA: (an existing file name)
        path/name of file with the fractional anisotropy
L1: (an existing file name)
        path/name of file with the 1st eigenvalue
L2: (an existing file name)
        path/name of file with the 2nd eigenvalue
L3: (an existing file name)
        path/name of file with the 3rd eigenvalue
MD: (an existing file name)
        path/name of file with the mean diffusivity
MO: (an existing file name)
        path/name of file with the mode of anisotropy
S0: (an existing file name)
        path/name of file with the raw T2 signal with no diffusion weighting
V1: (an existing file name)
        path/name of file with the 1st eigenvector
V2: (an existing file name)
        path/name of file with the 2nd eigenvector
V3: (an existing file name)
        path/name of file with the 3rd eigenvector
tensor: (an existing file name)
        path/name of file with the 4D tensor volume
```

80.3 DistanceMap

Link to code

Wraps command **distancemap**

Use FSL's distancemap to generate a map of the distance to the nearest nonzero voxel.

80.3.1 Example

```
>>> import nipype.interfaces.fsl as fsl
>>> mapper = fsl.DistanceMap()
>>> mapper.inputs.in_file = "skeleton_mask.nii.gz"
>>> mapper.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        image to calculate distance values for
        flag: --in=%s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
distance_map: (a file name)
        distance map to write
        flag: --out=%s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
invert_input: (a boolean)
        invert input image
        flag: --invert
local_max_file: (a boolean or a file name)
        write an image of the local maxima
        flag: --localmax=%s
mask_file: (an existing file name)
        binary mask to contrain calculations
        flag: --mask=%s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
distance_map: (an existing file name)
        value is distance to nearest nonzero voxels
local_max_file: (a file name)
        image of local maxima
```

80.4 FindTheBiggest

Link to code

Wraps 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.

80.4.1 Example

```
>>> from nipype.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 an existing file name)
        a list of input volumes or a singleMatrixFile
        flag: %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        file with the resulting segmentation
        flag: %s, position: 2
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output file indexed in order of input files
        flag: %s
```

80.5 MakeDyadicVectors

Link to code

Wraps command **make_dyadic_vectors**

Create vector volume representing mean principal diffusion direction and its uncertainty (dispersion)

Inputs:

```
[Mandatory]
phi_vol: (an existing file name)
        flag: %s, position: 1
theta_vol: (an existing file name)
        flag: %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
```

```
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        flag: %s, position: 2
output: (a file name, nipype default value: dyads)
        flag: %s, position: 3
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
perc: (a float)
        the {perc}% angle of the output cone of uncertainty (output will be
        in degrees)
        flag: %f, position: 4
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
dispersion: (an existing file name)
dyads: (an existing file name)
```

80.6 ProbTrackX

Link to code

Wraps command **probtrackx**

Use FSL probtrackx for tractography on bedpostx results

80.6.1 Examples

```
>>> from nipype.interfaces import fsl
>>> pbx = fsl.ProbTrackX(samples_base_name='merged', mask='mask.nii',     seed='MASK_average_tha
>>> pbx.cmdline
'probtrackx --forcedir -m mask.nii --mode=seedmask --nsamples=3 --nsteps=10 --opd --os2t --dir=.
```

Inputs:

```
[Mandatory]
fsamples: (a list of items which are an existing file name)
mask: (an existing file name)
        bet binary mask file in diffusion space
        flag: -m %s
phsamples: (a list of items which are an existing file name)
seed: (an existing file name or a list of items which are an existing
         file name 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
        flag: --seed=%s
thsamples: (a list of items which are an existing file name)
```

```
    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    avoid_mp: (an existing file name)
            reject pathways passing through locations given by this mask
            flag: --avoid=%s
    c_thresh: (a float)
            curvature threshold - default=0.2
            flag: --cthr=%.3f
    correct_path_distribution: (a boolean)
            correct path distribution for the length of the pathways
            flag: --pd
    dist_thresh: (a float)
            discards samples shorter than this threshold (in mm - default=0)
            flag: --distthresh=%.3f
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    fibst: (an integer (int or long))
            force a starting fibre for tracking - default=1, i.e. first fibre
            orientation. Only works if randfib==0
            flag: --fibst=%d
    force_dir: (a boolean, nipype default value: True)
            use the actual directory name given - i.e. do not add + to make a
            new directory
            flag: --forcedir
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inv_xfm: (a file name)
            transformation matrix taking DTI space to seed space (compulsory
            when using a warp_field for seeds_to_dti)
            flag: --invxfm=%s
    loop_check: (a boolean)
            perform loop_checks on paths - slower, but allows lower curvature
            threshold
            flag: --loopcheck
    mask2: (an existing file name)
            second bet binary mask (in diffusion space) in twomask_symm mode
            flag: --mask2=%s
    mesh: (an existing file name)
            Freesurfer-type surface descriptor (in ascii format)
            flag: --mesh=%s
    mod_euler: (a boolean)
            use modified euler streamlining
            flag: --modeuler
    mode: ('simple' or 'two_mask_symm' or 'seedmask')
            options: simple (single seed voxel), seedmask (mask of seed voxels),
            twomask_symm (two bet binary masks)
            flag: --mode=%s
    n_samples: (an integer (int or long), nipype default value: 5000)
            number of samples - default=5000
            flag: --nsamples=%d
    n_steps: (an integer (int or long))
            number of steps per sample - default=2000
            flag: --nsteps=%d
```

```
    network: (a boolean)
            activate network mode - only keep paths going through at least one
            seed mask (required if multiple seed masks)
            flag: --network
    opd: (a boolean, nipype default value: True)
            outputs path distributions
            flag: --opd
    os2t: (a boolean)
            Outputs seeds to targets
            flag: --os2t
    out_dir: (an existing directory name)
            directory to put the final volumes in
            flag: --dir=%s
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    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)
            flag: --randfib=%d
    random_seed: (a boolean)
            random seed
            flag: --rseed
    s2tastext: (a boolean)
            output seed-to-target counts as a text file (useful when seeding
            from a mesh)
            flag: --s2tastext
    sample_random_points: (a boolean)
            sample random points within seed voxels
            flag: --sampvox
    samples_base_name: (a string, nipype default value: merged)
            the rootname/base_name for samples files
            flag: --samples=%s
    seed_ref: (an existing file name)
            reference vol to define seed space in simple mode - diffusion space
            assumed if absent
            flag: --seedref=%s
    step_length: (a float)
            step_length in mm - default=0.5
            flag: --steplength=%.3f
    stop_mask: (an existing file name)
            stop tracking at locations given by this mask file
            flag: --stop=%s
    target_masks: (a list of items which are a file name)
            list of target masks - required for seeds_to_targets classification
            flag: --targetmasks=%s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    use_anisotropy: (a boolean)
            use anisotropy to constrain tracking
            flag: --usef
    verbose: (0 or 1 or 2)
            Verbose level, [0-2].Level 2 is required to output particle files.
            flag: --verbose=%d
    waypoints: (an existing file name)
```

```
        waypoint mask or ascii list of waypoint masks - only keep paths
        going through ALL the masks
        flag: --waypoints=%s
xfm: (an existing file name)
        transformation matrix taking seed space to DTI space (either FLIRT
        matrix or FNIRT warp_field) - default is identity
        flag: --xfm=%s
```

Outputs:

```
fdt_paths: (a list of items which are an existing file name)
        path/name of a 3D image file containing the output connectivity
        distribution to the seed mask
log: (an existing file name)
        path/name of a text record of the command that was run
particle_files: (a list of items which are an existing file name)
        Files describing all of the tract samples. Generated only if verbose
        is set to 2
targets: (a list of items which are an existing file name)
        a list with all generated seeds_to_target files
way_total: (an existing file name)
        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
```

80.7 ProbTrackX2

Link to code

Wraps command **probtrackx2**

Use FSL probtrackx2 for tractography on bedpostx results

80.7.1 Examples

```
>>> from nipype.interfaces import fsl
>>> pbx2 = fsl.ProbTrackX2()
>>> pbx2.inputs.seed = 'seed_source.nii.gz'
>>> pbx2.inputs.thsamples = 'merged_th1samples.nii.gz'
>>> pbx2.inputs.fsamples = 'merged_f1samples.nii.gz'
>>> pbx2.inputs.phsamples = 'merged_ph1samples.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=. --samp
```

Inputs:

```
[Mandatory]
fsamples: (a list of items which are an existing file name)
mask: (an existing file name)
        bet binary mask file in diffusion space
        flag: -m %s
phsamples: (a list of items which are an existing file name)
seed: (an existing file name or a list of items which are an existing
         file name 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
```

```
        flag: --seed=%s
thsamples: (a list of items which are an existing file name)

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
avoid_mp: (an existing file name)
        reject pathways passing through locations given by this mask
        flag: --avoid=%s
c_thresh: (a float)
        curvature threshold - default=0.2
        flag: --cthr=%.3f
colmask4: (an existing file name)
        Mask for columns of matrix4 (default=seed mask)
        flag: --colmask4=%s
correct_path_distribution: (a boolean)
        correct path distribution for the length of the pathways
        flag: --pd
dist_thresh: (a float)
        discards samples shorter than this threshold (in mm - default=0)
        flag: --distthresh=%.3f
distthresh1: (a float)
        Discards samples (in matrix1) shorter than this threshold (in mm -
        default=0)
        flag: --distthresh1=%.3f
distthresh3: (a float)
        Discards samples (in matrix3) shorter than this threshold (in mm -
        default=0)
        flag: --distthresh3=%.3f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fibst: (an integer (int or long))
        force a starting fibre for tracking - default=1, i.e. first fibre
        orientation. Only works if randfib==0
        flag: --fibst=%d
fopd: (an existing file name)
        Other mask for binning tract distribution
        flag: --fopd=%s
force_dir: (a boolean, nipype default value: True)
        use the actual directory name given - i.e. do not add + to make a
        new directory
        flag: --forcedir
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inv_xfm: (a file name)
        transformation matrix taking DTI space to seed space (compulsory
        when using a warp_field for seeds_to_dti)
        flag: --invxfm=%s
loop_check: (a boolean)
        perform loop_checks on paths - slower, but allows lower curvature
        threshold
        flag: --loopcheck
lrtarget3: (an existing file name)
        Column-space mask used for Nxn connectivity matrix
```

```
        flag: --lrtarget3=%s
meshspace: ('caret' or 'freesurfer' or 'first' or 'vox')
        Mesh reference space - either "caret" (default) or "freesurfer" or
        "first" or "vox"
        flag: --meshspace=%s
mod_euler: (a boolean)
        use modified euler streamlining
        flag: --modeuler
n_samples: (an integer (int or long), nipype default value: 5000)
        number of samples - default=5000
        flag: --nsamples=%d
n_steps: (an integer (int or long))
        number of steps per sample - default=2000
        flag: --nsteps=%d
network: (a boolean)
        activate network mode - only keep paths going through at least one
        seed mask (required if multiple seed masks)
        flag: --network
omatrix1: (a boolean)
        Output matrix1 - SeedToSeed Connectivity
        flag: --omatrix1
omatrix2: (a boolean)
        Output matrix2 - SeedToLowResMask
        flag: --omatrix2
        requires: target2
omatrix3: (a boolean)
        Output matrix3 (NxN connectivity matrix)
        flag: --omatrix3
        requires: target3, lrtarget3
omatrix4: (a boolean)
        Output matrix4 - DtiMaskToSeed (special Oxford Sparse Format)
        flag: --omatrix4
onewaycondition: (a boolean)
        Apply waypoint conditions to each half tract separately
        flag: --onewaycondition
opd: (a boolean, nipype default value: True)
        outputs path distributions
        flag: --opd
os2t: (a boolean)
        Outputs seeds to targets
        flag: --os2t
out_dir: (an existing directory name)
        directory to put the final volumes in
        flag: --dir=%s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
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)
        flag: --randfib=%d
random_seed: (a boolean)
        random seed
        flag: --rseed
s2tastext: (a boolean)
        output seed-to-target counts as a text file (useful when seeding
        from a mesh)
```

```
        flag: --s2tastext
    sample_random_points: (a boolean)
        sample random points within seed voxels
        flag: --sampvox
    samples_base_name: (a string, nipype default value: merged)
        the rootname/base_name for samples files
        flag: --samples=%s
    seed_ref: (an existing file name)
        reference vol to define seed space in simple mode - diffusion space
        assumed if absent
        flag: --seedref=%s
    simple: (a boolean)
        rack from a list of voxels (seed must be a ASCII list of
        coordinates)
        flag: --simple
    step_length: (a float)
        step_length in mm - default=0.5
        flag: --steplength=%.3f
    stop_mask: (an existing file name)
        stop tracking at locations given by this mask file
        flag: --stop=%s
    target2: (an existing file name)
        Low resolution binary brain mask for storing connectivity
        distribution in matrix2 mode
        flag: --target2=%s
    target3: (an existing file name)
        Mask used for NxN connectivity matrix (or Nxn if lrtarget3 is set)
        flag: --target3=%s
    target4: (an existing file name)
        Brain mask in DTI space
        flag: --target4=%s
    target_masks: (a list of items which are a file name)
        list of target masks - required for seeds_to_targets classification
        flag: --targetmasks=%s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
    use_anisotropy: (a boolean)
        use anisotropy to constrain tracking
        flag: --usef
    verbose: (0 or 1 or 2)
        Verbose level, [0-2].Level 2 is required to output particle files.
        flag: --verbose=%d
    waycond: ('OR' or 'AND')
        Waypoint condition. Either "AND" (default) or "OR"
        flag: --waycond=%s
    wayorder: (a boolean)
        Reject streamlines that do not hit waypoints in given order. Only
        valid if waycond=AND
        flag: --wayorder
    waypoints: (an existing file name)
        waypoint mask or ascii list of waypoint masks - only keep paths
        going through ALL the masks
        flag: --waypoints=%s
    xfm: (an existing file name)
        transformation matrix taking seed space to DTI space (either FLIRT
        matrix or FNIRT warp_field) - default is identity
```

```
        flag: --xfm=%s
```

Outputs:

```
fdt_paths: (a list of items which are an existing file name)
        path/name of a 3D image file containing the output connectivity
        distribution to the seed mask
log: (an existing file name)
        path/name of a text record of the command that was run
lookup_tractspace: (an existing file name)
        lookup_tractspace generated by --omatrix2 option
matrix1_dot: (an existing file name)
        Output matrix1.dot - SeedToSeed Connectivity
matrix2_dot: (an existing file name)
        Output matrix2.dot - SeedToLowResMask
matrix3_dot: (an existing file name)
        Output matrix3 - NxN connectivity matrix
network_matrix: (an existing file name)
        the network matrix generated by --omatrix1 option
particle_files: (a list of items which are an existing file name)
        Files describing all of the tract samples. Generated only if verbose
        is set to 2
targets: (a list of items which are an existing file name)
        a list with all generated seeds_to_target files
way_total: (an existing file name)
        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
```

80.8 ProjThresh

Link to code

Wraps command **proj_thresh**

Use FSL proj_thresh for thresholding some outputs of probtrack For complete details, see the FDT Documentation <http://www.fmrib.ox.ac.uk/fsl/fdt/fdt_thresh.html>

80.8.1 Example

```
>>> from nipype.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 an existing file name)
        a list of input volumes
        flag: %s, position: 0
threshold: (an integer (int or long))
        threshold indicating minimum number of seed voxels entering this
        mask region
        flag: %d, position: 1

[Optional]
args: (a string)
```

```
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_files: (a list of items which are an existing file name)
        path/name of output volume after thresholding
```

80.9 TractSkeleton

Link to code

Wraps 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 perpindicular direction.

80.9.1 Example

```
>>> import nipype.interfaces.fsl as fsl
>>> skeletor = fsl.TractSkeleton()
>>> skeletor.inputs.in_file = "all_FA.nii.gz"
>>> skeletor.inputs.skeleton_file = True
>>> skeletor.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input image (typcially mean FA volume)
        flag: -i %s

[Optional]
alt_data_file: (an existing file name)
        4D non-FA data to project onto skeleton
        flag: -a %s
alt_skeleton: (an existing file name)
        alternate skeleton to use
        flag: -s %s
args: (a string)
```

```
        Additional parameters to the command
        flag: %s
data_file: (an existing file name)
        4D data to project onto skeleton (usually FA)
distance_map: (an existing file name)
        distance map image
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
project_data: (a boolean)
        project data onto skeleton
        flag: -p %.3f %s %s %s %s
        requires: threshold, distance_map, data_file
projected_data: (a file name)
        input data projected onto skeleton
search_mask_file: (an existing file name)
        mask in which to use alternate search rule
        mutually_exclusive: use_cingulum_mask
skeleton_file: (a boolean or a file name)
        write out skeleton image
        flag: -o %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
threshold: (a float)
        skeleton threshold value
use_cingulum_mask: (a boolean, nipype default value: True)
        perform alternate search using built-in cingulum mask
        mutually_exclusive: search_mask_file
```

Outputs:

```
projected_data: (a file name)
        input data projected onto skeleton
skeleton_file: (a file name)
        tract skeleton image
```

80.10 VecReg

Link to code

Wraps 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>

80.10.1 Example

```
>>> from nipype.interfaces import fsl
>>> vreg = fsl.VecReg(in_file='diffusion.nii',                    affine_mat='trans.mat',
```

```
>>> vreg.cmdline
'vecreg -t trans.mat -i diffusion.nii -o diffusion_vreg.nii -r mni.nii'
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        filename for input vector or tensor field
        flag: -i %s
ref_vol: (an existing file name)
        filename for reference (target) volume
        flag: -r %s

[Optional]
affine_mat: (an existing file name)
        filename for affine transformation matrix
        flag: -t %s
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interpolation: ('nearestneighbour' or 'trilinear' or 'sinc' or
         'spline')
        interpolation method : nearestneighbour, trilinear (default), sinc
        or spline
        flag: --interp=%s
mask: (an existing file name)
        brain mask in input space
        flag: -m %s
out_file: (a file name)
        filename for output registered vector or tensor field
        flag: -o %s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
ref_mask: (an existing file name)
        brain mask in output space (useful for speed up of nonlinear reg)
        flag: --refmask=%s
rotation_mat: (an existing file name)
        filename for secondary affine matrixif set, this will be used for
        the rotation of the vector/tensor field
        flag: --rotmat=%s
rotation_warp: (an existing file name)
        filename for secondary warp fieldif set, this will be used for the
        rotation of the vector/tensor field
        flag: --rotwarp=%s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
warp_field: (an existing file name)
        filename for 4D warp field for nonlinear registration
        flag: -w %s
```

Outputs:

```
out_file: (an existing file name)
        path/name of filename for the registered vector or tensor field
```

80.11 XFibres5

Link to code
Wraps command **xfibres**
Perform model parameters estimation for local (voxelwise) diffusion parameters
Inputs:

```
[Mandatory]
bvals: (an existing file name)
        b values file
        flag: --bvals=%s
bvecs: (an existing file name)
        b vectors file
        flag: --bvecs=%s
dwi: (an existing file name)
        diffusion weighted image data file
        flag: --data=%s
mask: (an existing file name)
        brain binary mask file (i.e. from BET)
        flag: --mask=%s
n_fibres: (an integer >= 1, nipype default value: 1)
        Maximum number of fibres to fit in each voxel
        flag: --nfibres=%d

[Optional]
all_ard: (a boolean)
        Turn ARD on on all fibres
        flag: --allard
        mutually_exclusive: no_ard, all_ard
args: (a string)
        Additional parameters to the command
        flag: %s
burn_in: (an integer >= 0)
        Total num of jumps at start of MCMC to be discarded
        flag: --burnin=%d
burn_in_no_ard: (an integer >= 0)
        num of burnin jumps before the ard is imposed
        flag: --burninnoard=%d
cnlinear: (a boolean)
        Initialise with constrained nonlinear fitting
        flag: --cnonlinear
        mutually_exclusive: no_spat, non_linear, cnlinear
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
f0_ard: (a boolean)
        Noise floor model: add to the model an unattenuated signal
        compartment f0
        flag: --f0 --ardf0
        mutually_exclusive: f0_noard, f0_ard, all_ard
f0_noard: (a boolean)
        Noise floor model: add to the model an unattenuated signal
```

```
        compartment f0
        flag: --f0
        mutually_exclusive: f0_noard, f0_ard
force_dir: (a boolean, nipype default value: True)
        use the actual directory name given (do not add + to make a new
        directory)
        flag: --forcedir
fudge: (an integer (int or long))
        ARD fudge factor
        flag: --fudge=%d
gradnonlin: (an existing file name)
        gradient file corresponding to slice
        flag: --gradnonlin=%s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
logdir: (a directory name, nipype default value: .)
        flag: --logdir=%s
model: (1 or 2 or 3)
        use monoexponential (1, default, required for single-shell) or
        multiexponential (2, multi-shell) model
        flag: --model=%d
n_jumps: (an integer (int or long))
        Num of jumps to be made by MCMC
        flag: --njumps=%d
no_ard: (a boolean)
        Turn ARD off on all fibres
        flag: --noard
        mutually_exclusive: no_ard, all_ard
no_spat: (a boolean)
        Initialise with tensor, not spatially
        flag: --nospat
        mutually_exclusive: no_spat, non_linear, cnlinear
non_linear: (a boolean)
        Initialise with nonlinear fitting
        flag: --nonlinear
        mutually_exclusive: no_spat, non_linear, cnlinear
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
rician: (a boolean)
        use Rician noise modeling
        flag: --rician
sample_every: (an integer >= 0)
        Num of jumps for each sample (MCMC)
        flag: --sampleevery=%d
seed: (an integer (int or long))
        seed for pseudo random number generator
        flag: --seed=%d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
update_proposal_every: (an integer >= 1)
        Num of jumps for each update to the proposal density std (MCMC)
        flag: --updateproposalevery=%d
```

Outputs:

```
    dyads: (a list of items which are an existing file name)
            Mean of PDD distribution in vector form.
    fsamples: (a list of items which are an existing file name)
            Samples from the distribution on f anisotropy
    mean_S0samples: (an existing file name)
            Mean of distribution on T2wbaseline signal intensity S0
    mean_dsamples: (an existing file name)
            Mean of distribution on diffusivity d
    mean_fsamples: (a list of items which are an existing file name)
            Mean of distribution on f anisotropy
    mean_tausamples: (an existing file name)
            Mean of distribution on tau samples (only with rician noise)
    phsamples: (a list of items which are an existing file name)
            phi samples, per fiber
    thsamples: (a list of items which are an existing file name)
            theta samples, per fiber
```

CHAPTER 81

interfaces.fsl.epi

81.1 ApplyTOPUP

Link to code
Wraps command **applytopup**
Interface for FSL topup, a tool for estimating and correcting susceptibility induced distortions. General reference and use example.

81.1.1 Examples

```
>>> from nipype.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
'applytopup --datain=topup_encoding.txt --imain=epi.nii,epi_rev.nii --inindex=1,2 --topup=topup
>>> res = applytopup.run()
```

Inputs:

```
[Mandatory]
encoding_file: (an existing file name)
        name of text file with PE directions/times
        flag: --datain=%s
in_files: (a list of items which are an existing file name)
        name of 4D file with images
        flag: --imain=%s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
datatype: ('char' or 'short' or 'int' or 'float' or 'double')
        force output data type
        flag: -d=%s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

```
    in_index: (a list of items which are an integer (int or long))
            comma separated list of indices corresponding to --datain
            flag: --inindex=%s
    in_topup_fieldcoef: (an existing file name)
            topup file containing the field coefficients
            flag: --topup=%s
            requires: in_topup_movpar
    in_topup_movpar: (an existing file name)
            topup movpar.txt file
            requires: in_topup_fieldcoef
    interp: ('trilinear' or 'spline')
            interpolation method
            flag: --interp=%s
    method: ('jac' or 'lsr')
            use jacobian modulation (jac) or least-squares resampling (lsr)
            flag: --method=%s
    out_corrected: (a file name)
            output (warped) image
            flag: --out=%s
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_corrected: (an existing file name)
            name of 4D image file with unwarped images
```

81.2 EPIDeWarp

Link to code

Wraps command **epidewarp.fsl**

Wraps the unwarping script epidewarp.fsl.

Warning: deprecated in FSL, please use `nipype.workflows.dmri.preprocess.epi.sdc_fmb()` instead.

81.2.1 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
'epidewarp.fsl --mag magnitude.nii --dph phase.nii --epi functional.nii --esp 0.58 --exfdw .../e
>>> res = dewarp.run()
```

Inputs:

```
    [Mandatory]
    dph_file: (an existing file name)
```

```
        Phase file assumed to be scaled from 0 to 4095
        flag: --dph %s
mag_file: (an existing file name)
        Magnitude file
        flag: --mag %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
cleanup: (a boolean)
        cleanup
        flag: --cleanup
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
epi_file: (an existing file name)
        EPI volume to unwarp
        flag: --epi %s
epidw: (a string)
        dewarped epi volume
        flag: --epidw %s
esp: (a float, nipype default value: 0.58)
        EPI echo spacing
        flag: --esp %s
exf_file: (an existing file name)
        example func volume (or use epi)
        flag: --exf %s
exfdw: (a string)
        dewarped example func volume
        flag: --exfdw %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
nocleanup: (a boolean, nipype default value: True)
        no cleanup
        flag: --nocleanup
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
sigma: (an integer (int or long), nipype default value: 2)
        2D spatial gaussing smoothing stdev (default = 2mm)
        flag: --sigma %s
tediff: (a float, nipype default value: 2.46)
        difference in B0 field map TEs
        flag: --tediff %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tmpdir: (a string)
        tmpdir
        flag: --tmpdir %s
vsm: (a string)
        voxel shift map
        flag: --vsm %s
```

Outputs:

```
    exf_mask: (a file name)
            Mask from example functional volume
    exfdw: (a file name)
            dewarped functional volume example
    unwarped_file: (a file name)
            unwarped epi file
    vsm_file: (a file name)
            voxel shift map
```

81.3 Eddy

Link to code
Wraps command **eddy**
Interface for FSL eddy, a tool for estimating and correcting eddy currents induced distortions. User guide and more info regarding acqp file.

81.3.1 Examples

```
    >>> from nipype.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.cmdline
    'eddy --acqp=epi_acqp.txt --bvals=bvals.scheme --bvecs=bvecs.scheme --imain=epi.nii --index=epi_
    >>> res = eddy.run()
```

Inputs:

```
    [Mandatory]
    in_acqp: (an existing file name)
            File containing acquisition parameters
            flag: --acqp=%s
    in_bval: (an existing file name)
            File containing the b-values for all volumes in --imain
            flag: --bvals=%s
    in_bvec: (an existing file name)
            File containing the b-vectors for all volumes in --imain
            flag: --bvecs=%s
    in_file: (an existing file name)
            File containing all the images to estimate distortions for
            flag: --imain=%s
    in_index: (an existing file name)
            File containing indices for all volumes in --imain into --acqp and
            --topup
            flag: --index=%s
    in_mask: (an existing file name)
            Mask to indicate brain
            flag: --mask=%s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
```

```
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    flm: ('linear' or 'quadratic' or 'cubic')
            First level EC model
            flag: --flm=%s
    fwhm: (a float)
            FWHM for conditioning filter when estimating the parameters
            flag: --fwhm=%s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    in_topup_fieldcoef: (an existing file name)
            topup file containing the field coefficients
            flag: --topup=%s
            requires: in_topup_movpar
    in_topup_movpar: (an existing file name)
            topup movpar.txt file
            requires: in_topup_fieldcoef
    method: ('jac' or 'lsr')
            Final resampling method (jacobian/least squares)
            flag: --resamp=%s
    niter: (an integer (int or long))
            Number of iterations
            flag: --niter=%s
    num_threads: (an integer (int or long), nipype default value: 1)
            Number of openmp threads to use
    out_base: (a string, nipype default value: eddy_corrected)
            basename for output (warped) image
            flag: --out=%s
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    repol: (a boolean)
            Detect and replace outlier slices
            flag: --repol
    session: (an existing file name)
            File containing session indices for all volumes in --imain
            flag: --session=%s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_corrected: (an existing file name)
            4D image file containing all the corrected volumes
    out_parameter: (an existing file name)
            text file with parameters definining the field and movement for each
            scan
```

81.4 EddyCorrect

Link to code

Wraps command **eddy_correct**

Warning: Deprecated in FSL. Please use `nipype.interfaces.fsl.epi.Eddy` instead

81.4.1 Example

```
>>> from nipype.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: (an existing file name)
        4D input file
        flag: %s, position: 0
ref_num: (an integer (int or long), nipype default value: 0)
        reference number
        flag: %d, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        4D output file
        flag: %s, position: 1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
eddy_corrected: (an existing file name)
        path/name of 4D eddy corrected output file
```

81.5 EpiReg

Link to code

Wraps command **epi_reg**

Runs FSL epi_reg script for simultaneous coregistration and fieldmap unwarping.

81.5.1 Examples

```
>>> from nipype.interfaces.fsl import EpiReg
>>> epireg = EpiReg()
>>> epireg.inputs.epi='epi.nii'
>>> epireg.inputs.t1_head='T1.nii'
>>> epireg.inputs.t1_brain='T1_brain.nii'
>>> epireg.inputs.out_base='epi2struct'
>>> epireg.inputs.fmap='fieldmap_phase_fslprepared.nii'
>>> epireg.inputs.fmapmag='fieldmap_mag.nii'
>>> epireg.inputs.fmapmagbrain='fieldmap_mag_brain.nii'
>>> epireg.inputs.echospacing=0.00067
>>> epireg.inputs.pedir='y'
>>> epireg.cmdline
'epi_reg --echospacing=0.000670 --fmap=fieldmap_phase_fslprepared.nii --fmapmag=fieldmap_mag.nii
>>> epireg.run()
```

Inputs:

```
[Mandatory]
epi: (an existing file name)
        EPI image
        flag: --epi=%s, position: -4
t1_brain: (an existing file name)
        brain extracted T1 image
        flag: --t1brain=%s, position: -2
t1_head: (an existing file name)
        wholehead T1 image
        flag: --t1=%s, position: -3

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
echospacing: (a float)
        Effective EPI echo spacing (sometimes called dwell time) - in
        seconds
        flag: --echospacing=%f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fmap: (an existing file name)
        fieldmap image (in rad/s)
        flag: --fmap=%s
fmapmag: (an existing file name)
        fieldmap magnitude image - wholehead
        flag: --fmapmag=%s
fmapmagbrain: (an existing file name)
        fieldmap magnitude image - brain extracted
        flag: --fmapmagbrain=%s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
no_clean: (a boolean, nipype default value: True)
        do not clean up intermediate files
        flag: --noclean
no_fmapreg: (a boolean)
        do not perform registration of fmap to T1 (use if fmap already
```

```
        registered)
        flag: --nofmapreg
out_base: (a string, nipype default value: epi2struct)
        output base name
        flag: --out=%s, position: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
pedir: ('x' or 'y' or 'z' or '-x' or '-y' or '-z')
        phase encoding direction, dir = x/y/z/-x/-y/-z
        flag: --pedir=%s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
weight_image: (an existing file name)
        weighting image (in T1 space)
        flag: --weight=%s
wmseg: (an existing file name)
        white matter segmentation of T1 image, has to be named like the
        t1brain and end on _wmseg
        flag: --wmseg=%s
```

Outputs:

```
epi2str_inv: (an existing file name)
        rigid structural-to-epi transform
epi2str_mat: (an existing file name)
        rigid epi-to-structural transform
fmap2epi_mat: (an existing file name)
        rigid fieldmap-to-epi transform
fmap2str_mat: (an existing file name)
        rigid fieldmap-to-structural transform
fmap_epi: (an existing file name)
        fieldmap in epi space
fmap_str: (an existing file name)
        fieldmap in structural space
fmapmag_str: (an existing file name)
        fieldmap magnitude image in structural space
fullwarp: (an existing file name)
        warpfield to unwarp epi and transform into structural space
out_1vol: (an existing file name)
        unwarped and coregistered single volume
out_file: (an existing file name)
        unwarped and coregistered epi input
shiftmap: (an existing file name)
        shiftmap in epi space
wmedge: (an existing file name)
        white matter edges for visualization
wmseg: (an existing file name)
        white matter segmentation used in flirt bbr
```

81.6 PrepareFieldmap

Link to code

Wraps 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 for-

mat (e.g. 'fsl_prepare_fieldmap SIEMENS images_3_gre_field_mapping images_4_gre_field_mapping fmap_rads 2.65').

81.6.1 Examples

```
>>> from nipype.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
'fsl_prepare_fieldmap SIEMENS phase.nii magnitude.nii .../phase_fslprepared.nii.gz 2.460000'
>>> res = prepare.run()
```

Inputs:

```
[Mandatory]
delta_TE: (a float, nipype default value: 2.46)
        echo time difference of the fieldmap sequence in ms. (usually 2.46ms
        in Siemens)
        flag: %f, position: -2
in_magnitude: (an existing file name)
        Magnitude difference map, brain extracted
        flag: %s, position: 3
in_phase: (an existing file name)
        Phase difference map, in SIEMENS format range from 0-4096 or 0-8192)
        flag: %s, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
nocheck: (a boolean, nipype default value: False)
        do not perform sanity checks for image size/range/dimensions
        flag: --nocheck, position: -1
out_fieldmap: (a file name)
        output name for prepared fieldmap
        flag: %s, position: 4
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
scanner: (a string, nipype default value: SIEMENS)
        must be SIEMENS
        flag: %s, position: 1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_fieldmap: (an existing file name)
        output name for prepared fieldmap
```

81.7 SigLoss

Link to code
Wraps command **sigloss**
Estimates signal loss from a field map (in rad/s)

81.7.1 Examples

```
>>> from nipype.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
'sigloss --te=0.030000 -i phase.nii -s .../phase_sigloss.nii.gz'
>>> res = sigloss.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        b0 fieldmap file
        flag: -i %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
echo_time: (a float)
        echo time in seconds
        flag: --te=%f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask_file: (an existing file name)
        brain mask file
        flag: -m %s
out_file: (a file name)
        output signal loss estimate file
        flag: -s %s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
slice_direction: ('x' or 'y' or 'z')
        slicing direction
        flag: -d %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        signal loss estimate file
```

81.8 TOPUP

Link to code
Wraps 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.

81.8.1 Examples

```
>>> from nipype.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
'topup --config=b02b0.cnf --datain=topup_encoding.txt --imain=b0_b0rev.nii --out=b0_b0rev_base -
>>> res = topup.run()
```

Inputs:

```
[Mandatory]
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
        flag: --datain=%s
        mutually_exclusive: encoding_file
        requires: readout_times
encoding_file: (an existing file name)
        name of text file with PE directions/times
        flag: --datain=%s
        mutually_exclusive: encoding_direction
in_file: (an existing file name)
        name of 4D file with images
        flag: --imain=%s
readout_times: (a list of items which are a float)
        readout times (dwell times by # phase-encode steps minus 1)
        mutually_exclusive: encoding_file
        requires: encoding_direction

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
config: (a string, nipype default value: b02b0.cnf)
        Name of config file specifying command line arguments
        flag: --config=%s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
estmov: (1 or 0)
        estimate movements if set
```

```
        flag: --estmov=%d
fwhm: (a float)
        FWHM (in mm) of gaussian smoothing kernel
        flag: --fwhm=%f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interp: ('spline' or 'linear')
        Image interpolation model, linear or spline.
        flag: --interp=%s
max_iter: (an integer (int or long))
        max # of non-linear iterations
        flag: --miter=%d
minmet: (0 or 1)
        Minimisation method 0=Levenberg-Marquardt, 1=Scaled Conjugate
        Gradient
        flag: --minmet=%d
numprec: ('double' or 'float')
        Precision for representing Hessian, double or float.
        flag: --numprec=%s
out_base: (a file name)
        base-name of output files (spline coefficients (Hz) and movement
        parameters)
        flag: --out=%s
out_corrected: (a file name)
        name of 4D image file with unwarped images
        flag: --iout=%s
out_field: (a file name)
        name of image file with field (Hz)
        flag: --fout=%s
out_logfile: (a file name)
        name of log-file
        flag: --logout=%s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
reg_lambda: (a float)
        lambda weighting value of the regularisation term
        flag: --miter=%0.f
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
        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.
        flag: --regmod=%s
regrid: (1 or 0)
        If set (=1), the calculations are done in a different grid
        flag: --regrid=%d
scale: (0 or 1)
        If set (=1), the images are individually scaled to a common mean
        flag: --scale=%d
splineorder: (an integer (int or long))
        order of spline, 2->Qadratic spline, 3->Cubic spline
        flag: --splineorder=%d
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.
        flag: --ssqlambda=%d
subsamp: (an integer (int or long))
        sub-sampling scheme
        flag: --subsamp=%d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
warp_res: (a float)
        (approximate) resolution (in mm) of warp basis for the different
        sub-sampling levels.
        flag: --warpres=%f
```

Outputs:

```
out_corrected: (a file name)
        name of 4D image file with unwarped images
out_enc_file: (a file name)
        encoding directions file output for applytopup
out_field: (a file name)
        name of image file with field (Hz)
out_fieldcoef: (an existing file name)
        file containing the field coefficients
out_logfile: (a file name)
        name of log-file
out_movpar: (an existing file name)
        movpar.txt output file
```

CHAPTER 82

interfaces.fsl.maths

82.1 ApplyMask

Link to code
Wraps command **fslmaths**
Use fslmaths to apply a binary mask to another image.
Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            image to operate on
            flag: %s, position: 2
    mask_file: (an existing file name)
            binary image defining mask space
            flag: -mas %s, position: 4

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
             or 'input')
            datatype to use for calculations (default is float)
            flag: -dt %s, position: 1
    nan2zeros: (a boolean)
            change NaNs to zeros before doing anything
            flag: -nan, position: 3
    out_file: (a file name)
            image to write
            flag: %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)
            flag: -odt %s, position: -1
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
```

```
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image written after calculations
```

82.2 BinaryMaths

Link to code

Wraps command **fslmaths**

Use fslmaths to perform mathematical operations using a second image or a numeric value.

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        image to operate on
        flag: %s, position: 2
operand_file: (an existing file name)
        second image to perform operation with
        flag: %s, position: 5
        mutually_exclusive: operand_value
operand_value: (a float)
        value to perform operation with
        flag: %.8f, position: 5
        mutually_exclusive: operand_file
operation: ('add' or 'sub' or 'mul' or 'div' or 'rem' or 'max' or
         'min')
        operation to perform
        flag: -%s, position: 4

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
         or 'input')
        datatype to use for calculations (default is float)
        flag: -dt %s, position: 1
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
        flag: -nan, position: 3
out_file: (a file name)
        image to write
        flag: %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)
        flag: -odt %s, position: -1
```

```
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
            image written after calculations
```

82.3 ChangeDataType

Link to code

Wraps command **fslmaths**

Use fslmaths to change the datatype of an image.

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            image to operate on
            flag: %s, position: 2
    output_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
             or 'input')
            output data type
            flag: -odt %s, position: -1

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
             or 'input')
            datatype to use for calculations (default is float)
            flag: -dt %s, position: 1
    nan2zeros: (a boolean)
            change NaNs to zeros before doing anything
            flag: -nan, position: 3
    out_file: (a file name)
            image to write
            flag: %s, position: -2
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
            image written after calculations
```

82.4 DilateImage

Link to code

Wraps command **fslmaths**

Use fslmaths to perform a spatial dilation of an image.

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            image to operate on
            flag: %s, position: 2
    operation: ('mean' or 'modal' or 'max')
            filtering operation to perfoem in dilation
            flag: -dil%s, position: 6

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
             or 'input')
            datatype to use for calculations (default is float)
            flag: -dt %s, position: 1
    kernel_file: (an existing file name)
            use external file for kernel
            flag: %s, position: 5
            mutually_exclusive: kernel_size
    kernel_shape: ('3D' or '2D' or 'box' or 'boxv' or 'gauss' or 'sphere'
             or 'file')
            kernel shape to use
            flag: -kernel %s, position: 4
    kernel_size: (a float)
            kernel size - voxels for box/boxv, mm for sphere, mm sigma for gauss
            flag: %.4f, position: 5
            mutually_exclusive: kernel_file
    nan2zeros: (a boolean)
            change NaNs to zeros before doing anything
            flag: -nan, position: 3
    out_file: (a file name)
            image to write
            flag: %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)
            flag: -odt %s, position: -1
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
```

```
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image written after calculations
```

82.5 ErodeImage

Link to code

Wraps command **fslmaths**

Use fslmaths to perform a spatial erosion of an image.

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        image to operate on
        flag: %s, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
         or 'input')
        datatype to use for calculations (default is float)
        flag: -dt %s, position: 1
kernel_file: (an existing file name)
        use external file for kernel
        flag: %s, position: 5
        mutually_exclusive: kernel_size
kernel_shape: ('3D' or '2D' or 'box' or 'boxv' or 'gauss' or 'sphere'
         or 'file')
        kernel shape to use
        flag: -kernel %s, position: 4
kernel_size: (a float)
        kernel size - voxels for box/boxv, mm for sphere, mm sigma for gauss
        flag: %.4f, position: 5
        mutually_exclusive: kernel_file
minimum_filter: (a boolean, nipype default value: False)
        if true, minimum filter rather than erosion by zeroing-out
        flag: %s, position: 6
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
        flag: -nan, position: 3
out_file: (a file name)
        image to write
```

```
        flag: %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)
        flag: -odt %s, position: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image written after calculations
```

82.6 IsotropicSmooth

Link to code

Wraps command **fslmaths**

Use fslmaths to spatially smooth an image with a gaussian kernel.

Inputs:

```
[Mandatory]
fwhm: (a float)
        fwhm of smoothing kernel [mm]
        flag: -s %.5f, position: 4
        mutually_exclusive: sigma
in_file: (an existing file name)
        image to operate on
        flag: %s, position: 2
sigma: (a float)
        sigma of smoothing kernel [mm]
        flag: -s %.5f, position: 4
        mutually_exclusive: fwhm

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
         or 'input')
        datatype to use for calculations (default is float)
        flag: -dt %s, position: 1
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
        flag: -nan, position: 3
out_file: (a file name)
        image to write
```

```
        flag: %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)
        flag: -odt %s, position: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image written after calculations
```

82.7 MathsCommand

Link to code

Wraps command **fslmaths**

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        image to operate on
        flag: %s, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
         or 'input')
        datatype to use for calculations (default is float)
        flag: -dt %s, position: 1
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
        flag: -nan, position: 3
out_file: (a file name)
        image to write
        flag: %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)
        flag: -odt %s, position: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
```

```
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image written after calculations
```

82.8 MaxImage

Link to code

Wraps command **fslmaths**

Use fslmaths to generate a max image across a given dimension.

82.8.1 Examples

```
>>> from nipype.interfaces.fsl.maths import MaxImage
>>> maxer = MaxImage()
>>> maxer.inputs.in_file = "functional.nii"
>>> maxer.dimension = "T"
>>> maxer.cmdline
'fslmaths functional.nii -Tmax functional_max.nii'
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        image to operate on
        flag: %s, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
dimension: ('T' or 'X' or 'Y' or 'Z', nipype default value: T)
        dimension to max across
        flag: -%smax, position: 4
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
         or 'input')
        datatype to use for calculations (default is float)
        flag: -dt %s, position: 1
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
        flag: -nan, position: 3
out_file: (a file name)
        image to write
        flag: %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)
        flag: -odt %s, position: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image written after calculations
```

82.9 MeanImage

Link to code

Wraps command **fslmaths**

Use fslmaths to generate a mean image across a given dimension.

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        image to operate on
        flag: %s, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
dimension: ('T' or 'X' or 'Y' or 'Z', nipype default value: T)
        dimension to mean across
        flag: -%smean, position: 4
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
         or 'input')
        datatype to use for calculations (default is float)
        flag: -dt %s, position: 1
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
        flag: -nan, position: 3
out_file: (a file name)
        image to write
        flag: %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)
        flag: -odt %s, position: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
```

```
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image written after calculations
```

82.10 MultiImageMaths

Link to code
Wraps command **fslmaths**
Use fslmaths to perform a sequence of mathematical operations.

82.10.1 Examples

```
>>> from nipype.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]
in_file: (an existing file name)
        image to operate on
        flag: %s, position: 2
op_string: (a string)
        python formatted string of operations to perform
        flag: %s, position: 4
operand_files: (a list of items which are an existing file name)
        list of file names to plug into op string

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
         or 'input')
        datatype to use for calculations (default is float)
        flag: -dt %s, position: 1
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
        flag: -nan, position: 3
out_file: (a file name)
```

```
        image to write
        flag: %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)
        flag: -odt %s, position: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image written after calculations
```

82.11 SpatialFilter

Link to code

Wraps command **fslmaths**

Use fslmaths to spatially filter an image.

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        image to operate on
        flag: %s, position: 2
operation: ('mean' or 'median' or 'meanu')
        operation to filter with
        flag: -f%s, position: 6

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
         or 'input')
        datatype to use for calculations (default is float)
        flag: -dt %s, position: 1
kernel_file: (an existing file name)
        use external file for kernel
        flag: %s, position: 5
        mutually_exclusive: kernel_size
kernel_shape: ('3D' or '2D' or 'box' or 'boxv' or 'gauss' or 'sphere'
         or 'file')
        kernel shape to use
        flag: -kernel %s, position: 4
kernel_size: (a float)
```

```
        kernel size - voxels for box/boxv, mm for sphere, mm sigma for gauss
        flag: %.4f, position: 5
        mutually_exclusive: kernel_file
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
        flag: -nan, position: 3
out_file: (a file name)
        image to write
        flag: %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)
        flag: -odt %s, position: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image written after calculations
```

82.12 StdImage

Link to code

Wraps command **fslmaths**

Use fslmaths to generate a standard deviation in an image across a given dimension.

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        image to operate on
        flag: %s, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
dimension: ('T' or 'X' or 'Y' or 'Z', nipype default value: T)
        dimension to standard deviate across
        flag: -%sstd, position: 4
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
         or 'input')
        datatype to use for calculations (default is float)
        flag: -dt %s, position: 1
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
```

```
        flag: -nan, position: 3
out_file: (a file name)
        image to write
        flag: %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)
        flag: -odt %s, position: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image written after calculations
```

82.13 TemporalFilter

Link to code

Wraps command **fslmaths**

Use fslmaths to apply a low, high, or bandpass temporal filter to a timeseries.

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        image to operate on
        flag: %s, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
highpass_sigma: (a float, nipype default value: -1)
        highpass filter sigma (in volumes)
        flag: -bptf %.6f, position: 4
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
         or 'input')
        datatype to use for calculations (default is float)
        flag: -dt %s, position: 1
lowpass_sigma: (a float, nipype default value: -1)
        lowpass filter sigma (in volumes)
        flag: %.6f, position: 5
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
        flag: -nan, position: 3
out_file: (a file name)
```

```
        image to write
        flag: %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)
        flag: -odt %s, position: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image written after calculations
```

82.14 Threshold

Link to code

Wraps command **fslmaths**

Use fslmaths to apply a threshold to an image in a variety of ways.

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        image to operate on
        flag: %s, position: 2
thresh: (a float)
        threshold value
        flag: %s, position: 4

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
direction: ('below' or 'above', nipype default value: below)
        zero-out either below or above thresh value
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
         or 'input')
        datatype to use for calculations (default is float)
        flag: -dt %s, position: 1
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
        flag: -nan, position: 3
out_file: (a file name)
        image to write
        flag: %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)
        flag: -odt %s, position: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
use_nonzero_voxels: (a boolean)
        use nonzero voxels to calculate robust range
        requires: use_robust_range
use_robust_range: (a boolean)
        interpret thresh as percentage (0-100) of robust range
```

Outputs:

```
out_file: (an existing file name)
        image written after calculations
```

82.15 UnaryMaths

Link to code

Wraps command **fslmaths**

Use fslmaths to perorm a variety of mathematical operations on an image.

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        image to operate on
        flag: %s, position: 2
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
        flag: -%s, position: 4

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
internal_datatype: ('float' or 'char' or 'int' or 'short' or 'double'
         or 'input')
        datatype to use for calculations (default is float)
        flag: -dt %s, position: 1
nan2zeros: (a boolean)
        change NaNs to zeros before doing anything
        flag: -nan, position: 3
out_file: (a file name)
```

```
        image to write
        flag: %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)
        flag: -odt %s, position: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image written after calculations
```

CHAPTER 83

interfaces.fsl.model

83.1 Cluster

Link to code
Wraps command **cluster**
Uses FSL cluster to perform clustering on statistical output

83.1.1 Examples

```
>>> cl = Cluster()
>>> cl.inputs.threshold = 2.3
>>> cl.inputs.in_file = 'zstat1.nii.gz'
>>> cl.inputs.out_localmax_txt_file = 'stats.txt'
>>> cl.cmdline
'cluster --in=zstat1.nii.gz --olmax=stats.txt --thresh=2.3000000000'
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input volume
        flag: --in=%s
threshold: (a float)
        threshold for input volume
        flag: --thresh=%.10f

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
connectivity: (an integer (int or long))
        the connectivity of voxels (default 26)
        flag: --connectivity=%d
cope_file: (a file name)
        cope volume
        flag: --cope=%s
dlh: (a float)
        smoothness estimate = sqrt(det(Lambda))
        flag: --dlh=%.10f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
find_min: (a boolean)
        find minima instead of maxima
```

```
    fractional: (a boolean)
            interprets the threshold as a fraction of the robust range
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    minclustersize: (a boolean)
            prints out minimum significant cluster size
            flag: --minclustersize
    no_table: (a boolean)
            suppresses printing of the table info
    num_maxima: (an integer (int or long))
            no of local maxima to report
            flag: --num=%d
    out_index_file: (a boolean or a file name)
            output of cluster index (in size order)
            flag: --oindex=%s
    out_localmax_txt_file: (a boolean or a file name)
            local maxima text file
            flag: --olmax=%s
    out_localmax_vol_file: (a boolean or a file name)
            output of local maxima volume
            flag: --olmaxim=%s
    out_max_file: (a boolean or a file name)
            filename for output of max image
            flag: --omax=%s
    out_mean_file: (a boolean or a file name)
            filename for output of mean image
            flag: --omean=%s
    out_pval_file: (a boolean or a file name)
            filename for image output of log pvals
            flag: --opvals=%s
    out_size_file: (a boolean or a file name)
            filename for output of size image
            flag: --osize=%s
    out_threshold_file: (a boolean or a file name)
            thresholded image
            flag: --othresh=%s
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    peak_distance: (a float)
            minimum distance between local maxima/minima, in mm (default 0)
            flag: --peakdist=%.10f
    pthreshold: (a float)
            p-threshold for clusters
            flag: --pthresh=%.10f
            requires: dlh, volume
    std_space_file: (a file name)
            filename for standard-space volume
            flag: --stdvol=%s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    use_mm: (a boolean)
            use mm, not voxel, coordinates
    volume: (an integer (int or long))
            number of voxels in the mask
```

```
        flag: --volume=%d
warpfield_file: (a file name)
        file contining warpfield
        flag: --warpvol=%s
xfm_file: (a file name)
        filename for Linear: input->standard-space transform. Non-linear:
        input->highres transform
        flag: --xfm=%s
```

Outputs:

```
index_file: (a file name)
        output of cluster index (in size order)
localmax_txt_file: (a file name)
        local maxima text file
localmax_vol_file: (a file name)
        output of local maxima volume
max_file: (a file name)
        filename for output of max image
mean_file: (a file name)
        filename for output of mean image
pval_file: (a file name)
        filename for image output of log pvals
size_file: (a file name)
        filename for output of size image
threshold_file: (a file name)
        thresholded image
```

83.2 ContrastMgr

Link to code

Wraps 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.

Inputs:

```
[Mandatory]
corrections: (an existing file name)
        statistical corrections used within FILM modelling
dof_file: (an existing file name)
        degrees of freedom
param_estimates: (a list of items which are an existing file name)
        Parameter estimates for each column of the design matrix
sigmasquareds: (an existing file name)
        summary of residuals, See Woolrich, et. al., 2001
tcon_file: (an existing file name)
        contrast file containing T-contrasts
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
contrast_num: (an integer >= 1)
        contrast number to start labeling copes from
        flag: -cope
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
```

```
          {})
         Environment variables
fcon_file: (an existing file name)
         contrast file containing F-contrasts
         flag: -f %s
ignore_exception: (a boolean, nipype default value: False)
         Print an error message instead of throwing an exception in case the
         interface fails to run
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
          'NIFTI')
         FSL output type
suffix: (a string)
         suffix to put on the end of the cope filename before the contrast
         number, default is nothing
         flag: -suffix %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
         Control terminal output: `stream` - displays to terminal immediately
         (default), `allatonce` - waits till command is finished to display
         output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
copes: (a list of items which are an existing file name)
         Contrast estimates for each contrast
fstats: (a list of items which are an existing file name)
         f-stat file for each contrast
neffs: (a list of items which are an existing file name)
         neff file ?? for each contrast
tstats: (a list of items which are an existing file name)
         t-stat file for each contrast
varcopes: (a list of items which are an existing file name)
         Variance estimates for each contrast
zfstats: (a list of items which are an existing file name)
         z-stat file for each F contrast
zstats: (a list of items which are an existing file name)
         z-stat file for each contrast
```

83.3 FEAT

Link to code

Wraps command **feat**

Uses FSL feat to calculate first level stats

Inputs:

```
[Mandatory]
fsf_file: (an existing file name)
         File specifying the feat design spec file
         flag: %s, position: 0

[Optional]
args: (a string)
         Additional parameters to the command
         flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
          with values which are a value of type 'str', nipype default value:
          {})
         Environment variables
ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
feat_dir: (an existing directory name)
```

83.4 FEATModel

Link to code

Wraps command **feat_model**

Uses FSL feat_model to generate design.mat files

Inputs:

```
[Mandatory]
ev_files: (a list of items which are an existing file name)
        Event spec files generated by level1design
        flag: %s, position: 1
fsf_file: (an existing file name)
        File specifying the feat design spec file
        flag: %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
con_file: (an existing file name)
        Contrast file containing contrast vectors
design_cov: (an existing file name)
        Graphical representation of design covariance
design_file: (an existing file name)
        Mat file containing ascii matrix for design
design_image: (an existing file name)
        Graphical representation of design matrix
```

```
    fcon_file: (a file name)
            Contrast file containing contrast vectors
```

83.5 FEATRegister

Link to code

Register feat directories to a specific standard

Inputs:

```
    [Mandatory]
    feat_dirs: (a list of items which are an existing directory name)
            Lower level feat dirs
    reg_image: (an existing file name)
            image to register to (will be treated as standard)

    [Optional]
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    reg_dof: (an integer (int or long), nipype default value: 12)
            registration degrees of freedom
```

Outputs:

```
    fsf_file: (an existing file name)
            FSL feat specification file
```

83.6 FILMGLS

Link to code

Wraps command **film_gls**

Use FSL film_gls command to fit a design matrix to voxel timeseries

83.6.1 Examples

Initialize with no options, assigning them when calling run:

```
    >>> from nipype.interfaces import fsl
    >>> fgls = fsl.FILMGLS()
    >>> res = fgls.run('in_file', 'design_file', 'thresh', rn='stats')
```

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
    >>> fgls.inputs.results_dir = 'stats'
    >>> res = fgls.run()
```

Specify options when creating an instance:

```
    >>> fgls = fsl.FILMGLS(in_file='functional.nii', design_file='design.mat', threshold=10, results
    >>> res = fgls.run()
```

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            input data file
            flag: %s, position: -3

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    autocorr_estimate_only: (a boolean)
            perform autocorrelation estimatation only
            flag: -ac
            mutually_exclusive: autocorr_estimate_only, fit_armodel,
             tukey_window, multitaper_product, use_pava, autocorr_noestimate
    autocorr_noestimate: (a boolean)
            do not estimate autocorrs
            flag: -noest
            mutually_exclusive: autocorr_estimate_only, fit_armodel,
             tukey_window, multitaper_product, use_pava, autocorr_noestimate
    brightness_threshold: (an integer >= 0)
            susan brightness threshold, otherwise it is estimated
            flag: -epith %d
    design_file: (an existing file name)
            design matrix file
            flag: %s, position: -2
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    fit_armodel: (a boolean)
            fits autoregressive model - default is to use tukey with
            M=sqrt(numvols)
            flag: -ar
            mutually_exclusive: autocorr_estimate_only, fit_armodel,
             tukey_window, multitaper_product, use_pava, autocorr_noestimate
    full_data: (a boolean)
            output full data
            flag: -v
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    mask_size: (an integer (int or long))
            susan mask size
            flag: -ms %d
    multitaper_product: (an integer (int or long))
            multitapering with slepian tapers and num is the time-bandwidth
            product
            flag: -mt %d
            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
            flag: -output_pwdata
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    results_dir: (a directory name, nipype default value: results)
            directory to store results in
```

```
        flag: -rn %s
smooth_autocorr: (a boolean)
        Smooth auto corr estimates
        flag: -sa
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
threshold: (a floating point number >= 0.0, nipype default value:
         0.0)
        threshold
        flag: %f, position: -1
tukey_window: (an integer (int or long))
        tukey window size to estimate autocorr
        flag: -tukey %d
        mutually_exclusive: autocorr_estimate_only, fit_armodel,
         tukey_window, multitaper_product, use_pava, autocorr_noestimate
use_pava: (a boolean)
        estimates autocorr using PAVA
        flag: -pava
```

Outputs:

```
corrections: (an existing file name)
        statistical corrections used within FILM modelling
dof_file: (an existing file name)
        degrees of freedom
logfile: (an existing file name)
        FILM run logfile
param_estimates: (a list of items which are an existing file name)
        Parameter estimates for each column of the design matrix
residual4d: (an existing file name)
        Model fit residual mean-squared error for each time point
results_dir: (an existing directory name)
        directory storing model estimation output
sigmasquareds: (an existing file name)
        summary of residuals, See Woolrich, et. al., 2001
thresholdac: (an existing file name)
        The FILM autocorrelation parameters
```

83.7 FLAMEO

Link to code

Wraps command **flameo**

Use FSL flameo command to perform higher level model fits

83.7.1 Examples

Initialize FLAMEO with no options, assigning them when calling run:

```
>>> from nipype.interfaces import fsl
>>> import os
>>> flameo = fsl.FLAMEO(cope_file='cope.nii.gz',                                    var_cope_file='varc
>>> flameo.cmdline
'flameo --copefile=cope.nii.gz --covsplitfile=cov_split.mat --designfile=design.mat --ld=stats -
```

Inputs:

```
    [Mandatory]
    cope_file: (an existing file name)
            cope regressor data file
            flag: --copefile=%s
    cov_split_file: (an existing file name)
            ascii matrix specifying the groups the covariance is split into
            flag: --covsplitfile=%s
    design_file: (an existing file name)
            design matrix file
            flag: --designfile=%s
    mask_file: (an existing file name)
            mask file
            flag: --maskfile=%s
    run_mode: ('fe' or 'ols' or 'flame1' or 'flame12')
            inference to perform
            flag: --runmode=%s
    t_con_file: (an existing file name)
            ascii matrix specifying t-contrasts
            flag: --tcontrastsfile=%s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    burnin: (an integer (int or long))
            number of jumps at start of mcmc to be discarded
            flag: --burnin=%d
    dof_var_cope_file: (an existing file name)
            dof data file for varcope data
            flag: --dofvarcopefile=%s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    f_con_file: (an existing file name)
            ascii matrix specifying f-contrasts
            flag: --fcontrastsfile=%s
    fix_mean: (a boolean)
            fix mean for tfit
            flag: --fixmean
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    infer_outliers: (a boolean)
            infer outliers - not for fe
            flag: --inferoutliers
    log_dir: (a directory name, nipype default value: stats)
            flag: --ld=%s
    n_jumps: (an integer (int or long))
            number of jumps made by mcmc
            flag: --njumps=%d
    no_pe_outputs: (a boolean)
            do not output pe files
            flag: --nopeoutput
    outlier_iter: (an integer (int or long))
            Number of max iterations to use when inferring outliers. Default is
            12.
            flag: --ioni=%d
```

```
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    sample_every: (an integer (int or long))
            number of jumps for each sample
            flag: --sampleevery=%d
    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
            flag: --sigma_dofs=%d
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    var_cope_file: (an existing file name)
            varcope weightings data file
            flag: --varcopefile=%s
```

Outputs:

```
    copes: (a list of items which are an existing file name)
            Contrast estimates for each contrast
    fstats: (a list of items which are an existing file name)
            f-stat file for each contrast
    mrefvars: (a list of items which are an existing file name)
            mean random effect variances for each contrast
    pes: (a list of items which are an existing file name)
            Parameter estimates for each column of the design matrix for each
            voxel
    res4d: (a list of items which are an existing file name)
            Model fit residual mean-squared error for each time point
    stats_dir: (a directory name)
            directory storing model estimation output
    tdof: (a list of items which are an existing file name)
            temporal dof file for each contrast
    tstats: (a list of items which are an existing file name)
            t-stat file for each contrast
    var_copes: (a list of items which are an existing file name)
            Variance estimates for each contrast
    weights: (a list of items which are an existing file name)
            weights file for each contrast
    zfstats: (a list of items which are an existing file name)
            z stat file for each f contrast
    zstats: (a list of items which are an existing file name)
            z-stat file for each contrast
```

83.8 GLM

Link to code
Wraps command **fsl_glm**
FSL GLM:

83.8.1 Example

```
>>> import nipype.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]
design: (an existing file name)
        file name of the GLM design matrix (text time courses for temporal
        regression or an image file for spatial regression)
        flag: -d %s, position: 2
in_file: (an existing file name)
        input file name (text matrix or 3D/4D image file)
        flag: -i %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
contrasts: (an existing file name)
        matrix of t-statics contrasts
        flag: -c %s
dat_norm: (a boolean)
        switch on normalization of the data time series to unit std
        deviation
        flag: --dat_norm
demean: (a boolean)
        switch on demeaining of design and data
        flag: --demean
des_norm: (a boolean)
        switch on normalization of the design matrix columns to unit std
        deviation
        flag: --des_norm
dof: (an integer (int or long))
        set degrees of freedom explicitly
        flag: --dof=%d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        mask image file name if input is image
        flag: -m %s
out_cope: (a file name)
        output file name for COPE (either as txt or image
        flag: --out_cope=%s
out_data_name: (a file name)
        output file name for pre-processed data
        flag: --out_data=%s
out_f_name: (a file name)
        output file name for F-value of full model fit
        flag: --out_f=%s
out_file: (a file name)
        filename for GLM parameter estimates (GLM betas)
        flag: -o %s, position: 3
out_p_name: (a file name)
        output file name for p-values of Z-stats (either as text file or
```

```
        image)
        flag: --out_p=%s
out_pf_name: (a file name)
        output file name for p-value for full model fit
        flag: --out_pf=%s
out_res_name: (a file name)
        output file name for residuals
        flag: --out_res=%s
out_sigsq_name: (a file name)
        output file name for residual noise variance sigma-square
        flag: --out_sigsq=%s
out_t_name: (a file name)
        output file name for t-stats (either as txt or image
        flag: --out_t=%s
out_varcb_name: (a file name)
        output file name for variance of COPEs
        flag: --out_varcb=%s
out_vnscales_name: (a file name)
        output file name for scaling factors for variance normalisation
        flag: --out_vnscales=%s
out_z_name: (a file name)
        output file name for Z-stats (either as txt or image
        flag: --out_z=%s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
var_norm: (a boolean)
        perform MELODIC variance-normalisation on data
        flag: --vn
```

Outputs:

```
out_cope: (a list of items which are an existing file name)
        output file name for COPEs (either as text file or image)
out_data: (a list of items which are an existing file name)
        output file for preprocessed data
out_f: (a list of items which are an existing file name)
        output file name for F-value of full model fit
out_file: (an existing file name)
        file name of GLM parameters (if generated)
out_p: (a list of items which are an existing file name)
        output file name for p-values of Z-stats (either as text file or
        image)
out_pf: (a list of items which are an existing file name)
        output file name for p-value for full model fit
out_res: (a list of items which are an existing file name)
        output file name for residuals
out_sigsq: (a list of items which are an existing file name)
        output file name for residual noise variance sigma-square
out_t: (a list of items which are an existing file name)
        output file name for t-stats (either as text file or image)
out_varcb: (a list of items which are an existing file name)
        output file name for variance of COPEs
out_vnscales: (a list of items which are an existing file name)
        output file name for scaling factors for variance normalisation
```

```
out_z: (a list of items which are an existing file name)
        output file name for COPEs (either as text file or image)
```

83.9 L2Model

Link to code
Generate subject specific second level model

83.9.1 Examples

```
>>> from nipype.interfaces.fsl import L2Model
>>> model = L2Model(num_copes=3) # 3 sessions
```

Inputs:

```
[Mandatory]
num_copes: (an integer >= 1)
        number of copes to be combined

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
design_con: (an existing file name)
        design contrast file
design_grp: (an existing file name)
        design group file
design_mat: (an existing file name)
        design matrix file
```

83.10 Level1Design

Link to code
Generate FEAT specific files

83.10.1 Examples

```
>>> level1design = Level1Design()
>>> level1design.inputs.interscan_interval = 2.5
>>> level1design.inputs.bases = {'dgamma':{'derivs': False}}
>>> level1design.inputs.session_info = 'session_info.npz'
>>> level1design.run()
```

Inputs:

```
[Mandatory]
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' and
         with values which are a boolean 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}}
interscan_interval: (a float)
        Interscan interval (in secs)
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
session_info: (any value)
        Session specific information generated by ``modelgen.SpecifyModel``

[Optional]
contrasts: (a list of items which are a tuple of the form: (a string,
         'T', a list of items which are a string, a list of items which are
         a float) or a tuple of the form: (a string, 'T', a list of items
         which are a string, a list of items which are a float, a list of
         items which are a float) or a tuple of the form: (a string, 'F', a
         list of items which are a tuple of the form: (a string, 'T', a list
         of items which are a string, a list of items which are a float) or
         a tuple of the form: (a string, 'T', a list of items which are a
         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.
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
ev_files: (a list of items which are a list of items which are an
         existing file name)
        condition information files
fsf_files: (a list of items which are an existing file name)
        FSL feat specification files
```

83.11 MELODIC

Link to code

Wraps command **melodic**

Multivariate Exploratory Linear Optimised Decomposition into Independent Components

83.11.1 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 --mmt
>>> melodic_setup.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        input file names (either single file name or a list)
        flag: -i %s, position: 0

[Optional]
ICs: (an existing file name)
        filename of the IC components file for mixture modelling
        flag: --ICs=%s
approach: (a string)
        approach for decomposition, 2D: defl, symm (default), 3D: tica
        (default), concat
        flag: -a %s
args: (a string)
        Additional parameters to the command
        flag: %s
bg_image: (an existing file name)
        specify background image for report (default: mean image)
        flag: --bgimage=%s
bg_threshold: (a float)
        brain/non-brain threshold used to mask non-brain voxels, as a
        percentage (only if --nobet selected)
        flag: --bgthreshold=%f
cov_weight: (a float)
        voxel-wise weights for the covariance matrix (e.g. segmentation
        information)
        flag: --covarweight=%f
dim: (an integer (int or long))
        dimensionality reduction into #num dimensions(default: automatic
        estimation)
        flag: -d %d
dim_est: (a string)
        use specific dim. estimation technique: lap, bic, mdl, aic, mean
        (default: lap)
        flag: --dimest=%s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
epsilon: (a float)
        minimum error change
        flag: --eps=%f
epsilonS: (a float)
        minimum error change for rank-1 approximation in TICA
        flag: --epsS=%f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
log_power: (a boolean)
```

```
        calculate log of power for frequency spectrum
        flag: --logPower
mask: (an existing file name)
        file name of mask for thresholding
        flag: -m %s
max_restart: (an integer (int or long))
        maximum number of restarts
        flag: --maxrestart=%d
maxit: (an integer (int or long))
        maximum number of iterations before restart
        flag: --maxit=%d
mix: (an existing file name)
        mixing matrix for mixture modelling / filtering
        flag: --mix=%s
mm_thresh: (a float)
        threshold for Mixture Model based inference
        flag: --mmthresh=%f
no_bet: (a boolean)
        switch off BET
        flag: --nobet
no_mask: (a boolean)
        switch off masking
        flag: --nomask
no_mm: (a boolean)
        switch off mixture modelling on IC maps
        flag: --no_mm
non_linearity: (a string)
        nonlinearity: gauss, tanh, pow3, pow4
        flag: --nl=%s
num_ICs: (an integer (int or long))
        number of IC's to extract (for deflation approach)
        flag: -n %d
out_all: (a boolean)
        output everything
        flag: --Oall
out_dir: (a directory name)
        output directory name
        flag: -o %s
out_mean: (a boolean)
        output mean volume
        flag: --Omean
out_orig: (a boolean)
        output the original ICs
        flag: --Oorig
out_pca: (a boolean)
        output PCA results
        flag: --Opca
out_stats: (a boolean)
        output thresholded maps and probability maps
        flag: --Ostats
out_unmix: (a boolean)
        output unmixing matrix
        flag: --Ounmix
out_white: (a boolean)
        output whitening/dewhitening matrices
        flag: --Owhite
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
```

```
        FSL output type
pbsc: (a boolean)
        switch off conversion to percent BOLD signal change
        flag: --pbsc
rem_cmp: (a list of items which are an integer (int or long))
        component numbers to remove
        flag: -f %d
remove_deriv: (a boolean)
        removes every second entry in paradigm file (EV derivatives)
        flag: --remove_deriv
report: (a boolean)
        generate Melodic web report
        flag: --report
report_maps: (a string)
        control string for spatial map images (see slicer)
        flag: --report_maps=%s
s_con: (an existing file name)
        t-contrast matrix across subject-domain
        flag: --Scon=%s
s_des: (an existing file name)
        design matrix across subject-domain
        flag: --Sdes=%s
sep_vn: (a boolean)
        switch off joined variance normalization
        flag: --sep_vn
sep_whiten: (a boolean)
        switch on separate whitening
        flag: --sep_whiten
smode: (an existing file name)
        matrix of session modes for report generation
        flag: --smode=%s
t_con: (an existing file name)
        t-contrast matrix across time-domain
        flag: --Tcon=%s
t_des: (an existing file name)
        design matrix across time-domain
        flag: --Tdes=%s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tr_sec: (a float)
        TR in seconds
        flag: --tr=%f
update_mask: (a boolean)
        switch off mask updating
        flag: --update_mask
var_norm: (a boolean)
        switch off variance normalization
        flag: --vn
```

Outputs:

```
out_dir: (an existing directory name)
report_dir: (an existing directory name)
```

83.12 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.

83.12.1 Examples

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
contrasts: (a list of items which are a tuple of the form: (a string,
         'T', a list of items which are a string, a list of items which are
         a float) or a tuple of the form: (a string, 'F', a list of items
         which are a tuple of the form: (a string, 'T', a list of items
         which are a string, 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])]. 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 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)
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
design_con: (an existing file name)
        design t-contrast file
design_fts: (an existing file name)
        design f-contrast file
design_grp: (an existing file name)
        design group file
design_mat: (an existing file name)
        design matrix file
```

83.13 Randomise

Link to code
Wraps 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

83.13.1 Example

```
>>> import nipype.interfaces.fsl as fsl
>>> rand = fsl.Randomise(in_file='allFA.nii', mask = 'mask.nii', tcon='design.con', design_mat='
>>> rand.cmdline
'randomise -i allFA.nii -o "tbss_" -d design.mat -t design.con -m mask.nii'
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        4D input file
        flag: -i %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
base_name: (a string, nipype default value: tbss_)
        the rootname that all generated files will have
        flag: -o "%s", position: 1
c_thresh: (a float)
        carry out cluster-based thresholding
        flag: -c %.2f
cm_thresh: (a float)
        carry out cluster-mass-based thresholding
        flag: -C %.2f
demean: (a boolean)
        demean data temporally before model fitting
        flag: -D
design_mat: (an existing file name)
        design matrix file
        flag: -d %s, position: 2
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
f_c_thresh: (a float)
        carry out f cluster thresholding
        flag: -F %.2f
f_cm_thresh: (a float)
        carry out f cluster-mass thresholding
        flag: -S %.2f
f_only: (a boolean)
        calculate f-statistics only
        flag: --f_only
fcon: (an existing file name)
        f contrasts file
        flag: -f %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        mask image
        flag: -m %s
num_perm: (an integer (int or long))
        number of permutations (default 5000, set to 0 for exhaustive)
        flag: -n %d
one_sample_group_mean: (a boolean)
```

```
        perform 1-sample group-mean test instead of generic permutation test
        flag: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
     'NIFTI')
        FSL output type
p_vec_n_dist_files: (a boolean)
        output permutation vector and null distribution text files
        flag: -P
raw_stats_imgs: (a boolean)
        output raw ( unpermuted ) statistic images
        flag: -R
seed: (an integer (int or long))
        specific integer seed for random number generator
        flag: --seed=%d
show_info_parallel_mode: (a boolean)
        print out information required for parallel mode and exit
        flag: -Q
show_total_perms: (a boolean)
        print out how many unique permutations would be generated and exit
        flag: -q
tcon: (an existing file name)
        t contrasts file
        flag: -t %s, position: 3
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tfce: (a boolean)
        carry out Threshold-Free Cluster Enhancement
        flag: -T
tfce2D: (a boolean)
        carry out Threshold-Free Cluster Enhancement with 2D optimisation
        flag: --T2
tfce_C: (a float)
        TFCE connectivity (6 or 26; default=6)
        flag: --tfce_C=%.2f
tfce_E: (a float)
        TFCE extent parameter (default=0.5)
        flag: --tfce_E=%.2f
tfce_H: (a float)
        TFCE height parameter (default=2)
        flag: --tfce_H=%.2f
var_smooth: (an integer (int or long))
        use variance smoothing (std is in mm)
        flag: -v %d
vox_p_values: (a boolean)
        output voxelwise (corrected and uncorrected) p-value images
        flag: -x
x_block_labels: (an existing file name)
        exchangeability block labels file
        flag: -e %s
```

Outputs:

```
f_corrected_p_files: (a list of items which are an existing file
     name)
        f contrast FWE (Family-wise error) corrected p values files
f_p_files: (a list of items which are an existing file name)
        f contrast uncorrected p values files
```

```
    fstat_files: (a list of items which are an existing file name)
            f contrast raw statistic
    t_corrected_p_files: (a list of items which are an existing file
             name)
            t contrast FWE (Family-wise error) corrected p values files
    t_p_files: (a list of items which are an existing file name)
            f contrast uncorrected p values files
    tstat_files: (a list of items which are an existing file name)
            t contrast raw statistic
```

83.14 SMM

Link to code

Wraps 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]
    mask: (an existing file name)
            mask file
            flag: --mask="%s", position: 1
    spatial_data_file: (an existing file name)
            statistics spatial map
            flag: --sdf="%s", position: 0

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    no_deactivation_class: (a boolean)
            enforces no deactivation class
            flag: --zfstatmode, position: 2
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    activation_p_map: (an existing file name)
    deactivation_p_map: (an existing file name)
    null_p_map: (an existing file name)
```

83.15 SmoothEstimate

Link to code
Wraps command **smoothest**
Estimates the smoothness of an image

83.15.1 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
        flag: --dof=%d
        mutually_exclusive: zstat_file
mask_file: (an existing file name)
        brain mask volume
        flag: --mask=%s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
residual_fit_file: (an existing file name)
        residual-fit image file
        flag: --res=%s
        requires: dof
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
zstat_file: (an existing file name)
        zstat image file
        flag: --zstat=%s
        mutually_exclusive: dof
```

Outputs:

```
dlh: (a float)
        smoothness estimate sqrt(det(Lambda))
resels: (a float)
        number of resels
volume: (an integer (int or long))
```

```
        number of voxels in mask
```

interfaces.fsl.preprocess

84.1 ApplyWarp

Link to code
Wraps command **applywarp**
Use FSL's applywarp to apply the results of a FNIRT registration

84.1.1 Examples

```
>>> from nipype.interfaces import fsl
>>> from nipype.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_filed.nii'
>>> res = aw.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        image to be warped
        flag: --in=%s, position: 0
ref_file: (an existing file name)
        reference image
        flag: --ref=%s, position: 1

[Optional]
abswarp: (a boolean)
        treat warp field as absolute: x' = w(x)
        flag: --abs
        mutually_exclusive: relwarp
args: (a string)
        Additional parameters to the command
        flag: %s
datatype: ('char' or 'short' or 'int' or 'float' or 'double')
        Force output data type [char short int float double].
        flag: --datatype=%s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
field_file: (an existing file name)
        file containing warp field
        flag: --warp=%s
```

```
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    interp: ('nn' or 'trilinear' or 'sinc' or 'spline')
            interpolation method
            flag: --interp=%s, position: -2
    mask_file: (an existing file name)
            filename for mask image (in reference space)
            flag: --mask=%s
    out_file: (a file name)
            output filename
            flag: --out=%s, position: 2
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    postmat: (an existing file name)
            filename for post-transform (affine matrix)
            flag: --postmat=%s
    premat: (an existing file name)
            filename for pre-transform (affine matrix)
            flag: --premat=%s
    relwarp: (a boolean)
            treat warp field as relative: x' = x + w(x)
            flag: --rel, position: -1
            mutually_exclusive: abswarp
    superlevel: ('a' or an integer (int or long))
            level of intermediary supersampling, a for 'automatic' or integer
            level. Default = 2
            flag: --superlevel=%s
    supersample: (a boolean)
            intermediary supersampling of output, default is off
            flag: --super
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
            Warped output file
```

84.2 ApplyXfm

Link to code

Wraps command **flirt**

Currently just a light wrapper around FLIRT, with no modifications

ApplyXfm is used to apply an existing tranform to an image

84.2.1 Examples

```
>>> import nipype.interfaces.fsl as fsl
>>> from nipype.testing import example_data
>>> applyxfm = fsl.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file
        flag: -in %s, position: 0
reference: (an existing file name)
        reference file
        flag: -ref %s, position: 1

[Optional]
angle_rep: ('quaternion' or 'euler')
        representation of rotation angles
        flag: -anglerep %s
apply_isoxfm: (a float)
        as applyxfm but forces isotropic resampling
        flag: -applyisoxfm %f
        mutually_exclusive: apply_xfm
apply_xfm: (a boolean, nipype default value: True)
        apply transformation supplied by in_matrix_file
        flag: -applyxfm
        requires: in_matrix_file
args: (a string)
        Additional parameters to the command
        flag: %s
bbrslope: (a float)
        value of bbr slope
        flag: -bbrslope %f
bbrtype: ('signed' or 'global_abs' or 'local_abs')
        type of bbr cost function: signed [default], global_abs, local_abs
        flag: -bbrtype %s
bgvalue: (a float)
        use specified background value for points outside FOV
        flag: -setbackground %f
bins: (an integer (int or long))
        number of histogram bins
        flag: -bins %d
coarse_search: (an integer (int or long))
        coarse search delta angle
        flag: -coarsesearch %d
cost: ('mutualinfo' or 'corratio' or 'normcorr' or 'normmi' or
         'leastsq' or 'labeldiff' or 'bbr')
        cost function
        flag: -cost %s
cost_func: ('mutualinfo' or 'corratio' or 'normcorr' or 'normmi' or
         'leastsq' or 'labeldiff' or 'bbr')
        cost function
        flag: -searchcost %s
datatype: ('char' or 'short' or 'int' or 'float' or 'double')
        force output data type
        flag: -datatype %s
display_init: (a boolean)
        display initial matrix
        flag: -displayinit
dof: (an integer (int or long))
```

```
        number of transform degrees of freedom
        flag: -dof %d
echospacing: (a float)
        value of EPI echo spacing - units of seconds
        flag: -echospacing %f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fieldmap: (a file name)
        fieldmap image in rads/s - must be already registered to the
        reference image
        flag: -fieldmap %s
fieldmapmask: (a file name)
        mask for fieldmap image
        flag: -fieldmapmask %s
fine_search: (an integer (int or long))
        fine search delta angle
        flag: -finesearch %d
force_scaling: (a boolean)
        force rescaling even for low-res images
        flag: -forcescaling
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_matrix_file: (a file name)
        input 4x4 affine matrix
        flag: -init %s
in_weight: (an existing file name)
        File for input weighting volume
        flag: -inweight %s
interp: ('trilinear' or 'nearestneighbour' or 'sinc' or 'spline')
        final interpolation method used in reslicing
        flag: -interp %s
min_sampling: (a float)
        set minimum voxel dimension for sampling
        flag: -minsampling %f
no_clamp: (a boolean)
        do not use intensity clamping
        flag: -noclamp
no_resample: (a boolean)
        do not change input sampling
        flag: -noresample
no_resample_blur: (a boolean)
        do not use blurring on downsampling
        flag: -noresampblur
no_search: (a boolean)
        set all angular searches to ranges 0 to 0
        flag: -nosearch
out_file: (a file name)
        registered output file
        flag: -out %s, position: 2
out_log: (a file name)
        output log
        requires: save_log
out_matrix_file: (a file name)
        output affine matrix in 4x4 asciii format
        flag: -omat %s, position: 3
```

```
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    padding_size: (an integer (int or long))
            for applyxfm: interpolates outside image by size
            flag: -paddingsize %d
    pedir: (an integer (int or long))
            phase encode direction of EPI - 1/2/3=x/y/z & -1/-2/-3=-x/-y/-z
            flag: -pedir %d
    ref_weight: (an existing file name)
            File for reference weighting volume
            flag: -refweight %s
    rigid2D: (a boolean)
            use 2D rigid body mode - ignores dof
            flag: -2D
    save_log: (a boolean)
            save to log file
    schedule: (an existing file name)
            replaces default schedule
            flag: -schedule %s
    searchr_x: (a list of from 2 to 2 items which are an integer (int or
             long))
            search angles along x-axis, in degrees
            flag: -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
            flag: -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
            flag: -searchrz %s
    sinc_width: (an integer (int or long))
            full-width in voxels
            flag: -sincwidth %d
    sinc_window: ('rectangular' or 'hanning' or 'blackman')
            sinc window
            flag: -sincwindow %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    uses_qform: (a boolean)
            initialize using sform or qform
            flag: -usesqform
    verbose: (an integer (int or long))
            verbose mode, 0 is least
            flag: -verbose %d
    wm_seg: (a file name)
            white matter segmentation volume needed by BBR cost function
            flag: -wmseg %s
    wmcoords: (a file name)
            white matter boundary coordinates for BBR cost function
            flag: -wmcoords %s
    wmnorms: (a file name)
            white matter boundary normals for BBR cost function
            flag: -wmnorms %s
```

Outputs:

```
    out_file: (an existing file name)
            path/name of registered file (if generated)
    out_log: (a file name)
            path/name of output log (if generated)
    out_matrix_file: (an existing file name)
            path/name of calculated affine transform (if generated)
```

84.3 BET

Link to code
Wraps command **bet**
Use FSL BET command for skull stripping.
For complete details, see the BET Documentation.

84.3.1 Examples

```
    >>> from nipype.interfaces import fsl
    >>> from nipype.testing import  example_data
    >>> btr = fsl.BET()
    >>> btr.inputs.in_file = example_data('structural.nii')
    >>> btr.inputs.frac = 0.7
    >>> res = btr.run()
```

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            input file to skull strip
            flag: %s, position: 0

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    center: (a list of at most 3 items which are an integer (int or
             long))
            center of gravity in voxels
            flag: -c %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    frac: (a float)
            fractional intensity threshold
            flag: -f %.2f
    functional: (a boolean)
            apply to 4D fMRI data
            flag: -F
            mutually_exclusive: functional, reduce_bias, robust, padding,
             remove_eyes, surfaces, t2_guided
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    mask: (a boolean)
            create binary mask image
            flag: -m
    mesh: (a boolean)
```

```
        generate a vtk mesh brain surface
        flag: -e
no_output: (a boolean)
        Don't generate segmented output
        flag: -n
out_file: (a file name)
        name of output skull stripped image
        flag: %s, position: 1
outline: (a boolean)
        create surface outline image
        flag: -o
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
padding: (a boolean)
        improve BET if FOV is very small in Z (by temporarily padding end
        slices)
        flag: -Z
        mutually_exclusive: functional, reduce_bias, robust, padding,
         remove_eyes, surfaces, t2_guided
radius: (an integer (int or long))
        head radius
        flag: -r %d
reduce_bias: (a boolean)
        bias field and neck cleanup
        flag: -B
        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)
        flag: -S
        mutually_exclusive: functional, reduce_bias, robust, padding,
         remove_eyes, surfaces, t2_guided
robust: (a boolean)
        robust brain centre estimation (iterates BET several times)
        flag: -R
        mutually_exclusive: functional, reduce_bias, robust, padding,
         remove_eyes, surfaces, t2_guided
skull: (a boolean)
        create skull image
        flag: -s
surfaces: (a boolean)
        run bet2 and then betsurf to get additional skull and scalp surfaces
        (includes registrations)
        flag: -A
        mutually_exclusive: functional, reduce_bias, robust, padding,
         remove_eyes, surfaces, t2_guided
t2_guided: (a file name)
        as with creating surfaces, when also feeding in non-brain-extracted
        T2 (includes registrations)
        flag: -A2 %s
        mutually_exclusive: functional, reduce_bias, robust, padding,
         remove_eyes, surfaces, t2_guided
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
threshold: (a boolean)
```

```
        apply thresholding to segmented brain image and mask
        flag: -t
vertical_gradient: (a float)
        vertical gradient in fractional intensity threshold (-1, 1)
        flag: -g %.2f
```

Outputs:

```
inskull_mask_file: (a file name)
        path/name of inskull mask (if generated)
inskull_mesh_file: (a file name)
        path/name of inskull mesh outline (if generated)
mask_file: (a file name)
        path/name of binary brain mask (if generated)
meshfile: (a file name)
        path/name of vtk mesh file (if generated)
out_file: (a file name)
        path/name of skullstripped file (if generated)
outline_file: (a file name)
        path/name of outline file (if generated)
outskin_mask_file: (a file name)
        path/name of outskin mask (if generated)
outskin_mesh_file: (a file name)
        path/name of outskin mesh outline (if generated)
outskull_mask_file: (a file name)
        path/name of outskull mask (if generated)
outskull_mesh_file: (a file name)
        path/name of outskull mesh outline (if generated)
skull_mask_file: (a file name)
        path/name of skull mask (if generated)
```

84.4 FAST

Link to code
Wraps command **fast**
Use FSL FAST for segmenting and bias correction.
For complete details, see the FAST Documentation.

84.4.1 Examples

```
>>> from nipype.interfaces import fsl
>>> from nipype.testing import example_data
```

Assign options through the `inputs` attribute:

```
>>> fastr = fsl.FAST()
>>> fastr.inputs.in_files = example_data('structural.nii')
>>> out = fastr.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        image, or multi-channel set of images, to be segmented
        flag: %s, position: -1

[Optional]
args: (a string)
```

```
        Additional parameters to the command
        flag: %s
bias_iters: (1 <= an integer <= 10)
        number of main-loop iterations during bias-field removal
        flag: -I %d
bias_lowpass: (4 <= an integer <= 40)
        bias field smoothing extent (FWHM) in mm
        flag: -l %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
hyper: (0.0 <= a floating point number <= 1.0)
        segmentation spatial smoothness
        flag: -H %.2f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
img_type: (1 or 2 or 3)
        int specifying type of image: (1 = T1, 2 = T2, 3 = PD)
        flag: -t %d
init_seg_smooth: (0.0001 <= a floating point number <= 0.1)
        initial segmentation spatial smoothness (during bias field
        estimation)
        flag: -f %.3f
init_transform: (an existing file name)
        <standard2input.mat> initialise using priors
        flag: -a %s
iters_afterbias: (1 <= an integer <= 20)
        number of main-loop iterations after bias-field removal
        flag: -O %d
manual_seg: (an existing file name)
        Filename containing intensities
        flag: -s %s
mixel_smooth: (0.0 <= a floating point number <= 1.0)
        spatial smoothness for mixeltype
        flag: -R %.2f
no_bias: (a boolean)
        do not remove bias field
        flag: -N
no_pve: (a boolean)
        turn off PVE (partial volume estimation)
        flag: --nopve
number_classes: (1 <= an integer <= 10)
        number of tissue-type classes
        flag: -n %d
other_priors: (a list of from 3 to 3 items which are a file name)
        alternative prior images
        flag: -A %s
out_basename: (a file name)
        base name of output files
        flag: -o %s
output_biascorrected: (a boolean)
        output restored image (bias-corrected image)
        flag: -B
output_biasfield: (a boolean)
        output estimated bias field
        flag: -b
```

```
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    probability_maps: (a boolean)
            outputs individual probability maps
            flag: -p
    segment_iters: (1 <= an integer <= 50)
            number of segmentation-initialisation iterations
            flag: -W %d
    segments: (a boolean)
            outputs a separate binary image for each tissue type
            flag: -g
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    use_priors: (a boolean)
            use priors throughout
            flag: -P
    verbose: (a boolean)
            switch on diagnostic messages
            flag: -v
```

Outputs:

```
    bias_field: (a list of items which are a file name)
    mixeltype: (a file name)
            path/name of mixeltype volume file _mixeltype
    partial_volume_files: (a list of items which are a file name)
    partial_volume_map: (a file name)
            path/name of partial volume file _pveseg
    probability_maps: (a list of items which are a file name)
    restored_image: (a list of items which are a file name)
    tissue_class_files: (a list of items which are a file name)
    tissue_class_map: (an existing file name)
            path/name of binary segmented volume file one val for each class
            _seg
```

84.5 FIRST

Link to code
Wraps command **run_first_all**
Use FSL's run_first_all command to segment subcortical volumes
http://www.fmrib.ox.ac.uk/fsl/first/index.html

84.5.1 Examples

```
    >>> from nipype.interfaces import fsl
    >>> first = fsl.FIRST()
    >>> first.inputs.in_file = 'structural.nii'
    >>> first.inputs.out_file = 'segmented.nii'
    >>> res = first.run()
```

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
```

```
        input data file
        flag: -i %s, position: -2
out_file: (a file name, nipype default value: segmented)
        output data file
        flag: -o %s, position: -1

[Optional]
affine_file: (an existing file name)
        Affine matrix to use (e.g. img2std.mat) (does not re-run
        registration)
        flag: -a %s, position: 6
args: (a string)
        Additional parameters to the command
        flag: %s
brain_extracted: (a boolean)
        Input structural image is already brain-extracted
        flag: -b, position: 2
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
list_of_specific_structures: (a list of at least 1 items which are a
         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
        flag: -s %s, position: 5
method: ('auto' or 'fast' or 'none', nipype default value: auto)
        Method must be one of auto, fast, none, or it can be entered using
        the 'method_as_numerical_threshold' input
        flag: -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
        flag: -m %.4f, position: 4
no_cleanup: (a boolean)
        Input structural image is already brain-extracted
        flag: -d, position: 3
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        Use verbose logging.
        flag: -v, position: 1
```

Outputs:

```
bvars: (a list of items which are an existing file name)
        bvars for each subcortical region
original_segmentations: (an existing file name)
        3D image file containing the segmented regions as integer values.
```

```
        Uses CMA labelling
segmentation_file: (an existing file name)
        4D image file containing a single volume per segmented region
vtk_surfaces: (a list of items which are an existing file name)
        VTK format meshes for each subcortical region
```

84.6 FLIRT

Link to code
Wraps command **flirt**
Use FSL FLIRT for coregistration.
For complete details, see the FLIRT Documentation.
To print out the command line help, use: fsl.FLIRT().inputs_help()

84.6.1 Examples

```
>>> from nipype.interfaces import fsl
>>> from nipype.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
'flirt -in structural.nii -ref mni.nii -out structural_flirt.nii.gz -omat structural_flirt.mat -
>>> res = flt.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file
        flag: -in %s, position: 0
reference: (an existing file name)
        reference file
        flag: -ref %s, position: 1

[Optional]
angle_rep: ('quaternion' or 'euler')
        representation of rotation angles
        flag: -anglerep %s
apply_isoxfm: (a float)
        as applyxfm but forces isotropic resampling
        flag: -applyisoxfm %f
        mutually_exclusive: apply_xfm
apply_xfm: (a boolean)
        apply transformation supplied by in_matrix_file
        flag: -applyxfm
        requires: in_matrix_file
args: (a string)
        Additional parameters to the command
        flag: %s
bbrslope: (a float)
        value of bbr slope
        flag: -bbrslope %f
bbrtype: ('signed' or 'global_abs' or 'local_abs')
        type of bbr cost function: signed [default], global_abs, local_abs
```

```
        flag: -bbrtype %s
    bgvalue: (a float)
        use specified background value for points outside FOV
        flag: -setbackground %f
    bins: (an integer (int or long))
        number of histogram bins
        flag: -bins %d
    coarse_search: (an integer (int or long))
        coarse search delta angle
        flag: -coarsesearch %d
    cost: ('mutualinfo' or 'corratio' or 'normcorr' or 'normmi' or
         'leastsq' or 'labeldiff' or 'bbr')
        cost function
        flag: -cost %s
    cost_func: ('mutualinfo' or 'corratio' or 'normcorr' or 'normmi' or
         'leastsq' or 'labeldiff' or 'bbr')
        cost function
        flag: -searchcost %s
    datatype: ('char' or 'short' or 'int' or 'float' or 'double')
        force output data type
        flag: -datatype %s
    display_init: (a boolean)
        display initial matrix
        flag: -displayinit
    dof: (an integer (int or long))
        number of transform degrees of freedom
        flag: -dof %d
    echospacing: (a float)
        value of EPI echo spacing - units of seconds
        flag: -echospacing %f
    environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
    fieldmap: (a file name)
        fieldmap image in rads/s - must be already registered to the
        reference image
        flag: -fieldmap %s
    fieldmapmask: (a file name)
        mask for fieldmap image
        flag: -fieldmapmask %s
    fine_search: (an integer (int or long))
        fine search delta angle
        flag: -finesearch %d
    force_scaling: (a boolean)
        force rescaling even for low-res images
        flag: -forcescaling
    ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
    in_matrix_file: (a file name)
        input 4x4 affine matrix
        flag: -init %s
    in_weight: (an existing file name)
        File for input weighting volume
        flag: -inweight %s
    interp: ('trilinear' or 'nearestneighbour' or 'sinc' or 'spline')
        final interpolation method used in reslicing
```

```
        flag: -interp %s
    min_sampling: (a float)
        set minimum voxel dimension for sampling
        flag: -minsampling %f
    no_clamp: (a boolean)
        do not use intensity clamping
        flag: -noclamp
    no_resample: (a boolean)
        do not change input sampling
        flag: -noresample
    no_resample_blur: (a boolean)
        do not use blurring on downsampling
        flag: -noresampblur
    no_search: (a boolean)
        set all angular searches to ranges 0 to 0
        flag: -nosearch
    out_file: (a file name)
        registered output file
        flag: -out %s, position: 2
    out_log: (a file name)
        output log
        requires: save_log
    out_matrix_file: (a file name)
        output affine matrix in 4x4 asciii format
        flag: -omat %s, position: 3
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
    padding_size: (an integer (int or long))
        for applyxfm: interpolates outside image by size
        flag: -paddingsize %d
    pedir: (an integer (int or long))
        phase encode direction of EPI - 1/2/3=x/y/z & -1/-2/-3=-x/-y/-z
        flag: -pedir %d
    ref_weight: (an existing file name)
        File for reference weighting volume
        flag: -refweight %s
    rigid2D: (a boolean)
        use 2D rigid body mode - ignores dof
        flag: -2D
    save_log: (a boolean)
        save to log file
    schedule: (an existing file name)
        replaces default schedule
        flag: -schedule %s
    searchr_x: (a list of from 2 to 2 items which are an integer (int or
         long))
        search angles along x-axis, in degrees
        flag: -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
        flag: -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
        flag: -searchrz %s
    sinc_width: (an integer (int or long))
```

```
        full-width in voxels
        flag: -sincwidth %d
sinc_window: ('rectangular' or 'hanning' or 'blackman')
        sinc window
        flag: -sincwindow %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
uses_qform: (a boolean)
        initialize using sform or qform
        flag: -usesqform
verbose: (an integer (int or long))
        verbose mode, 0 is least
        flag: -verbose %d
wm_seg: (a file name)
        white matter segmentation volume needed by BBR cost function
        flag: -wmseg %s
wmcoords: (a file name)
        white matter boundary coordinates for BBR cost function
        flag: -wmcoords %s
wmnorms: (a file name)
        white matter boundary normals for BBR cost function
        flag: -wmnorms %s
```

Outputs:

```
out_file: (an existing file name)
        path/name of registered file (if generated)
out_log: (a file name)
        path/name of output log (if generated)
out_matrix_file: (an existing file name)
        path/name of calculated affine transform (if generated)
```

84.7 FNIRT

Link to code
Wraps command **fnirt**
Use FSL FNIRT for non-linear registration.

84.7.1 Examples

```
>>> from nipype.interfaces import fsl
>>> from nipype.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'))
```

T1 -> Mni153

```
>>> from nipype.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
```

We can check the command line and confirm that it's what we expect.

```
>>> fnirt_mprage.cmdline
'fnirt --cout=fieldcoeff.nii --in=structural.nii --infwhm=8,4,2,2 --ref=mni.nii --subsamp=4,2,1,
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        name of input image
        flag: --in=%s
ref_file: (an existing file name)
        name of reference image
        flag: --ref=%s

[Optional]
affine_file: (an existing file name)
        name of file containing affine transform
        flag: --aff=%s
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)
        flag: --applyinmask=%s
        mutually_exclusive: skip_inmask
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)
        flag: --estint=%s
        mutually_exclusive: skip_intensity_mapping
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)
        flag: --applyrefmask=%s
        mutually_exclusive: skip_refmask
args: (a string)
        Additional parameters to the command
        flag: %s
bias_regularization_lambda: (a float)
        Weight of regularisation for bias-field, default 10000
        flag: --biaslambda=%f
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
        flag: --biasres=%d,%d,%d
config_file: ('T1_2_MNI152_2mm' or 'FA_2_FMRIB58_1mm' or an existing
         file name)
        Name of config file specifying command line arguments
        flag: --config=%s
derive_from_ref: (a boolean)
        If true, ref image is used to calculate derivatives. Default false
        flag: --refderiv
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
field_file: (a boolean or a file name)
        name of output file with field or true
        flag: --fout=%s
fieldcoeff_file: (a boolean or a file name)
        name of output file with field coefficients or true
        flag: --cout=%s
```

```
    hessian_precision: ('double' or 'float')
            Precision for representing Hessian, double or float. Default double
            flag: --numprec=%s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    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]
            flag: --infwhm=%s
    in_intensitymap_file: (an existing file name)
            name of file/files containing initial intensity mapingusually
            generated by previos fnirt run
            flag: --intin=%s
    inmask_file: (an existing file name)
            name of file with mask in input image space
            flag: --inmask=%s
    inmask_val: (a float)
            Value to mask out in --in image. Default =0.0
            flag: --impinval=%f
    intensity_mapping_model: ('none' or 'global_linear' or
             'global_non_linearlocal_linear' or 'global_non_linear_with_bias' or
             'local_non_linear')
            Model for intensity-mapping
            flag: --intmod=%s
    intensity_mapping_order: (an integer (int or long))
            Order of poynomial for mapping intensities, default 5
            flag: --intorder=%d
    inwarp_file: (an existing file name)
            name of file containing initial non-linear warps
            flag: --inwarp=%s
    jacobian_file: (a boolean or a file name)
            name of file for writing out the Jacobianof the field (for
            diagnostic or VBM purposes)
            flag: --jout=%s
    jacobian_range: (a tuple of the form: (a float, a float))
            Allowed range of Jacobian determinants, default 0.01, 100.0
            flag: --jacrange=%f,%f
    log_file: (a file name)
            Name of log-file
            flag: --logout=%s
    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]
            flag: --miter=%s
    modulatedref_file: (a boolean or a file name)
            name of file for writing out intensity modulated--ref (for
            diagnostic purposes)
            flag: --refout=%s
    out_intensitymap_file: (a boolean or a file name)
            name of files for writing information pertaining to intensity
            mapping
            flag: --intout=%s
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    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]
```

```
        flag: --reffwhm=%s
refmask_file: (an existing file name)
        name of file with mask in reference space
        flag: --refmask=%s
refmask_val: (a float)
        Value to mask out in --ref image. Default =0.0
        flag: --imprefval=%f
regularization_lambda: (a list of items which are a float)
        Weight of regularisation, default depending on --ssqlambda and
        --regmod switches. See user documetation.
        flag: --lambda=%s
regularization_model: ('membrane_energy' or 'bending_energy')
        Model for regularisation of warp-field [membrane_energy
        bending_energy], default bending_energy
        flag: --regmod=%s
skip_implicit_in_masking: (a boolean)
        skip implicit masking based on valuein --in image. Default = 0
        flag: --impinm=0
skip_implicit_ref_masking: (a boolean)
        skip implicit masking based on valuein --ref image. Default = 0
        flag: --imprefm=0
skip_inmask: (a boolean)
        skip specified inmask if set, default false
        flag: --applyinmask=0
        mutually_exclusive: apply_inmask
skip_intensity_mapping: (a boolean)
        Skip estimate intensity-mapping default false
        flag: --estint=0
        mutually_exclusive: apply_intensity_mapping
skip_lambda_ssq: (a boolean)
        If true, lambda is not weighted by current ssq, default false
        flag: --ssqlambda=0
skip_refmask: (a boolean)
        Skip specified refmask if set, default false
        flag: --applyrefmask=0
        mutually_exclusive: apply_refmask
spline_order: (an integer (int or long))
        Order of spline, 2->Qadratic spline, 3->Cubic spline. Default=3
        flag: --splineorder=%d
subsampling_scheme: (a list of items which are an integer (int or
         long))
        sub-sampling scheme, list, default [4, 2, 1, 1]
        flag: --subsamp=%s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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
        flag: --warpres=%d,%d,%d
warped_file: (a file name)
        name of output image
        flag: --iout=%s
```

Outputs:

```
    field_file: (a file name)
            file with warp field
    fieldcoeff_file: (an existing file name)
            file with field coefficients
    jacobian_file: (a file name)
            file containing Jacobian of the field
    log_file: (a file name)
            Name of log-file
    modulatedref_file: (a file name)
            file containing intensity modulated --ref
    out_intensitymap_file: (a file name)
            file containing info pertaining to intensity mapping
    warped_file: (an existing file name)
            warped image
```

84.8 FUGUE

Link to code

Wraps command **fugue**

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.

84.8.1 Examples

Unwarping an input image (shift map is known)

```
    >>> from nipype.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
    'fugue --in=epi.nii --mask=epi_mask.nii --loadshift=vsm.nii --unwarpdir=y --unwarp=epi_unwarped.
    >>> fugue.run()
```

Warping an input image (shift map is known)

```
    >>> from nipype.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'
    >>> 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
    'fugue --in=epi.nii --mask=epi_mask.nii --loadshift=vsm.nii --unwarpdir=y --warp=epi_warped.nii.
    >>> fugue.run()
```

Computing the vsm (unwrapped phase map is known)

```
    >>> from nipype.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
'fugue --dwelltoasym=0.9390243902 --mask=epi_mask.nii --phasemap=epi_phasediff.nii --saveshift=e
>>> fugue.run()
```

Inputs:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
asym_se_time: (a float)
        set the fieldmap asymmetric spin echo time (sec)
        flag: --asym=%.10f
despike_2dfilter: (a boolean)
        apply a 2D de-spiking filter
        flag: --despike
despike_threshold: (a float)
        specify the threshold for de-spiking (default=3.0)
        flag: --despikethreshold=%s
dwell_time: (a float)
        set the EPI dwell time per phase-encode line - same as echo spacing
        - (sec)
        flag: --dwell=%.10f
dwell_to_asym_ratio: (a float)
        set the dwell to asym time ratio
        flag: --dwelltoasym=%.10f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fmap_in_file: (an existing file name)
        filename for loading fieldmap (rad/s)
        flag: --loadfmap=%s
fmap_out_file: (a file name)
        filename for saving fieldmap (rad/s)
        flag: --savefmap=%s
forward_warping: (a boolean, nipype default value: False)
        apply forward warping instead of unwarping
fourier_order: (an integer (int or long))
        apply Fourier (sinusoidal) fitting of order N
        flag: --fourier=%d
icorr: (a boolean)
        apply intensity correction to unwarping (pixel shift method only)
        flag: --icorr
        requires: shift_in_file
icorr_only: (a boolean)
        apply intensity correction only
        flag: --icorronly
        requires: unwarped_file
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
```

```
        interface fails to run
in_file: (an existing file name)
        filename of input volume
        flag: --in=%s
mask_file: (an existing file name)
        filename for loading valid mask
        flag: --mask=%s
median_2dfilter: (a boolean)
        apply 2D median filtering
        flag: --median
no_extend: (a boolean)
        do not apply rigid-body extrapolation to the fieldmap
        flag: --noextend
no_gap_fill: (a boolean)
        do not apply gap-filling measure to the fieldmap
        flag: --nofill
nokspace: (a boolean)
        do not use k-space forward warping
        flag: --nokspace
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
pava: (a boolean)
        apply monotonic enforcement via PAVA
        flag: --pava
phase_conjugate: (a boolean)
        apply phase conjugate method of unwarping
        flag: --phaseconj
phasemap_in_file: (an existing file name)
        filename for input phase image
        flag: --phasemap=%s
poly_order: (an integer (int or long))
        apply polynomial fitting of order N
        flag: --poly=%d
save_fmap: (a boolean)
        write field map volume
        mutually_exclusive: save_unmasked_fmap
save_shift: (a boolean)
        write pixel shift volume
        mutually_exclusive: save_unmasked_shift
save_unmasked_fmap: (a boolean)
        saves the unmasked fieldmap when using --savefmap
        flag: --unmaskfmap
        mutually_exclusive: save_fmap
save_unmasked_shift: (a boolean)
        saves the unmasked shiftmap when using --saveshift
        flag: --unmaskshift
        mutually_exclusive: save_shift
shift_in_file: (an existing file name)
        filename for reading pixel shift volume
        flag: --loadshift=%s
shift_out_file: (a file name)
        filename for saving pixel shift volume
        flag: --saveshift=%s
smooth2d: (a float)
        apply 2D Gaussian smoothing of sigma N (in mm)
        flag: --smooth2=%.2f
smooth3d: (a float)
```

```
        apply 3D Gaussian smoothing of sigma N (in mm)
        flag: --smooth3=%.2f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
unwarp_direction: ('x' or 'y' or 'z' or 'x-' or 'y-' or 'z-')
        specifies direction of warping (default y)
        flag: --unwarpdir=%s
unwarped_file: (a file name)
        apply unwarping and save as filename
        flag: --unwarp=%s
        mutually_exclusive: warped_file
        requires: in_file
warped_file: (a file name)
        apply forward warping and save as filename
        flag: --warp=%s
        mutually_exclusive: unwarped_file
        requires: in_file
```

Outputs:

```
fmap_out_file: (a file name)
        fieldmap file
shift_out_file: (a file name)
        voxel shift map file
unwarped_file: (a file name)
        unwarped file
warped_file: (a file name)
        forward warped file
```

84.9 MCFLIRT

Link to code

Wraps command **mcflirt**

Use FSL MCFLIRT to do within-modality motion correction.

For complete details, see the MCFLIRT Documentation.

84.9.1 Examples

```
>>> from nipype.interfaces import fsl
>>> from nipype.testing import example_data
>>> mcflt = fsl.MCFLIRT(in_file=example_data('functional.nii'), cost='mutualinfo')
>>> res = mcflt.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        timeseries to motion-correct
        flag: -in %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
bins: (an integer (int or long))
```

```
        number of histogram bins
        flag: -bins %d
cost: ('mutualinfo' or 'woods' or 'corratio' or 'normcorr' or
         'normmi' or 'leastsquares')
        cost function to optimize
        flag: -cost %s
dof: (an integer (int or long))
        degrees of freedom for the transformation
        flag: -dof %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
init: (an existing file name)
        inital transformation matrix
        flag: -init %s
interpolation: ('spline' or 'nn' or 'sinc')
        interpolation method for transformation
        flag: -%s_final
mean_vol: (a boolean)
        register to mean volume
        flag: -meanvol
out_file: (a file name)
        file to write
        flag: -out %s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
ref_file: (an existing file name)
        target image for motion correction
        flag: -reffile %s
ref_vol: (an integer (int or long))
        volume to align frames to
        flag: -refvol %d
rotation: (an integer (int or long))
        scaling factor for rotation tolerances
        flag: -rotation %d
save_mats: (a boolean)
        save transformation matrices
        flag: -mats
save_plots: (a boolean)
        save transformation parameters
        flag: -plots
save_rms: (a boolean)
        save rms displacement parameters
        flag: -rmsabs -rmsrel
scaling: (a float)
        scaling factor to use
        flag: -scaling %.2f
smooth: (a float)
        smoothing factor for the cost function
        flag: -smooth %.2f
stages: (an integer (int or long))
        stages (if 4, perform final search with sinc interpolation
        flag: -stages %d
```

```
    stats_imgs: (a boolean)
            produce variance and std. dev. images
            flag: -stats
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    use_contour: (a boolean)
            run search on contour images
            flag: -edge
    use_gradient: (a boolean)
            run search on gradient images
            flag: -gdt
```

Outputs:

```
    mat_file: (a list of items which are an existing file name)
            transformation matrices
    mean_img: (an existing file name)
            mean timeseries image
    out_file: (an existing file name)
            motion-corrected timeseries
    par_file: (an existing file name)
            text-file with motion parameters
    rms_files: (a list of items which are an existing file name)
            absolute and relative displacement parameters
    std_img: (an existing file name)
            standard deviation image
    variance_img: (an existing file name)
            variance image
```

84.10 PRELUDE

Link to code

Wraps command **prelude**

Use FSL prelude to do phase unwrapping

84.10.1 Examples

Please insert examples for use of this command

Inputs:

```
    [Mandatory]
    complex_phase_file: (an existing file name)
            complex phase input volume
            flag: --complex=%s
            mutually_exclusive: magnitude_file, phase_file
    magnitude_file: (an existing file name)
            file containing magnitude image
            flag: --abs=%s
            mutually_exclusive: complex_phase_file
    phase_file: (an existing file name)
            raw phase file
            flag: --phase=%s
            mutually_exclusive: complex_phase_file

    [Optional]
```

```
    args: (a string)
            Additional parameters to the command
            flag: %s
    end: (an integer (int or long))
            final image number to process (default Inf)
            flag: --end=%d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    label_file: (a file name)
            saving the area labels output
            flag: --labels=%s
    labelprocess2d: (a boolean)
            does label processing in 2D (slice at a time)
            flag: --labelslices
    mask_file: (an existing file name)
            filename of mask input volume
            flag: --mask=%s
    num_partitions: (an integer (int or long))
            number of phase partitions to use
            flag: --numphasesplit=%d
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    process2d: (a boolean)
            does all processing in 2D (slice at a time)
            flag: --slices
            mutually_exclusive: labelprocess2d
    process3d: (a boolean)
            forces all processing to be full 3D
            flag: --force3D
            mutually_exclusive: labelprocess2d, process2d
    rawphase_file: (a file name)
            saving the raw phase output
            flag: --rawphase=%s
    removeramps: (a boolean)
            remove phase ramps during unwrapping
            flag: --removeramps
    savemask_file: (a file name)
            saving the mask volume
            flag: --savemask=%s
    start: (an integer (int or long))
            first image number to process (default 0)
            flag: --start=%d
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    threshold: (a float)
            intensity threshold for masking
            flag: --thresh=%.10f
    unwrapped_phase_file: (a file name)
            file containing unwrapepd phase
            flag: --unwrap=%s
```

Outputs:

```
unwrapped_phase_file: (an existing file name)
        unwrapped phase file
```

84.11 SUSAN

Link to code
Wraps command **susan**
use FSL SUSAN to perform smoothing

84.11.1 Examples

```
>>> from nipype.interfaces import fsl
>>> from nipype.testing import example_data
>>> anatfile
anatomical.nii
>>> 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()
```

Inputs:

```
[Mandatory]
brightness_threshold: (a float)
        brightness threshold and should be greater than noise level and less
        than contrast of edges to be preserved.
        flag: %.10f, position: 2
fwhm: (a float)
        fwhm of smoothing, in mm, gets converted using sqrt(8*log(2))
        flag: %.10f, position: 3
in_file: (an existing file name)
        filename of input timeseries
        flag: %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
dimension: (3 or 2, nipype default value: 3)
        within-plane (2) or fully 3D (3)
        flag: %d, position: 4
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output file name
        flag: %s, position: -1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
```

```
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
usans: (a list of at most 2 items which are a tuple of the form: (an
         existing file name, a float), nipype 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
use_median: (1 or 0, nipype default value: 1)
        whether to use a local median filter in the cases where single-point
        noise is detected
        flag: %d, position: 5
```

Outputs:

```
smoothed_file: (an existing file name)
        smoothed output file
```

84.12 SliceTimer

Link to code

Wraps command **slicetimer**

use FSL slicetimer to perform slice timing correction.

84.12.1 Examples

```
>>> from nipype.interfaces import fsl
>>> from nipype.testing import example_data
>>> st = fsl.SliceTimer()
>>> st.inputs.in_file = example_data('functional.nii')
>>> st.inputs.interleaved = True
>>> result = st.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        filename of input timeseries
        flag: --in=%s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
custom_order: (an existing file name)
        filename of single-column custom interleave order file (first slice
        is referred to as 1 not 0)
        flag: --ocustom=%s
custom_timings: (an existing file name)
        slice timings, in fractions of TR, range 0:1 (default is 0.5 = no
        shift)
        flag: --tcustom=%s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
global_shift: (a float)
```

```
            shift in fraction of TR, range 0:1 (default is 0.5 = no shift)
            flag: --tglobal
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    index_dir: (a boolean)
            slice indexing from top to bottom
            flag: --down
    interleaved: (a boolean)
            use interleaved acquisition
            flag: --odd
    out_file: (a file name)
            filename of output timeseries
            flag: --out=%s
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    slice_direction: (1 or 2 or 3)
            direction of slice acquisition (x=1, y=2, z=3) - default is z
            flag: --direction=%d
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    time_repetition: (a float)
            Specify TR of data - default is 3s
            flag: --repeat=%f
```

Outputs:

```
    slice_time_corrected_file: (an existing file name)
            slice time corrected file
```

CHAPTER 85

interfaces.fsl.utils

85.1 AvScale

Link to code
Wraps command **avscale**
Use FSL avscale command to extract info from mat file output of FLIRT

85.1.1 Examples

```
>>> avscale = AvScale()
>>> avscale.inputs.mat_file = 'flirt.mat'
>>> res = avscale.run()
```

Inputs:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mat_file: (an existing file name)
        mat file to read
        flag: %s, position: 0
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
average_scaling: (any value)
        Average Scaling
backward_half_transform: (any value)
        Backwards Half Transform
determinant: (any value)
```

```
        Determinant
forward_half_transform: (any value)
        Forward Half Transform
left_right_orientation_preserved: (a boolean)
        True if LR orientation preserved
rotation_translation_matrix: (any value)
        Rotation and Translation Matrix
scales: (any value)
        Scales (x,y,z)
skews: (any value)
        Skews
```

85.2 Complex

Link to code

Wraps command **fslcomplex**

fslcomplex is a tool for converting complex data

85.2.1 Examples

```
>>> cplx = Complex()
>>> cplx.inputs.complex_in_file = "complex.nii"
>>> cplx.real_polar = True
>>> res = cplx.run()
```

Inputs:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
complex_cartesian: (a boolean)
        flag: -complex, position: 1
        mutually_exclusive: real_polar, real_cartesian, complex_cartesian,
         complex_polar, complex_split, complex_merge
complex_in_file: (an existing file name)
        flag: %s, position: 2
complex_in_file2: (an existing file name)
        flag: %s, position: 3
complex_merge: (a boolean)
        flag: -complexmerge, position: 1
        mutually_exclusive: real_polar, real_cartesian, complex_cartesian,
         complex_polar, complex_split, complex_merge, start_vol, end_vol
complex_out_file: (a file name)
        flag: %s, position: -3
        mutually_exclusive: complex_out_file, magnitude_out_file,
         phase_out_file, real_out_file, imaginary_out_file, real_polar,
         real_cartesian
complex_polar: (a boolean)
        flag: -complexpolar, position: 1
        mutually_exclusive: real_polar, real_cartesian, complex_cartesian,
         complex_polar, complex_split, complex_merge
complex_split: (a boolean)
        flag: -complexsplit, position: 1
        mutually_exclusive: real_polar, real_cartesian, complex_cartesian,
```

```
         complex_polar, complex_split, complex_merge
end_vol: (an integer (int or long))
        flag: %d, position: -1
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
imaginary_in_file: (an existing file name)
        flag: %s, position: 3
imaginary_out_file: (a file name)
        flag: %s, position: -3
        mutually_exclusive: complex_out_file, magnitude_out_file,
         phase_out_file, real_polar, complex_cartesian, complex_polar,
         complex_split, complex_merge
magnitude_in_file: (an existing file name)
        flag: %s, position: 2
magnitude_out_file: (a file name)
        flag: %s, position: -4
        mutually_exclusive: complex_out_file, real_out_file,
         imaginary_out_file, real_cartesian, complex_cartesian,
         complex_polar, complex_split, complex_merge
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
phase_in_file: (an existing file name)
        flag: %s, position: 3
phase_out_file: (a file name)
        flag: %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_cartesian: (a boolean)
        flag: -realcartesian, position: 1
        mutually_exclusive: real_polar, real_cartesian, complex_cartesian,
         complex_polar, complex_split, complex_merge
real_in_file: (an existing file name)
        flag: %s, position: 2
real_out_file: (a file name)
        flag: %s, position: -4
        mutually_exclusive: complex_out_file, magnitude_out_file,
         phase_out_file, real_polar, complex_cartesian, complex_polar,
         complex_split, complex_merge
real_polar: (a boolean)
        flag: -realpolar, position: 1
        mutually_exclusive: real_polar, real_cartesian, complex_cartesian,
         complex_polar, complex_split, complex_merge
start_vol: (an integer (int or long))
        flag: %d, position: -2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
complex_out_file: (a file name)
imaginary_out_file: (a file name)
magnitude_out_file: (a file name)
phase_out_file: (a file name)
real_out_file: (a file name)
```

85.3 ConvertWarp

Link to code
Wraps command **convertwarp**
Use FSL convertwarp for combining multiple transforms into one.

85.3.1 Examples

```
>>> from nipype.interfaces.fsl import ConvertWarp
>>> warputils = ConvertWarp()
>>> warputils.inputs.warp1 = "warpfield.nii"
>>> warputils.inputs.reference = "T1.nii"
>>> warputils.inputs.relwarp = True
>>> warputils.inputs.output_type = "NIFTI_GZ"
>>> warputils.cmdline
'convertwarp --ref=T1.nii --rel --warp1=warpfield.nii --out=T1_concatwarp.nii.gz'
>>> res = warputils.run()
```

Inputs:

```
[Mandatory]
reference: (an existing file name)
        Name of a file in target space of the full transform.
        flag: --ref=%s, position: 1

[Optional]
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.
        flag: --abs
        mutually_exclusive: relwarp
args: (a string)
        Additional parameters to the command
        flag: %s
cons_jacobian: (a boolean)
        Constrain the Jacobian of the warpfield to lie within specified
        min/max limits.
        flag: --constrainj
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
jacobian_max: (a float)
        Maximum acceptable Jacobian value for constraint (default 100.0)
        flag: --jmax=%f
```

```
    jacobian_min: (a float)
            Minimum acceptable Jacobian value for constraint (default 0.01)
            flag: --jmin=%f
    midmat: (an existing file name)
            Name of file containing mid-warp-affine transform
            flag: --midmat=%s
    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.
            flag: --absout
            mutually_exclusive: out_relwarp
    out_file: (a file name)
            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.
            flag: --out=%s, position: -1
    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.
            flag: --relout
            mutually_exclusive: out_abswarp
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    postmat: (an existing file name)
            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).
            flag: --postmat=%s
    premat: (an existing file name)
            filename for pre-transform (affine matrix)
            flag: --premat=%s
    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.
            flag: --rel
            mutually_exclusive: abswarp
    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.
            flag: --shiftdir=%s
            requires: shift_in_file
    shift_in_file: (an existing file name)
            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).
            flag: --shiftmap=%s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    warp1: (an existing file name)
            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.
        flag: --warp1=%s
warp2: (an existing file name)
        Name of file containing secondary warp-fields/coefficients (after
        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).
        flag: --warp2=%s
```

Outputs:

```
out_file: (an existing file name)
        Name of output file, containing the warp as field or coefficients.
```

85.4 ConvertXFM

Link to code

Wraps command **convert_xfm**

Use the FSL utility convert_xfm to modify FLIRT transformation matrices.

85.4.1 Examples

```
>>> import nipype.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: (an existing file name)
        input transformation matrix
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
concat_xfm: (a boolean)
        write joint transformation of two input matrices
        flag: -concat, position: -3
        mutually_exclusive: invert_xfm, concat_xfm, fix_scale_skew
        requires: in_file2
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fix_scale_skew: (a boolean)
        use secondary matrix to fix scale and skew
        flag: -fixscaleskew, position: -3
        mutually_exclusive: invert_xfm, concat_xfm, fix_scale_skew
        requires: in_file2
ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_file2: (an existing file name)
        second input matrix (for use with fix_scale_skew or concat_xfm
        flag: %s, position: -2
invert_xfm: (a boolean)
        invert input transformation
        flag: -inverse, position: -3
        mutually_exclusive: invert_xfm, concat_xfm, fix_scale_skew
out_file: (a file name)
        final transformation matrix
        flag: -omat %s, position: 1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        output transformation matrix
```

85.5 CopyGeom

Link to code

Wraps 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]
dest_file: (an existing file name)
        destination image
        flag: %s, position: 1
in_file: (an existing file name)
        source image
        flag: %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_dims: (a boolean)
        Do not copy image dimensions
        flag: -d, position: -1
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

```
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
            image with new geometry header
```

85.6 ExtractROI

Link to code

Wraps 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).

85.6.1 Examples

```
    >>> from nipype.interfaces.fsl import ExtractROI
    >>> from nipype.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: (an existing file name)
            input file
            flag: %s, position: 0

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    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
            flag: %s, position: 2
            mutually_exclusive: x_min, x_size, y_min, y_size, z_min, z_size,
             t_min, t_size
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
```

```
          'NIFTI')
        FSL output type
roi_file: (a file name)
        output file
        flag: %s, position: 1
t_min: (an integer (int or long))
        flag: %d, position: 8
t_size: (an integer (int or long))
        flag: %d, position: 9
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
x_min: (an integer (int or long))
        flag: %d, position: 2
x_size: (an integer (int or long))
        flag: %d, position: 3
y_min: (an integer (int or long))
        flag: %d, position: 4
y_size: (an integer (int or long))
        flag: %d, position: 5
z_min: (an integer (int or long))
        flag: %d, position: 6
z_size: (an integer (int or long))
        flag: %d, position: 7
```

Outputs:

```
roi_file: (an existing file name)
```

85.7 FilterRegressor

Link to code

Wraps command **fsl_regfilt**

Data de-noising by regressing out part of a design matrix

Uses simple OLS regression on 4D images

Inputs:

```
[Mandatory]
design_file: (an existing file name)
        name of the matrix with time courses (e.g. GLM design or MELODIC
        mixing matrix)
        flag: -d %s, position: 3
filter_all: (a boolean)
        use all columns in the design file in denoising
        flag: -f '%s', position: 4
        mutually_exclusive: filter_columns
filter_columns: (a list of items which are an integer (int or long))
        (1-based) column indices to filter out of the data
        flag: -f '%s', position: 4
        mutually_exclusive: filter_all
in_file: (an existing file name)
        input file name (4D image)
        flag: -i %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
```

```
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (an existing file name)
        mask image file name
        flag: -m %s
out_file: (a file name)
        output file name for the filtered data
        flag: -o %s, position: 2
out_vnscales: (a boolean)
        output scaling factors for variance normalization
        flag: --out_vnscales
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
var_norm: (a boolean)
        perform variance-normalization on data
        flag: --vn
```

Outputs:

```
out_file: (an existing file name)
        output file name for the filtered data
```

85.8 ImageMaths

Link to code

Wraps command **fslmaths**

Use FSL fslmaths command to allow mathematical manipulation of images FSL info

85.8.1 Examples

```
>>> from nipype.interfaces import fsl
>>> from nipype.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: (an existing file name)
        flag: %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
```

```
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    in_file2: (an existing file name)
            flag: %s, position: 3
    op_string: (a string)
            string defining the operation, i. e. -add
            flag: %s, position: 2
    out_data_type: ('char' or 'short' or 'int' or 'float' or 'double' or
             'input')
            output datatype, one of (char, short, int, float, double, input)
            flag: -odt %s, position: 5
    out_file: (a file name)
            flag: %s, position: 4
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    suffix: (a string)
            out_file suffix
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
```

85.9 ImageMeants

Link to code

Wraps 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: (an existing file name)
            input file for computing the average timeseries
            flag: -i %s, position: 0

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    eig: (a boolean)
            calculate Eigenvariate(s) instead of mean (output will have 0 mean)
            flag: --eig
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
```

```
        interface fails to run
mask: (an existing file name)
        input 3D mask
        flag: -m %s
nobin: (a boolean)
        do not binarise the mask for calculation of Eigenvariates
        flag: --no_bin
order: (an integer (int or long), nipype default value: 1)
        select number of Eigenvariates
        flag: --order=%d
out_file: (a file name)
        name of output text matrix
        flag: -o %s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
show_all: (a boolean)
        show all voxel time series (within mask) instead of averaging
        flag: --showall
spatial_coord: (a list of items which are an integer (int or long))
        <x y z> requested spatial coordinate (instead of mask)
        flag: -c %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transpose: (a boolean)
        output results in transpose format (one row per voxel/mean)
        flag: --transpose
use_mm: (a boolean)
        use mm instead of voxel coordinates (for -c option)
        flag: --usemm
```

Outputs:

```
out_file: (an existing file name)
        path/name of output text matrix
```

85.10 ImageStats

Link to code

Wraps command **fslstats**

Use FSL fslstats command to calculate stats from images FSL info

85.10.1 Examples

```
>>> from nipype.interfaces.fsl import ImageStats
>>> from nipype.testing import funcfile
>>> stats = ImageStats(in_file=funcfile, op_string= '-M')
>>> stats.cmdline == 'fslstats %s -M'%funcfile
True
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to generate stats of
        flag: %s, position: 2
```

```
    op_string: (a 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
            flag: %s, position: 3

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    mask_file: (an existing file name)
            mask file used for option -k %s
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    split_4d: (a boolean)
            give a separate output line for each 3D volume of a 4D timeseries
            flag: -t, position: 1
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_stat: (any value)
            stats output
```

85.11 InvWarp

Link to code
Wraps command **invwarp**
Use FSL Invwarp to invert a FNIRT warp

85.11.1 Examples

```
    >>> from nipype.interfaces.fsl import InvWarp
    >>> invwarp = InvWarp()
    >>> invwarp.inputs.warp = "struct2mni.nii"
    >>> invwarp.inputs.reference = "anatomical.nii"
    >>> invwarp.inputs.output_type = "NIFTI_GZ"
    >>> invwarp.cmdline
    'invwarp --out=struct2mni_inverse.nii.gz --ref=anatomical.nii --warp=struct2mni.nii'
    >>> res = invwarp.run()
```

Inputs:

```
    [Mandatory]
    reference: (an existing file name)
            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.
        flag: --ref=%s
warp: (an existing file name)
        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).
        flag: --warp=%s

[Optional]
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.
        flag: --abs
        mutually_exclusive: relative
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inverse_warp: (a file name)
        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.
        flag: --out=%s
jacobian_max: (a float)
        Maximum acceptable Jacobian value for constraint (default 100.0)
        flag: --jmax=%f
jacobian_min: (a float)
        Minimum acceptable Jacobian value for constraint (default 0.01)
        flag: --jmin=%f
niter: (an integer (int or long))
        Determines how many iterations of the gradient-descent search that
        should be run.
        flag: --niter=%d
noconstraint: (a boolean)
        Do not apply Jacobian constraint
        flag: --noconstraint
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
regularise: (a float)
        Regularization strength (deafult=1.0).
        flag: --regularise=%f
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.
```

```
        flag: --rel
        mutually_exclusive: absolute
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
inverse_warp: (an existing file name)
        Name of output file, containing warps that are the "reverse" of
        those in --warp.
```

85.12 Merge

Link to code

Wraps 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'.

85.12.1 Examples

```
>>> from nipype.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]
dimension: ('t' or 'x' or 'y' or 'z' or 'a')
        dimension along which to merge, optionally set tr input when
        dimension is t
        flag: -%s, position: 0
in_files: (a list of items which are an existing file name)
        flag: %s, position: 2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

```
    merged_file: (a file name)
            flag: %s, position: 1
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    tr: (a float)
            use to specify TR in seconds (default is 1.00 sec), overrides
            dimension and sets it to tr
            flag: %.2f, position: -1
```

Outputs:

```
    merged_file: (an existing file name)
```

85.13 MotionOutliers

Link to code

Wraps 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 nipype.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: (an existing file name)
            unfiltered 4D image
            flag: -i %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    dummy: (an integer (int or long))
            number of dummy scans to delete (before running anything and
            creating EVs)
            flag: --dummy=%d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    mask: (an existing file name)
            mask image for calculating metric
            flag: -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
```

```
        flag: --%s
no_motion_correction: (a boolean)
        do not run motion correction (assumed already done)
        flag: --nomoco
out_file: (a file name)
        output outlier file name
        flag: -o %s
out_metric_plot: (a file name)
        output metric values plot (DVARS etc.) file name
        flag: -p %s
out_metric_values: (a file name)
        output metric values (DVARS etc.) file name
        flag: -s %s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
threshold: (a float)
        specify absolute threshold value (otherwise use box-plot cutoff =
        P75 + 1.5*IQR)
        flag: --thresh=%g
```

Outputs:

```
out_file: (an existing file name)
out_metric_plot: (an existing file name)
out_metric_values: (an existing file name)
```

85.14 Overlay

Link to code

Wraps command **overlay**

Use FSL's overlay command to combine background and statistical images into one volume

85.14.1 Examples

```
>>> from nipype.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)
>>> combine.inputs.show_negative_stats = True
>>> res = combine.run()
```

Inputs:

```
[Mandatory]
auto_thresh_bg: (a boolean)
        automatically threshold the background image
        flag: -a, position: 5
        mutually_exclusive: auto_thresh_bg, full_bg_range, bg_thresh
background_image: (an existing file name)
        image to use as background
        flag: %s, position: 4
```

```
    bg_thresh: (a tuple of the form: (a float, a float))
            min and max values for background intensity
            flag: %.3f %.3f, position: 5
            mutually_exclusive: auto_thresh_bg, full_bg_range, bg_thresh
    full_bg_range: (a boolean)
            use full range of background image
            flag: -A, position: 5
            mutually_exclusive: auto_thresh_bg, full_bg_range, bg_thresh
    stat_image: (an existing file name)
            statistical image to overlay in color
            flag: %s, position: 6
    stat_thresh: (a tuple of the form: (a float, a float))
            min and max values for the statistical overlay
            flag: %.2f %.2f, position: 7

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    out_file: (a file name)
            combined image volume
            flag: %s, position: -1
    out_type: ('float' or 'int', nipype default value: float)
            write output with float or int
            flag: %s, position: 2
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    show_negative_stats: (a boolean)
            display negative statistics in overlay
            flag: %s, position: 8
            mutually_exclusive: stat_image2
    stat_image2: (an existing file name)
            second statistical image to overlay in color
            flag: %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
            flag: %.2f %.2f, position: 10
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    transparency: (a boolean, nipype default value: True)
            make overlay colors semi-transparent
            flag: %s, position: 1
    use_checkerboard: (a boolean)
            use checkerboard mask for overlay
            flag: -c, position: 3
```

Outputs:

```
    out_file: (an existing file name)
            combined image volume
```

85.15 PlotMotionParams

Link to code
Wraps command **fsl_tsplot**
Use fsl_tsplot to plot the estimated motion parameters from a realignment program.

85.15.1 Examples

```
>>> import nipype.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()
```

85.15.2 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 flexibilty, see the `fsl.PlotTimeSeries` interface.
Inputs:

```
    [Mandatory]
    in_file: (an existing file name or a list of items which are an
             existing file name)
            file with motion parameters
            flag: %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
            flag: %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    out_file: (a file name)
            image to write
            flag: -o %s
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    plot_size: (a tuple of the form: (an integer (int or long), an
```

```
          integer (int or long)))
        plot image height and width
        flag: %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image to write
```

85.16 PlotTimeSeries

Link to code

Wraps command **fsl_tsplot**

Use fsl_tsplot to create images of time course plots.

85.16.1 Examples

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name or a list of items which are an
         existing file name)
        file or list of files with columns of timecourse information
        flag: %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
labels: (a string or a list of items which are a string)
        label or list of labels
        flag: %s
legend_file: (an existing file name)
        legend file
        flag: --legend=%s
out_file: (a file name)
        image to write
        flag: -o %s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
```

```
          'NIFTI')
        FSL output type
plot_finish: (an integer (int or long))
        final column from in-file to plot
        flag: --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
        flag: %s
        mutually_exclusive: plot_start, plot_finish
plot_size: (a tuple of the form: (an integer (int or long), an
         integer (int or long)))
        plot image height and width
        flag: %s
plot_start: (an integer (int or long))
        first column from in-file to plot
        flag: --start=%d
        mutually_exclusive: plot_range
sci_notation: (a boolean)
        switch on scientific notation
        flag: --sci
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
title: (a string)
        plot title
        flag: %s
x_precision: (an integer (int or long))
        precision of x-axis labels
        flag: --precision=%d
x_units: (an integer (int or long), nipype default value: 1)
        scaling units for x-axis (between 1 and length of in file)
        flag: -u %d
y_max: (a float)
        maximum y value
        flag: --ymax=%.2f
        mutually_exclusive: y_range
y_min: (a float)
        minumum y value
        flag: --ymin=%.2f
        mutually_exclusive: y_range
y_range: (a tuple of the form: (a float, a float))
        min and max y axis values
        flag: %s
        mutually_exclusive: y_min, y_max
```

Outputs:

```
out_file: (an existing file name)
        image to write
```

85.17 PowerSpectrum

Link to code

Wraps command **fslpspec**

Use FSL PowerSpectrum command for power spectrum estimation.

85.17.1 Examples

```
>>> from nipype.interfaces import fsl
>>> pspec = fsl.PowerSpectrum()
>>> pspec.inputs.in_file = 'functional.nii'
>>> res = pspec.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input 4D file to estimate the power spectrum
        flag: %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        name of output 4D file for power spectrum
        flag: %s, position: 1
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        path/name of the output 4D power spectrum file
```

85.18 Reorient2Std

Link to code

Wraps command **fslreorient2std**

fslreorient2std is a tool for reorienting the image to match the approximate orientation of the standard template images (MNI152).

85.18.1 Examples

```
>>> reorient = Reorient2Std()
>>> reorient.inputs.in_file = "functional.nii"
>>> res = reorient.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
```

```
        flag: %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    out_file: (a file name)
            flag: %s
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
```

85.19 RobustFOV

Link to code

Wraps command **robustfov**

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input filename
        flag: -i %s, position: 0

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_roi: (a file name)
        ROI volume output name
        flag: -r %s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
```

```
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_roi: (an existing file name)
        ROI volume output name
```

85.20 SigLoss

Link to code
Wraps command **sigloss**
Estimates signal loss from a field map (in rad/s)

85.20.1 Examples

```
>>> sigloss = SigLoss()
>>> sigloss.inputs.in_file = "phase.nii"
>>> sigloss.inputs.echo_time = 0.03
>>> res = sigloss.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        b0 fieldmap file
        flag: -i %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
echo_time: (a float)
        echo time in seconds
        flag: --te=%f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask_file: (an existing file name)
        brain mask file
        flag: -m %s
out_file: (a file name)
        output signal loss estimate file
        flag: -s %s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
slice_direction: ('x' or 'y' or 'z')
        slicing direction
        flag: -d %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        signal loss estimate file
```

85.21 Slicer

Link to code
Wraps command **slicer**
Use FSL's slicer command to output a png image from a volume.

85.21.1 Examples

```
>>> from nipype.interfaces import fsl
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input volume
        flag: %s, position: 1

[Optional]
all_axial: (a boolean)
        output all axial slices into one picture
        flag: -A, position: 10
        mutually_exclusive: single_slice, middle_slices, all_axial,
         sample_axial
        requires: image_width
args: (a string)
        Additional parameters to the command
        flag: %s
colour_map: (an existing file name)
        use different colour map from that stored in nifti header
        flag: -l %s, position: 4
dither_edges: (a boolean)
        produce semi-transparent (dithered) edges
        flag: -t, position: 7
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
image_edges: (an existing file name)
        volume to display edge overlay for (useful for checking registration
        flag: %s, position: 2
image_width: (an integer (int or long))
        max picture width
        flag: %d, position: -2
```

```
    intensity_range: (a tuple of the form: (a float, a float))
            min and max intensities to display
            flag: -i %.3f %.3f, position: 5
    label_slices: (a boolean, nipype default value: True)
            display slice number
            flag: -L, position: 3
    middle_slices: (a boolean)
            output picture of mid-sagittal, axial, and coronal slices
            flag: -a, position: 10
            mutually_exclusive: single_slice, middle_slices, all_axial,
             sample_axial
    nearest_neighbour: (a boolean)
            use nearest neighbor interpolation for output
            flag: -n, position: 8
    out_file: (a file name)
            picture to write
            flag: %s, position: -1
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    sample_axial: (an integer (int or long))
            output every n axial slices into one picture
            flag: -S %d, position: 10
            mutually_exclusive: single_slice, middle_slices, all_axial,
             sample_axial
            requires: image_width
    scaling: (a float)
            image scale
            flag: -s %f, position: 0
    show_orientation: (a boolean, nipype default value: True)
            label left-right orientation
            flag: %s, position: 9
    single_slice: ('x' or 'y' or 'z')
            output picture of single slice in the x, y, or z plane
            flag: -%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
            flag: -%d, position: 11
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    threshold_edges: (a float)
            use threshold for edges
            flag: -e %.3f, position: 6
```

Outputs:

```
    out_file: (an existing file name)
            picture to write
```

85.22 Smooth

Link to code
Wraps command **fslmaths**

Use fslmaths to smooth the image

85.22.1 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
'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
'fslmaths functional2.nii -kernel gauss 3.397 -fmean functional2_smooth.nii.gz'
```

One of sigma or fwhm must be set:

```
>>> from nipype.interfaces.fsl import Smooth
>>> sm = Smooth()
>>> sm.inputs.output_type = 'NIFTI_GZ'
>>> sm.inputs.in_file = 'functional2.nii'
>>> sm.cmdline
Traceback (most recent call last):
 ~~~
ValueError: Smooth requires a value for one of the inputs ...
```

Inputs:

```
[Mandatory]
fwhm: (a float)
        gaussian kernel fwhm, will be converted to sigma in mm (not voxels)
        flag: -kernel gauss %.03f -fmean, position: 1
        mutually_exclusive: sigma
in_file: (an existing file name)
        flag: %s, position: 0
sigma: (a float)
        gaussian kernel sigma in mm (not voxels)
        flag: -kernel gauss %.03f -fmean, position: 1
        mutually_exclusive: fwhm

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
```

```
    smoothed_file: (a file name)
            flag: %s, position: 2
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    smoothed_file: (an existing file name)
```

85.23 Split

Link to code

Wraps command **fslsplit**

Uses FSL Fslsplit command to separate a volume into images in time, x, y or z dimension.

Inputs:

```
    [Mandatory]
    dimension: ('t' or 'x' or 'y' or 'z')
            dimension along which the file will be split
            flag: -%s, position: 2
    in_file: (an existing file name)
            input filename
            flag: %s, position: 0

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    out_base_name: (a string)
            outputs prefix
            flag: %s, position: 1
    output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
             'NIFTI')
            FSL output type
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_files: (a list of items which are an existing file name)
```

85.24 SwapDimensions

Link to code

Wraps 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-syle dimension codes (RL, LR, AP, PA, IS, SI).
Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input image
        flag: %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
        flag: %s %s %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        image to write
        flag: %s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        image with new dimensions
```

85.25 WarpPoints

Link to code
Wraps 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

85.25.1 Examples

```
>>> from nipype.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
'img2imgcoord -mm -dest T1.nii -src epi.nii -warp warpfield.nii surf.txt'
>>> res = warppoints.run()
```

Inputs:

```
[Mandatory]
dest_file: (an existing file name)
        filename of destination image
        flag: -dest %s
in_coords: (an existing file name)
        filename of file containing coordinates
        flag: %s, position: -1
src_file: (an existing file name)
        filename of source image
        flag: -src %s

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
coord_mm: (a boolean)
        all coordinates in mm
        flag: -mm
        mutually_exclusive: coord_vox
coord_vox: (a boolean)
        all coordinates in voxels - default
        flag: -vox
        mutually_exclusive: coord_mm
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output file name
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
warp_file: (an existing file name)
        filename of warpfield (e.g. intermediate2dest_warp.nii.gz)
        flag: -warp %s
        mutually_exclusive: xfm_file
xfm_file: (an existing file name)
        filename of affine transform (e.g. source2dest.mat)
        flag: -xfm %s
        mutually_exclusive: warp_file
```

Outputs:

```
    out_file: (an existing file name)
            Name of output file, containing the warp as field or coefficients.
```

85.26 WarpPointsToStd

Link to code
Wraps 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

---

85.26.1 Examples

```
>>> from nipype.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
'img2stdcoord -mm -img T1.nii -std mni.nii -warp warpfield.nii surf.txt'
>>> res = warppoints.run()
```

Inputs:

```
    [Mandatory]
    img_file: (an existing file name)
            filename of input image
            flag: -img %s
    in_coords: (an existing file name)
            filename of file containing coordinates
            flag: %s, position: -1
    std_file: (an existing file name)
            filename of destination image
            flag: -std %s

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    coord_mm: (a boolean)
            all coordinates in mm
            flag: -mm
            mutually_exclusive: coord_vox
    coord_vox: (a boolean)
            all coordinates in voxels - default
            flag: -vox
            mutually_exclusive: coord_mm
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output file name
premat_file: (an existing file name)
        filename of pre-warp affine transform (e.g.
        example_func2highres.mat)
        flag: -premat %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
warp_file: (an existing file name)
        filename of warpfield (e.g. intermediate2dest_warp.nii.gz)
        flag: -warp %s
        mutually_exclusive: xfm_file
xfm_file: (an existing file name)
        filename of affine transform (e.g. source2dest.mat)
        flag: -xfm %s
        mutually_exclusive: warp_file
```

Outputs:

```
out_file: (an existing file name)
        Name of output file, containing the warp as field or coefficients.
```

85.27 WarpUtils

Link to code

Wraps command **fnirtfileutils**

Use FSL fnirtfileutils to convert field->coefficients, coefficients->field, coefficients->other_coefficients etc

85.27.1 Examples

```
>>> from nipype.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
'fnirtfileutils --in=warpfield.nii --outformat=spline --ref=T1.nii --warpres=10.0000,10.0000,10.
>>> res = invwarp.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        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).
        flag: --in=%s
reference: (an existing file name)
        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.
        flag: --ref=%s
write_jacobian: (a boolean, nipype default value: False)
        Switch on --jac flag with automatically generated filename

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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.
        flag: --knotspace=%d,%d,%d
out_file: (a file name)
        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.
        flag: --out=%s, position: -1
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.
        flag: --outformat=%s
out_jacobian: (a file name)
        Specifies that a (3D) file of Jacobian determinants corresponding to
        --in should be produced and written to filename.
        flag: --jac=%s
output_type: ('NIFTI_PAIR' or 'NIFTI_PAIR_GZ' or 'NIFTI_GZ' or
         'NIFTI')
        FSL output type
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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.
        flag: --warpres=%0.4f,%0.4f,%0.4f
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).
            flag: --withaff
```

Outputs:

```
    out_file: (a file name)
            Name of output file, containing the warp as field or coefficients.
    out_jacobian: (a file name)
            Name of output file, containing the map of the determinant of the
            Jacobian
```

CHAPTER 86

interfaces.io

86.1 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 ouputs of the same name.

86.1.1 Examples

```
>>> from nipype.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()
>>> result.outputs.out_paths
['./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
['027-ep2d_fid_T1_Gd4',
 '018-ep2d_fid_T1_Gd2',
 '016-ep2d_fid_T1_Gd1',
 '013-ep2d_fid_T1_pre']
>>> result.outputs.basename
['acquisition',
 'acquisition'
 'acquisition',
 'acquisition']
```

Inputs:

```
[Mandatory]
root_paths: (a list of items which are any value or a string)

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
ignore_regexes: (a list of items which are any value)
        List of regular expressions, if any match the path it will be
        ignored.
match_regex: (a string, nipype default value: (.+))
```

```
        Regular expression for matching paths.
max_depth: (an integer (int or long))
        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, nipype default value: False)
        Unpack single results from list
```

Outputs:

```
None
```

86.2 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

86.2.1 Examples

```
>>> from nipype.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 string)
            Layout used to get files. relative to base directory if defined

    [Optional]
    base_directory: (an existing directory name)
            Path to the base directory consisting of subject data.
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    raise_on_empty: (a boolean, nipype default value: True)
            Generate exception if list is empty for a given field
    template_args: (a dictionary with keys which are a 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
```

86.3 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 comesfrom 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.

86.3.1 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()
```

To use DataSink in a MapNode, its inputs have to be defined at the time the interface is created.

```
>>> ds = DataSink(infields=['contasts.@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()
```

Inputs:

```
[Mandatory]

[Optional]
_outputs: (a dictionary with keys which are a string and with values
          which are any value, nipype default value: {})
base_directory: (a directory name)
        Path to the base directory for storing data.
bucket: (any value)
        Boto3 S3 bucket for manual override of bucket
container: (a string)
        Folder within base directory in which to store output
creds_path: (a 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
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
local_copy: (a string)
        Copy files locally as well as to S3 bucket
parameterization: (a boolean, nipype default value: True)
        store output in parametrized structure
regexp_substitutions: (a list of items which are a tuple of the form:
          (a string, a string))
        List of 2-tuples reflecting a pair of a Python regexp pattern and a
        replacement string. Invoked after string `substitutions`
remove_dest_dir: (a boolean, nipype default value: False)
        remove dest directory when copying dirs
strip_dir: (a directory name)
        path to strip out of filename
substitutions: (a list of items which are a tuple of the form: (a
          string, a string))
        List of 2-tuples reflecting string to substitute and string to
        replace it with
```

Outputs:

```
out_file: (any value)
        datasink output
```

86.4 FreeSurferSource

Link to code

Generates freesurfer subject info from their directories

86.4.1 Examples

```
>>> from nipype.interfaces.io import FreeSurferSource
>>> fs = FreeSurferSource()
>>> #fs.inputs.subjects_dir = '.'
>>> fs.inputs.subject_id = 'PWS04'
>>> res = fs.run()
```

```
>>> fs.inputs.hemi = 'lh'
>>> res = fs.run()
```

Inputs:

```
[Mandatory]
subject_id: (a string)
        Subject name for whom to retrieve data
subjects_dir: (a directory name)
        Freesurfer subjects directory.

[Optional]
hemi: ('both' or 'lh' or 'rh', nipype default value: both)
        Selects hemisphere specific outputs
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
BA_stats: (a list of items which are an existing file name)
        Brodmann Area statistics files
T1: (an existing file name)
        Intensity normalized whole-head volume
annot: (a list of items which are an existing file name)
        Surface annotation files
aparc_a2009s_stats: (a list of items which are an existing file name)
        Aparc a2009s parcellation statistics files
aparc_aseg: (a list of items which are an existing file name)
        Aparc parcellation projected into aseg volume
aparc_stats: (a list of items which are an existing file name)
        Aparc parcellation statistics files
aseg: (an existing file name)
        Volumetric map of regions from automatic segmentation
aseg_stats: (a list of items which are an existing file name)
        Automated segmentation statistics file
brain: (an existing file name)
        Intensity normalized brain-only volume
brainmask: (an existing file name)
        Skull-stripped (brain-only) volume
curv: (a list of items which are an existing file name)
        Maps of surface curvature
curv_stats: (a list of items which are an existing file name)
        Curvature statistics files
entorhinal_exvivo_stats: (a list of items which are an existing file
         name)
        Entorhinal exvivo statistics files
filled: (an existing file name)
        Subcortical mass volume
inflated: (a list of items which are an existing file name)
        Inflated surface meshes
label: (a list of items which are an existing file name)
```

```
        Volume and surface label files
norm: (an existing file name)
        Normalized skull-stripped volume
nu: (an existing file name)
        Non-uniformity corrected whole-head volume
orig: (an existing file name)
        Base image conformed to Freesurfer space
pial: (a list of items which are an existing file name)
        Gray matter/pia mater surface meshes
rawavg: (an existing file name)
        Volume formed by averaging input images
ribbon: (a list of items which are an existing file name)
        Volumetric maps of cortical ribbons
smoothwm: (a list of items which are an existing file name)
        Smoothed original surface meshes
sphere: (a list of items which are an existing file name)
        Spherical surface meshes
sphere_reg: (a list of items which are an existing file name)
        Spherical registration file
sulc: (a list of items which are an existing file name)
        Surface maps of sulcal depth
thickness: (a list of items which are an existing file name)
        Surface maps of cortical thickness
volume: (a list of items which are an existing file name)
        Surface maps of cortical volume
white: (a list of items which are an existing file name)
        White/gray matter surface meshes
wm: (an existing file name)
        Segmented white-matter volume
wmparc: (an existing file name)
        Aparc parcellation projected into subcortical white matter
wmparc_stats: (a list of items which are an existing file name)
        White matter parcellation statistics file
```

86.5 IOBase

Link to code

Inputs:

```
[Mandatory]

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
None
```

86.6 JSONFileGrabber

Link to code

Datagrabber interface that loads a json file and generates an output for every first-level object

86.6.1 Example

```
>>> import pprint
>>> from nipype.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 = 'jsongrabber.txt'
>>> res = jsonSource.run()
>>> pprint.pprint(res.outputs.get())
{'param1': ...'exampleStr', 'param2': 4, 'param3': 1.0}
```

Inputs:

```
[Mandatory]

[Optional]
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
ignore_exception: (a boolean, nipype default value: False)
         Print an error message instead of throwing an exception in case the
         interface fails to run
in_file: (an existing file name)
         JSON source file
```

Outputs:

```
None
```

86.7 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()
```

Using a dictionary as input:

```
>>> dictsink = JSONFileSink()
>>> dictsink.inputs.in_dict = {'subject_id': 's1',
...                            'some_measurement': 11.4}
>>> dictsink.run()
```

Inputs:

```
[Mandatory]

[Optional]
```

```
    _outputs: (a dictionary with keys which are any value and with values
             which are any value, nipype default value: {})
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    in_dict: (a dictionary with keys which are any value and with values
             which are any value, nipype default value: {})
            input JSON dictionary
    out_file: (a file name)
            JSON sink file
```

Outputs:

```
    out_file: (a file name)
            JSON sink file
```

86.8 MySQLSink

Link to code

Very simple frontend for storing values into MySQL database.

86.8.1 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()
```

Inputs:

```
    [Mandatory]
    config: (a file name)
            MySQL Options File (same format as my.cnf)
            mutually_exclusive: host
    database_name: (a string)
            Otherwise known as the schema name
    host: (a string, nipype default value: localhost)
            mutually_exclusive: config
            requires: username, password
    table_name: (a string)

    [Optional]
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    password: (a string)
    username: (a string)
```

Outputs:

```
    None
```

86.9 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.

Inputs:

```
[Mandatory]
bucket: (a string)
        Amazon S3 bucket where your data is stored
sort_filelist: (a boolean)
        Sort the filelist that matches the template
template: (a string)
        Layout used to get files. Relative to bucket_path if defined.Uses
        regex rather than glob style formatting.

[Optional]
anon: (a boolean, nipype 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.
bucket_path: (a string, nipype default value: )
        Location within your bucket for subject data.
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
local_directory: (an existing directory name)
        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, nipype default value: True)
        Generate exception if list is empty for a given field
region: (a string, nipype default value: us-east-1)
        Region of s3 bucket
template_args: (a dictionary with keys which are a 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
```

86.10 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.

86.10.1 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'
>>> sql.inputs.some_measurement = 11.4
>>> sql.run()
```

Inputs:

```
[Mandatory]
database_file: (an existing file name)
table_name: (a string)

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
None
```

86.11 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

86.11.1 Examples

```
>>> from nipype.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]
base_directory: (a string)
        Path to the base directory consisting of subject data.
hostname: (a string)
        Server hostname.
sort_filelist: (a boolean)
        Sort the filelist that matches the template
template: (a string)
        Layout used to get files. relative to base directory if defined

[Optional]
download_files: (a boolean, nipype default value: True)
        If false it will return the file names without downloading them
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
password: (a string)
        Server password.
raise_on_empty: (a boolean, nipype default value: True)
        Generate exception if list is empty for a given field
ssh_log_to_file: (a string, nipype default value: )
        If set SSH commands will be logged to the given file
template_args: (a dictionary with keys which are a 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
template_expression: ('fnmatch' or 'regexp', nipype default value:
         fnmatch)
        Use either fnmatch or regexp to express templates
username: (a string)
        Server username.
```

Outputs:

```
None
```

86.12 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 persistant 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.

86.12.1 Examples

```
>>> import pprint
>>> from nipype 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())
{'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:

```
[Mandatory]

[Optional]
base_directory: (an existing directory name)
        Root path common to templates.
force_lists: (a boolean or a list of items which are a string, nipype
         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
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
raise_on_empty: (a boolean, nipype default value: True)
        Raise an exception if a template pattern matches no files.
sort_filelist: (a boolean, nipype default value: True)
        When matching mutliple files, return them in sorted order.
```

Outputs:

```
None
```

86.13 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]
config: (a file name)
        mutually_exclusive: server
experiment_id: (a string)
        Set to workflow name
```

```
    project_id: (a string)
            Project in which to store the outputs
    server: (a string)
            mutually_exclusive: config
            requires: user, pwd
    subject_id: (a string)
            Set to subject id

    [Optional]
    _outputs: (a dictionary with keys which are a string and with values
             which are any value, nipype default value: {})
    assessor_id: (a string)
            Option to customize ouputs representation in XNAT - assessor level
            will be used with specified id
            mutually_exclusive: reconstruction_id
    cache_dir: (a directory name)
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    pwd: (a string)
    reconstruction_id: (a string)
            Option to customize ouputs representation in XNAT - reconstruction
            level will be used with specified id
            mutually_exclusive: assessor_id
    share: (a boolean, nipype default value: False)
            Option to share the subjects from the original projectinstead of
            creating new ones when possible - the created experiments are then
            shared back to the original project
    user: (a string)
```

Outputs:

```
    None
```

86.14 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.

86.14.1 Examples

```
    >>> from nipype.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'                    '/as
    >>> 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]
config: (a file name)
        mutually_exclusive: server
query_template: (a string)
        Layout used to get files. Relative to base directory if defined
server: (a string)
        mutually_exclusive: config
        requires: user, pwd

[Optional]
cache_dir: (a directory name)
        Cache directory
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
pwd: (a string)
query_template_args: (a dictionary with keys which are a string and
         with values which are a list of items which are a list of items
         which are any value, nipype default value: {'outfiles': []})
        Information to plug into template
user: (a string)
```

Outputs:

```
None
```

86.15 add_traits()

Link to code

Add traits to a traited class.
All traits are set to Undefined by default

86.16 copytree()

Link to code

Recursively copy a directory tree using nipype.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.

86.17 push_file()

Link to code

86.18 quote_id()

Link to code

86.19 unquote_id()

Link to code

CHAPTER 87

interfaces.meshfix

87.1 MeshFix

Link to code
Wraps 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.

87.1.1 Example

```
>>> import nipype.interfaces.meshfix as mf
>>> fix = mf.MeshFix()
>>> fix.inputs.in_file1 = 'lh-pial.stl'
>>> fix.inputs.in_file2 = 'rh-pial.stl'
>>> fix.run()
>>> fix.cmdline
'meshfix lh-pial.stl rh-pial.stl -o lh-pial_fixed.off'
```

Inputs:

```
[Mandatory]
in_file1: (an existing file name)
        flag: %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
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.
        flag: --cut-inner %d
cut_outer: (an integer (int or long))
        Remove triangles of 1st that are outside of the 2nd shell.
        flag: --cut-outer %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.
        flag: --decouple-inin %d
```

```
    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.
            flag: --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.
            flag: --decouple-outout %d
    dilation: (an integer (int or long))
            Dilate the surface by d. d < 0 means shrinking.
            flag: --dilate %d
    dont_clean: (a boolean)
            Don't Clean
            flag: --no-clean
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    epsilon_angle: (0.0 <= a floating point number <= 2.0)
            Epsilon angle in degrees (must be between 0 and 2)
            flag: -a %f
    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)
            flag: %f
            requires: finetuning_substeps
    finetuning_inwards: (a boolean)
            flag: --fineTuneIn
            requires: finetuning_distance, finetuning_substeps
    finetuning_outwards: (a boolean)
            Similar to finetuning_inwards, but ensures minimal distance in the
            other direction
            flag: --fineTuneIn
            mutually_exclusive: finetuning_inwards
            requires: finetuning_distance, 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)
            flag: %d
            requires: finetuning_distance
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    in_file2: (an existing file name)
            flag: %s, position: 2
    join_closest_components: (a boolean)
            Join the closest pair of components.
            flag: -jc
            mutually_exclusive: join_closest_components
    join_overlapping_largest_components: (a boolean)
            Join 2 biggest components if they overlap, remove the rest.
            flag: -j
```

```
        mutually_exclusive: join_closest_components
laplacian_smoothing_steps: (an integer (int or long))
        The number of laplacian smoothing steps to apply
        flag: --smooth %d
number_of_biggest_shells: (an integer (int or long))
        Only the N biggest shells are kept
        flag: --shells %d
out_filename: (a file name)
        The output filename for the fixed mesh file
        flag: -o %s
output_type: ('stl' or 'msh' or 'wrl' or 'vrml' or 'fs' or 'off',
         nipype default value: off)
        The output type to save the file as.
quiet_mode: (a boolean)
        Quiet mode, don't write much to stdout.
        flag: -q
remove_handles: (a boolean)
        Remove handles
        flag: --remove-handles
save_as_freesurfer_mesh: (a boolean)
        Result is saved in freesurfer mesh format
        flag: --fsmesh
        mutually_exclusive: save_as_vrml, save_as_stl
save_as_stl: (a boolean)
        Result is saved in stereolithographic format (.stl)
        flag: --stl
        mutually_exclusive: save_as_vmrl, save_as_freesurfer_mesh
save_as_vmrl: (a boolean)
        Result is saved in VRML1.0 format (.wrl)
        flag: --wrl
        mutually_exclusive: save_as_stl, save_as_freesurfer_mesh
set_intersections_to_one: (a boolean)
        If the mesh contains intersections, return value = 1.If saved in
        gmsh format, intersections will be highlighted.
        flag: --intersect
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
uniform_remeshing_steps: (an integer (int or long))
        Number of steps for uniform remeshing of the whole mesh
        flag: -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
        flag: --vertices %d
        requires: uniform_remeshing_steps
x_shift: (an integer (int or long))
        Shifts the coordinates of the vertices when saving. Output must be
        in FreeSurfer format
        flag: --smooth %d
```

Outputs:

```
mesh_file: (an existing file name)
        The output mesh file
```

CHAPTER 88

interfaces.minc.base

88.1 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.

88.1.1 Examples

```
>>> from nipype.interfaces.minc.base import aggregate_filename
>>> f = aggregate_filename(['/tmp/foo1.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/foo1.mnc', '/tmp/blah1.mnc'], 'averaged')
>>> os.path.split(f)[1] # This has a full path, so just check the filename.
'foo1_averaged.mnc'
```

interfaces.minc.minc

89.1 Average

Link to code
Wraps command **mincaverage**
Average a number of MINC files.

89.1.1 Examples

```
>>> from nipype.interfaces.minc import Average
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
filelist: (a file name)
        Specify the name of a file containing input file names.
        flag: -filelist %s
        mutually_exclusive: input_files, filelist
input_files: (a list of items which are a file name)
        input file(s)
        flag: %s, position: -2
        mutually_exclusive: input_files, filelist

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
avgdim: (a string)
        Specify a dimension along which we wish to average.
        flag: -avgdim %s
binarize: (a boolean)
        Binarize the volume by looking for values in a given range.
        flag: -binarize
binrange: (a tuple of the form: (a float, a float))
        Specify a range for binarization. Default value: 1.79769e+308
        -1.79769e+308.
        flag: -binrange %s %s
binvalue: (a float)
        Specify a target value (+/- 0.5) forbinarization. Default value:
        -1.79769e+308
```

```
        flag: -binvalue %s
check_dimensions: (a boolean)
        Check that dimension info matches across files (default).
        flag: -check_dimensions
        mutually_exclusive: check_dimensions, no_check_dimensions
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: -clobber
copy_header: (a boolean)
        Copy all of the header from the first file (default for one file).
        flag: -copy_header
        mutually_exclusive: copy_header, no_copy_header
debug: (a boolean)
        Print out debugging messages.
        flag: -debug
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
format_byte: (a boolean)
        Write out byte data.
        flag: -byte
        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.
        flag: -double
        mutually_exclusive: format_filetype, format_byte, format_short,
         format_int, format_long, format_float, format_double,
         format_signed, format_unsigned
format_filetype: (a boolean)
        Use data type of first file (default).
        flag: -filetype
        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.
        flag: -float
        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.
        flag: -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.
        flag: -long
        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.
        flag: -short
```

```
        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.
        flag: -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).
        flag: -unsigned
        mutually_exclusive: format_filetype, format_byte, format_short,
         format_int, format_long, format_float, format_double,
         format_signed, format_unsigned
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
max_buffer_size_in_kb: (an integer >= 0)
        Specify the maximum size of the internal buffers (in kbytes).
        flag: -max_buffer_size_in_kb %d
no_check_dimensions: (a boolean)
        Do not check dimension info.
        flag: -nocheck_dimensions
        mutually_exclusive: check_dimensions, no_check_dimensions
no_copy_header: (a boolean)
        Do not copy all of the header from the first file (default for many
        files)).
        flag: -nocopy_header
        mutually_exclusive: copy_header, no_copy_header
nonormalize: (a boolean)
        Do not normalize data sets (default).
        flag: -nonormalize
        mutually_exclusive: normalize, nonormalize
normalize: (a boolean)
        Normalize data sets for mean intensity.
        flag: -normalize
        mutually_exclusive: normalize, nonormalize
output_file: (a file name)
        output file
        flag: %s, position: -1
quiet: (a boolean)
        Do not print out log messages.
        flag: -quiet
        mutually_exclusive: verbose, quiet
sdfile: (a file name)
        Specify an output sd file (default=none).
        flag: -sdfile %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
two: (a boolean)
        Create a MINC 2 output file.
        flag: -2
verbose: (a boolean)
        Print out log messages (default).
        flag: -verbose
```

```
        mutually_exclusive: verbose, quiet
voxel_range: (a tuple of the form: (an integer (int or long), an
         integer (int or long)))
        Valid range for output data.
        flag: -range %d %d
weights: (a list of items which are a string)
        Specify weights for averaging ("<w1>,<w2>,...").
        flag: -weights %s
width_weighted: (a boolean)
        Weight by dimension widths when -avgdim is used.
        flag: -width_weighted
        requires: avgdim
```

Outputs:

```
output_file: (an existing file name)
        output file
```

89.2 BBox

Link to code

Wraps command **mincbbox**

Determine a bounding box of image.

89.2.1 Examples

```
>>> from nipype.interfaces.minc import BBox
>>> from nipype.interfaces.minc.testdata import nonempty_minc_data
```

```
>>> file0 = nonempty_minc_data(0)
>>> bbox = BBox(input_file=file0)
>>> bbox.run()
```

Inputs:

```
[Mandatory]
input_file: (an existing file name)
        input file
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
format_minccrop: (a boolean)
        Output format for minccrop: (-xlim x1 x2 -ylim y1 y2 -zlim z1 z2
        flag: -minccrop
format_mincresample: (a boolean)
        Output format for mincresample: (-step x y z -start x y z -nelements
        x y z
        flag: -mincresample
format_mincreshape: (a boolean)
        Output format for mincreshape: (-start x,y,z -count dx,dy,dz
```

```
        flag: -mincreshape
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
one_line: (a boolean)
        Output on one line (default): start_x y z width_x y z
        flag: -one_line
        mutually_exclusive: one_line, two_lines
out_file: (a file name)
        flag: > %s, position: -1
output_file: (a file name)
        output file containing bounding box corners
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
threshold: (an integer (int or long))
        VIO_Real value threshold for bounding box. Default value: 0.
        flag: -threshold
two_lines: (a boolean)
        Output on two lines: start_x y z
         width_x y z
        flag: -two_lines
        mutually_exclusive: one_line, two_lines
```

Outputs:

```
output_file: (an existing file name)
        output file containing bounding box corners
```

89.3 Beast

Link to code

Wraps command **mincbeast**

Extract brain image using BEaST (Brain Extraction using non-local Segmentation Technique).

89.3.1 Examples

```
>>> from nipype.interfaces.minc import Beast
>>> from nipype.interfaces.minc.testdata import nonempty_minc_data
```

```
>>> file0 = nonempty_minc_data(0)
>>> beast = Beast(input_file=file0)
>>> beast .run()
```

Inputs:

```
[Mandatory]
input_file: (a file name)
        input file
        flag: %s, position: -2
library_dir: (a directory name)
        library directory
        flag: %s, position: -3

[Optional]
abspath: (a boolean, nipype default value: True)
```

```
        File paths in the library are absolute (default is relative to
        library root).
        flag: -abspath
args: (a string)
        Additional parameters to the command
        flag: %s
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: -clobber
confidence_level_alpha: (a float)
        Specify confidence level Alpha. Default value: 0.5
        flag: -alpha %s
configuration_file: (a file name)
        Specify configuration file.
        flag: -configuration %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fill_holes: (a boolean)
        Fill holes in the binary output.
        flag: -fill
flip_images: (a boolean)
        Flip images around the mid-sagittal plane to increase patch count.
        flag: -flip
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
load_moments: (a boolean)
        Do not calculate moments instead use precalculatedlibrary moments.
        (for optimization purposes)
        flag: -load_moments
median_filter: (a boolean)
        Apply a median filter on the probability map.
        flag: -median
nlm_filter: (a boolean)
        Apply an NLM filter on the probability map (experimental).
        flag: -nlm_filter
number_selected_images: (an integer (int or long))
        Specify number of selected images. Default value: 20
        flag: -selection_num %s
output_file: (a file name)
        output file
        flag: %s, position: -1
patch_size: (an integer (int or long))
        Specify patch size for single scale approach. Default value: 1.
        flag: -patch_size %s
probability_map: (a boolean)
        Output the probability map instead of crisp mask.
        flag: -probability
same_resolution: (a boolean)
        Output final mask with the same resolution as input file.
        flag: -same_resolution
search_area: (an integer (int or long))
        Specify size of search area for single scale approach. Default
        value: 2.
        flag: -search_area %s
smoothness_factor_beta: (a float)
```

```
        Specify smoothness factor Beta. Default value: 0.25
        flag: -beta %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
threshold_patch_selection: (a float)
        Specify threshold for patch selection. Default value: 0.95
        flag: -threshold %s
voxel_size: (an integer (int or long))
        Specify voxel size for calculations (4, 2, or 1).Default value: 4.
        Assumes no multiscale. Use configurationfile for multiscale.
        flag: -voxel_size %s
```

Outputs:

```
output_file: (an existing file name)
        output mask file
```

89.4 BestLinReg

Link to code
Wraps 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

89.4.1 Examples

```
>>> from nipype.interfaces.minc import BestLinReg
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
source: (an existing file name)
        source Minc file
        flag: %s, position: -4
target: (an existing file name)
        target Minc file
        flag: %s, position: -3

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: -clobber
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
```

```
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_mnc: (a file name)
        output mnc file
        flag: %s, position: -1
output_xfm: (a file name)
        output xfm file
        flag: %s, position: -2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        Print out log messages. Default: False.
        flag: -verbose
```

Outputs:

```
output_mnc: (an existing file name)
        output mnc file
output_xfm: (an existing file name)
        output xfm file
```

89.5 BigAverage

Link to code

Wraps 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

89.5.1 Examples

```
>>> from nipype.interfaces.minc import BigAverage
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
input_files: (a list of items which are a file name)
```

```
        input file(s)
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: --clobber
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_file: (a file name)
        output file
        flag: %s, position: -1
output_float: (a boolean)
        Output files with float precision.
        flag: --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 alarge
        number of input files.
        flag: -robust
sd_file: (a file name)
        Place standard deviation image in specified file.
        flag: --sdfile %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tmpdir: (a directory name)
        temporary files directory
        flag: -tmpdir %s
verbose: (a boolean)
        Print out log messages. Default: False.
        flag: --verbose
```

Outputs:

```
output_file: (an existing file name)
        output file
sd_file: (an existing file name)
        standard deviation image
```

89.6 Blob

Link to code

Wraps command **mincblob**

Calculate blobs from minc deformation grids.

89.6.1 Examples

```
>>> from nipype.interfaces.minc import Blob
>>> from nipype.interfaces.minc.testdata import minc2Dfile
```

```
>>> blob = Blob(input_file=minc2Dfile, output_file='/tmp/tmp.mnc', trace=True)
>>> blob.run()
```

Inputs:

```
[Mandatory]
input_file: (an existing file name)
        input file to blob
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
determinant: (a boolean)
        compute the determinant (exact growth and shrinkage) -- SLOW
        flag: -determinant
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
magnitude: (a boolean)
        compute the magnitude of the displacement vector
        flag: -magnitude
output_file: (a file name)
        output file
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
trace: (a boolean)
        compute the trace (approximate growth and shrinkage) -- FAST
        flag: -trace
translation: (a boolean)
        compute translation (structure displacement)
        flag: -translation
```

Outputs:

```
output_file: (an existing file name)
        output file
```

89.7 Blur

Link to code

Wraps 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.

89.7.1 Examples

```
>>> from nipype.interfaces.minc import Blur
>>> from nipype.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()
```

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()
```

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()
```

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]
fwhm: (a float)
        Full-width-half-maximum of gaussian kernel. Default value: 0.
        flag: -fwhm %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.
        flag: -3dfwhm %s %s %s
        mutually_exclusive: fwhm, fwhm3d, standard_dev
input_file: (an existing file name)
        input file
        flag: %s, position: -2
standard_dev: (a float)
        Standard deviation of gaussian kernel. Default value: 0.
        flag: -standarddev %s
        mutually_exclusive: fwhm, fwhm3d, standard_dev

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: -clobber
dimensions: (1 or 2 or 3)
        Number of dimensions to blur (either 1,2 or 3). Default value: 3.
        flag: -dimensions %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
gaussian: (a boolean)
        Use a gaussian smoothing kernel (default).
        flag: -gaussian
        mutually_exclusive: gaussian, rect
```

```
    gradient: (a boolean)
            Create the gradient magnitude volume as well.
            flag: -gradient
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    no_apodize: (a boolean)
            Do not apodize the data before blurring.
            flag: -no_apodize
    output_file_base: (a file name)
            output file base
            flag: %s, position: -1
    partial: (a boolean)
            Create the partial derivative and gradient magnitude volumes as
            well.
            flag: -partial
    rect: (a boolean)
            Use a rect (box) smoothing kernel.
            flag: -rect
            mutually_exclusive: gaussian, rect
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    gradient_dxyz: (a file name)
            Gradient dxyz.
    output_file: (an existing file name)
            Blurred output file.
    partial_dx: (a file name)
            Partial gradient dx.
    partial_dxyz: (a file name)
            Partial gradient dxyz.
    partial_dy: (a file name)
            Partial gradient dy.
    partial_dz: (a file name)
            Partial gradient dz.
```

89.8 Calc

Link to code

Wraps command **minccalc**

Compute an expression using MINC files as input.

89.8.1 Examples

```
    >>> from nipype.interfaces.minc import Calc
    >>> from nipype.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]
    >>> calc.run()
```

Inputs:

```
    [Mandatory]
    expfile: (a file name)
            Name of file containing expression.
            flag: -expfile %s
            mutually_exclusive: expression, expfile
    expression: (a string)
            Expression to use in calculations.
            flag: -expression '%s'
            mutually_exclusive: expression, expfile
    filelist: (a file name)
            Specify the name of a file containing input file names.
            flag: -filelist %s
            mutually_exclusive: input_files, filelist
    input_files: (a list of items which are a file name)
            input file(s) for calculation
            flag: %s, position: -2

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    check_dimensions: (a boolean)
            Check that files have matching dimensions (default).
            flag: -check_dimensions
            mutually_exclusive: check_dimensions, no_check_dimensions
    clobber: (a boolean, nipype default value: True)
            Overwrite existing file.
            flag: -clobber
    copy_header: (a boolean)
            Copy all of the header from the first file.
            flag: -copy_header
            mutually_exclusive: copy_header, no_copy_header
    debug: (a boolean)
            Print out debugging messages.
            flag: -debug
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    eval_width: (an integer (int or long))
            Number of voxels to evaluate simultaneously.
            flag: -eval_width %s
    format_byte: (a boolean)
            Write out byte data.
            flag: -byte
            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.
            flag: -double
            mutually_exclusive: format_filetype, format_byte, format_short,
             format_int, format_long, format_float, format_double,
             format_signed, format_unsigned
    format_filetype: (a boolean)
            Use data type of first file (default).
            flag: -filetype
            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.
        flag: -float
        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.
        flag: -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.
        flag: -long
        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.
        flag: -short
        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.
        flag: -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).
        flag: -unsigned
        mutually_exclusive: format_filetype, format_byte, format_short,
         format_int, format_long, format_float, format_double,
         format_signed, format_unsigned
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
ignore_nan: (a boolean)
        Ignore invalid data (NaN) for accumulations.
        flag: -ignore_nan
max_buffer_size_in_kb: (an integer >= 0)
        Specify the maximum size of the internal buffers (in kbytes).
        flag: -max_buffer_size_in_kb %d
no_check_dimensions: (a boolean)
        Do not check that files have matching dimensions.
        flag: -nocheck_dimensions
        mutually_exclusive: check_dimensions, no_check_dimensions
no_copy_header: (a boolean)
        Do not copy all of the header from the first file.
        flag: -nocopy_header
        mutually_exclusive: copy_header, no_copy_header
outfiles: (a list of items which are a tuple of the form: (a string,
         a file name))
output_file: (a file name)
```

```
        output file
        flag: %s, position: -1
output_illegal: (a boolean)
        Value to write out when an illegal operation is done. Default value:
        1.79769e+308
        flag: -illegal_value
        mutually_exclusive: output_nan, output_zero, output_illegal_value
output_nan: (a boolean)
        Output NaN when an illegal operation is done (default).
        flag: -nan
        mutually_exclusive: output_nan, output_zero, output_illegal_value
output_zero: (a boolean)
        Output zero when an illegal operation is done.
        flag: -zero
        mutually_exclusive: output_nan, output_zero, output_illegal_value
propagate_nan: (a boolean)
        Invalid data in any file at a voxel produces a NaN (default).
        flag: -propagate_nan
quiet: (a boolean)
        Do not print out log messages.
        flag: -quiet
        mutually_exclusive: verbose, quiet
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
two: (a boolean)
        Create a MINC 2 output file.
        flag: -2
verbose: (a boolean)
        Print out log messages (default).
        flag: -verbose
        mutually_exclusive: verbose, quiet
voxel_range: (a tuple of the form: (an integer (int or long), an
         integer (int or long)))
        Valid range for output data.
        flag: -range %d %d
```

Outputs:

```
output_file: (an existing file name)
        output file
```

89.9 Convert

Link to code

Wraps command **mincconvert**

convert between MINC 1 to MINC 2 format.

89.9.1 Examples

```
>>> from nipype.interfaces.minc import Convert
>>> from nipype.interfaces.minc.testdata import minc2Dfile
>>> c = Convert(input_file=minc2Dfile, output_file='/tmp/out.mnc', two=True) # Convert to MINC2
>>> c.run()
```

Inputs:

```
    [Mandatory]
    input_file: (an existing file name)
            input file for converting
            flag: %s, position: -2

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    chunk: (an integer >= 0)
            Set the target block size for chunking (0 default, >1 block size).
            flag: -chunk %d
    clobber: (a boolean, nipype default value: True)
            Overwrite existing file.
            flag: -clobber
    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).
            flag: -compress %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    output_file: (a file name)
            output file
            flag: %s, position: -1
    template: (a boolean)
            Create a template file. The dimensions, variables, andattributes of
            the input file are preserved but all data it set to zero.
            flag: -template
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    two: (a boolean)
            Create a MINC 2 output file.
            flag: -2
```

Outputs:

```
    output_file: (an existing file name)
            output file
```

89.10 Copy

Link to code

Wraps 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 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: (an existing file name)
```

```
        input file to copy
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_file: (a file name)
        output file
        flag: %s, position: -1
pixel_values: (a boolean)
        Copy pixel values as is.
        flag: -pixel_values
        mutually_exclusive: pixel_values, real_values
real_values: (a boolean)
        Copy real pixel intensities (default).
        flag: -real_values
        mutually_exclusive: pixel_values, real_values
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
output_file: (an existing file name)
        output file
```

89.11 Dump

Link to code

Wraps command **mincdump**

Dump a MINC file. Typically used in conjunction with mincgen (see Gen).

89.11.1 Examples

```
>>> from nipype.interfaces.minc import Dump
>>> from nipype.interfaces.minc.testdata import minc2Dfile
```

```
>>> dump = Dump(input_file=minc2Dfile)
>>> dump.run()
```

```
>>> dump = Dump(input_file=minc2Dfile, output_file='/tmp/out.txt', precision=(3, 4))
>>> dump.run()
```

Inputs:

```
[Mandatory]
input_file: (an existing file name)
        input file
```

```
        flag: %s, position: -2

[Optional]
annotations_brief: ('c' or 'f')
        Brief annotations for C or Fortran indices in data.
        flag: -b %s
        mutually_exclusive: annotations_brief, annotations_full
annotations_full: ('c' or 'f')
        Full annotations for C or Fortran indices in data.
        flag: -f %s
        mutually_exclusive: annotations_brief, annotations_full
args: (a string)
        Additional parameters to the command
        flag: %s
coordinate_data: (a boolean)
        Coordinate variable data and header information.
        flag: -c
        mutually_exclusive: coordinate_data, header_data
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
header_data: (a boolean)
        Header information only, no data.
        flag: -h
        mutually_exclusive: coordinate_data, header_data
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
line_length: (an integer >= 0)
        Line length maximum in data section (default 80).
        flag: -l %d
netcdf_name: (a string)
        Name for netCDF (default derived from file name).
        flag: -n %s
out_file: (a file name)
        flag: > %s, position: -1
output_file: (a file name)
        output file
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
        flag: %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
variables: (a list of items which are a string)
        Output data for specified variables only.
        flag: -v %s
```

Outputs:

```
output_file: (an existing file name)
        output file
```

89.12 Extract

Link to code
Wraps command **mincextract**
Dump a hyperslab of MINC file data.

89.12.1 Examples

```
>>> from nipype.interfaces.minc import Extract
>>> from nipype.interfaces.minc.testdata import minc2Dfile
```

```
>>> extract = Extract(input_file=minc2Dfile)
>>> extract.run()
```

```
>>> extract = Extract(input_file=minc2Dfile, start=[3, 10, 5], count=[4, 4, 4]) # extract a 4x4x
>>> extract.run()
```

Inputs:

```
[Mandatory]
input_file: (an existing file name)
        input file
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
count: (a list of items which are an integer (int or long))
        Specifies edge lengths of hyperslab to read.
        flag: -count %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
flip_any_direction: (a boolean)
        Do not flip images (Default).
        flag: -any_direction
        mutually_exclusive: flip_positive_direction,
         flip_negative_direction, flip_any_direction
flip_negative_direction: (a boolean)
        Flip images to always have negative direction.
        flag: -negative_direction
        mutually_exclusive: flip_positive_direction,
         flip_negative_direction, flip_any_direction
flip_positive_direction: (a boolean)
        Flip images to always have positive direction.
        flag: -positive_direction
        mutually_exclusive: flip_positive_direction,
         flip_negative_direction, flip_any_direction
flip_x_any: (a boolean)
        Don't flip images along x-axis (default).
        flag: -xanydirection
        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).
        flag: -xdirection
        mutually_exclusive: flip_x_positive, flip_x_negative, flip_x_any
```

```
    flip_x_positive: (a boolean)
            Flip images to give positive xspace:step value (left-to-right).
            flag: +xdirection
            mutually_exclusive: flip_x_positive, flip_x_negative, flip_x_any
    flip_y_any: (a boolean)
            Don't flip images along y-axis (default).
            flag: -yanydirection
            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).
            flag: -ydirection
            mutually_exclusive: flip_y_positive, flip_y_negative, flip_y_any
    flip_y_positive: (a boolean)
            Flip images to give positive yspace:step value (post-to-ant).
            flag: +ydirection
            mutually_exclusive: flip_y_positive, flip_y_negative, flip_y_any
    flip_z_any: (a boolean)
            Don't flip images along z-axis (default).
            flag: -zanydirection
            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).
            flag: -zdirection
            mutually_exclusive: flip_z_positive, flip_z_negative, flip_z_any
    flip_z_positive: (a boolean)
            Flip images to give positive zspace:step value (inf-to-sup).
            flag: +zdirection
            mutually_exclusive: flip_z_positive, flip_z_negative, flip_z_any
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    image_maximum: (a float)
            Specify the maximum real image value for normalization.Default
            value: 1.79769e+308.
            flag: -image_maximum %s
    image_minimum: (a float)
            Specify the minimum real image value for normalization.Default
            value: 1.79769e+308.
            flag: -image_minimum %s
    image_range: (a tuple of the form: (a float, a float))
            Specify the range of real image values for normalization.
            flag: -image_range %s %s
    nonormalize: (a boolean)
            Turn off pixel normalization.
            flag: -nonormalize
            mutually_exclusive: normalize, nonormalize
    normalize: (a boolean)
            Normalize integer pixel values to file max and min.
            flag: -normalize
            mutually_exclusive: normalize, nonormalize
    out_file: (a file name)
            flag: > %s, position: -1
    output_file: (a file name)
            output file
    start: (a list of items which are an integer (int or long))
            Specifies corner of hyperslab (C conventions for indices).
            flag: -start %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
```

```
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
    write_ascii: (a boolean)
        Write out data as ascii strings (default).
        flag: -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.
        flag: -byte
        mutually_exclusive: write_ascii, write_ascii, write_byte,
         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.
        flag: -double
        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.
        flag: -float
        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.
        flag: -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.
        flag: -long
        mutually_exclusive: write_ascii, write_ascii, write_byte,
         write_short, write_int, write_long, write_float, write_double,
         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.
        flag: -range %s %s
    write_short: (a boolean)
        Write out data as short integers.
        flag: -short
        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.
        flag: -signed
        mutually_exclusive: write_signed, write_unsigned
    write_unsigned: (a boolean)
        Write out unsigned data.
        flag: -unsigned
        mutually_exclusive: write_signed, write_unsigned
```

Outputs:

```
    output_file: (an existing file name)
            output file in raw/text format
```

89.13 Gennlxfm

Link to code
Wraps 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

89.13.1 Examples

```
>>> from nipype.interfaces.minc import Gennlxfm
>>> from nipype.interfaces.minc.testdata import minc2Dfile
>>> gennlxfm = Gennlxfm(step=1, like=minc2Dfile)
>>> gennlxfm.run()
```

Inputs:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    clobber: (a boolean, nipype default value: True)
            Overwrite existing file.
            flag: -clobber
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ident: (a boolean)
            Generate an identity xfm. Default: False.
            flag: -ident
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    like: (an existing file name)
            Generate a nlxfm like this file.
            flag: -like %s
    output_file: (a file name)
            output file
            flag: %s, position: -1
    step: (an integer (int or long))
            Output ident xfm step [default: 1].
            flag: -step %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    verbose: (a boolean)
            Print out log messages. Default: False.
            flag: -verbose
```

Outputs:

```
output_file: (an existing file name)
        output file
output_grid: (an existing file name)
        output grid
```

89.14 Math

Link to code
Wraps command **mincmath**
Various mathematical operations supplied by mincmath.

89.14.1 Examples

```
>>> from nipype.interfaces.minc import Math
>>> from nipype.interfaces.minc.testdata import minc2Dfile
```

Scale: volume*3.0 + 2:

```
>>> scale = Math(input_files=[minc2Dfile], scale=(3.0, 2))
>>> scale.run()
```

Test if >= 1.5:

```
>>> gt = Math(input_files=[minc2Dfile], test_gt=1.5)
>>> gt.run()
```

Inputs:

```
[Mandatory]
filelist: (a file name)
        Specify the name of a file containing input file names.
        flag: -filelist %s
        mutually_exclusive: input_files, filelist
input_files: (a list of items which are a file name)
        input file(s) for calculation
        flag: %s, position: -2
        mutually_exclusive: input_files, filelist

[Optional]
abs: (a boolean)
        Take absolute value of a volume.
        flag: -abs
args: (a string)
        Additional parameters to the command
        flag: %s
calc_add: (a boolean or a float)
        Add N volumes or volume + constant.
        flag: -add
calc_and: (a boolean)
        Calculate vol1 && vol2 (&& ...).
        flag: -and
calc_div: (a boolean or a float)
        Divide 2 volumes or volume / constant.
        flag: -div
calc_mul: (a boolean or a float)
        Multiply N volumes or volume * constant.
        flag: -mult
calc_not: (a boolean)
```

```
        Calculate !vol1.
        flag: -not
calc_or: (a boolean)
        Calculate vol1 || vol2 (|| ...).
        flag: -or
calc_sub: (a boolean or a float)
        Subtract 2 volumes or volume - constant.
        flag: -sub
check_dimensions: (a boolean)
        Check that dimension info matches across files (default).
        flag: -check_dimensions
        mutually_exclusive: check_dimensions, no_check_dimensions
clamp: (a tuple of the form: (a float, a float))
        Clamp a volume to lie between two values.
        flag: -clamp -const2 %s %s
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: -clobber
copy_header: (a boolean)
        Copy all of the header from the first file (default for one file).
        flag: -copy_header
        mutually_exclusive: copy_header, no_copy_header
count_valid: (a boolean)
        Count the number of valid values in N volumes.
        flag: -count_valid
dimension: (a string)
        Specify a dimension along which we wish to perform a calculation.
        flag: -dimension %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
exp: (a tuple of the form: (a float, a float))
        Calculate c2*exp(c1*x). Both constants must be specified.
        flag: -exp -const2 %s %s
format_byte: (a boolean)
        Write out byte data.
        flag: -byte
        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.
        flag: -double
        mutually_exclusive: format_filetype, format_byte, format_short,
         format_int, format_long, format_float, format_double,
         format_signed, format_unsigned
format_filetype: (a boolean)
        Use data type of first file (default).
        flag: -filetype
        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.
        flag: -float
        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.
            flag: -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.
            flag: -long
            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.
            flag: -short
            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.
            flag: -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).
            flag: -unsigned
            mutually_exclusive: format_filetype, format_byte, format_short,
             format_int, format_long, format_float, format_double,
             format_signed, format_unsigned
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    ignore_nan: (a boolean)
            Ignore invalid data (NaN) for accumulations.
            flag: -ignore_nan
    invert: (a float)
            Calculate 1/c.
            flag: -invert -const %s
    isnan: (a boolean)
            Test for NaN values in vol1.
            flag: -isnan
    log: (a tuple of the form: (a float, a float))
            Calculate log(x/c2)/c1. The constants c1 and c2 default to 1.
            flag: -log -const2 %s %s
    max_buffer_size_in_kb: (an integer >= 0)
            Specify the maximum size of the internal buffers (in kbytes).
            flag: -max_buffer_size_in_kb %d
    maximum: (a boolean)
            Find maximum of N volumes.
            flag: -maximum
    minimum: (a boolean)
            Find minimum of N volumes.
            flag: -minimum
    nisnan: (a boolean)
            Negation of -isnan.
            flag: -nisnan
```

```
    no_check_dimensions: (a boolean)
            Do not check dimension info.
            flag: -nocheck_dimensions
            mutually_exclusive: check_dimensions, no_check_dimensions
    no_copy_header: (a boolean)
            Do not copy all of the header from the first file (default for many
            files)).
            flag: -nocopy_header
            mutually_exclusive: copy_header, no_copy_header
    nsegment: (a tuple of the form: (a float, a float))
            Opposite of -segment: within range = 0, outside range = 1.
            flag: -nsegment -const2 %s %s
    output_file: (a file name)
            output file
            flag: %s, position: -1
    output_illegal: (a boolean)
            Value to write out when an illegal operationis done. Default value:
            1.79769e+308
            flag: -illegal_value
            mutually_exclusive: output_nan, output_zero, output_illegal_value
    output_nan: (a boolean)
            Output NaN when an illegal operation is done (default).
            flag: -nan
            mutually_exclusive: output_nan, output_zero, output_illegal_value
    output_zero: (a boolean)
            Output zero when an illegal operation is done.
            flag: -zero
            mutually_exclusive: output_nan, output_zero, output_illegal_value
    percentdiff: (a float)
            Percent difference between 2 volumes, thresholded (const def=0.0).
            flag: -percentdiff
    propagate_nan: (a boolean)
            Invalid data in any file at a voxel produces a NaN (default).
            flag: -propagate_nan
    scale: (a tuple of the form: (a float, a float))
            Scale a volume: volume * c1 + c2.
            flag: -scale -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.
            flag: -segment -const2 %s %s
    sqrt: (a boolean)
            Take square root of a volume.
            flag: -sqrt
    square: (a boolean)
            Take square of a volume.
            flag: -square
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    test_eq: (a boolean or a float)
            Test for integer vol1 == vol2 or vol1 == constant.
            flag: -eq
    test_ge: (a boolean or a float)
            Test for vol1 >= vol2 or vol1 >= const.
            flag: -ge
    test_gt: (a boolean or a float)
```

```
        Test for vol1 > vol2 or vol1 > constant.
        flag: -gt
test_le: (a boolean or a float)
        Test for vol1 <= vol2 or vol1 <= const.
        flag: -le
test_lt: (a boolean or a float)
        Test for vol1 < vol2 or vol1 < constant.
        flag: -lt
test_ne: (a boolean or a float)
        Test for integer vol1 != vol2 or vol1 != const.
        flag: -ne
two: (a boolean)
        Create a MINC 2 output file.
        flag: -2
voxel_range: (a tuple of the form: (an integer (int or long), an
         integer (int or long)))
        Valid range for output data.
        flag: -range %d %d
```

Outputs:

```
output_file: (an existing file name)
        output file
```

89.15 NlpFit

Link to code

Wraps command **nlpfit**

Hierarchial non-linear fitting with bluring.

This tool is part of the minc-widgets package:

https://github.com/BIC-MNI/minc-widgets/blob/master/nlpfit/nlpfit

89.15.1 Examples

```
>>> from nipype.interfaces.minc import NlpFit
>>> from nipype.interfaces.minc.testdata import nonempty_minc_data, nlp_config
>>> from nipype.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
>>> nlpfit.run()
```

Inputs:

```
[Mandatory]
config_file: (an existing file name)
        File containing the fitting configuration use.
        flag: -config_file %s
init_xfm: (an existing file name)
        Initial transformation (default identity).
        flag: -init_xfm %s
source: (an existing file name)
        source Minc file
```

```
        flag: %s, position: -3
source_mask: (an existing file name)
        Source mask to use during fitting.
        flag: -source_mask %s
target: (an existing file name)
        target Minc file
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: -clobber
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
input_grid_files: (a list of items which are a file name)
        input grid file(s)
output_xfm: (a file name)
        output xfm file
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        Print out log messages. Default: False.
        flag: -verbose
```

Outputs:

```
output_grid: (an existing file name)
        output grid file
output_xfm: (an existing file name)
        output xfm file
```

89.16 Norm

Link to code

Wraps command **mincnorm**

Normalise a file between a max and minimum (possibly) using two histogram pct's.

89.16.1 Examples

```
>>> from nipype.interfaces.minc import Norm
>>> from nipype.interfaces.minc.testdata import minc2Dfile
>>> n = Norm(input_file=minc2Dfile, output_file='/tmp/out.mnc') # Normalise the file.
>>> n.run()
```

Inputs:

```
    [Mandatory]
    input_file: (an existing file name)
            input file to normalise
            flag: %s, position: -2

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    clamp: (a boolean, nipype default value: True)
            Force the ouput range between limits [default].
            flag: -clamp
    clobber: (a boolean, nipype default value: True)
            Overwrite existing file.
            flag: -clobber
    cutoff: (0.0 <= a floating point number <= 100.0)
            Cutoff value to use to calculate thresholds by a histogram PcT in %.
            [default: 0.01]
            flag: -cutoff %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    lower: (a float)
            Lower real value to use.
            flag: -lower %s
    mask: (a file name)
            Calculate the image normalisation within a mask.
            flag: -mask %s
    out_ceil: (a float)
            Output files minimum [default: 100]
            flag: -out_ceil %s
    out_floor: (a float)
            Output files maximum [default: 0]
            flag: -out_floor %s
    output_file: (a file name)
            output file
            flag: %s, position: -1
    output_threshold_mask: (a file name)
            File in which to store the threshold mask.
            flag: -threshold_mask %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    threshold: (a boolean)
            Threshold the image (set values below threshold_perc to -out_floor).
            flag: -threshold
    threshold_blur: (a float)
            Blur FWHM for intensity edges then thresholding [default: 2].
            flag: -threshold_blur %s
    threshold_bmt: (a boolean)
            Use the resulting image BiModalT as the threshold.
            flag: -threshold_bmt
    threshold_perc: (0.0 <= a floating point number <= 100.0)
```

```
        Threshold percentage (0.1 == lower 10% of intensity range) [default:
        0.1].
        flag: -threshold_perc %s
upper: (a float)
        Upper real value to use.
        flag: -upper %s
```

Outputs:

```
output_file: (an existing file name)
        output file
output_threshold_mask: (a file name)
        threshold mask file
```

89.17 Pik

Link to code
Wraps command **mincpik**
Generate images from minc files.
Mincpik uses Imagemagick to generate images from Minc files.

89.17.1 Examples

```
>>> from nipype.interfaces.minc import Pik
>>> from nipype.interfaces.minc.testdata import nonempty_minc_data
```

```
>>> file0 = nonempty_minc_data(0)
>>> pik = Pik(input_file=file0, title='foo')
>>> pik .run()
```

Inputs:

```
[Mandatory]
input_file: (an existing file name)
        input file
        flag: %s, position: -2

[Optional]
annotated_bar: (a boolean)
        create an annotated bar to match the image (use height of the output
        image)
        flag: --anot_bar
args: (a string)
        Additional parameters to the command
        flag: %s
auto_range: (a boolean)
        Automatically determine image range using a 5 and 95% PcT.
        (histogram)
        flag: --auto_range
        mutually_exclusive: image_range, auto_range
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: -clobber
depth: (8 or 16)
        Bitdepth for resulting image 8 or 16 (MSB machines only!)
        flag: --depth %s
environ: (a dictionary with keys which are a value of type 'str' and
```

```
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
horizontal_triplanar_view: (a boolean)
        Create a horizontal triplanar view.
        flag: --horizontal
        mutually_exclusive: vertical_triplanar_view,
         horizontal_triplanar_view
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
image_range: (a tuple of the form: (a float, a float))
        Range of image values to use for pixel intensity.
        flag: --image_range %s %s
        mutually_exclusive: image_range, auto_range
jpg: (a boolean)
        Output a jpg file.
        mutually_exclusive: jpg, png
lookup: (a string)
        Arguments to pass to minclookup
        flag: --lookup %s
minc_range: (a tuple of the form: (a float, a float))
        Valid range of values for MINC file.
        flag: --range %s %s
output_file: (a file name)
        output file
        flag: %s, position: -1
png: (a boolean)
        Output a png file (default).
        mutually_exclusive: jpg, png
sagittal_offset: (an integer (int or long))
        Offset the sagittal slice from the centre.
        flag: --sagittal_offset %s
sagittal_offset_perc: (0 <= an integer <= 100)
        Offset the sagittal slice by a percentage from the centre.
        flag: --sagittal_offset_perc %d
scale: (an integer (int or long))
        Scaling factor for resulting image. By default images areoutput at
        twice their original resolution.
        flag: --scale %s
slice_x: (a boolean)
        Get a sagittal (x) slice.
        flag: -x
        mutually_exclusive: slice_z, slice_y, slice_x
slice_y: (a boolean)
        Get a coronal (y) slice.
        flag: -y
        mutually_exclusive: slice_z, slice_y, slice_x
slice_z: (a boolean)
        Get an axial/transverse (z) slice.
        flag: -z
        mutually_exclusive: slice_z, slice_y, slice_x
start: (an integer (int or long))
        Slice number to get. (note this is in voxel co-ordinates).
        flag: --slice %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
```

```
        output, `file` - writes output to file, `none` - output is ignored
tile_size: (an integer (int or long))
        Pixel size for each image in a triplanar.
        flag: --tilesize %s
title: (a boolean or a string)
        flag: %s
title_size: (an integer (int or long))
        Font point size for the title.
        flag: --title_size %s
        requires: title
triplanar: (a boolean)
        Create a triplanar view of the input file.
        flag: --triplanar
vertical_triplanar_view: (a boolean)
        Create a vertical triplanar view (Default).
        flag: --vertical
        mutually_exclusive: vertical_triplanar_view,
         horizontal_triplanar_view
width: (an integer (int or long))
        Autoscale the resulting image to have a fixed image width (in
        pixels).
        flag: --width %s
```

Outputs:

```
output_file: (an existing file name)
        output image
```

89.18 Resample

Link to code

Wraps command **mincresample**

Resample a minc file.'

89.18.1 Examples

```
>>> from nipype.interfaces.minc import Resample
>>> from nipype.interfaces.minc.testdata import minc2Dfile
>>> r = Resample(input_file=minc2Dfile, output_file='/tmp/out.mnc') # Resample the file.
>>> r.run()
```

Inputs:

```
[Mandatory]
input_file: (an existing file name)
        input file for resampling
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: -clobber
coronal_slices: (a boolean)
        Write out coronal slices
```

```
        flag: -coronal
        mutually_exclusive: transverse, sagittal, coronal
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.
        flag: -dircos %s %s %s
        mutually_exclusive: nelements, nelements_x_y_or_z
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fill: (a boolean)
        Use a fill value for points outside of input volume.
        flag: -fill
        mutually_exclusive: nofill, fill
fill_value: (a float)
        Specify a fill value for points outside of input volume.Default
        value: 1.79769e+308.
        flag: -fillvalue %s
        requires: fill
format_byte: (a boolean)
        Write out byte data.
        flag: -byte
        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.
        flag: -double
        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.
        flag: -float
        mutually_exclusive: 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.
        flag: -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.
        flag: -long
        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.
        flag: -short
        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.
        flag: -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).
        flag: -unsigned
        mutually_exclusive: format_byte, format_short, format_int,
         format_long, format_float, format_double, format_signed,
         format_unsigned
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.
        flag: -width %s
        requires: sinc_interpolation
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
input_grid_files: (a list of items which are a file name)
        input grid file(s)
invert_transformation: (a boolean)
        Invert the transformation before using it.
        flag: -invert_transformation
keep_real_range: (a boolean)
        Keep the real scale of the input volume.
        flag: -keep_real_range
        mutually_exclusive: keep_real_range, nokeep_real_range
like: (a file name)
        Specifies a model file for the resampling.
        flag: -like %s
nearest_neighbour_interpolation: (a boolean)
        Do nearest neighbour interpolation.
        flag: -nearest_neighbour
        mutually_exclusive: trilinear_interpolation, tricubic_interpolation,
         nearest_neighbour_interpolation, sinc_interpolation
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).
        flag: -nelements %s %s %s
        mutually_exclusive: nelements, nelements_x_y_or_z
no_fill: (a boolean)
        Use value zero for points outside of input volume.
        flag: -nofill
        mutually_exclusive: nofill, fill
no_input_sampling: (a boolean)
        Use the input sampling without transforming (old behaviour).
        flag: -use_input_sampling
        mutually_exclusive: vio_transform, no_input_sampling
nokeep_real_range: (a boolean)
        Do not keep the real scale of the data (default).
        flag: -nokeep_real_range
        mutually_exclusive: keep_real_range, nokeep_real_range
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.
        flag: -origin %s %s %s
output_file: (a file name)
```

```
        output file
        flag: %s, position: -1
output_range: (a tuple of the form: (a float, a float))
        Valid range for output data. Default value: -1.79769e+308
        -1.79769e+308.
        flag: -range %s %s
sagittal_slices: (a boolean)
        Write out sagittal slices
        flag: -sagittal
        mutually_exclusive: transverse, sagittal, coronal
sinc_interpolation: (a boolean)
        Do windowed sinc interpolation.
        flag: -sinc
        mutually_exclusive: trilinear_interpolation, tricubic_interpolation,
         nearest_neighbour_interpolation, sinc_interpolation
sinc_window_hamming: (a boolean)
        Set sinc window type to Hamming.
        flag: -hamming
        mutually_exclusive: sinc_window_hanning, sinc_window_hamming
        requires: sinc_interpolation
sinc_window_hanning: (a boolean)
        Set sinc window type to Hanning.
        flag: -hanning
        mutually_exclusive: sinc_window_hanning, sinc_window_hamming
        requires: sinc_interpolation
spacetype: (a string)
        Set the spacetype attribute to a specified string.
        flag: -spacetype %s
standard_sampling: (a boolean)
        Set the sampling to standard values (step, start and dircos).
        flag: -standard_sampling
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.
        flag: -start %s %s %s
        mutually_exclusive: nelements, nelements_x_y_or_z
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).
        flag: -step %s %s %s
        mutually_exclusive: nelements, nelements_x_y_or_z
talairach: (a boolean)
        Output is in Talairach space.
        flag: -talairach
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transformation: (a file name)
        File giving world transformation. (Default = identity).
        flag: -transformation %s
transverse_slices: (a boolean)
        Write out transverse slices.
        flag: -transverse
        mutually_exclusive: transverse, sagittal, coronal
tricubic_interpolation: (a boolean)
        Do tricubic interpolation.
        flag: -tricubic
```

```
        mutually_exclusive: trilinear_interpolation, tricubic_interpolation,
         nearest_neighbour_interpolation, sinc_interpolation
trilinear_interpolation: (a boolean)
        Do trilinear interpolation.
        flag: -trilinear
        mutually_exclusive: trilinear_interpolation, tricubic_interpolation,
         nearest_neighbour_interpolation, sinc_interpolation
two: (a boolean)
        Create a MINC 2 output file.
        flag: -2
units: (a string)
        Specify the units of the output sampling.
        flag: -units %s
vio_transform: (a boolean)
        VIO_Transform the input sampling with the transform (default).
        flag: -tfm_input_sampling
        mutually_exclusive: vio_transform, no_input_sampling
xdircos: (a float)
        Direction cosines along the X dimension.Default value: 1.79769e+308
        1.79769e+308 1.79769e+308.
        flag: -xdircos %s
        mutually_exclusive: dircos, dircos_x_y_or_z
        requires: ydircos, zdircos
xnelements: (an integer (int or long))
        Number of elements along the X dimension.
        flag: -xnelements %s
        mutually_exclusive: nelements, nelements_x_y_or_z
        requires: ynelements, znelements
xstart: (a float)
        Start point along the X dimension. Default value: 1.79769e+308.
        flag: -xstart %s
        mutually_exclusive: start, start_x_y_or_z
        requires: ystart, zstart
xstep: (an integer (int or long))
        Step size along the X dimension. Default value: 0.
        flag: -xstep %s
        mutually_exclusive: step, step_x_y_or_z
        requires: ystep, zstep
ydircos: (a float)
        Direction cosines along the Y dimension.Default value: 1.79769e+308
        1.79769e+308 1.79769e+308.
        flag: -ydircos %s
        mutually_exclusive: dircos, dircos_x_y_or_z
        requires: xdircos, zdircos
ynelements: (an integer (int or long))
        Number of elements along the Y dimension.
        flag: -ynelements %s
        mutually_exclusive: nelements, nelements_x_y_or_z
        requires: xnelements, znelements
ystart: (a float)
        Start point along the Y dimension. Default value: 1.79769e+308.
        flag: -ystart %s
        mutually_exclusive: start, start_x_y_or_z
        requires: xstart, zstart
ystep: (an integer (int or long))
        Step size along the Y dimension. Default value: 0.
        flag: -ystep %s
        mutually_exclusive: step, step_x_y_or_z
```

```
        requires: xstep, zstep
zdircos: (a float)
        Direction cosines along the Z dimension.Default value: 1.79769e+308
        1.79769e+308 1.79769e+308.
        flag: -zdircos %s
        mutually_exclusive: dircos, dircos_x_y_or_z
        requires: xdircos, ydircos
znelements: (an integer (int or long))
        Number of elements along the Z dimension.
        flag: -znelements %s
        mutually_exclusive: nelements, nelements_x_y_or_z
        requires: xnelements, ynelements
zstart: (a float)
        Start point along the Z dimension. Default value: 1.79769e+308.
        flag: -zstart %s
        mutually_exclusive: start, start_x_y_or_z
        requires: xstart, ystart
zstep: (an integer (int or long))
        Step size along the Z dimension. Default value: 0.
        flag: -zstep %s
        mutually_exclusive: step, step_x_y_or_z
        requires: xstep, ystep
```

Outputs:

```
output_file: (an existing file name)
        output file
```

89.19 Reshape

Link to code

Wraps 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).

89.19.1 Examples

```
>>> from nipype.interfaces.minc import Reshape
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
input_file: (a file name)
        input file
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
```

```
        flag: -clobber
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_file: (a file name)
        output file
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        Print out log messages. Default: False.
        flag: -verbose
write_short: (a boolean)
        Convert to short integer data.
        flag: -short
```

Outputs:

```
output_file: (an existing file name)
        output file
```

89.20 ToEcat

Link to code

Wraps 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.

89.20.1 Examples

```
>>> from nipype.interfaces.minc import ToEcat
>>> from nipype.interfaces.minc.testdata import minc2Dfile
```

```
>>> c = ToEcat(input_file=minc2Dfile)
>>> c.run()
```

```
>>> c = ToEcat(input_file=minc2Dfile, voxels_as_integers=True)
>>> c.run()
```

Inputs:

```
[Mandatory]
input_file: (an existing file name)
        input file to convert
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
```

```
          with values which are a value of type 'str', nipype default value:
          {})
        Environment variables
ignore_acquisition_variable: (a boolean)
        Ignore informations from the minc acquisition variable.
        flag: -ignore_acquisition_variable
ignore_ecat_acquisition_variable: (a boolean)
        Ignore informations from the minc ecat_acquisition variable.
        flag: -ignore_ecat_acquisition_variable
ignore_ecat_main: (a boolean)
        Ignore informations from the minc ecat-main variable.
        flag: -ignore_ecat_main
ignore_ecat_subheader_variable: (a boolean)
        Ignore informations from the minc ecat-subhdr variable.
        flag: -ignore_ecat_subheader_variable
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
ignore_patient_variable: (a boolean)
        Ignore informations from the minc patient variable.
        flag: -ignore_patient_variable
ignore_study_variable: (a boolean)
        Ignore informations from the minc study variable.
        flag: -ignore_study_variable
no_decay_corr_fctr: (a boolean)
        Do not compute the decay correction factors
        flag: -no_decay_corr_fctr
output_file: (a file name)
        output file
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
voxels_as_integers: (a boolean)
        Voxel values are treated as integers, scale andcalibration factors
        are set to unity
        flag: -label
```

Outputs:

```
output_file: (an existing file name)
        output file
```

89.21 ToRaw

Link to code

Wraps command **minctoraw**

Dump a chunk of MINC file data. This program is largely superceded by mincextract (see Extract).

89.21.1 Examples

```
>>> from nipype.interfaces.minc import ToRaw
>>> from nipype.interfaces.minc.testdata import minc2Dfile
```

```
>>> toraw = ToRaw(input_file=minc2Dfile)
>>> toraw.run()
```

```
>>> toraw = ToRaw(input_file=minc2Dfile, write_range=(0, 100))
>>> toraw.run()
```

Inputs:

```
[Mandatory]
input_file: (an existing file name)
        input file
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
nonormalize: (a boolean)
        Turn off pixel normalization.
        flag: -nonormalize
        mutually_exclusive: normalize, nonormalize
normalize: (a boolean)
        Normalize integer pixel values to file max and min.
        flag: -normalize
        mutually_exclusive: normalize, nonormalize
out_file: (a file name)
        flag: > %s, position: -1
output_file: (a file name)
        output file
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
write_byte: (a boolean)
        Write out data as bytes.
        flag: -byte
        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.
        flag: -double
        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.
        flag: -float
        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.
        flag: -int
        mutually_exclusive: write_byte, write_short, write_int, write_long,
```

```
          write_float, write_double
write_long: (a boolean)
        Superseded by write_int.
        flag: -long
        mutually_exclusive: write_byte, write_short, write_int, write_long,
         write_float, write_double
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.
        flag: -range %s %s
write_short: (a boolean)
        Write out data as short integers.
        flag: -short
        mutually_exclusive: write_byte, write_short, write_int, write_long,
         write_float, write_double
write_signed: (a boolean)
        Write out signed data.
        flag: -signed
        mutually_exclusive: write_signed, write_unsigned
write_unsigned: (a boolean)
        Write out unsigned data.
        flag: -unsigned
        mutually_exclusive: write_signed, write_unsigned
```

Outputs:

```
output_file: (an existing file name)
        output file in raw format
```

89.22 VolSymm

Link to code

Wraps 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

89.22.1 Examples

```
>>> from nipype.interfaces.minc import VolSymm
>>> from nipype.interfaces.minc.testdata import nonempty_minc_data
```

```
>>> input_file = nonempty_minc_data(0)
>>> volsymm = VolSymm(input_file=input_file)
>>> volsymm.run()
```

Inputs:

```
[Mandatory]
input_file: (a file name)
        input file
        flag: %s, position: -3

[Optional]
args: (a string)
        Additional parameters to the command
```

```
        flag: %s
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: -clobber
config_file: (an existing file name)
        File containing the fitting configuration (nlpfit -help for info).
        flag: -config_file %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fit_linear: (a boolean)
        Fit using a linear xfm.
        flag: -linear
fit_nonlinear: (a boolean)
        Fit using a non-linear xfm.
        flag: -nonlinear
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
input_grid_files: (a list of items which are a file name)
        input grid file(s)
nofit: (a boolean)
        Use the input transformation instead of generating one.
        flag: -nofit
output_file: (a file name)
        output file
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
trans_file: (a file name)
        output xfm trans file
        flag: %s, position: -2
verbose: (a boolean)
        Print out log messages. Default: False.
        flag: -verbose
x: (a boolean)
        Flip volume in x-plane (default).
        flag: -x
y: (a boolean)
        Flip volume in y-plane.
        flag: -y
z: (a boolean)
        Flip volume in z-plane.
        flag: -z
```

Outputs:

```
output_file: (an existing file name)
        output file
output_grid: (an existing file name)
        output grid file
trans_file: (an existing file name)
        xfm trans file
```

89.23 Volcentre

Link to code
Wraps command **volcentre**
Centre a MINC image's sampling about a point, typically (0,0,0).

89.23.1 Example

```
>>> from nipype.interfaces.minc import Volcentre
>>> from nipype.interfaces.minc.testdata import minc2Dfile
>>> vc = Volcentre(input_file=minc2Dfile)
>>> vc.run()
```

Inputs:

```
[Mandatory]
input_file: (an existing file name)
        input file to centre
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
centre: (a tuple of the form: (a float, a float, a float))
        Centre to use (x,y,z) [default: 0 0 0].
        flag: -centre %s %s %s
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: -clobber
com: (a boolean)
        Use the CoM of the volume for the new centre (via mincstats).
        Default: False
        flag: -com
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_file: (a file name)
        output file
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        Print out log messages. Default: False.
        flag: -verbose
zero_dircos: (a boolean)
        Set the direction cosines to identity [default].
        flag: -zero_dircos
```

Outputs:

```
output_file: (an existing file name)
        output file
```

89.24 Voliso

Link to code
Wraps command **voliso**
Changes the steps and starts in order that the output volume has isotropic sampling.

89.24.1 Examples

```
>>> from nipype.interfaces.minc import Voliso
>>> from nipype.interfaces.minc.testdata import minc2Dfile
>>> viso = Voliso(input_file=minc2Dfile, minstep=0.1, avgstep=True)
>>> viso.run()
```

Inputs:

```
[Mandatory]
input_file: (an existing file name)
        input file to convert to isotropic sampling
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
avgstep: (a boolean)
        Calculate the maximum step from the average steps of the input
        volume.
        flag: --avgstep
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: --clobber
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
maxstep: (a float)
        The target maximum step desired in the output volume.
        flag: --maxstep %s
minstep: (a float)
        The target minimum step desired in the output volume.
        flag: --minstep %s
output_file: (a file name)
        output file
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        Print out log messages. Default: False.
        flag: --verbose
```

Outputs:

```
output_file: (an existing file name)
        output file
```

89.25 Volpad

Link to code
Wraps command **volpad**
Centre a MINC image's sampling about a point, typically (0,0,0).

89.25.1 Examples

```
>>> from nipype.interfaces.minc import Volpad
>>> from nipype.interfaces.minc.testdata import minc2Dfile
>>> vp = Volpad(input_file=minc2Dfile, smooth=True, smooth_distance=4)
>>> vp.run()
```

Inputs:

```
[Mandatory]
input_file: (an existing file name)
        input file to centre
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
auto: (a boolean)
        Automatically determine padding distances (uses -distance as max).
        Default: False.
        flag: -auto
auto_freq: (a float)
        Frequency of voxels over bimodalt threshold to stop at [default:
        500].
        flag: -auto_freq %s
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: -clobber
distance: (an integer (int or long))
        Padding distance (in voxels) [default: 4].
        flag: -distance %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_file: (a file name)
        output file
        flag: %s, position: -1
smooth: (a boolean)
        Smooth (blur) edges before padding. Default: False.
        flag: -smooth
smooth_distance: (an integer (int or long))
        Smoothing distance (in voxels) [default: 4].
        flag: -smooth_distance %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

```
verbose: (a boolean)
        Print out log messages. Default: False.
        flag: -verbose
```

Outputs:

```
output_file: (an existing file name)
        output file
```

89.26 XfmAvg

Link to code

Wraps 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

89.26.1 Examples

```
>>> from nipype.interfaces.minc import XfmAvg
>>> from nipype.interfaces.minc.testdata import nonempty_minc_data, nlp_config
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
input_files: (a list of items which are a file name)
        input file(s)
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
avg_linear: (a boolean)
        average the linear part [default].
        flag: -avg_linear
avg_nonlinear: (a boolean)
        average the non-linear part [default].
        flag: -avg_nonlinear
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: -clobber
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
ignore_linear: (a boolean)
```

```
        opposite of -avg_linear.
        flag: -ignore_linear
ignore_nonlinear: (a boolean)
        opposite of -avg_nonlinear.
        flag: -ignore_nonline
input_grid_files: (a list of items which are a file name)
        input grid file(s)
output_file: (a file name)
        output file
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        Print out log messages. Default: False.
        flag: -verbose
```

Outputs:

```
output_file: (an existing file name)
        output file
output_grid: (an existing file name)
        output grid file
```

89.27 XfmConcat

Link to code

Wraps command **xfmconcat**

Concatenate transforms together. The output transformation is equivalent to applying input1.xfm, then input2.xfm, ..., in that order.

89.27.1 Examples

```
>>> from nipype.interfaces.minc import XfmConcat
>>> from nipype.interfaces.minc.testdata import minc2Dfile
>>> conc = XfmConcat(input_files=['input1.xfm', 'input1.xfm'])
>>> conc.run()
```

Inputs:

```
[Mandatory]
input_files: (a list of items which are a file name)
        input file(s)
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
clobber: (a boolean, nipype default value: True)
        Overwrite existing file.
        flag: -clobber
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
```

```
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    input_grid_files: (a list of items which are a file name)
            input grid file(s)
    output_file: (a file name)
            output file
            flag: %s, position: -1
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    verbose: (a boolean)
            Print out log messages. Default: False.
            flag: -verbose
```

Outputs:

```
    output_file: (an existing file name)
            output file
    output_grids: (a list of items which are an existing file name)
            output grids
```

89.28 XfmInvert

Link to code

Wraps command **xfminvert**

Invert an xfm transform file.

89.28.1 Examples

```
>>> from nipype.interfaces.minc import XfmAvg
>>> from nipype.testing import example_data
```

```
>>> xfm = example_data('minc_initial.xfm')
>>> invert = XfmInvert(input_file=xfm)
>>> invert.run()
```

Inputs:

```
    [Mandatory]
    input_file: (a file name)
            input file
            flag: %s, position: -2

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    clobber: (a boolean, nipype default value: True)
            Overwrite existing file.
            flag: -clobber
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
output_file: (a file name)
        output file
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        Print out log messages. Default: False.
        flag: -verbose
```

Outputs:

```
output_file: (an existing file name)
        output file
output_grid: (an existing file name)
        output grid file
```

CHAPTER 90

interfaces.minc.testdata

90.1 nonempty_minc_data()

Link to code

interfaces.mipav.developer

91.1 JistBrainMgdmSegmentation

Link to code
Wraps command **java edu.jhu.ece.iacl.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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inAdjust: ('true' or 'false')
        Adjust intensity priors
        flag: --inAdjust %s
inAtlas: (an existing file name)
        Atlas file
        flag: --inAtlas %s
inCompute: ('true' or 'false')
        Compute posteriors
        flag: --inCompute %s
inCurvature: (a float)
        Curvature weight
        flag: --inCurvature %f
inData: (a float)
        Data weight
        flag: --inData %f
inFLAIR: (an existing file name)
        FLAIR Image
        flag: --inFLAIR %s
inMP2RAGE: (an existing file name)
        MP2RAGE T1 Map Image
        flag: --inMP2RAGE %s
```

```
    inMP2RAGE2: (an existing file name)
            MP2RAGE T1-weighted Image
            flag: --inMP2RAGE2 %s
    inMPRAGE: (an existing file name)
            MPRAGE T1-weighted Image
            flag: --inMPRAGE %s
    inMax: (an integer (int or long))
            Max iterations
            flag: --inMax %d
    inMin: (a float)
            Min change
            flag: --inMin %f
    inOutput: ('segmentation' or 'memberships')
            Output images
            flag: --inOutput %s
    inPV: (an existing file name)
            PV / Dura Image
            flag: --inPV %s
    inPosterior: (a float)
            Posterior scale (mm)
            flag: --inPosterior %f
    inSteps: (an integer (int or long))
            Steps
            flag: --inSteps %d
    inTopology: ('26/6' or '6/26' or '18/6' or '6/18' or '6/6' or 'wcs'
             or 'wco' or 'no')
            Topology
            flag: --inTopology %s
    null: (a string)
            Execution Time
            flag: --null %s
    outLevelset: (a boolean or a file name)
            Levelset Boundary Image
            flag: --outLevelset %s
    outPosterior2: (a boolean or a file name)
            Posterior Maximum Memberships (4D)
            flag: --outPosterior2 %s
    outPosterior3: (a boolean or a file name)
            Posterior Maximum Labels (4D)
            flag: --outPosterior3 %s
    outSegmented: (a boolean or a file name)
            Segmented Brain Image
            flag: --outSegmented %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    xDefaultMem: (an integer (int or long))
            Set default maximum heap size
            flag: -xDefaultMem %d
    xMaxProcess: (an integer (int or long), nipype default value: 1)
            Set default maximum number of processes.
            flag: -xMaxProcess %d
    xPrefExt: ('nrrd')
            Output File Type
            flag: --xPrefExt %s
```

Outputs:

```
    outLevelset: (an existing file name)
            Levelset Boundary Image
    outPosterior2: (an existing file name)
            Posterior Maximum Memberships (4D)
    outPosterior3: (an existing file name)
            Posterior Maximum Labels (4D)
    outSegmented: (an existing file name)
            Segmented Brain Image
```

91.2 JistBrainMp2rageDuraEstimation

Link to code
Wraps command **java edu.jhu.ece.iacl.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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inDistance: (a float)
            Distance to background (mm)
            flag: --inDistance %f
    inSecond: (an existing file name)
            Second inversion (Inv2) Image
            flag: --inSecond %s
    inSkull: (an existing file name)
            Skull Stripping Mask
            flag: --inSkull %s
    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.
            flag: --inoutput %s
    null: (a string)
            Execution Time
            flag: --null %s
    outDura: (a boolean or a file name)
            Dura Image
            flag: --outDura %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    xDefaultMem: (an integer (int or long))
```

```
        Set default maximum heap size
        flag: -xDefaultMem %d
xMaxProcess: (an integer (int or long), nipype default value: 1)
        Set default maximum number of processes.
        flag: -xMaxProcess %d
xPrefExt: ('nrrd')
        Output File Type
        flag: --xPrefExt %s
```

Outputs:

```
outDura: (an existing file name)
        Dura Image
```

91.3 JistBrainMp2rageSkullStripping

Link to code

Wraps command **java edu.jhu.ece.iacl.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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inFilter: (an existing file name)
        Filter Image (opt)
        flag: --inFilter %s
inSecond: (an existing file name)
        Second inversion (Inv2) Image
        flag: --inSecond %s
inSkip: ('true' or 'false')
        Skip zero values
        flag: --inSkip %s
inT1: (an existing file name)
        T1 Map (T1_Images) Image (opt)
        flag: --inT1 %s
inT1weighted: (an existing file name)
        T1-weighted (UNI) Image (opt)
        flag: --inT1weighted %s
null: (a string)
        Execution Time
        flag: --null %s
outBrain: (a boolean or a file name)
```

```
        Brain Mask Image
        flag: --outBrain %s
outMasked: (a boolean or a file name)
        Masked T1 Map Image
        flag: --outMasked %s
outMasked2: (a boolean or a file name)
        Masked T1-weighted Image
        flag: --outMasked2 %s
outMasked3: (a boolean or a file name)
        Masked Filter Image
        flag: --outMasked3 %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
xDefaultMem: (an integer (int or long))
        Set default maximum heap size
        flag: -xDefaultMem %d
xMaxProcess: (an integer (int or long), nipype default value: 1)
        Set default maximum number of processes.
        flag: -xMaxProcess %d
xPrefExt: ('nrrd')
        Output File Type
        flag: --xPrefExt %s
```

Outputs:

```
outBrain: (an existing file name)
        Brain Mask Image
outMasked: (an existing file name)
        Masked T1 Map Image
outMasked2: (an existing file name)
        Masked T1-weighted Image
outMasked3: (an existing file name)
        Masked Filter Image
```

91.4 JistBrainPartialVolumeFilter

Link to code

Wraps command **java edu.jhu.ece.iacl.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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
inInput: (an existing file name)
        Input Image
        flag: --inInput %s
inPV: ('bright' or 'dark' or 'both')
        Outputs the raw intensity values or a probability score for the
        partial volume regions.
        flag: --inPV %s
inoutput: ('probability' or 'intensity')
        output
        flag: --inoutput %s
null: (a string)
        Execution Time
        flag: --null %s
outPartial: (a boolean or a file name)
        Partial Volume Image
        flag: --outPartial %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
xDefaultMem: (an integer (int or long))
        Set default maximum heap size
        flag: -xDefaultMem %d
xMaxProcess: (an integer (int or long), nipype default value: 1)
        Set default maximum number of processes.
        flag: -xMaxProcess %d
xPrefExt: ('nrrd')
        Output File Type
        flag: --xPrefExt %s
```

Outputs:

```
outPartial: (an existing file name)
        Partial Volume Image
```

91.5 JistCortexSurfaceMeshInflation

Link to code

Wraps command **java edu.jhu.ece.iacl.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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
```

```
          with values which are a value of type 'str', nipype default value:
          {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inLevelset: (an existing file name)
        Levelset Image
        flag: --inLevelset %s
inLorentzian: ('true' or 'false')
        Lorentzian Norm
        flag: --inLorentzian %s
inMax: (an integer (int or long))
        Max Iterations
        flag: --inMax %d
inMean: (a float)
        Mean Curvature Threshold
        flag: --inMean %f
inSOR: (a float)
        SOR Parameter
        flag: --inSOR %f
inStep: (an integer (int or long))
        Step Size
        flag: --inStep %d
inTopology: ('26/6' or '6/26' or '18/6' or '6/18' or '6/6' or 'wcs'
         or 'wco' or 'no')
        Topology
        flag: --inTopology %s
null: (a string)
        Execution Time
        flag: --null %s
outInflated: (a boolean or a file name)
        Inflated Surface
        flag: --outInflated %s
outOriginal: (a boolean or a file name)
        Original Surface
        flag: --outOriginal %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
xDefaultMem: (an integer (int or long))
        Set default maximum heap size
        flag: -xDefaultMem %d
xMaxProcess: (an integer (int or long), nipype default value: 1)
        Set default maximum number of processes.
        flag: -xMaxProcess %d
xPrefExt: ('nrrd')
        Output File Type
        flag: --xPrefExt %s
```

Outputs:

```
outInflated: (an existing file name)
        Inflated Surface
outOriginal: (an existing file name)
        Original Surface
```

91.6 JistIntensityMp2rageMasking

Link to code
Wraps command **java edu.jhu.ece.iacl.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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inBackground: ('exponential' or 'half-normal')
            Model distribution for background noise (default is half-normal,
            exponential is more stringent).
            flag: --inBackground %s
    inMasking: ('binary' or 'proba')
            Whether to use a binary threshold or a weighted average based on the
            probability.
            flag: --inMasking %s
    inQuantitative: (an existing file name)
            Quantitative T1 Map (T1_Images) Image
            flag: --inQuantitative %s
    inSecond: (an existing file name)
            Second inversion (Inv2) Image
            flag: --inSecond %s
    inSkip: ('true' or 'false')
            Skip zero values
            flag: --inSkip %s
    inT1weighted: (an existing file name)
            T1-weighted (UNI) Image
            flag: --inT1weighted %s
    null: (a string)
            Execution Time
            flag: --null %s
    outMasked: (a boolean or a file name)
            Masked T1 Map Image
            flag: --outMasked %s
    outMasked2: (a boolean or a file name)
            Masked Iso Image
            flag: --outMasked2 %s
    outSignal: (a boolean or a file name)
            Signal Proba Image
            flag: --outSignal %s
    outSignal2: (a boolean or a file name)
            Signal Mask Image
            flag: --outSignal2 %s
```

```
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
xDefaultMem: (an integer (int or long))
        Set default maximum heap size
        flag: -xDefaultMem %d
xMaxProcess: (an integer (int or long), nipype default value: 1)
        Set default maximum number of processes.
        flag: -xMaxProcess %d
xPrefExt: ('nrrd')
        Output File Type
        flag: --xPrefExt %s
```

Outputs:

```
outMasked: (an existing file name)
        Masked T1 Map Image
outMasked2: (an existing file name)
        Masked Iso Image
outSignal: (an existing file name)
        Signal Proba Image
outSignal2: (an existing file name)
        Signal Mask Image
```

91.7 JistLaminarProfileCalculator

Link to code

Wraps command **java edu.jhu.ece.iacl.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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inIntensity: (an existing file name)
        Intensity Profile Image
        flag: --inIntensity %s
inMask: (an existing file name)
        Mask Image (opt, 3D or 4D)
        flag: --inMask %s
incomputed: ('mean' or 'stdev' or 'skewness' or 'kurtosis')
        computed statistic
        flag: --incomputed %s
```

```
    null: (a string)
            Execution Time
            flag: --null %s
    outResult: (a boolean or a file name)
            Result
            flag: --outResult %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    xDefaultMem: (an integer (int or long))
            Set default maximum heap size
            flag: -xDefaultMem %d
    xMaxProcess: (an integer (int or long), nipype default value: 1)
            Set default maximum number of processes.
            flag: -xMaxProcess %d
    xPrefExt: ('nrrd')
            Output File Type
            flag: --xPrefExt %s
```

Outputs:

```
    outResult: (an existing file name)
            Result
```

91.8 JistLaminarProfileGeometry

Link to code

Wraps command **java edu.jhu.ece.iacl.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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inProfile: (an existing file name)
            Profile Surface Image
            flag: --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
            flag: --incomputed %s
    inoutside: (a float)
            outside extension (mm)
```

```
        flag: --inoutside %f
inregularization: ('none' or 'Gaussian')
        regularization
        flag: --inregularization %s
insmoothing: (a float)
        smoothing parameter
        flag: --insmoothing %f
null: (a string)
        Execution Time
        flag: --null %s
outResult: (a boolean or a file name)
        Result
        flag: --outResult %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
xDefaultMem: (an integer (int or long))
        Set default maximum heap size
        flag: -xDefaultMem %d
xMaxProcess: (an integer (int or long), nipype default value: 1)
        Set default maximum number of processes.
        flag: -xMaxProcess %d
xPrefExt: ('nrrd')
        Output File Type
        flag: --xPrefExt %s
```

Outputs:

```
outResult: (an existing file name)
        Result
```

91.9 JistLaminarProfileSampling

Link to code

Wraps command **java edu.jhu.ece.iacl.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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inCortex: (an existing file name)
        Cortex Mask (opt)
        flag: --inCortex %s
```

```
    inIntensity: (an existing file name)
            Intensity Image
            flag: --inIntensity %s
    inProfile: (an existing file name)
            Profile Surface Image
            flag: --inProfile %s
    null: (a string)
            Execution Time
            flag: --null %s
    outProfile2: (a boolean or a file name)
            Profile 4D Mask
            flag: --outProfile2 %s
    outProfilemapped: (a boolean or a file name)
            Profile-mapped Intensity Image
            flag: --outProfilemapped %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    xDefaultMem: (an integer (int or long))
            Set default maximum heap size
            flag: -xDefaultMem %d
    xMaxProcess: (an integer (int or long), nipype default value: 1)
            Set default maximum number of processes.
            flag: -xMaxProcess %d
    xPrefExt: ('nrrd')
            Output File Type
            flag: --xPrefExt %s
```

Outputs:

```
    outProfile2: (an existing file name)
            Profile 4D Mask
    outProfilemapped: (an existing file name)
            Profile-mapped Intensity Image
```

91.10 JistLaminarROIAveraging

Link to code

Wraps command **java edu.jhu.ece.iacl.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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
inIntensity: (an existing file name)
        Intensity Profile Image
        flag: --inIntensity %s
inMask: (an existing file name)
        Mask Image (opt, 3D or 4D)
        flag: --inMask %s
inROI: (an existing file name)
        ROI Mask
        flag: --inROI %s
inROI2: (a string)
        ROI Name
        flag: --inROI2 %s
null: (a string)
        Execution Time
        flag: --null %s
outROI3: (a boolean or a file name)
        ROI Average
        flag: --outROI3 %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
xDefaultMem: (an integer (int or long))
        Set default maximum heap size
        flag: -xDefaultMem %d
xMaxProcess: (an integer (int or long), nipype default value: 1)
        Set default maximum number of processes.
        flag: -xMaxProcess %d
xPrefExt: ('nrrd')
        Output File Type
        flag: --xPrefExt %s
```

Outputs:

```
outROI3: (an existing file name)
        ROI Average
```

91.11 JistLaminarVolumetricLayering

Link to code

Wraps command **java edu.jhu.ece.iacl.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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
```

```
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inInner: (an existing file name)
        Inner Distance Image (GM/WM boundary)
        flag: --inInner %s
inLayering: ('distance-preserving' or 'volume-preserving')
        Layering method
        flag: --inLayering %s
inLayering2: ('outward' or 'inward')
        Layering direction
        flag: --inLayering2 %s
inMax: (an integer (int or long))
        Max iterations for narrow band evolution
        flag: --inMax %d
inMin: (a float)
        Min change ratio for narrow band evolution
        flag: --inMin %f
inNumber: (an integer (int or long))
        Number of layers
        flag: --inNumber %d
inOuter: (an existing file name)
        Outer Distance Image (CSF/GM boundary)
        flag: --inOuter %s
inTopology: ('26/6' or '6/26' or '18/6' or '6/18' or '6/6' or 'wcs'
         or 'wco' or 'no')
        Topology
        flag: --inTopology %s
incurvature: (an integer (int or long))
        curvature approximation scale (voxels)
        flag: --incurvature %d
inpresmooth: ('true' or 'false')
        pre-smooth cortical surfaces
        flag: --inpresmooth %s
inratio: (a float)
        ratio smoothing kernel size (voxels)
        flag: --inratio %f
null: (a string)
        Execution Time
        flag: --null %s
outContinuous: (a boolean or a file name)
        Continuous depth measurement
        flag: --outContinuous %s
outDiscrete: (a boolean or a file name)
        Discrete sampled layers
        flag: --outDiscrete %s
outLayer: (a boolean or a file name)
        Layer boundary surfaces
        flag: --outLayer %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

```
    xDefaultMem: (an integer (int or long))
            Set default maximum heap size
            flag: -xDefaultMem %d
    xMaxProcess: (an integer (int or long), nipype default value: 1)
            Set default maximum number of processes.
            flag: -xMaxProcess %d
    xPrefExt: ('nrrd')
            Output File Type
            flag: --xPrefExt %s
```

Outputs:

```
    outContinuous: (an existing file name)
            Continuous depth measurement
    outDiscrete: (an existing file name)
            Discrete sampled layers
    outLayer: (an existing file name)
            Layer boundary surfaces
```

91.12 MedicAlgorithmImageCalculator

Link to code
Wraps command **java edu.jhu.ece.iacl.jist.cli.run edu.jhu.ece.iacl.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.iacl.ece.jhu.edu/
Inputs:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inOperation: ('Add' or 'Subtract' or 'Multiply' or 'Divide' or 'Min'
             or 'Max')
            Operation
            flag: --inOperation %s
    inVolume: (an existing file name)
            Volume 1
            flag: --inVolume %s
    inVolume2: (an existing file name)
            Volume 2
            flag: --inVolume2 %s
    null: (a string)
            Execution Time
```

```
        flag: --null %s
outResult: (a boolean or a file name)
        Result Volume
        flag: --outResult %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
xDefaultMem: (an integer (int or long))
        Set default maximum heap size
        flag: -xDefaultMem %d
xMaxProcess: (an integer (int or long), nipype default value: 1)
        Set default maximum number of processes.
        flag: -xMaxProcess %d
xPrefExt: ('nrrd')
        Output File Type
        flag: --xPrefExt %s
```

Outputs:

```
outResult: (an existing file name)
        Result Volume
```

91.13 MedicAlgorithmLesionToads

Link to code

Wraps command **java edu.jhu.ece.iacl.jist.cli.run edu.jhu.ece.iacl.plugins.classification.MedicAlgorithmLesionToads **

title: Lesion TOADS
category: Developer Tools
description: Algorithm for simulataneous 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://iacl.ece.jhu.edu/~nshiee/
Inputs:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inAtlas: ('With Lesion' or 'No Lesion')
        Atlas to Use
        flag: --inAtlas %s
inAtlas2: (an existing file name)
        Atlas File - With Lesions
        flag: --inAtlas2 %s
```

```
    inAtlas3: (an existing file name)
            Atlas File - No Lesion - T1 and FLAIR
            flag: --inAtlas3 %s
    inAtlas4: (an existing file name)
            Atlas File - No Lesion - T1 Only
            flag: --inAtlas4 %s
    inAtlas5: (a float)
            Controls the effect of the statistical atlas on the segmentation
            flag: --inAtlas5 %f
    inAtlas6: ('rigid' or 'multi_fully_affine')
            Atlas alignment
            flag: --inAtlas6 %s
    inConnectivity: ('(26,6)' or '(6,26)' or '(6,18)' or '(18,6)')
            Connectivity (foreground,background)
            flag: --inConnectivity %s
    inCorrect: ('true' or 'false')
            Correct MR field inhomogeneity.
            flag: --inCorrect %s
    inFLAIR: (an existing file name)
            FLAIR Image
            flag: --inFLAIR %s
    inInclude: ('true' or 'false')
            Include lesion in WM class in hard classification
            flag: --inInclude %s
    inMaximum: (an integer (int or long))
            Maximum distance from the interventricular WM boundary to downweight
            the lesion membership to avoid false postives
            flag: --inMaximum %d
    inMaximum2: (an integer (int or long))
            Maximum Ventircle Distance
            flag: --inMaximum2 %d
    inMaximum3: (an integer (int or long))
            Maximum InterVentricular Distance
            flag: --inMaximum3 %d
    inMaximum4: (a float)
            Maximum amount of relative change in the energy function considered
            as the convergence criteria
            flag: --inMaximum4 %f
    inMaximum5: (an integer (int or long))
            Maximum iterations
            flag: --inMaximum5 %d
    inOutput: ('hard segmentation' or 'hard segmentation+memberships' or
             'cruise inputs' or 'dura removal inputs')
            Output images
            flag: --inOutput %s
    inOutput2: ('true' or 'false')
            Output the hard classification using maximum membership (not
            neceesarily topologically correct)
            flag: --inOutput2 %s
    inOutput3: ('true' or 'false')
            Output the estimated inhomogeneity field
            flag: --inOutput3 %s
    inSmooting: (a float)
            Controls the effect of neighberhood voxels on the membership
            flag: --inSmooting %f
    inT1_MPRAGE: (an existing file name)
            T1_MPRAGE Image
            flag: --inT1_MPRAGE %s
```

```
    inT1_SPGR: (an existing file name)
            T1_SPGR Image
            flag: --inT1_SPGR %s
    null: (a string)
            Execution Time
            flag: --null %s
    outCortical: (a boolean or a file name)
            Cortical GM Membership
            flag: --outCortical %s
    outFilled: (a boolean or a file name)
            Filled WM Membership
            flag: --outFilled %s
    outHard: (a boolean or a file name)
            Hard segmentation
            flag: --outHard %s
    outHard2: (a boolean or a file name)
            Hard segmentationfrom memberships
            flag: --outHard2 %s
    outInhomogeneity: (a boolean or a file name)
            Inhomogeneity Field
            flag: --outInhomogeneity %s
    outLesion: (a boolean or a file name)
            Lesion Segmentation
            flag: --outLesion %s
    outMembership: (a boolean or a file name)
            Membership Functions
            flag: --outMembership %s
    outSulcal: (a boolean or a file name)
            Sulcal CSF Membership
            flag: --outSulcal %s
    outWM: (a boolean or a file name)
            WM Mask
            flag: --outWM %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    xDefaultMem: (an integer (int or long))
            Set default maximum heap size
            flag: -xDefaultMem %d
    xMaxProcess: (an integer (int or long), nipype default value: 1)
            Set default maximum number of processes.
            flag: -xMaxProcess %d
    xPrefExt: ('nrrd')
            Output File Type
            flag: --xPrefExt %s
```

Outputs:

```
    outCortical: (an existing file name)
            Cortical GM Membership
    outFilled: (an existing file name)
            Filled WM Membership
    outHard: (an existing file name)
            Hard segmentation
    outHard2: (an existing file name)
            Hard segmentationfrom memberships
    outInhomogeneity: (an existing file name)
            Inhomogeneity Field
```

```
    outLesion: (an existing file name)
            Lesion Segmentation
    outMembership: (an existing file name)
            Membership Functions
    outSulcal: (an existing file name)
            Sulcal CSF Membership
    outWM: (an existing file name)
            WM Mask
```

91.14 MedicAlgorithmMipavReorient

Link to code
Wraps command **java edu.jhu.ece.iacl.jist.cli.run edu.jhu.ece.iacl.plugins.utilities.volume.MedicAlgorithmMipavReorient **
title: Reorient Volume
category: Developer Tools
description: Reorient a volume to a particular anatomical orientation.
version: .alpha
Inputs:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    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
            flag: --inInterpolation %s
    inNew: ('Dicom axial' or 'Dicom coronal' or 'Dicom sagittal' or 'User
             defined')
            New image orientation
            flag: --inNew %s
    inResolution: ('Unchanged' or 'Finest cubic' or 'Coarsest cubic' or
             'Same as template')
            Resolution
            flag: --inResolution %s
    inSource: (a list of items which are a file name)
            Source
            flag: --inSource %s
    inTemplate: (an existing file name)
            Template
            flag: --inTemplate %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)
```

```
        flag: --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)
        flag: --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)
        flag: --inUser3 %s
inUser4: ('Axial' or 'Coronal' or 'Sagittal' or 'Unknown')
        User defined Image Orientation
        flag: --inUser4 %s
null: (a string)
        Execution Time
        flag: --null %s
outReoriented: (a list of items which are a file name)
        Reoriented Volume
        flag: --outReoriented %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
xDefaultMem: (an integer (int or long))
        Set default maximum heap size
        flag: -xDefaultMem %d
xMaxProcess: (an integer (int or long), nipype default value: 1)
        Set default maximum number of processes.
        flag: -xMaxProcess %d
xPrefExt: ('nrrd')
        Output File Type
        flag: --xPrefExt %s
```

Outputs:

```
None
```

91.15 MedicAlgorithmN3

Link to code

Wraps command **java edu.jhu.ece.iacl.jist.cli.run edu.jhu.ece.iacl.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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
```

```
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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.
        flag: --inAutomatic %s
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.
        flag: --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.
        flag: --inField %f
inInput: (an existing file name)
        Input Volume
        flag: --inInput %s
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.
        flag: --inKernel %f
inMaximum: (an integer (int or long))
        Maximum number of Iterations
        flag: --inMaximum %d
inSignal: (a float)
        Default = min + 1, Values at less than threshold are treated as part
        of the background
        flag: --inSignal %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.
        flag: --inSubsample %f
inWeiner: (a float)
        Usually between 0.0-1.0
        flag: --inWeiner %f
null: (a string)
        Execution Time
        flag: --null %s
outInhomogeneity: (a boolean or a file name)
        Inhomogeneity Corrected Volume
        flag: --outInhomogeneity %s
outInhomogeneity2: (a boolean or a file name)
        Inhomogeneity Field
        flag: --outInhomogeneity2 %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

```
    xDefaultMem: (an integer (int or long))
            Set default maximum heap size
            flag: -xDefaultMem %d
    xMaxProcess: (an integer (int or long), nipype default value: 1)
            Set default maximum number of processes.
            flag: -xMaxProcess %d
    xPrefExt: ('nrrd')
            Output File Type
            flag: --xPrefExt %s
```

Outputs:

```
    outInhomogeneity: (an existing file name)
            Inhomogeneity Corrected Volume
    outInhomogeneity2: (an existing file name)
            Inhomogeneity Field
```

91.16 MedicAlgorithmSPECTRE2010

Link to code
Wraps command **java edu.jhu.ece.iacl.jist.cli.run edu.jhu.ece.iacl.plugins.segmentation.skull_strip.MedicAlgorithmSPECTRE2
**
title: SPECTRE 2010
category: Developer Tools

91.16.1 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.iacl.ece.jhu.edu/
contributor: Aaron Carass (aaron_carass@jhu.edu) http://www.iacl.ece.jhu.edu/ Hanlin Wan (hanlin-wan@gmail.com)
Inputs:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inApply: ('All' or 'X' or 'Y' or 'Z')
            Apply rotation
            flag: --inApply %s
    inAtlas: (an existing file name)
```

```
        SPECTRE atlas description file. A text file enumerating atlas files
        and landmarks.
        flag: --inAtlas %s
inBackground: (a float)
        flag: --inBackground %f
inCoarse: (a float)
        Coarse angle increment
        flag: --inCoarse %f
inCost: ('Correlation ratio' or 'Least squares' or 'Normalized cross
         correlation' or 'Normalized mutual information')
        Cost function
        flag: --inCost %s
inDegrees: ('Rigid - 6' or 'Global rescale - 7' or 'Specific rescale
         - 9' or 'Affine - 12')
        Degrees of freedom
        flag: --inDegrees %s
inFind: ('true' or 'false')
        Find Midsaggital Plane
        flag: --inFind %s
inFine: (a float)
        Fine angle increment
        flag: --inFine %f
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.
        flag: --inImage %s
inInhomogeneity: ('true' or 'false')
        Set to false by default, this parameter will make FANTASM try to do
        inhomogeneity correction during it's iterative cycle.
        flag: --inInhomogeneity %s
inInitial: (an integer (int or long))
        Erosion of the inital mask, which is based on the probability mask
        and the classification., The initial mask is ouput as the d0 volume
        at the conclusion of SPECTRE.
        flag: --inInitial %d
inInitial2: (a float)
        Initial probability threshold
        flag: --inInitial2 %f
inInput: (an existing file name)
        Input volume to be skullstripped.
        flag: --inInput %s
inMMC: (an integer (int or long))
        The size of the dilation step within the Modified Morphological
        Closing.
        flag: --inMMC %d
inMMC2: (an integer (int or long))
        The size of the erosion step within the Modified Morphological
        Closing.
        flag: --inMMC2 %d
inMaximum: (a float)
        Maximum angle
        flag: --inMaximum %f
inMinimum: (a float)
        Minimum probability threshold
        flag: --inMinimum %f
inMinimum2: (a float)
        Minimum angle
        flag: --inMinimum2 %f
```

```
    inMultiple: (an integer (int or long))
            Multiple of tolerance to bracket the minimum
            flag: --inMultiple %d
    inMultithreading: ('true' or 'false')
            Set to false by default, this parameter controls the multithreaded
            behavior of the linear registration.
            flag: --inMultithreading %s
    inNumber: (an integer (int or long))
            Number of iterations
            flag: --inNumber %d
    inNumber2: (an integer (int or long))
            Number of minima from Level 8 to test at Level 4
            flag: --inNumber2 %d
    inOutput: ('true' or 'false')
            Determines if the output results are transformed back into the space
            of the original input image.
            flag: --inOutput %s
    inOutput2: ('true' or 'false')
            Output Plane?
            flag: --inOutput2 %s
    inOutput3: ('true' or 'false')
            Output Split-Halves?
            flag: --inOutput3 %s
    inOutput4: ('true' or 'false')
            Output Segmentation on Plane?
            flag: --inOutput4 %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
            flag: --inOutput5 %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
            flag: --inRegistration %s
    inResample: ('true' or 'false')
            Determines if the data is resampled to be isotropic during the
            processing.
            flag: --inResample %s
    inRun: ('true' or 'false')
            Run Smooth Brain Mask
            flag: --inRun %s
    inSkip: ('true' or 'false')
            Skip multilevel search (Assume images are close to alignment)
            flag: --inSkip %s
    inSmoothing: (a float)
            flag: --inSmoothing %f
    inSubsample: ('true' or 'false')
            Subsample image for speed
            flag: --inSubsample %s
    inUse: ('true' or 'false')
            Use the max of the min resolutions of the two datasets when
            resampling
            flag: --inUse %s
    null: (a string)
            Execution Time
            flag: --null %s
```

```
    outFANTASM: (a boolean or a file name)
            Tissue classification of of the whole input volume.
            flag: --outFANTASM %s
    outMask: (a boolean or a file name)
            Binary Mask of the skullstripped result with just the brain
            flag: --outMask %s
    outMidsagittal: (a boolean or a file name)
            Plane dividing the brain hemispheres
            flag: --outMidsagittal %s
    outOriginal: (a boolean or a file name)
            If Output in Original Space Flag is true then outputs the original
            input volume. Otherwise outputs the axialy reoriented input volume.
            flag: --outOriginal %s
    outPrior: (a boolean or a file name)
            Probability prior from the atlas registrations
            flag: --outPrior %s
    outSegmentation: (a boolean or a file name)
            2D image showing the tissue classification on the midsagittal plane
            flag: --outSegmentation %s
    outSplitHalves: (a boolean or a file name)
            Skullstripped mask of the brain with the hemispheres divided.
            flag: --outSplitHalves %s
    outStripped: (a boolean or a file name)
            Skullstripped result of the input volume with just the brain.
            flag: --outStripped %s
    outd0: (a boolean or a file name)
            Initial Brainmask
            flag: --outd0 %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    xDefaultMem: (an integer (int or long))
            Set default maximum heap size
            flag: -xDefaultMem %d
    xMaxProcess: (an integer (int or long), nipype default value: 1)
            Set default maximum number of processes.
            flag: -xMaxProcess %d
    xPrefExt: ('nrrd')
            Output File Type
            flag: --xPrefExt %s
```

Outputs:

```
    outFANTASM: (an existing file name)
            Tissue classification of of the whole input volume.
    outMask: (an existing file name)
            Binary Mask of the skullstripped result with just the brain
    outMidsagittal: (an existing file name)
            Plane dividing the brain hemispheres
    outOriginal: (an existing file name)
            If Output in Original Space Flag is true then outputs the original
            input volume. Otherwise outputs the axialy reoriented input volume.
    outPrior: (an existing file name)
            Probability prior from the atlas registrations
    outSegmentation: (an existing file name)
            2D image showing the tissue classification on the midsagittal plane
    outSplitHalves: (an existing file name)
            Skullstripped mask of the brain with the hemispheres divided.
```

```
    outStripped: (an existing file name)
            Skullstripped result of the input volume with just the brain.
    outd0: (an existing file name)
            Initial Brainmask
```

91.17 MedicAlgorithmThresholdToBinaryMask

Link to code
Wraps command **java edu.jhu.ece.iacl.jist.cli.run edu.jhu.ece.iacl.plugins.utilities.volume.MedicAlgorithmThresholdToBinaryM
**
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.iacl.ece.jhu.edu/
Inputs:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inLabel: (a list of items which are a file name)
            Input volumes
            flag: --inLabel %s
    inMaximum: (a float)
            Maximum threshold value.
            flag: --inMaximum %f
    inMinimum: (a float)
            Minimum threshold value.
            flag: --inMinimum %f
    inUse: ('true' or 'false')
            Use the images max intensity as the max value of the range.
            flag: --inUse %s
    null: (a string)
            Execution Time
            flag: --null %s
    outBinary: (a list of items which are a file name)
            Binary Mask
            flag: --outBinary %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    xDefaultMem: (an integer (int or long))
            Set default maximum heap size
            flag: -xDefaultMem %d
    xMaxProcess: (an integer (int or long), nipype default value: 1)
```

```
        Set default maximum number of processes.
        flag: -xMaxProcess %d
xPrefExt: ('nrrd')
        Output File Type
        flag: --xPrefExt %s
```

Outputs:

```
None
```

91.18 RandomVol

Link to code
Wraps command **java edu.jhu.ece.iacl.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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inField: ('Uniform' or 'Normal' or 'Exponential')
        Field
        flag: --inField %s
inLambda: (a float)
        Lambda Value for Exponential Distribution
        flag: --inLambda %f
inMaximum: (an integer (int or long))
        Maximum Value
        flag: --inMaximum %d
inMinimum: (an integer (int or long))
        Minimum Value
        flag: --inMinimum %d
inSize: (an integer (int or long))
        Size of Volume in X direction
        flag: --inSize %d
inSize2: (an integer (int or long))
        Size of Volume in Y direction
        flag: --inSize2 %d
inSize3: (an integer (int or long))
        Size of Volume in Z direction
        flag: --inSize3 %d
inSize4: (an integer (int or long))
        Size of Volume in t direction
        flag: --inSize4 %d
```

```
    inStandard: (an integer (int or long))
            Standard Deviation for Normal Distribution
            flag: --inStandard %d
    null: (a string)
            Execution Time
            flag: --null %s
    outRand1: (a boolean or a file name)
            Rand1
            flag: --outRand1 %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    xDefaultMem: (an integer (int or long))
            Set default maximum heap size
            flag: -xDefaultMem %d
    xMaxProcess: (an integer (int or long), nipype default value: 1)
            Set default maximum number of processes.
            flag: -xMaxProcess %d
    xPrefExt: ('nrrd')
            Output File Type
            flag: --xPrefExt %s
```

Outputs:

```
    outRand1: (an existing file name)
            Rand1
```

interfaces.mne.base

92.1 WatershedBEM

Link to code
Wraps command **mne_watershed_bem**
Uses mne_watershed_bem to get information from dicom directories

92.1.1 Examples

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
subject_id: (a string)
        Subject ID (must have a complete Freesurfer directory)
        flag: --subject %s
subjects_dir: (an existing directory name, nipype default value: )
        Path to Freesurfer subjects directory

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
atlas_mode: (a boolean)
        Use atlas mode for registration (default: no rigid alignment)
        flag: --atlas
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
overwrite: (a boolean, nipype default value: True)
        Overwrites the existing files
        flag: --overwrite
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
```

```
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
volume: ('T1' or 'aparc+aseg' or 'aseg' or 'brain' or 'orig' or
         'brainmask' or 'ribbon', nipype default value: T1)
        The volume from the "mri" directory to use (defaults to T1)
        flag: --volume %s
```

Outputs:

```
brain_surface: (an existing file name)
        Brain surface (in Freesurfer format)
cor_files: (a list of items which are an existing file name)
        "COR" format files
fif_file: (an existing file name)
        "fif" format file for EEG processing in MNE
inner_skull_surface: (an existing file name)
        Inner skull surface (in Freesurfer format)
mesh_files: (a list of items which are an existing file name)
        Paths to the output meshes (brain, inner skull, outer skull, outer
        skin)
outer_skin_surface: (an existing file name)
        Outer skin surface (in Freesurfer format)
outer_skull_surface: (an existing file name)
        Outer skull surface (in Freesurfer format)
```

CHAPTER 93

interfaces.mrtrix.convert

93.1 MRTrix2TrackVis

Link to code

Converts MRtrix (.tck) tract files into TrackVis (.trk) format using functions from dipy

93.1.1 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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        The input file for the tracks in MRTrix (.tck) format

[Optional]
image_file: (an existing file name)
        The image the tracks were generated from
matrix_file: (an existing file name)
        A transformation matrix to apply to the tracts after they have been
        generated (from FLIRT - affine transformation from image_file to
        registration_image_file)
out_filename: (a file name, nipype default value: converted.trk)
        The output filename for the tracks in TrackVis (.trk) format
registration_image_file: (an existing file name)
        The final image the tracks should be registered to.
```

Outputs:

```
out_file: (an existing file name)
```

93.2 read_mrtrix_header()

Link to code

93.3 read_mrtrix_streamlines()

Link to code

93.4 read_mrtrix_tracks()

Link to code

93.5 transform_to_affine()

Link to code

CHAPTER 94

interfaces.mrtrix.preprocess

94.1 DWI2Tensor

Link to code
Wraps command **dwi2tensor**
Converts diffusion-weighted images to tensor images.

94.1.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (a list of items which are an existing file name)
        Diffusion-weighted images
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
debug: (a boolean)
        Display debugging messages.
        flag: -debug, position: 1
encoding_file: (a file name)
        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()
        flag: -grad %s, position: 2
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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.
        flag: -ignoreslices %s, position: 2
ignore_volumes: (a list of at least 1 items which are an integer (int
         or long))
        Requires two values (i.e. [2 5 6] for [Volumes] Ignores the image
        volumes specified when computing the tensor.
        flag: -ignorevolumes %s, position: 2
out_filename: (a file name)
        Output tensor filename
        flag: %s, position: -1
quiet: (a boolean)
        Do not display information messages or progress status.
        flag: -quiet, position: 1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
tensor: (an existing file name)
        path/name of output diffusion tensor image
```

94.2 Erode

Link to code

Wraps command **erode**

Erode (or dilates) a mask (i.e. binary) image

94.2.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> erode = mrt.Erode()
>>> erode.inputs.in_file = 'mask.mif'
>>> erode.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Input mask image to be eroded
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
debug: (a boolean)
        Display debugging messages.
        flag: -debug, position: 1
dilate: (a boolean)
        Perform dilation rather than erosion
        flag: -dilate, position: 1
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
```

```
          {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
number_of_passes: (an integer (int or long))
        the number of passes (default: 1)
        flag: -npass %s
out_filename: (a file name)
        Output image filename
        flag: %s, position: -1
quiet: (a boolean)
        Do not display information messages or progress status.
        flag: -quiet, position: 1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        the output image
```

94.3 GenerateWhiteMatterMask

Link to code

Wraps command **gen_WM_mask**

Generates a white matter probability mask from the DW images.

94.3.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> genWM = mrt.GenerateWhiteMatterMask()
>>> genWM.inputs.in_file = 'dwi.mif'
>>> genWM.inputs.encoding_file = 'encoding.txt'
>>> genWM.run()
```

Inputs:

```
[Mandatory]
binary_mask: (an existing file name)
        Binary brain mask
        flag: %s, position: -2
encoding_file: (an existing file name)
        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
        flag: -grad %s, position: 1
in_file: (an existing file name)
        Diffusion-weighted images
        flag: %s, position: -3

[Optional]
args: (a string)
        Additional parameters to the command
```

```
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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)
        flag: -margin %s
out_WMProb_filename: (a file name)
        Output WM probability image filename
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
WMprobabilitymap: (an existing file name)
        WMprobabilitymap
```

94.4 MRConvert

Link to code

Wraps 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.

94.4.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> mrconvert = mrt.MRConvert()
>>> mrconvert.inputs.in_file = 'dwi_FA.mif'
>>> mrconvert.inputs.out_filename = 'dwi_FA.nii'
>>> mrconvert.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        voxel-order data filename
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
```

```
    extension: ('mif' or 'nii' or 'float' or 'char' or 'short' or 'int'
             or 'long' or 'double', nipype default value: mif)
            "i.e. Bfloat". Can be "char", "short", "int", "long", "float" or
            "double"
    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.
            flag: -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.
            flag: %s, position: 2
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    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.
            flag: -output %s, position: 2
    offset_bias: (a float)
            Apply offset to the intensity values.
            flag: -scale %d, position: 3
    out_filename: (a file name)
            Output filename
            flag: %s, position: -1
    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"
            flag: -output %s, position: 2
    prs: (a boolean)
            Assume that the DW gradients are specified in the PRS frame (Siemens
            DICOM only).
            flag: -prs, position: 3
    replace_NaN_with_zero: (a boolean)
            Replace all NaN values with zero.
            flag: -zero, position: 3
    resample: (a float)
            Apply scaling to the intensity values.
            flag: -scale %d, position: 3
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    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.
            flag: -vox %s, position: 3
```

Outputs:

```
    converted: (an existing file name)
            path/name of 4D volume in voxel order
```

94.5 MRMultiply

Link to code
Wraps command **mrmult**
Multiplies two images.

94.5.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> MRmult = mrt.MRMultiply()
>>> MRmult.inputs.in_files = ['dwi.mif', 'dwi_WMProb.mif']
>>> MRmult.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        Input images to be multiplied
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
debug: (a boolean)
        Display debugging messages.
        flag: -debug, position: 1
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_filename: (a file name)
        Output image filename
        flag: %s, position: -1
quiet: (a boolean)
        Do not display information messages or progress status.
        flag: -quiet, position: 1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        the output image of the multiplication
```

94.6 MRTransform

Link to code
Wraps command **mrtransform**
Apply spatial transformations or reslice images

94.6.1 Example

```
>>> MRxform = MRTransform()
>>> MRxform.inputs.in_files = 'anat_coreg.mif'
>>> MRxform.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        Input images to be transformed
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
debug: (a boolean)
        Display debugging messages.
        flag: -debug, position: 1
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
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.
        flag: -flipx, position: 1
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
invert: (a boolean)
        Invert the specified transform before using it
        flag: -inverse, position: 1
out_filename: (a file name)
        Output image
        flag: %s, position: -1
quiet: (a boolean)
        Do not display information messages or progress status.
        flag: -quiet, position: 1
reference_image: (an existing file name)
        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.
        flag: -reference %s, position: 1
replace_transform: (a boolean)
        replace the current transform by that specified, rather than
        applying it to the current transform
        flag: -replace, position: 1
template_image: (an existing file name)
        Reslice the input image to match the specified template image.
        flag: -template %s, position: 1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

```
transformation_file: (an existing file name)
        The transform to apply, in the form of a 4x4 ascii file.
        flag: -transform %s, position: 1
```

Outputs:

```
out_file: (an existing file name)
        the output image of the transformation
```

94.7 MRTrixViewer

Link to code

Wraps command **mrview**

Loads the input images in the MRTrix Viewer.

94.7.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> MRview = mrt.MRTrixViewer()
>>> MRview.inputs.in_files = 'dwi.mif'
>>> MRview.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        Input images to be viewed
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
debug: (a boolean)
        Display debugging messages.
        flag: -debug, position: 1
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
quiet: (a boolean)
        Do not display information messages or progress status.
        flag: -quiet, position: 1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
None
```

94.8 MedianFilter3D

Link to code

Wraps command **median3D**
Smooth images using a 3x3x3 median filter.

94.8.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> median3d = mrt.MedianFilter3D()
>>> median3d.inputs.in_file = 'mask.mif'
>>> median3d.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Input images to be smoothed
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
debug: (a boolean)
        Display debugging messages.
        flag: -debug, position: 1
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_filename: (a file name)
        Output image filename
        flag: %s, position: -1
quiet: (a boolean)
        Do not display information messages or progress status.
        flag: -quiet, position: 1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        the output image
```

94.9 Tensor2ApparentDiffusion

Link to code
Wraps command **tensor2ADC**
Generates a map of the apparent diffusion coefficient (ADC) in each voxel

94.9.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> tensor2ADC = mrt.Tensor2ApparentDiffusion()
```

```
>>> tensor2ADC.inputs.in_file = 'dwi_tensor.mif'
>>> tensor2ADC.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Diffusion tensor image
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
debug: (a boolean)
        Display debugging messages.
        flag: -debug, position: 1
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_filename: (a file name)
        Output Fractional Anisotropy filename
        flag: %s, position: -1
quiet: (a boolean)
        Do not display information messages or progress status.
        flag: -quiet, position: 1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
ADC: (an existing file name)
        the output image of the major eigenvectors of the diffusion tensor
        image.
```

94.10 Tensor2FractionalAnisotropy

Link to code

Wraps command **tensor2FA**

Generates a map of the fractional anisotropy in each voxel.

94.10.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> tensor2FA = mrt.Tensor2FractionalAnisotropy()
>>> tensor2FA.inputs.in_file = 'dwi_tensor.mif'
>>> tensor2FA.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
```

```
        Diffusion tensor image
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
debug: (a boolean)
        Display debugging messages.
        flag: -debug, position: 1
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_filename: (a file name)
        Output Fractional Anisotropy filename
        flag: %s, position: -1
quiet: (a boolean)
        Do not display information messages or progress status.
        flag: -quiet, position: 1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
FA: (an existing file name)
        the output image of the major eigenvectors of the diffusion tensor
        image.
```

94.11 Tensor2Vector

Link to code

Wraps command **tensor2vector**

Generates a map of the major eigenvectors of the tensors in each voxel.

94.11.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> tensor2vector = mrt.Tensor2Vector()
>>> tensor2vector.inputs.in_file = 'dwi_tensor.mif'
>>> tensor2vector.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Diffusion tensor image
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
```

```
    debug: (a boolean)
            Display debugging messages.
            flag: -debug, position: 1
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    out_filename: (a file name)
            Output vector filename
            flag: %s, position: -1
    quiet: (a boolean)
            Do not display information messages or progress status.
            flag: -quiet, position: 1
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    vector: (an existing file name)
            the output image of the major eigenvectors of the diffusion tensor
            image.
```

94.12 Threshold

Link to code

Wraps 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.

94.12.1 Example

```
    >>> import nipype.interfaces.mrtrix as mrt
    >>> thresh = mrt.Threshold()
    >>> thresh.inputs.in_file = 'wm_mask.mif'
    >>> thresh.run()
```

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            The input image to be thresholded
            flag: %s, position: -2

    [Optional]
    absolute_threshold_value: (a float)
            Specify threshold value as absolute intensity.
            flag: -abs %s
    args: (a string)
            Additional parameters to the command
            flag: %s
```

```
    debug: (a boolean)
            Display debugging messages.
            flag: -debug, position: 1
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    invert: (a boolean)
            Invert output binary mask
            flag: -invert, position: 1
    out_filename: (a file name)
            The output binary image mask.
            flag: %s, position: -1
    percentage_threshold_value: (a float)
            Specify threshold value as a percentage of the peak intensity in the
            input image.
            flag: -percent %s
    quiet: (a boolean)
            Do not display information messages or progress status.
            flag: -quiet, position: 1
    replace_zeros_with_NaN: (a boolean)
            Replace all zero values with NaN
            flag: -nan, position: 1
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
            The output binary image mask.
```

CHAPTER 95

interfaces.mrtrix.tensors

95.1 ConstrainedSphericalDeconvolution

Link to code

Wraps 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] Im {Y(2,2)}
- [2] Im {Y(2,1)}
- [3] Y(2,0)
- [4] Re {Y(2,1)}
- [5] Re {Y(2,2)}
- [6] Im {Y(4,4)}
- [7] Im {Y(4,3)}

95.1.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> csdeconv = mrt.ConstrainedSphericalDeconvolution()
>>> csdeconv.inputs.in_file = 'dwi.mif'
>>> csdeconv.inputs.encoding_file = 'encoding.txt'
>>> csdeconv.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        diffusion-weighted image
        flag: %s, position: -3
response_file: (an existing file name)
        the diffusion-weighted signal response function for a single fibre
        population (see EstimateResponse)
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
```

```
        flag: %s
debug: (a boolean)
        Display debugging messages.
        flag: -debug
directions_file: (an existing file name)
        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)
        flag: -directions %s, position: -2
encoding_file: (an existing file name)
        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
        flag: -grad %s, position: 1
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
filter_file: (an existing file name)
        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 ]).
        flag: -filter %s, position: -2
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
iterations: (an integer (int or long))
        the maximum number of iterations to perform for each voxel (default
        = 50)
        flag: -niter %s
lambda_value: (a float)
        the regularisation parameter lambda that controls the strength of
        the constraint (default = 1.0).
        flag: -lambda %s
mask_image: (an existing file name)
        only perform computation within the specified binary brain mask
        image
        flag: -mask %s, position: 2
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.
        flag: -lmax %s
normalise: (a boolean)
        normalise the DW signal to the b=0 image
        flag: -normalise, position: 3
out_filename: (a file name)
        Output filename
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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)
        flag: -threshold %s
```

Outputs:

```
spherical_harmonics_image: (an existing file name)
        Spherical harmonics image
```

95.2 DWI2SphericalHarmonicsImage

Link to code

Wraps 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] Im {Y(2,2)}
- [2] Im {Y(2,1)}
- [3] Y(2,0)
- [4] Re {Y(2,1)}
- [5] Re {Y(2,2)}
- [6] Im {Y(4,4)}
- [7] Im {Y(4,3)}

95.2.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> dwi2SH = mrt.DWI2SphericalHarmonicsImage()
>>> dwi2SH.inputs.in_file = 'diffusion.nii'
>>> dwi2SH.inputs.encoding_file = 'encoding.txt'
>>> dwi2SH.run()
```

Inputs:

```
[Mandatory]
encoding_file: (an existing file name)
        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
        flag: -grad %s, position: 1
in_file: (an existing file name)
        Diffusion-weighted images
        flag: %s, position: -2
```

```
    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    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.
            flag: -lmax %s
    normalise: (a boolean)
            normalise the DW signal to the b=0 image
            flag: -normalise, position: 3
    out_filename: (a file name)
            Output filename
            flag: %s, position: -1
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    spherical_harmonics_image: (an existing file name)
            Spherical harmonics image
```

95.3 Directions2Amplitude

Link to code

Wraps command **dir2amp**

convert directions image to amplitudes

95.3.1 Example

```
    >>> import nipype.interfaces.mrtrix as mrt
    >>> amplitudes = mrt.Directions2Amplitude()
    >>> amplitudes.inputs.in_file = 'peak_directions.mif'
    >>> amplitudes.run()
```

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            the input directions image. Each volume corresponds to the x, y & z
            component of each direction vector in turn.
            flag: %s, position: -2

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
```

```
    display_debug: (a boolean)
            Display debugging messages.
            flag: -debug
    display_info: (a boolean)
            Display information messages.
            flag: -info
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    num_peaks: (an integer (int or long))
            the number of peaks to extract (default is 3)
            flag: -num %s
    out_file: (a file name)
            the output amplitudes image
            flag: %s, position: -1
    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)
            flag: -direction %s
    peaks_image: (an existing file name)
            the program will try to find the peaks that most closely match those
            in the image provided
            flag: -peaks %s
    quiet_display: (a boolean)
            do not display information messages or progress status.
            flag: -quiet
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
            amplitudes image
```

95.4 EstimateResponseForSH

Link to code

Wraps command **estimate_response**

Estimates the fibre response function for use in spherical deconvolution.

95.4.1 Example

```
    >>> import nipype.interfaces.mrtrix as mrt
    >>> estresp = mrt.EstimateResponseForSH()
    >>> estresp.inputs.in_file = 'dwi.mif'
    >>> estresp.inputs.mask_image = 'dwi_WMProb.mif'
    >>> estresp.inputs.encoding_file = 'encoding.txt'
    >>> estresp.run()
```

Inputs:

```
[Mandatory]
encoding_file: (an existing file name)
        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
        flag: -grad %s, position: 1
in_file: (an existing file name)
        Diffusion-weighted images
        flag: %s, position: -3
mask_image: (an existing file name)
        only perform computation within the specified binary brain mask
        image
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
debug: (a boolean)
        Display debugging messages.
        flag: -debug
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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.
        flag: -lmax %s
normalise: (a boolean)
        normalise the DW signal to the b=0 image
        flag: -normalise
out_filename: (a file name)
        Output filename
        flag: %s, position: -1
quiet: (a boolean)
        Do not display information messages or progress status.
        flag: -quiet
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
response: (an existing file name)
        Spherical harmonics image
```

95.5 FindShPeaks

Link to code
Wraps command **find_SH_peaks**

identify the orientations of the N largest peaks of a SH profile

95.5.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
directions_file: (an existing file name)
        the set of directions to use as seeds for the peak finding
        flag: %s, position: -2
in_file: (an existing file name)
        the input image of SH coefficients.
        flag: %s, position: -3

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
display_debug: (a boolean)
        Display debugging messages.
        flag: -debug
display_info: (a boolean)
        Display information messages.
        flag: -info
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
num_peaks: (an integer (int or long))
        the number of peaks to extract (default is 3)
        flag: -num %s
out_file: (a file name)
        the output image. Each volume corresponds to the x, y & z component
        of each peak direction vector in turn
        flag: %s, position: -1
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)
        flag: -direction %s
peak_threshold: (a float)
        only peak amplitudes greater than the threshold will be considered
        flag: -threshold %s
peaks_image: (an existing file name)
        the program will try to find the peaks that most closely match those
        in the image provided
        flag: -peaks %s
```

```
quiet_display: (a boolean)
        do not display information messages or progress status.
        flag: -quiet
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        Peak directions image
```

95.6 GenerateDirections

Link to code

Wraps command **gendir**

generate a set of directions evenly distributed over a hemisphere.

95.6.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> gendir = mrt.GenerateDirections()
>>> gendir.inputs.num_dirs = 300
>>> gendir.run()
```

Inputs:

```
[Mandatory]
num_dirs: (an integer (int or long))
        the number of directions to generate.
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
display_debug: (a boolean)
        Display debugging messages.
        flag: -debug
display_info: (a boolean)
        Display information messages.
        flag: -info
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
niter: (an integer (int or long))
        specify the maximum number of iterations to perform.
        flag: -niter %s
out_file: (a file name)
        the text file to write the directions to, as [ az el ] pairs.
        flag: %s, position: -1
power: (a float)
```

```
        specify exponent to use for repulsion power law.
        flag: -power %s
quiet_display: (a boolean)
        do not display information messages or progress status.
        flag: -quiet
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        directions file
```

95.7 concat_files()

Link to code

CHAPTER 96

interfaces.mrtrix.tracking

96.1 DiffusionTensorStreamlineTrack

Link to code

Wraps 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'

96.1.1 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()
```

Inputs:

```
[Mandatory]
gradient_encoding_file: (an existing file name)
        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
        flag: -grad %s, position: -2
in_file: (an existing file name)
        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.
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
cutoff_value: (a float)
        Set the FA or FOD amplitude cutoff for terminating tracks (default
        is 0.1).
        flag: -cutoff %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).
```

```
        flag: -number %d
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.
        flag: -noprecomputed
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
exclude_file: (an existing file name)
        exclusion file
        flag: -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)
        flag: -exclude %s, position: 2
        mutually_exclusive: exclude_file, exclude_spec
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
include_file: (an existing file name)
        inclusion file
        flag: -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)
        flag: -include %s, position: 2
        mutually_exclusive: include_file, include_spec
initial_cutoff_value: (a float)
        Sets the minimum FA or FOD amplitude for initiating tracks (default
        is twice the normal cutoff).
        flag: -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
        flag: -initdirection %s
inputmodel: ('DT_STREAM' or 'SD_PROB' or 'SD_STREAM', nipype default
         value: DT_STREAM)
        input model type
        flag: %s, position: -3
mask_file: (an existing file name)
        mask file. Only tracks within mask.
        flag: -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.
        flag: -mask %s, position: 2
        mutually_exclusive: mask_file, mask_spec
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).
        flag: -maxnum %d
maximum_tract_length: (a float)
        Sets the maximum length of any track in millimeters (default is 200
        mm).
        flag: -length %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)
            flag: -curvature %s
    minimum_tract_length: (a float)
            Sets the minimum length of any track in millimeters (default is 10
            mm).
            flag: -minlength %s
    no_mask_interpolation: (a boolean)
            Turns off trilinear interpolation of mask images.
            flag: -nomaskinterp
    out_file: (a file name)
            output data file
            flag: %s, position: -1
    seed_file: (an existing file name)
            seed file
            flag: -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)
            flag: -seed %s, position: 2
            mutually_exclusive: seed_file, seed_spec
    step_size: (a float)
            Set the step size of the algorithm in mm (default is 0.2).
            flag: -step %s
    stop: (a boolean)
            stop track as soon as it enters any of the include regions.
            flag: -stop
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    unidirectional: (a boolean)
            Track from the seed point in one direction only (default is to track
            in both directions).
            flag: -unidirectional
```

Outputs:

```
    tracked: (an existing file name)
            output file containing reconstructed tracts
```

96.2 FilterTracks

Link to code

Wraps command **filter_tracks**

Use regions-of-interest to select a subset of tracks from a given MRtrix track file.

96.2.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> filt = mrt.FilterTracks()
>>> filt.inputs.in_file = 'tracks.tck'
>>> filt.run()
```

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            input tracks to be filtered
            flag: %s, position: -2

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    debug: (a boolean)
            Display debugging messages.
            flag: -debug, position: 1
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    exclude_file: (an existing file name)
            exclusion file
            flag: -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)
            flag: -exclude %s, position: 2
            mutually_exclusive: exclude_file, exclude_spec
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    include_file: (an existing file name)
            inclusion file
            flag: -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)
            flag: -include %s, position: 2
            mutually_exclusive: include_file, include_spec
    invert: (a boolean)
            invert the matching process, so that tracks that wouldotherwise have
            been included are now excluded and vice-versa.
            flag: -invert
    minimum_tract_length: (a float)
            Sets the minimum length of any track in millimeters (default is 10
            mm).
            flag: -minlength %s
    no_mask_interpolation: (a boolean)
            Turns off trilinear interpolation of mask images.
            flag: -nomaskinterp
    out_file: (a file name)
            Output filtered track filename
            flag: %s, position: -1
    quiet: (a boolean)
            Do not display information messages or progress status.
            flag: -quiet, position: 1
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        the output filtered tracks
```

96.3 ProbabilisticSphericallyDeconvolutedStreamlineTrack

Link to code

Wraps 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'

96.3.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> sdprobtrack = mrt.ProbabilisticSphericallyDeconvolutedStreamlineTrack()
>>> sdprobtrack.inputs.in_file = 'data.Bfloat'
>>> sdprobtrack.inputs.seed_file = 'seed_mask.nii'
>>> sdprobtrack.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        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.
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
cutoff_value: (a float)
        Set the FA or FOD amplitude cutoff for terminating tracks (default
        is 0.1).
        flag: -cutoff %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).
        flag: -number %d
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.
        flag: -noprecomputed
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
exclude_file: (an existing file name)
        exclusion file
        flag: -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)
        flag: -exclude %s, position: 2
        mutually_exclusive: exclude_file, exclude_spec
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
include_file: (an existing file name)
        inclusion file
        flag: -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)
        flag: -include %s, position: 2
        mutually_exclusive: include_file, include_spec
initial_cutoff_value: (a float)
        Sets the minimum FA or FOD amplitude for initiating tracks (default
        is twice the normal cutoff).
        flag: -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
        flag: -initdirection %s
inputmodel: ('DT_STREAM' or 'SD_PROB' or 'SD_STREAM', nipype default
         value: DT_STREAM)
        input model type
        flag: %s, position: -3
mask_file: (an existing file name)
        mask file. Only tracks within mask.
        flag: -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.
        flag: -mask %s, position: 2
        mutually_exclusive: mask_file, mask_spec
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).
        flag: -maxnum %d
maximum_number_of_trials: (an integer (int or long))
        Set the maximum number of sampling trials at each point (only used
        for probabilistic tracking).
        flag: -trials %s
maximum_tract_length: (a float)
        Sets the maximum length of any track in millimeters (default is 200
        mm).
        flag: -length %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)
        flag: -curvature %s
minimum_tract_length: (a float)
        Sets the minimum length of any track in millimeters (default is 10
        mm).
        flag: -minlength %s
no_mask_interpolation: (a boolean)
        Turns off trilinear interpolation of mask images.
```

```
        flag: -nomaskinterp
out_file: (a file name)
        output data file
        flag: %s, position: -1
seed_file: (an existing file name)
        seed file
        flag: -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)
        flag: -seed %s, position: 2
        mutually_exclusive: seed_file, seed_spec
step_size: (a float)
        Set the step size of the algorithm in mm (default is 0.2).
        flag: -step %s
stop: (a boolean)
        stop track as soon as it enters any of the include regions.
        flag: -stop
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
unidirectional: (a boolean)
        Track from the seed point in one direction only (default is to track
        in both directions).
        flag: -unidirectional
```

Outputs:

```
tracked: (an existing file name)
        output file containing reconstructed tracts
```

96.4 SphericallyDeconvolutedStreamlineTrack

Link to code

Wraps 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'

96.4.1 Example

```
>>> import nipype.interfaces.mrtrix as mrt
>>> sdtrack = mrt.SphericallyDeconvolutedStreamlineTrack()
>>> sdtrack.inputs.in_file = 'data.Bfloat'
>>> sdtrack.inputs.seed_file = 'seed_mask.nii'
>>> sdtrack.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        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.
        flag: %s, position: -2
```

```
    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    cutoff_value: (a float)
            Set the FA or FOD amplitude cutoff for terminating tracks (default
            is 0.1).
            flag: -cutoff %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).
            flag: -number %d
    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.
            flag: -noprecomputed
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    exclude_file: (an existing file name)
            exclusion file
            flag: -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)
            flag: -exclude %s, position: 2
            mutually_exclusive: exclude_file, exclude_spec
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    include_file: (an existing file name)
            inclusion file
            flag: -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)
            flag: -include %s, position: 2
            mutually_exclusive: include_file, include_spec
    initial_cutoff_value: (a float)
            Sets the minimum FA or FOD amplitude for initiating tracks (default
            is twice the normal cutoff).
            flag: -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
            flag: -initdirection %s
    inputmodel: ('DT_STREAM' or 'SD_PROB' or 'SD_STREAM', nipype default
             value: DT_STREAM)
            input model type
            flag: %s, position: -3
    mask_file: (an existing file name)
            mask file. Only tracks within mask.
            flag: -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.
        flag: -mask %s, position: 2
        mutually_exclusive: mask_file, mask_spec
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).
        flag: -maxnum %d
maximum_tract_length: (a float)
        Sets the maximum length of any track in millimeters (default is 200
        mm).
        flag: -length %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)
        flag: -curvature %s
minimum_tract_length: (a float)
        Sets the minimum length of any track in millimeters (default is 10
        mm).
        flag: -minlength %s
no_mask_interpolation: (a boolean)
        Turns off trilinear interpolation of mask images.
        flag: -nomaskinterp
out_file: (a file name)
        output data file
        flag: %s, position: -1
seed_file: (an existing file name)
        seed file
        flag: -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)
        flag: -seed %s, position: 2
        mutually_exclusive: seed_file, seed_spec
step_size: (a float)
        Set the step size of the algorithm in mm (default is 0.2).
        flag: -step %s
stop: (a boolean)
        stop track as soon as it enters any of the include regions.
        flag: -stop
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
unidirectional: (a boolean)
        Track from the seed point in one direction only (default is to track
        in both directions).
        flag: -unidirectional
```

Outputs:

```
tracked: (an existing file name)
        output file containing reconstructed tracts
```

96.5 StreamlineTrack

Link to code

Wraps 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.

96.5.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        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.
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
cutoff_value: (a float)
        Set the FA or FOD amplitude cutoff for terminating tracks (default
        is 0.1).
        flag: -cutoff %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).
        flag: -number %d
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.
        flag: -noprecomputed
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
exclude_file: (an existing file name)
        exclusion file
        flag: -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)
        flag: -exclude %s, position: 2
        mutually_exclusive: exclude_file, exclude_spec
ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
include_file: (an existing file name)
        inclusion file
        flag: -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)
        flag: -include %s, position: 2
        mutually_exclusive: include_file, include_spec
initial_cutoff_value: (a float)
        Sets the minimum FA or FOD amplitude for initiating tracks (default
        is twice the normal cutoff).
        flag: -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
        flag: -initdirection %s
inputmodel: ('DT_STREAM' or 'SD_PROB' or 'SD_STREAM', nipype default
         value: DT_STREAM)
        input model type
        flag: %s, position: -3
mask_file: (an existing file name)
        mask file. Only tracks within mask.
        flag: -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.
        flag: -mask %s, position: 2
        mutually_exclusive: mask_file, mask_spec
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).
        flag: -maxnum %d
maximum_tract_length: (a float)
        Sets the maximum length of any track in millimeters (default is 200
        mm).
        flag: -length %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)
        flag: -curvature %s
minimum_tract_length: (a float)
        Sets the minimum length of any track in millimeters (default is 10
        mm).
        flag: -minlength %s
no_mask_interpolation: (a boolean)
        Turns off trilinear interpolation of mask images.
        flag: -nomaskinterp
out_file: (a file name)
        output data file
        flag: %s, position: -1
seed_file: (an existing file name)
        seed file
        flag: -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)
            flag: -seed %s, position: 2
            mutually_exclusive: seed_file, seed_spec
    step_size: (a float)
            Set the step size of the algorithm in mm (default is 0.2).
            flag: -step %s
    stop: (a boolean)
            stop track as soon as it enters any of the include regions.
            flag: -stop
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    unidirectional: (a boolean)
            Track from the seed point in one direction only (default is to track
            in both directions).
            flag: -unidirectional
```

Outputs:

```
    tracked: (an existing file name)
            output file containing reconstructed tracts
```

96.6 Tracks2Prob

Link to code

Wraps 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.

96.6.1 Example

```
    >>> import nipype.interfaces.mrtrix as mrt
    >>> tdi = mrt.Tracks2Prob()
    >>> tdi.inputs.in_file = 'dwi_CSD_tracked.tck'
    >>> tdi.inputs.colour = True
    >>> tdi.run()
```

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            tract file
            flag: %s, position: -2

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    colour: (a boolean)
            add colour to the output image according to the direction of the
            tracks.
            flag: -colour, position: 3
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
```

```
          {})
         Environment variables
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.
         flag: -fraction, position: 3
ignore_exception: (a boolean, nipype default value: False)
         Print an error message instead of throwing an exception in case the
         interface fails to run
out_filename: (a file name)
         output data file
         flag: %s, position: -1
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"
         flag: -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.
         flag: -resample %d, position: 3
template_file: (an existing file name)
         an image file to be used as a template for the output (the output
         image wil have the same transform and field of view)
         flag: -template %s, position: 1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
         Control terminal output: `stream` - displays to terminal immediately
         (default), `allatonce` - waits till command is finished to display
         output, `file` - writes output to file, `none` - output is ignored
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.
         flag: -vox %s, position: 2
```

Outputs:

```
tract_image: (an existing file name)
         Output tract count or track density image
```

CHAPTER 97

interfaces.mrtrix3.base

97.1 MRTrix3Base

Link to code
Wraps command **None**
Inputs:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
None
```

interfaces.mrtrix3.connectivity

98.1 BuildConnectome

Link to code
Wraps command **tck2connectome**
Generate a connectome matrix from a streamlines file and a node parcellation image

98.1.1 Example

```
>>> import nipype.interfaces.mrtrix3 as mrt
>>> mat = mrt.BuildConnectome()
>>> mat.inputs.in_file = 'tracks.tck'
>>> mat.inputs.in_parc = 'aparc+aseg.nii'
>>> mat.cmdline
'tck2connectome tracks.tck aparc+aseg.nii connectome.csv'
>>> mat.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input tractography
        flag: %s, position: -3
out_file: (a file name, nipype default value: connectome.csv)
        output file after processing
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_parc: (an existing file name)
        parcellation file
        flag: %s, position: -2
in_scalar: (an existing file name)
        provide the associated image for the mean_scalar metric
        flag: -image %s
in_weights: (an existing file name)
```

```
        specify a text scalar file containing the streamline weights
        flag: -tck_weights_in %s
keep_unassigned: (a boolean)
        By default, the program discards the information regarding those
        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)
        flag: -keep_unassigned
metric: ('count' or 'meanlength' or 'invlength' or 'invnodevolume' or
         'mean_scalar' or 'invlength_invnodevolume')
        specify the edge weight metric
        flag: -metric %s
nthreads: (an integer (int or long))
        number of threads. if zero, the number of available cpus will be
        used
        flag: -nthreads %d
search_forward: (a float)
        project the streamline forwards from the endpoint in search of
        aparcellation node voxel. Argument is the maximum traversal length
        in mm.
        flag: -assignment_forward_search %f
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.
        flag: -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).
        flag: -assignment_reverse_search %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
vox_lookup: (a boolean)
        use a simple voxel lookup value at each streamline endpoint
        flag: -assignment_voxel_lookup
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)
        flag: -zero_diagonal
```

Outputs:

```
out_file: (an existing file name)
        the output response file
```

98.2 LabelConfig

Link to code

Wraps command **labelconfig**

Re-configure parcellation to be incrementally defined.

98.2.1 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
'labelconfig aparc+aseg.nii mrtrix3_labelconfig.txt parcellation.mif'
>>> labels.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input anatomical image
        flag: %s, position: -3
out_file: (a file name, nipype default value: parcellation.mif)
        output file after processing
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_config: (an existing file name)
        connectome configuration file
        flag: %s, position: -2
lut_aal: (a file name)
        get information from the AAL lookup table (typically
        "ROI_MNI_V4.txt")
        flag: -lut_aal %s
lut_basic: (a file name)
        get information from a basic lookup table consisting of index / name
        pairs
        flag: -lut_basic %s
lut_fs: (a file name)
        get information from a FreeSurfer lookup table(typically
        "FreeSurferColorLUT.txt")
        flag: -lut_freesurfer %s
lut_itksnap: (a file name)
        get information from an ITK - SNAP lookup table(this includes the
        IIT atlas file "LUT_GM.txt")
        flag: -lut_itksnap %s
nthreads: (an integer (int or long))
        number of threads. if zero, the number of available cpus will be
        used
        flag: -nthreads %d
spine: (a file name)
        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.
        flag: -spine %s
```

```
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        the output response file
```

interfaces.mrtrix3.preprocess

99.1 ResponseSD

Link to code
Wraps command **dwi2response**
Generate an appropriate response function from the image data for spherical deconvolution.

99.1.1 Example

```
>>> import nipype.interfaces.mrtrix3 as mrt
>>> resp = mrt.ResponseSD()
>>> resp.inputs.in_file = 'dwi.mif'
>>> resp.inputs.in_mask = 'mask.nii.gz'
>>> resp.inputs.grad_fsl = ('bvecs', 'bvals')
>>> resp.cmdline
'dwi2response -fslgrad bvecs bvals -mask mask.nii.gz dwi.mif response.txt'
>>> resp.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input diffusion weighted images
        flag: %s, position: -2
out_file: (a file name, nipype default value: response.txt)
        output file containing SH coefficients
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
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).
        flag: -bvalue_scaling %s
disp_mult: (a float)
        dispersion of FOD lobe must not exceed some threshold as determined
        by this multiplier and the FOD dispersion in other single-fibre
        voxels. The threshold is: (mean + (multiplier * (mean - min)));
        default = 1.0. Criterion is only applied in second pass of RF
        estimation.
```

```
        flag: -dispersion_multiplier %f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
grad_file: (an existing file name)
        dw gradient scheme (MRTrix format
        flag: -grad %s
grad_fsl: (a tuple of the form: (an existing file name, an existing
         file name))
        (bvecs, bvals) dw gradient scheme (FSL format
        flag: -fslgrad %s %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_bval: (an existing file name)
        bvals file in FSL format
in_bvec: (an existing file name)
        bvecs file in FSL format
        flag: -fslgrad %s %s
in_mask: (an existing file name)
        provide initial mask image
        flag: -mask %s
int_mult: (a float)
        integral of FOD lobe must not be outside some range as determined by
        this multiplier and FOD lobe integral in other single-fibre voxels.
        The range is: (mean +- (multiplier * stdev)); default = 2.0.
        Criterion is only applied in second pass of RF estimation.
        flag: -integral_multiplier %f
iterations: (an integer (int or long))
        maximum number of iterations per pass
        flag: -max_iters %d
max_change: (a float)
        maximum percentile change in any response function coefficient; if
        no individual coefficient changes by more than this fraction, the
        algorithm is terminated.
        flag: -max_change %f
max_sh: (an integer (int or long))
        maximum harmonic degree of response function
        flag: -lmax %d
nthreads: (an integer (int or long))
        number of threads. if zero, the number of available cpus will be
        used
        flag: -nthreads %d
out_sf: (a file name)
        write a mask containing single-fibre voxels
        flag: -sf %s
shell: (a list of items which are a float)
        specify one or more dw gradient shells
        flag: -shell %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
test_all: (a boolean)
        re-test all voxels at every iteration
        flag: -test_all
vol_ratio: (a float)
```

```
        maximal volume ratio between the sum of all other positive lobes in
        the voxel and the largest FOD lobe
        flag: -volume_ratio %f
```

Outputs:

```
out_file: (an existing file name)
        the output response file
out_sf: (a file name)
        mask containing single-fibre voxels
```

CHAPTER 100

interfaces.mrtrix3.reconst

100.1 EstimateFOD

Link to code

Wraps command **dwi2fod**

Convert diffusion-weighted images to tensor images

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. The spherical harmonic coefficients are stored as follows. First, since the signal attenuation profile is real, 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, only the even elements are computed.

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. Each volume will correspond to the following:

volume 0: l = 0, m = 0 volume 1: l = 2, m = -2 (imaginary part of m=2 SH) volume 2: l = 2, m = -1 (imaginary part of m=1 SH) volume 3: l = 2, m = 0 volume 4: l = 2, m = 1 (real part of m=1 SH) volume 5: l = 2, m = 2 (real part of m=2 SH) etc...

100.1.1 Example

```
>>> import nipype.interfaces.mrtrix3 as mrt
>>> fod = mrt.EstimateFOD()
>>> fod.inputs.in_file = 'dwi.mif'
>>> fod.inputs.response = 'response.txt'
>>> fod.inputs.in_mask = 'mask.nii.gz'
>>> fod.inputs.grad_fsl = ('bvecs', 'bvals')
>>> fod.cmdline
'dwi2fod -fslgrad bvecs bvals -mask mask.nii.gz dwi.mif response.txt fods.mif'
>>> fod.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input diffusion weighted images
        flag: %s, position: -3
out_file: (a file name, nipype default value: fods.mif)
        the output spherical harmonics coefficients image
```

```
        flag: %s, position: -1
response: (an existing file name)
        a text file containing the diffusion-weighted signal response
        function coefficients for a single fibre population
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
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).
        flag: -bvalue_scaling %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
grad_file: (an existing file name)
        dw gradient scheme (MRTrix format
        flag: -grad %s
grad_fsl: (a tuple of the form: (an existing file name, an existing
         file name))
        (bvecs, bvals) dw gradient scheme (FSL format
        flag: -fslgrad %s %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_bval: (an existing file name)
        bvals file in FSL format
in_bvec: (an existing file name)
        bvecs file in FSL format
        flag: -fslgrad %s %s
in_dirs: (an existing file name)
        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.
        flag: -directions %s
in_mask: (an existing file name)
        provide initial mask image
        flag: -mask %s
max_sh: (an integer (int or long))
        maximum harmonic degree of response function
        flag: -lmax %d
n_iter: (an integer (int or long))
        the maximum number of iterations to perform for each voxel
        flag: -niter %d
neg_lambda: (a float)
        the regularisation parameter lambda that controls the strength of
        the non-negativity constraint
        flag: -neg_lambda %f
nthreads: (an integer (int or long))
        number of threads. if zero, the number of available cpus will be
        used
```

```
        flag: -nthreads %d
sh_filter: (an existing file name)
        the linear frequency filtering parameters used for the initial
        linear spherical deconvolution step (default = [ 1 1 1 0 0 ]). These
        should be supplied as a text file containing the filtering
        coefficients for each even harmonic order.
        flag: -filter %s
shell: (a list of items which are a float)
        specify one or more dw gradient shells
        flag: -shell %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
thres: (a float)
        the threshold below which the amplitude of the FOD is assumed to be
        zero, expressed as an absolute amplitude
        flag: -threshold %f
```

Outputs:

```
out_file: (an existing file name)
        the output response file
```

100.2 FitTensor

Link to code

Wraps command **dwi2tensor**

Convert diffusion-weighted images to tensor images

100.2.1 Example

```
>>> import nipype.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
'dwi2tensor -fslgrad bvecs bvals -mask mask.nii.gz dwi.mif dti.mif'
>>> tsr.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input diffusion weighted images
        flag: %s, position: -2
out_file: (a file name, nipype default value: dti.mif)
        the output diffusion tensor image
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
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).
        flag: -bvalue_scaling %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
grad_file: (an existing file name)
        dw gradient scheme (MRTrix format
        flag: -grad %s
grad_fsl: (a tuple of the form: (an existing file name, an existing
         file name))
        (bvecs, bvals) dw gradient scheme (FSL format
        flag: -fslgrad %s %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_bval: (an existing file name)
        bvals file in FSL format
in_bvec: (an existing file name)
        bvecs file in FSL format
        flag: -fslgrad %s %s
in_mask: (an existing file name)
        only perform computation within the specified binary brain mask
        image
        flag: -mask %s
method: ('nonlinear' or 'loglinear' or 'sech' or 'rician')
        select method used to perform the fitting
        flag: -method %s
nthreads: (an integer (int or long))
        number of threads. if zero, the number of available cpus will be
        used
        flag: -nthreads %d
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
        flag: -regularisation %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        the output DTI file
```

CHAPTER 101

interfaces.mrtrix3.tracking

101.1 Tractography

Link to code
Wraps command **tckgen**
Performs streamlines tractography after selecting the appropriate algorithm.

101.1.1 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
'tckgen -algorithm iFOD2 -mask mask.nii.gz -seed_sphere 80.000000,100.000000,70.000000,10.000000
>>> tk.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input file to be processed
        flag: %s, position: -2
out_file: (a file name, nipype default value: tracked.tck)
        output file containing tracks
        flag: %s, position: -1

[Optional]
act_file: (an existing file name)
        use the Anatomically-Constrained Tractography framework during
        tracking; provided image must be in the 5TT (five - tissue - type)
        format
        flag: -act %s
algorithm: ('iFOD2' or 'FACT' or 'iFOD1' or 'Nulldist' or 'SD_Stream'
         or 'Tensor_Det' or 'Tensor_Prob', nipype default value: iFOD2)
        tractography algorithm to be used
        flag: -algorithm %s
angle: (a float)
        set the maximum angle between successive steps (default is 90deg x
        stepsize / voxelsize)
        flag: -angle %f
args: (a string)
        Additional parameters to the command
        flag: %s
```

```
    backtrack: (a boolean)
            allow tracks to be truncated
            flag: -backtrack
    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).
            flag: -bvalue_scaling %s
    crop_at_gmwmi: (a boolean)
            crop streamline endpoints more precisely as they cross the GM-WM
            interface
            flag: -crop_at_gmwmi
    cutoff: (a float)
            set the FA or FOD amplitude cutoff for terminating tracks (default
            is 0.1)
            flag: -cutoff %f
    cutoff_init: (a float)
            set the minimum FA or FOD amplitude for initiating tracks (default
            is the same as the normal cutoff)
            flag: -initcutoff %f
    downsample: (a float)
            downsample the generated streamlines to reduce output file size
            flag: -downsample %f
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    grad_file: (an existing file name)
            dw gradient scheme (MRTrix format
            flag: -grad %s
    grad_fsl: (a tuple of the form: (an existing file name, an existing
             file name))
            (bvecs, bvals) dw gradient scheme (FSL format
            flag: -fslgrad %s %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    in_bval: (an existing file name)
            bvals file in FSL format
    in_bvec: (an existing file name)
            bvecs file in FSL format
            flag: -fslgrad %s %s
    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
            flag: -initdirection %f,%f,%f
    max_length: (a float)
            set the maximum length of any track in mm (default is 100 x
            voxelsize)
            flag: -maxlength %f
    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
            flag: -max_seed_attempts %d
    max_tracks: (an integer (int or long))
```

```
        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)
        flag: -maxnum %d
min_length: (a float)
        set the minimum length of any track in mm (default is 5 x voxelsize)
        flag: -minlength %f
n_samples: (an integer (int or long))
        set the number of FOD samples to take per step for the 2nd order
        (iFOD2) method
        flag: -samples %d
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
        flag: -number %d
n_trials: (an integer (int or long))
        set the maximum number of sampling trials at each point (only used
        for probabilistic tracking)
        flag: -trials %d
noprecompt: (a boolean)
        do NOT pre-compute legendre polynomial values. Warning: this will
        slow down the algorithm by a factor of approximately 4
        flag: -noprecomputed
nthreads: (an integer (int or long))
        number of threads. if zero, the number of available cpus will be
        used
        flag: -nthreads %d
out_seeds: (a file name)
        output the seed location of all successful streamlines to a file
        flag: -output_seeds %s
power: (an integer (int or long))
        raise the FOD to the power specified (default is 1/nsamples)
        flag: -power %d
roi_excl: (an existing file name 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
        flag: -exclude %s
roi_incl: (an existing file name 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
        flag: -include %s
roi_mask: (an existing file name 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
        flag: -mask %s
seed_dynamic: (an existing file name)
        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.
        flag: -seed_dynamic %s
seed_gmwmi: (an existing file name)
        seed from the grey matter - white matter interface (only valid if
```

```
            using ACT framework)
            flag: -seed_gmwmi %s
            requires: act_file
    seed_grid_voxel: (a tuple of the form: (an existing file name, 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)
            flag: -seed_grid_per_voxel %s %d
            mutually_exclusive: seed_image, seed_rnd_voxel
    seed_image: (an existing file name)
            seed streamlines entirely at random within mask
            flag: -seed_image %s
    seed_rejection: (an existing file name)
            seed from an image using rejection sampling (higher values = more
            probable to seed from
            flag: -seed_rejection %s
    seed_rnd_voxel: (a tuple of the form: (an existing file name, an
             integer (int or long)))
            seed a fixed number of streamlines per voxel in a mask image; random
            placement of seeds in each voxel
            flag: -seed_random_per_voxel %s %d
            mutually_exclusive: seed_image, seed_grid_voxel
    seed_sphere: (a tuple of the form: (a float, a float, a float, a
             float))
            spherical seed
            flag: -seed_sphere %f,%f,%f,%f
    sph_trait: (a tuple of the form: (a float, a float, a float, a
             float))
            flag: %f,%f,%f,%f
    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)
            flag: -step %f
    stop: (a boolean)
            stop propagating a streamline once it has traversed all include
            regions
            flag: -stop
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    unidirectional: (a boolean)
            track from the seed point in one direction only (default is to track
            in both directions)
            flag: -unidirectional
    use_rk4: (a boolean)
            use 4th-order Runge-Kutta integration (slower, but eliminates
            curvature overshoot in 1st-order deterministic methods)
            flag: -rk4
```

Outputs:

```
    out_file: (an existing file name)
            the output filtered tracks
    out_seeds: (a file name)
            output the seed location of all successful streamlines to a file
```

interfaces.mrtrix3.utils

102.1 BrainMask

Link to code
Wraps command **dwi2mask**
Convert a mesh surface to a partial volume estimation image

102.1.1 Example

```
>>> import nipype.interfaces.mrtrix3 as mrt
>>> bmsk = mrt.BrainMask()
>>> bmsk.inputs.in_file = 'dwi.mif'
>>> bmsk.cmdline
'dwi2mask dwi.mif brainmask.mif'
>>> bmsk.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input diffusion weighted images
        flag: %s, position: -2
out_file: (a file name, nipype default value: brainmask.mif)
        output brain mask
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
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).
        flag: -bvalue_scaling %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
grad_file: (an existing file name)
        dw gradient scheme (MRTrix format
        flag: -grad %s
grad_fsl: (a tuple of the form: (an existing file name, an existing
```

```
            file name))
           (bvecs, bvals) dw gradient scheme (FSL format
           flag: -fslgrad %s %s
    ignore_exception: (a boolean, nipype default value: False)
           Print an error message instead of throwing an exception in case the
           interface fails to run
    in_bval: (an existing file name)
           bvals file in FSL format
    in_bvec: (an existing file name)
           bvecs file in FSL format
           flag: -fslgrad %s %s
    nthreads: (an integer (int or long))
           number of threads. if zero, the number of available cpus will be
           used
           flag: -nthreads %d
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
           Control terminal output: `stream` - displays to terminal immediately
           (default), `allatonce` - waits till command is finished to display
           output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
           the output response file
```

102.2 ComputeTDI

Link to code

Wraps 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)

102.2.1 Example

```
>>> import nipype.interfaces.mrtrix3 as mrt
>>> tdi = mrt.ComputeTDI()
>>> tdi.inputs.in_file = 'dti.mif'
>>> tdi.cmdline
'tckmap dti.mif tdi.mif'
>>> tdi.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input tractography
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
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
        flag: -constrast %s
data_type: ('float' or 'unsigned int')
        specify output image data type
        flag: -datatype %s
dixel: (a file name)
        map streamlines todixels within each voxel. Directions are stored
        asazimuth elevation pairs.
        flag: -dixel %s
ends_only: (a boolean)
        only map the streamline endpoints to the image
        flag: -ends_only
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
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
        flag: -fwhm_tck %f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_map: (an existing file name)
        provide thescalar image map for generating images with 'scalar_map'
        contrasts, or the SHs image for fod_amp
        flag: -image %s
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)
        flag: -map_zero
max_tod: (an integer (int or long))
        generate a Track Orientation Distribution (TOD) in each voxel.
```

```
        flag: -tod %d
nthreads: (an integer (int or long))
        number of threads. if zero, the number of available cpus will be
        used
        flag: -nthreads %d
out_file: (a file name, nipype default value: tdi.mif)
        output TDI file
        flag: %s, position: -1
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)
        flag: -precise
reference: (an existing file name)
        a referenceimage to be used as template
        flag: -template %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.
        flag: -stat_tck %s
stat_vox: ('sum' or 'min' or 'mean' or 'max')
        define the statistic for choosing the finalvoxel intesities for a
        given contrast
        flag: -stat_vox %s
tck_weights: (an existing file name)
        specify a text scalar file containing the streamline weights
        flag: -tck_weights_in %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
upsample: (an integer (int or long))
        upsample the tracks by some ratio using Hermite interpolation before
        mappping
        flag: -upsample %d
use_dec: (a boolean)
        perform mapping in DEC space
        flag: -dec
vox_size: (a list of items which are an integer (int or long))
        voxel dimensions
        flag: -vox %s
```

Outputs:

```
out_file: (a file name)
        output TDI file
```

102.3 Generate5tt

Link to code

Wraps command **5ttgen**

Concatenate segmentation results from FSL FAST and FIRST into the 5TT format required for ACT

102.3.1 Example

```
>>> import nipype.interfaces.mrtrix3 as mrt
>>> seg = mrt.Generate5tt()
>>> seg.inputs.in_fast = ['tpm_00.nii.gz',
...                       'tpm_01.nii.gz', 'tpm_02.nii.gz']
>>> seg.inputs.in_first = 'first_merged.nii.gz'
>>> seg.cmdline
'5ttgen tpm_00.nii.gz tpm_01.nii.gz tpm_02.nii.gz first_merged.nii.gz act-5tt.mif'
>>> seg.run()
```

Inputs:

```
[Mandatory]
in_fast: (a list of items which are an existing file name)
        list of PVE images from FAST
        flag: %s, position: -3
out_file: (a file name, nipype default value: act-5tt.mif)
        name of output file
        flag: %s, position: -1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_first: (an existing file name)
        combined segmentation file from FIRST
        flag: %s, position: -2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        segmentation for ACT in 5tt format
```

102.4 Mesh2PVE

Link to code
Wraps command **mesh2pve**
Convert a mesh surface to a partial volume estimation image

102.4.1 Example

```
>>> import nipype.interfaces.mrtrix3 as mrt
>>> m2p = mrt.Mesh2PVE()
>>> m2p.inputs.in_file = 'surf1.vtk'
>>> m2p.inputs.reference = 'dwi.mif'
>>> m2p.inputs.in_first = 'T1.nii.gz'
```

```
>>> m2p.cmdline
'mesh2pve -first T1.nii.gz surf1.vtk dwi.mif mesh2volume.nii.gz'
>>> m2p.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        input mesh
        flag: %s, position: -3
out_file: (a file name, nipype default value: mesh2volume.nii.gz)
        output file containing SH coefficients
        flag: %s, position: -1
reference: (an existing file name)
        input reference image
        flag: %s, position: -2

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_first: (an existing file name)
        indicates that the mesh file is provided by FSL FIRST
        flag: -first %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (an existing file name)
        the output response file
```

102.5 TCK2VTK

Link to code

Wraps command **tck2vtk**

Convert a track file to a vtk format, cave: coordinates are in XYZ coordinates not reference

102.5.1 Example

```
>>> import nipype.interfaces.mrtrix3 as mrt
>>> vtk = mrt.TCK2VTK()
>>> vtk.inputs.in_file = 'tracks.tck'
>>> vtk.inputs.reference = 'b0.nii'
>>> vtk.cmdline
'tck2vtk -image b0.nii tracks.tck tracks.vtk'
>>> vtk.run()
```

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            input tractography
            flag: %s, position: -2

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    nthreads: (an integer (int or long))
            number of threads. if zero, the number of available cpus will be
            used
            flag: -nthreads %d
    out_file: (a file name, nipype default value: tracks.vtk)
            output VTK file
            flag: %s, position: -1
    reference: (an existing file name)
            if specified, the properties of this image will be used to convert
            track point positions from real (scanner) coordinates into image
            coordinates (in mm).
            flag: -image %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    voxel: (an existing file name)
            if specified, the properties of this image will be used to convert
            track point positions from real (scanner) coordinates into image
            coordinates.
            flag: -image %s
```

Outputs:

```
    out_file: (a file name)
            output VTK file
```

102.6 TensorMetrics

Link to code
Wraps command **tensor2metric**
Compute metrics from tensors

102.6.1 Example

```
    >>> import nipype.interfaces.mrtrix3 as mrt
    >>> comp = mrt.TensorMetrics()
    >>> comp.inputs.in_file = 'dti.mif'
    >>> comp.inputs.out_fa = 'fa.mif'
    >>> comp.cmdline
```

```
    'tensor2metric -fa fa.mif dti.mif'
    >>> comp.run()
```

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            input DTI image
            flag: %s, position: -1

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    component: (a list of items which are any value)
            specify the desired eigenvalue/eigenvector(s). Note that several
            eigenvalues can be specified as a number sequence
            flag: -num %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    in_mask: (an existing file name)
            only perform computation within the specified binary brain mask
            image
            flag: -mask %s
    modulate: ('FA' or 'none' or 'eval')
            how to modulate the magnitude of the eigenvectors
            flag: -modulate %s
    out_adc: (a file name)
            output ADC file
            flag: -adc %s
    out_eval: (a file name)
            output selected eigenvalue(s) file
            flag: -value %s
    out_evec: (a file name)
            output selected eigenvector(s) file
            flag: -vector %s
    out_fa: (a file name)
            output FA file
            flag: -fa %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_adc: (a file name)
            output ADC file
    out_eval: (a file name)
            output selected eigenvalue(s) file
    out_evec: (a file name)
            output selected eigenvector(s) file
    out_fa: (a file name)
            output FA file
```

CHAPTER 103

interfaces.nipy.model

103.1 EstimateContrast

Link to code

Estimate contrast of a fitted model.

Inputs:

```
[Mandatory]
axis: (any value)
beta: (an existing file name)
        beta coefficients of the fitted model
constants: (any value)
contrasts: (a list of items which are a tuple of the form: (a string,
         'T', a list of items which are a string, a list of items which are
         a float) or a tuple of the form: (a string, 'T', a list of items
         which are a string, a list of items which are a float, a list of
         items which are a float) or a tuple of the form: (a string, 'F', a
         list of items which are a tuple of the form: (a string, 'T', a list
         of items which are a string, a list of items which are a float) or
         a tuple of the form: (a string, 'T', a list of items which are a
         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.
dof: (any value)
        degrees of freedom
nvbeta: (any value)
reg_names: (a list of items which are any value)
s2: (an existing file name)
        squared variance of the residuals

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (a file name)
```

Outputs:

```
p_maps: (a list of items which are an existing file name)
stat_maps: (a list of items which are an existing file name)
z_maps: (a list of items which are an existing file name)
```

103.2 FitGLM

Link to code

Fit GLM model based on the specified design. Supports only single or concatenated runs.
Inputs:

```
[Mandatory]
TR: (a float)
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 uless they are concatenated
        (see SpecifyModel options)

[Optional]
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'
hrf_model: ('Canonical' or 'Canonical With Derivative' or 'FIR',
         nipype default value: Canonical)
        that specifies the hemodynamic reponse function it can be
        'Canonical', 'Canonical With Derivative' or 'FIR'
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask: (a file name)
        restrict the fitting only to the region defined by this mask
method: ('kalman' or 'ols', nipype default value: kalman)
        method to fit the model, ols or kalma; kalman is more time consuming
        but it supports autoregressive model
model: ('ar1' or 'spherical', nipype default value: ar1)
        autoregressive mode is available only for the kalman method
normalize_design_matrix: (a boolean, nipype default value: False)
        normalize (zscore) the regressors before fitting
plot_design_matrix: (a boolean, nipype default value: False)
save_residuals: (a boolean, nipype default value: False)
```

Outputs:

```
a: (an existing file name)
axis: (any value)
beta: (an existing file name)
constants: (any value)
dof: (any value)
nvbeta: (any value)
reg_names: (a list of items which are any value)
residuals: (a file name)
s2: (an existing file name)
```

CHAPTER 104

interfaces.nipy.preprocess

104.1 ComputeMask

Link to code
Inputs:

```
[Mandatory]
mean_volume: (an existing file name)
        mean EPI image, used to compute the threshold for the mask

[Optional]
M: (a float)
        upper fraction of the histogram to be discarded
cc: (a boolean)
        Keep only the largest connected component
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
m: (a float)
        lower fraction of the histogram to be discarded
reference_volume: (an existing file name)
        reference volume used to compute the mask. If none is give, the mean
        volume is used.
```

Outputs:

```
brain_mask: (an existing file name)
```

104.2 FmriRealign4d

Link to code
Simultaneous motion and slice timing correction algorithm
This interface wraps nipy's FmriRealign4d algorithm [1].

104.2.1 Examples

```
>>> from nipype.interfaces.nipy.preprocess import FmriRealign4d
>>> realigner = FmriRealign4d()
>>> realigner.inputs.in_file = ['functional.nii']
>>> realigner.inputs.tr = 2
>>> realigner.inputs.slice_order = list(range(0,67))
>>> res = realigner.run()
```

[1] Roche A. A four-dimensional registration algorithm with application to joint correction of motion and slice timing in fMRI. IEEE Trans Med Imaging. 2011 Aug;30(8):1546-54. DOI.

104.2.2 References

Inputs:

```
[Mandatory]
in_file: (a list of items which are an existing file name)
        File to realign
tr: (a float)
        TR in seconds

[Optional]
between_loops: (a list of items which are an integer (int or long),
         nipype default value: [5])
        loops used to realign different runs
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
loops: (a list of items which are an integer (int or long), nipype
         default value: [5])
        loops within each run
slice_order: (a list of items which are an integer (int or long))
        0 based slice order. This would be equivalent to
        enteringnp.argsort(spm_slice_order) for this field. This
        effectsinterleaved acquisition. This field will be deprecated
        infuture Nipy releases and be replaced by actual sliceacquisition
        times.
        requires: time_interp
speedup: (a list of items which are an integer (int or long), nipype
         default value: [5])
        successive image sub-sampling factors for acceleration
start: (a float, nipype default value: 0.0)
        time offset into TR to align slices to
time_interp: (True)
        Assume smooth changes across time e.g., fmri series. If you don't
        want slice timing correction set this to undefined
        requires: slice_order
tr_slices: (a float)
        TR slices
        requires: time_interp
```

Outputs:

```
out_file: (a list of items which are an existing file name)
        Realigned files
par_file: (a list of items which are an existing file name)
        Motion parameter files
```

104.3 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.

104.3.1 Examples

```
>>> from nipype.interfaces.nipy import SpaceTimeRealigner
>>> #Run spatial realignment only
>>> realigner = SpaceTimeRealigner()
>>> realigner.inputs.in_file = ['functional.nii']
>>> res = realigner.run()
```

```
>>> 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()
```

104.3.2 References

Inputs:

```
[Mandatory]
in_file: (a list of items which are an existing file name)
        File to realign

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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
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.
tr: (a float)
        TR in seconds
        requires: slice_times
```

Outputs:

```
out_file: (a list of items which are an existing file name)
        Realigned files
par_file: (a list of items which are an existing file name)
        Motion parameter files. Angles are not euler angles
```

104.4 Trim

Link to code

Simple interface to trim a few volumes from a 4d fmri nifti file

104.4.1 Examples

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        EPI image to trim

[Optional]
begin_index: (an integer (int or long), nipype default value: 0)
        first volume
end_index: (an integer (int or long), nipype default value: 0)
        last volume indexed as in python (and 0 for last)
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output filename
suffix: (a string, nipype default value: _trim)
        suffix for out_file to use if no out_file provided
```

Outputs:

```
out_file: (an existing file name)
```

CHAPTER 105

interfaces.nipy.utils

105.1 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 `nipype.algorithms.metrics.Similarity` instead.

105.1.1 Example

```
>>> from nipype.interfaces.nipy.utils import Similarity
>>> similarity = Similarity()
>>> similarity.inputs.volume1 = 'rc1s1.nii'
>>> similarity.inputs.volume2 = 'rc1s2.nii'
>>> similarity.inputs.mask1 = 'mask.nii'
>>> similarity.inputs.mask2 = 'mask.nii'
>>> similarity.inputs.metric = 'cr'
>>> res = similarity.run()
```

Inputs:

```
[Mandatory]
volume1: (an existing file name)
        3D volume
volume2: (an existing file name)
        3D volume

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask1: (an existing file name)
        3D volume
mask2: (an existing file name)
        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 float)
        Similarity between volume 1 and 2
```

CHAPTER 106

interfaces.nitime.analysis

106.1 CoherenceAnalyzer

Link to code
Inputs:

```
[Mandatory]

[Optional]
NFFT: (an 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.)
TR: (a float)
        The TR used to collect the datain your csv file <in_file>
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'
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 overwhich the analysis will
        average.[low,high] (Default [0.02,0.15]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
in_TS: (any value)
        a nitime TimeSeries object
in_file: (an existing file name)
        csv file with ROIs on the columns and time-points on the rows. ROI
        names at the top row
        requires: TR
n_overlap: (an integer >= 0, nipype default value: 0)
        The number of samples which overlapbetween subsequent
        windows.(Defaults to 0)
output_csv_file: (a file name)
        File to write outputs (coherence,time-delay) with file-names:
        file_name_ {coherence,timedelay}
output_figure_file: (a file name)
        File to write output figures (coherence,time-delay) with file-names:
        file_name_{coherence,timedelay}. Possible formats:
        .png,.svg,.pdf,.jpg,...
```

Outputs:

```
coherence_array: (an array)
        The pairwise coherence valuesbetween the ROIs
```

```
    coherence_csv: (a file name)
            A csv file containing the pairwise coherence values
    coherence_fig: (a file name)
            Figure representing coherence values
    timedelay_array: (an array)
            The pairwise time delays between theROIs (in seconds)
    timedelay_csv: (a file name)
            A csv file containing the pairwise time delay values
    timedelay_fig: (a file name)
            Figure representing coherence values
```

interfaces.petpvc

107.1 PETPVC

Link to code
Wraps 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.
There is a publication waiting to be accepted for this software tool.
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)

107.1.1 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"

107.1.2 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()
```

Inputs:

```
[Mandatory]
fwhm_x: (a float)
        The full-width at half maximum in mm along x-axis
        flag: -x %.4f
fwhm_y: (a float)
        The full-width at half maximum in mm along y-axis
        flag: -y %.4f
fwhm_z: (a float)
        The full-width at half maximum in mm along z-axis
        flag: -z %.4f
in_file: (an existing file name)
        PET image file
        flag: -i %s
mask_file: (an existing file name)
        Mask image file
        flag: -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
        flag: -p %s

[Optional]
alpha: (a float)
        Alpha value
        flag: -a %.4f
args: (a string)
```

```
        Additional parameters to the command
        flag: %s
debug: (a boolean, nipype default value: False)
        Prints debug information
        flag: -d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
n_deconv: (an integer (int or long))
        Number of deconvolution iterations
        flag: -k %d
n_iter: (an integer (int or long))
        Number of iterations
        flag: -n %d
out_file: (a file name)
        Output file
        flag: -o %s
stop_crit: (a float)
        Stopping criterion
        flag: -a %.4f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
out_file: (a file name)
        Output file
```

interfaces.semtools.brains.classify

108.1 BRAINSPosteriorToContinuousClass

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputBasalGmVolume: (an existing file name)
            Basal Grey Matter Posterior Volume
            flag: --inputBasalGmVolume %s
    inputCrblGmVolume: (an existing file name)
            Cerebellum Grey Matter Posterior Volume
            flag: --inputCrblGmVolume %s
    inputCrblWmVolume: (an existing file name)
            Cerebellum White Matter Posterior Volume
            flag: --inputCrblWmVolume %s
    inputCsfVolume: (an existing file name)
            CSF Posterior Volume
            flag: --inputCsfVolume %s
    inputSurfaceGmVolume: (an existing file name)
            Surface Grey Matter Posterior Volume
            flag: --inputSurfaceGmVolume %s
```

```
    inputVbVolume: (an existing file name)
            Venous Blood Posterior Volume
            flag: --inputVbVolume %s
    inputWhiteVolume: (an existing file name)
            White Matter Posterior Volume
            flag: --inputWhiteVolume %s
    outputVolume: (a boolean or a file name)
            Output Continuous Tissue Classified Image
            flag: --outputVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputVolume: (an existing file name)
            Output Continuous Tissue Classified Image
```

interfaces.semtools.brains.segmentation

109.1 BRAINSTalairach

Link to code
Wraps 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 structred 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:

```
    [Mandatory]

    [Optional]
    AC: (a list of items which are a float)
            Location of AC Point
            flag: --AC %s
    ACisIndex: (a boolean)
            AC Point is Index
            flag: --ACisIndex
    IRP: (a list of items which are a float)
            Location of IRP Point
            flag: --IRP %s
    IRPisIndex: (a boolean)
            IRP Point is Index
            flag: --IRPisIndex
    PC: (a list of items which are a float)
            Location of PC Point
            flag: --PC %s
    PCisIndex: (a boolean)
            PC Point is Index
            flag: --PCisIndex
    SLA: (a list of items which are a float)
            Location of SLA Point
            flag: --SLA %s
```

```
    SLAisIndex: (a boolean)
            SLA Point is Index
            flag: --SLAisIndex
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
            Input image used to define physical space of images
            flag: --inputVolume %s
    outputBox: (a boolean or a file name)
            Name of the resulting Talairach Bounding Box file
            flag: --outputBox %s
    outputGrid: (a boolean or a file name)
            Name of the resulting Talairach Grid file
            flag: --outputGrid %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputBox: (an existing file name)
            Name of the resulting Talairach Bounding Box file
    outputGrid: (an existing file name)
            Name of the resulting Talairach Grid file
```

109.2 BRAINSTalairachMask

Link to code

Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
```

```
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    expand: (a boolean)
            Expand exterior box to include surface CSF
            flag: --expand
    hemisphereMode: ('left' or 'right' or 'both')
            Mode for box creation: left, right, both
            flag: --hemisphereMode %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
            Input image used to define physical space of resulting mask
            flag: --inputVolume %s
    outputVolume: (a boolean or a file name)
            Output filename for the resulting binary image
            flag: --outputVolume %s
    talairachBox: (an existing file name)
            Name of the Talairach box file.
            flag: --talairachBox %s
    talairachParameters: (an existing file name)
            Name of the Talairach parameter file.
            flag: --talairachParameters %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputVolume: (an existing file name)
            Output filename for the resulting binary image
```

109.3 SimilarityIndex

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    ANNContinuousVolume: (an existing file name)
            ANN Continuous volume to be compared to the manual volume
            flag: --ANNContinuousVolume %s
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
```

```
          with values which are a value of type 'str', nipype default value:
          {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputManualVolume: (an existing file name)
        input manual(reference) volume
        flag: --inputManualVolume %s
outputCSVFilename: (an existing file name)
        output CSV Filename
        flag: --outputCSVFilename %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
thresholdInterval: (a float)
        Threshold interval to compute similarity index between zero and one
        flag: --thresholdInterval %f
```

Outputs:

```
None
```

interfaces.semtools.brains.utilities

110.1 HistogramMatchingFilter

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    histogramAlgorithm: ('OtsuHistogramMatching')
             histogram algrithm selection
            flag: --histogramAlgorithm %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputBinaryVolume: (an existing file name)
            inputBinaryVolume
            flag: --inputBinaryVolume %s
    inputVolume: (an existing file name)
            The Input image to be computed for statistics
            flag: --inputVolume %s
    numberOfHistogramBins: (an integer (int or long))
             number of histogram bin
            flag: --numberOfHistogramBins %d
    numberOfMatchPoints: (an integer (int or long))
             number of histogram matching points
            flag: --numberOfMatchPoints %d
    outputVolume: (a boolean or a file name)
            Output Image File Name
            flag: --outputVolume %s
    referenceBinaryVolume: (an existing file name)
            referenceBinaryVolume
```

```
        flag: --referenceBinaryVolume %s
referenceVolume: (an existing file name)
        The Input image to be computed for statistics
        flag: --referenceVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
         verbose mode running for debbuging
        flag: --verbose
writeHistogram: (a string)
         decide if histogram data would be written with prefixe of the file
        name
        flag: --writeHistogram %s
```

Outputs:

```
outputVolume: (an existing file name)
        Output Image File Name
```

interfaces.semtools.converters

111.1 DWICompare

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume1: (an existing file name)
            First input volume (.nhdr or .nrrd)
            flag: --inputVolume1 %s
    inputVolume2: (an existing file name)
            Second input volume (.nhdr or .nrrd)
            flag: --inputVolume2 %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
None
```

111.2 DWISimpleCompare

Link to code
Wraps 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 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
checkDWIData: (a boolean)
        check for existence of DWI data, and if present, compare it
        flag: --checkDWIData
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume1: (an existing file name)
        First input volume (.nhdr or .nrrd)
        flag: --inputVolume1 %s
inputVolume2: (an existing file name)
        Second input volume (.nhdr or .nrrd)
        flag: --inputVolume2 %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
None
```

interfaces.semtools.diffusion.diffusion

112.1 DWIConvert

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    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.
            Use with caution!
            flag: --allowLossyConversion
    args: (a string)
            Additional parameters to the command
            flag: %s
    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.
            flag: --conversionMode %s
    environ: (a dictionary with keys which are a value of type 'str' and
```

```
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fMRI: (a boolean)
        Output a NRRD file, but without gradients
        flag: --fMRI
fslNIFTIFile: (an existing file name)
        4D NIfTI file containing gradient volumes
        flag: --fslNIFTIFile %s
gradientVectorFile: (a boolean or a file name)
        Text file giving gradient vectors
        flag: --gradientVectorFile %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputBValues: (an existing file name)
        The B Values are stored in FSL .bval text file format
        flag: --inputBValues %s
inputBVectors: (an existing file name)
        The Gradient Vectors are stored in FSL .bvec text file format
        flag: --inputBVectors %s
inputDicomDirectory: (an existing directory name)
        Directory holding Dicom series
        flag: --inputDicomDirectory %s
inputVolume: (an existing file name)
        Input DWI volume -- not used for DicomToNrrd mode.
        flag: --inputVolume %s
outputBValues: (a boolean or a file name)
        The B Values are stored in FSL .bval text file format (defaults to
        <outputVolume>.bval)
        flag: --outputBValues %s
outputBVectors: (a boolean or a file name)
        The Gradient Vectors are stored in FSL .bvec text file format
        (defaults to <outputVolume>.bvec)
        flag: --outputBVectors %s
outputDirectory: (a boolean or a directory name)
        Directory holding the output NRRD file
        flag: --outputDirectory %s
outputVolume: (a boolean or a file name)
        Output filename (.nhdr or .nrrd)
        flag: --outputVolume %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.
        flag: --smallGradientThreshold %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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.
        flag: --transposeInputBVectors
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.
        flag: --useBMatrixGradientDirections
useIdentityMeaseurementFrame: (a boolean)
        Adjust all the gradients so that the measurement frame is an
        identity matrix.
        flag: --useIdentityMeaseurementFrame
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.
        flag: --writeProtocolGradientsFile
```

Outputs:

```
gradientVectorFile: (an existing file name)
        Text file giving gradient vectors
outputBValues: (an existing file name)
        The B Values are stored in FSL .bval text file format (defaults to
        <outputVolume>.bval)
outputBVectors: (an existing file name)
        The Gradient Vectors are stored in FSL .bvec text file format
        (defaults to <outputVolume>.bvec)
outputDirectory: (an existing directory name)
        Directory holding the output NRRD file
outputVolume: (an existing file name)
        Output filename (.nhdr or .nrrd)
```

112.2 dtiaverage

Link to code

Wraps command ** dtiaverage **

title: DTIAverage (DTIProcess)

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 aft

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/DTIProcess

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contributor: Casey Goodlett

Inputs:

```
[Mandatory]

[Optional]
DTI_double: (a boolean)
        Tensor components are saved as doubles (cannot be visualized in
```

```
        Slicer)
        flag: --DTI_double
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputs: (a list of items which are an existing file name)
        List of all the tensor fields to be averaged
        flag: --inputs %s...
tensor_output: (a boolean or a file name)
        Averaged tensor volume
        flag: --tensor_output %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        produce verbose output
        flag: --verbose
```

Outputs:

```
tensor_output: (an existing file name)
        Averaged tensor volume
```

112.3 dtiestim

Link to code

Wraps 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/DTIProcess
license: Copyright (c) Casey Goodlett. All rights reserved.

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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 DTIProcess compatible with Slicer execution, and simplified the stand-alone build requirements by removing the dependancies on boost and a fortran compiler.
Inputs:

```
[Mandatory]

[Optional]
B0: (a boolean or a file name)
        Baseline image, average of all baseline images
        flag: --B0 %s
B0_mask_output: (a boolean or a file name)
        B0 mask used for the estimation. B0 thresholded either with the -t
        option value or the automatic OTSU value
        flag: --B0_mask_output %s
DTI_double: (a boolean)
        Tensor components are saved as doubles (cannot be visualized in
        Slicer)
        flag: --DTI_double
args: (a string)
        Additional parameters to the command
        flag: %s
bad_region_mask: (an existing file name)
        Bad region mask. Image where for every voxel > 0 the tensors are not
        estimated
        flag: --bad_region_mask %s
brain_mask: (an existing file name)
        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.
        flag: --brain_mask %s
correction: ('none' or 'zero' or 'abs' or 'nearest')
        Correct the tensors if computed tensor is not semi-definite positive
        flag: --correction %s
defaultTensor: (a list of items which are a float)
        Default tensor used if estimated tensor is below a given threshold
        flag: --defaultTensor %s
dwi_image: (an existing file name)
        DWI image volume (required)
        flag: --dwi_image %s
```

```
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    idwi: (a boolean or a file name)
            idwi output image. Image with isotropic diffusion-weighted
            information = geometric mean of diffusion images
            flag: --idwi %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    method: ('lls' or 'wls' or 'nls' or 'ml')
            Esitmation method (lls:linear least squares, wls:weighted least
            squares, nls:non-linear least squares, ml:maximum likelihood)
            flag: --method %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
            flag: --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).
            flag: --shiftNegCoeff %f
    sigma: (a float)
            flag: --sigma %f
    step: (a float)
            Gradient descent step size (for nls and ml methods)
            flag: --step %f
    tensor_output: (a boolean or a file name)
            Tensor OutputImage
            flag: --tensor_output %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    threshold: (an integer (int or long))
            Baseline threshold for estimation. If not specified calculated using
            an OTSU threshold on the baseline image.
            flag: --threshold %d
    verbose: (a boolean)
            produce verbose output
            flag: --verbose
    weight_iterations: (an integer (int or long))
            Number of iterations to recaluate weightings from tensor estimate
            flag: --weight_iterations %d
```

Outputs:

```
    B0: (an existing file name)
            Baseline image, average of all baseline images
    B0_mask_output: (an existing file name)
            B0 mask used for the estimation. B0 thresholded either with the -t
```

```
        option value or the automatic OTSU value
idwi: (an existing file name)
        idwi output image. Image with isotropic diffusion-weighted
        information = geometric mean of diffusion images
tensor_output: (an existing file name)
        Tensor OutputImage
```

112.4 dtiprocess

Link to code

Wraps command ** dtiprocess **
title: DTIProcess (DTIProcess)
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 subregion 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/DTIProcess
license: Copyright (c) Casey Goodlett. All rights reserved.

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contributor: Casey Goodlett
Inputs:

```
[Mandatory]

[Optional]
DTI_double: (a boolean)
        Tensor components are saved as doubles (cannot be visualized in
        Slicer)
```

```
        flag: --DTI_double
RD_output: (a boolean or a file name)
        RD (Radial Diffusivity 1/2*(lambda2+lambda3)) output
        flag: --RD_output %s
affineitk_file: (an existing file name)
        Transformation file for affine transformation. ITK format.
        flag: --affineitk_file %s
args: (a string)
        Additional parameters to the command
        flag: %s
color_fa_output: (a boolean or a file name)
        Color Fractional Anisotropy output file
        flag: --color_fa_output %s
correction: ('none' or 'zero' or 'abs' or 'nearest')
        Correct the tensors if computed tensor is not semi-definite positive
        flag: --correction %s
deformation_output: (a boolean or a file name)
        Warped tensor field based on a deformation field. This option
        requires the --forward,-F transformation to be specified.
        flag: --deformation_output %s
dof_file: (an existing file name)
        Transformation file for affine transformation. This can be ITK
        format (or the outdated RView).
        flag: --dof_file %s
dti_image: (an existing file name)
        DTI tensor volume
        flag: --dti_image %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fa_gradient_output: (a boolean or a file name)
        Fractional Anisotropy Gradient output file
        flag: --fa_gradient_output %s
fa_gradmag_output: (a boolean or a file name)
        Fractional Anisotropy Gradient Magnitude output file
        flag: --fa_gradmag_output %s
fa_output: (a boolean or a file name)
        Fractional Anisotropy output file
        flag: --fa_output %s
forward: (an existing file name)
        Forward transformation. Assumed to be a deformation field in world
        coordinates, unless the --h-field option is specified.
        flag: --forward %s
frobenius_norm_output: (a boolean or a file name)
        Frobenius Norm Output
        flag: --frobenius_norm_output %s
hField: (a boolean)
        forward and inverse transformations are h-fields instead of
        displacement fields
        flag: --hField
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interpolation: ('nearestneighbor' or 'linear' or 'cubic')
        Interpolation type (nearestneighbor, linear, cubic)
        flag: --interpolation %s
lambda1_output: (a boolean or a file name)
```

```
        Axial Diffusivity - Lambda 1 (largest eigenvalue) output
        flag: --lambda1_output %s
lambda2_output: (a boolean or a file name)
        Lambda 2 (middle eigenvalue) output
        flag: --lambda2_output %s
lambda3_output: (a boolean or a file name)
        Lambda 3 (smallest eigenvalue) output
        flag: --lambda3_output %s
mask: (an existing file name)
        Mask tensors. Specify --outmask if you want to save the masked
        tensor field, otherwise the mask is applied just for the current
        processing
        flag: --mask %s
md_output: (a boolean or a file name)
        Mean Diffusivity output file
        flag: --md_output %s
negative_eigenvector_output: (a boolean or a file name)
        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.
        flag: --negative_eigenvector_output %s
newdof_file: (an existing file name)
        Transformation file for affine transformation. RView NEW format.
        (txt file output of dof2mat)
        flag: --newdof_file %s
outmask: (a boolean or a file name)
        Name of the masked tensor field.
        flag: --outmask %s
principal_eigenvector_output: (a boolean or a file name)
        Principal Eigenvectors Output
        flag: --principal_eigenvector_output %s
reorientation: ('fs' or 'ppd')
        Reorientation type (fs, ppd)
        flag: --reorientation %s
rot_output: (a boolean or a file name)
        Rotated tensor output file. Must also specify the dof file.
        flag: --rot_output %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].
        flag: --scalar_float
sigma: (a float)
        Scale of gradients
        flag: --sigma %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        produce verbose output
        flag: --verbose
```

Outputs:

```
RD_output: (an existing file name)
        RD (Radial Diffusivity 1/2*(lambda2+lambda3)) output
color_fa_output: (an existing file name)
        Color Fractional Anisotropy output file
deformation_output: (an existing file name)
        Warped tensor field based on a deformation field. This option
```

```
        requires the --forward,-F transformation to be specified.
fa_gradient_output: (an existing file name)
        Fractional Anisotropy Gradient output file
fa_gradmag_output: (an existing file name)
        Fractional Anisotropy Gradient Magnitude output file
fa_output: (an existing file name)
        Fractional Anisotropy output file
frobenius_norm_output: (an existing file name)
        Frobenius Norm Output
lambda1_output: (an existing file name)
        Axial Diffusivity - Lambda 1 (largest eigenvalue) output
lambda2_output: (an existing file name)
        Lambda 2 (middle eigenvalue) output
lambda3_output: (an existing file name)
        Lambda 3 (smallest eigenvalue) output
md_output: (an existing file name)
        Mean Diffusivity output file
negative_eigenvector_output: (an existing file name)
        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.
outmask: (an existing file name)
        Name of the masked tensor field.
principal_eigenvector_output: (an existing file name)
        Principal Eigenvectors Output
rot_output: (an existing file name)
        Rotated tensor output file. Must also specify the dof file.
```

interfaces.semtools.diffusion.gtract

113.1 compareTractInclusion

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %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
            flag: --closeness %f
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    numberOfPoints: (an integer (int or long))
            Number of points in comparison fiber pairs
            flag: --numberOfPoints %d
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    standardFiber: (an existing file name)
            Required: standard fiber tract file name
```

```
        flag: --standardFiber %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
testFiber: (an existing file name)
        Required: test fiber tract file name
        flag: --testFiber %s
testForBijection: (a boolean)
        Flag to apply the closeness criterion both ways
        flag: --testForBijection
testForFiberCardinality: (a boolean)
        Flag to require the same number of fibers in both tracts
        flag: --testForFiberCardinality
writeXMLPolyDataFile: (a boolean)
        Flag to make use of XML files when reading and writing vtkPolyData.
        flag: --writeXMLPolyDataFile
```

Outputs:

```
None
```

113.2 extractNrrdVectorIndex

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Required: input file containing the vector that will be extracted
        flag: --inputVolume %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
```

```
    outputVolume: (a boolean or a file name)
            Required: name of output NRRD file containing the vector image at
            the given index
            flag: --outputVolume %s
    setImageOrientation: ('AsAcquired' or 'Axial' or 'Coronal' or
             'Sagittal')
            Sets the image orientation of the extracted vector (Axial, Coronal,
            Sagittal)
            flag: --setImageOrientation %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    vectorIndex: (an integer (int or long))
            Index in the vector image to extract
            flag: --vectorIndex %d
```

Outputs:

```
    outputVolume: (an existing file name)
            Required: name of output NRRD file containing the vector image at
            the given index
```

113.3 gtractAnisotropyMap

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    anisotropyType: ('ADC' or 'FA' or 'RA' or 'VR' or 'AD' or 'RD' or
             'LI')
            Anisotropy Mapping Type: ADC, FA, RA, VR, AD, RD, LI
            flag: --anisotropyType %s
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
```

```
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputTensorVolume: (an existing file name)
            Required: input file containing the diffusion tensor image
            flag: --inputTensorVolume %s
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputVolume: (a boolean or a file name)
            Required: name of output NRRD file containing the selected kind of
            anisotropy scalar.
            flag: --outputVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputVolume: (an existing file name)
            Required: name of output NRRD file containing the selected kind of
            anisotropy scalar.
```

113.4 gtractAverageBvalues

Link to code

Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    averageB0only: (a boolean)
            Average only baseline gradients. All other gradient directions are
            not averaged, but retained in the outputVolume
            flag: --averageB0only
    directionsTolerance: (a float)
            Tolerance for matching identical gradient direction pairs
            flag: --directionsTolerance %f
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
```

```
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
            Required: input image file name containing multiple baseline
            gradients to average
            flag: --inputVolume %s
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputVolume: (a boolean or a file name)
            Required: name of output NRRD file containing directly averaged
            baseline images
            flag: --outputVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputVolume: (an existing file name)
            Required: name of output NRRD file containing directly averaged
            baseline images
```

113.5 gtractClipAnisotropy

Link to code

Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    clipFirstSlice: (a boolean)
            Clip the first slice of the anisotropy image
            flag: --clipFirstSlice
    clipLastSlice: (a boolean)
            Clip the last slice of the anisotropy image
            flag: --clipLastSlice
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
```

```
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
            Required: input image file name
            flag: --inputVolume %s
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputVolume: (a boolean or a file name)
            Required: name of output NRRD file containing the clipped anisotropy
            image
            flag: --outputVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputVolume: (an existing file name)
            Required: name of output NRRD file containing the clipped anisotropy
            image
```

113.6 gtractCoRegAnatomy

Link to code

Wraps 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 shoud 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    borderSize: (an integer (int or long))
            Size of border
```

```
        flag: --borderSize %d
convergence: (a float)
        Convergence Factor
        flag: --convergence %f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
gradientTolerance: (a float)
        Gradient Tolerance
        flag: --gradientTolerance %f
gridSize: (a list of items which are an integer (int or long))
        Number of grid subdivisions in all 3 directions
        flag: --gridSize %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputAnatomicalVolume: (an existing file name)
        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.
        flag: --inputAnatomicalVolume %s
inputRigidTransform: (an existing file name)
        Required (for B-Spline type co-registration): input rigid transform
        file name. Used as a starting point for the anatomical B-Spline
        registration.
        flag: --inputRigidTransform %s
inputVolume: (an existing file name)
        Required: input vector image file name. It is recommended that the
        input volume is the skull stripped baseline image of the DWI scan.
        flag: --inputVolume %s
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.,
        flag: --maxBSplineDisplacement %f
maximumStepSize: (a float)
        Maximum permitted step size to move in the selected 3D fit
        flag: --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
        flag: --minimumStepSize %f
numberOfHistogramBins: (an integer (int or long))
        Number of histogram bins
        flag: --numberOfHistogramBins %d
numberOfIterations: (an integer (int or long))
        Number of iterations in the selected 3D fit
        flag: --numberOfIterations %d
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.
        flag: --numberOfSamples %d
```

```
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputTransformName: (a boolean or a file name)
            Required: filename for the fit transform.
            flag: --outputTransformName %s
    relaxationFactor: (a float)
            Fraction of gradient from Jacobian to attempt to move in the
            selected 3D fit
            flag: --relaxationFactor %f
    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.
            flag: --samplingPercentage %f
    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
            flag: --spatialScale %d
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    transformType: ('Rigid' or 'Bspline')
            Transform Type: Rigid|Bspline
            flag: --transformType %s
    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
            flag: --translationScale %f
    useCenterOfHeadAlign: (a boolean)
            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.
            flag: --useCenterOfHeadAlign
    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.
            flag: --useGeometryAlign
    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.
        flag: --useMomentsAlign
vectorIndex: (an integer (int or long))
        Vector image index in the moving image (within the DWI) to be used
        for registration.
        flag: --vectorIndex %d
```

Outputs:

```
outputTransformName: (an existing file name)
        Required: filename for the fit transform.
```

113.7 gtractConcatDwi

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignoreOrigins: (a boolean)
        If image origins are different force all images to origin of first
        image
        flag: --ignoreOrigins
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (a list of items which are an existing file name)
        Required: input file containing the first diffusion weighted image
        flag: --inputVolume %s...
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputVolume: (a boolean or a file name)
        Required: name of output NRRD file containing the combined diffusion
        weighted images.
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
```

```
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Required: name of output NRRD file containing the combined diffusion
        weighted images.
```

113.8 gtractCopyImageOrientation

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputReferenceVolume: (an existing file name)
        Required: input file containing orietation that will be cloned.
        flag: --inputReferenceVolume %s
inputVolume: (an existing file name)
        Required: input file containing the signed short image to reorient
        without resampling.
        flag: --inputVolume %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputVolume: (a boolean or a file name)
        Required: name of output NRRD or Nifti file containing the
        reoriented image in reference image space.
```

```
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Required: name of output NRRD or Nifti file containing the
        reoriented image in reference image space.
```

113.9 gtractCoregBvalues

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
debugLevel: (an integer (int or long))
        Display debug messages, and produce debug intermediate results.
        0=OFF, 1=Minimal, 10=Maximum debugging.
        flag: --debugLevel %d
eddyCurrentCorrection: (a boolean)
        Flag to perform eddy current corection in addition to motion
        correction (recommended)
        flag: --eddyCurrentCorrection
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fixedVolume: (an existing file name)
        Required: input fixed image file name. It is recommended that this
        image should either contain or be a b0 image.
        flag: --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.
            flag: --fixedVolumeIndex %d
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    maximumStepSize: (a float)
            Maximum permitted step size to move in each 3D fit step (adjust when
            eddyCurrentCorrection is enabled; suggested value = 0.1)
            flag: --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
            flag: --minimumStepSize %f
    movingVolume: (an existing file name)
            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.
            flag: --movingVolume %s
    numberOfIterations: (an integer (int or long))
            Number of iterations in each 3D fit
            flag: --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.
            flag: --numberOfSpatialSamples %d
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputTransform: (a boolean or a file name)
            Registration 3D transforms concatenated in a single output file.
            There are no tools that can use this, but can be used for debugging
            purposes.
            flag: --outputTransform %s
    outputVolume: (a boolean or a file name)
            Required: name of output NRRD file containing moving images
            individually resampled and fit to the specified fixed image index.
            flag: --outputVolume %s
    registerB0Only: (a boolean)
            Register the B0 images only
            flag: --registerB0Only
    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)
            flag: --relaxationFactor %f
    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.
            flag: --samplingPercentage %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
            flag: --spatialScale %f
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputTransform: (an existing file name)
            Registration 3D transforms concatenated in a single output file.
            There are no tools that can use this, but can be used for debugging
            purposes.
    outputVolume: (an existing file name)
            Required: name of output NRRD file containing moving images
            individually resampled and fit to the specified fixed image index.
```

113.10 gtractCostFastMarching

Link to code

Wraps 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:

```
    [Mandatory]

    [Optional]
    anisotropyWeight: (a float)
            Anisotropy weight used for vcl_cost function calculations
            flag: --anisotropyWeight %f
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputAnisotropyVolume: (an existing file name)
            Required: input anisotropy image file name
```

```
        flag: --inputAnisotropyVolume %s
inputStartingSeedsLabelMapVolume: (an existing file name)
        Required: input starting seeds LabelMap image file name
        flag: --inputStartingSeedsLabelMapVolume %s
inputTensorVolume: (an existing file name)
        Required: input tensor image file name
        flag: --inputTensorVolume %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputCostVolume: (a boolean or a file name)
        Output vcl_cost image
        flag: --outputCostVolume %s
outputSpeedVolume: (a boolean or a file name)
        Output speed image
        flag: --outputSpeedVolume %s
seedThreshold: (a float)
        Anisotropy threshold used for seed selection
        flag: --seedThreshold %f
startingSeedsLabel: (an integer (int or long))
        Label value for Starting Seeds
        flag: --startingSeedsLabel %d
stoppingValue: (a float)
        Terminiating value for vcl_cost function estimation
        flag: --stoppingValue %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputCostVolume: (an existing file name)
        Output vcl_cost image
outputSpeedVolume: (an existing file name)
        Output speed image
```

113.11 gtractCreateGuideFiber

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
```

```
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputFiber: (an existing file name)
        Required: input fiber tract file name
        flag: --inputFiber %s
numberOfPoints: (an integer (int or long))
        Number of points in output guide fiber
        flag: --numberOfPoints %d
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputFiber: (a boolean or a file name)
        Required: output guide fiber file name
        flag: --outputFiber %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
writeXMLPolyDataFile: (a boolean)
        Flag to make use of XML files when reading and writing vtkPolyData.
        flag: --writeXMLPolyDataFile
```

Outputs:

```
outputFiber: (an existing file name)
        Required: output guide fiber file name
```

113.12 gtractFastMarchingTracking

Link to code

Wraps 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:

```
[Mandatory]
```

```
    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    costStepSize: (a float)
            Cost image sub-voxel sampling
            flag: --costStepSize %f
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputAnisotropyVolume: (an existing file name)
            Required: input anisotropy image file name
            flag: --inputAnisotropyVolume %s
    inputCostVolume: (an existing file name)
            Required: input vcl_cost image file name
            flag: --inputCostVolume %s
    inputStartingSeedsLabelMapVolume: (an existing file name)
            Required: input starting seeds LabelMap image file name
            flag: --inputStartingSeedsLabelMapVolume %s
    inputTensorVolume: (an existing file name)
            Required: input tensor image file name
            flag: --inputTensorVolume %s
    maximumStepSize: (a float)
            Maximum step size to move when tracking
            flag: --maximumStepSize %f
    minimumStepSize: (a float)
            Minimum step size to move when tracking
            flag: --minimumStepSize %f
    numberOfIterations: (an integer (int or long))
            Number of iterations used for the optimization
            flag: --numberOfIterations %d
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputTract: (a boolean or a file name)
            Required: name of output vtkPolydata file containing tract lines and
            the point data collected along them.
            flag: --outputTract %s
    seedThreshold: (a float)
            Anisotropy threshold used for seed selection
            flag: --seedThreshold %f
    startingSeedsLabel: (an integer (int or long))
            Label value for Starting Seeds
            flag: --startingSeedsLabel %d
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    trackingThreshold: (a float)
            Anisotropy threshold used for fiber tracking
            flag: --trackingThreshold %f
    writeXMLPolyDataFile: (a boolean)
            Flag to make use of the XML format for vtkPolyData fiber tracts.
            flag: --writeXMLPolyDataFile
```

Outputs:

```
outputTract: (an existing file name)
        Required: name of output vtkPolydata file containing tract lines and
        the point data collected along them.
```

113.13 gtractFiberTracking

Link to code
Wraps 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 ther 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 severeal 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 original proposed by Basser et al. The tracking follows the primarty 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 ansiotropy, 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-ambigous regions and utilizes branching and a graph search algorithm in ambigous regions. Ambiguous tracking regions are defined based on two criteria: Branching Al Threshold (anisotropy values below this value and above the traching 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 seconadary 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 alogrithm 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 a 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    branchingAngle: (a float)
            Branching angle in degrees (recommended for GraphSearch fiber
            tracking method)
            flag: --branchingAngle %f
    branchingThreshold: (a float)
            Anisotropy Branching threshold (recommended for GraphSearch fiber
            tracking method)
            flag: --branchingThreshold %f
    curvatureThreshold: (a float)
            Curvature threshold in degrees (recommended for Free fiber tracking)
            flag: --curvatureThreshold %f
    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)
            flag: --endingSeedsLabel %d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    guidedCurvatureThreshold: (a float)
            Guided Curvature Threshold (Degrees)
            flag: --guidedCurvatureThreshold %f
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputAnisotropyVolume: (an existing file name)
            Required (for Free, Streamline, GraphSearch, and Guided fiber
            tracking methods): input anisotropy image file name
            flag: --inputAnisotropyVolume %s
    inputEndingSeedsLabelMapVolume: (an existing file name)
            Required (for Streamline, GraphSearch, and Guided fiber tracking
            methods): input ending seeds LabelMap image file name
            flag: --inputEndingSeedsLabelMapVolume %s
    inputStartingSeedsLabelMapVolume: (an existing file name)
            Required (for Free, Streamline, GraphSearch, and Guided fiber
            tracking methods): input starting seeds LabelMap image file name
            flag: --inputStartingSeedsLabelMapVolume %s
    inputTensorVolume: (an existing file name)
            Required (for Free, Streamline, GraphSearch, and Guided fiber
            tracking methods): input tensor image file name
            flag: --inputTensorVolume %s
    inputTract: (an existing file name)
```

```
        Required (for Guided fiber tracking method): guide fiber in
        vtkPolydata file containing one tract line.
        flag: --inputTract %s
maximumBranchPoints: (an integer (int or long))
        Maximum branch points (recommended for GraphSearch fiber tracking
        method)
        flag: --maximumBranchPoints %d
maximumGuideDistance: (a float)
        Maximum distance for using the guide fiber direction
        flag: --maximumGuideDistance %f
maximumLength: (a float)
        Maximum fiber length (voxels)
        flag: --maximumLength %f
minimumLength: (a float)
        Minimum fiber length. Helpful for filtering invalid tracts.
        flag: --minimumLength %f
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputTract: (a boolean or a file name)
        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.
        flag: --outputTract %s
randomSeed: (an integer (int or long))
        Random number generator seed
        flag: --randomSeed %d
seedThreshold: (a float)
        Anisotropy threshold for seed selection (recommended for Free fiber
        tracking)
        flag: --seedThreshold %f
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)
        flag: --startingSeedsLabel %d
stepSize: (a float)
        Fiber tracking step size
        flag: --stepSize %f
tendF: (a float)
        Tend F parameter
        flag: --tendF %f
tendG: (a float)
        Tend G parameter
        flag: --tendG %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
trackingMethod: ('Guided' or 'Free' or 'Streamline' or 'GraphSearch')
        Fiber tracking Filter Type: Guided|Free|Streamline|GraphSearch
        flag: --trackingMethod %s
trackingThreshold: (a float)
        Anisotropy threshold for fiber tracking (anisotropy values of the
        next point along the path)
        flag: --trackingThreshold %f
useLoopDetection: (a boolean)
        Flag to make use of loop detection.
        flag: --useLoopDetection
```

```
    useRandomWalk: (a boolean)
            Flag to use random walk.
            flag: --useRandomWalk
    useTend: (a boolean)
            Flag to make use of Tend F and Tend G parameters.
            flag: --useTend
    writeXMLPolyDataFile: (a boolean)
            Flag to make use of the XML format for vtkPolyData fiber tracts.
            flag: --writeXMLPolyDataFile
```

Outputs:

```
    outputTract: (an existing file name)
            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.
```

113.14 gtractImageConformity

Link to code

Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputReferenceVolume: (an existing file name)
            Required: input file containing the standard image to clone the
            characteristics of.
            flag: --inputReferenceVolume %s
    inputVolume: (an existing file name)
            Required: input file containing the signed short image to reorient
            without resampling.
            flag: --inputVolume %s
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputVolume: (a boolean or a file name)
```

```
        Required: name of output Nrrd or Nifti file containing the
        reoriented image in reference image space.
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Required: name of output Nrrd or Nifti file containing the
        reoriented image in reference image space.
```

113.15 gtractInvertBSplineTransform

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputReferenceVolume: (an existing file name)
        Required: input image file name to exemplify the anatomical space to
        interpolate over.
        flag: --inputReferenceVolume %s
inputTransform: (an existing file name)
        Required: input B-Spline transform file name
        flag: --inputTransform %s
landmarkDensity: (a list of items which are an integer (int or long))
        Number of landmark subdivisions in all 3 directions
        flag: --landmarkDensity %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputTransform: (a boolean or a file name)
        Required: output transform file name
```

```
        flag: --outputTransform %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputTransform: (an existing file name)
        Required: output transform file name
```

113.16 gtractInvertDisplacementField

Link to code

Wraps command ** gtractInvertDisplacementField **
title: Invert Displacement Field
category: Diffusion.GTRACT
description: This program will invert a deformatrion 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
baseImage: (an existing file name)
        Required: base image used to define the size of the inverse field
        flag: --baseImage %s
deformationImage: (an existing file name)
        Required: Displacement field image
        flag: --deformationImage %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputVolume: (a boolean or a file name)
        Required: Output deformation field
        flag: --outputVolume %s
subsamplingFactor: (an integer (int or long))
        Subsampling factor for the deformation field
        flag: --subsamplingFactor %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
```

```
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Required: Output deformation field
```

113.17 gtractInvertRigidTransform

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputTransform: (an existing file name)
        Required: input rigid transform file name
        flag: --inputTransform %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputTransform: (a boolean or a file name)
        Required: output transform file name
        flag: --outputTransform %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputTransform: (an existing file name)
        Required: output transform file name
```

113.18 gtractResampleAnisotropy

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputAnatomicalVolume: (an existing file name)
            Required: input file containing the anatomical image whose
            characteristics will be cloned.
            flag: --inputAnatomicalVolume %s
    inputAnisotropyVolume: (an existing file name)
            Required: input file containing the anisotropy image
            flag: --inputAnisotropyVolume %s
    inputTransform: (an existing file name)
            Required: input Rigid OR Bspline transform file name
            flag: --inputTransform %s
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputVolume: (a boolean or a file name)
            Required: name of output NRRD file containing the resampled
            transformed anisotropy image.
            flag: --outputVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    transformType: ('Rigid' or 'B-Spline')
            Transform type: Rigid, B-Spline
            flag: --transformType %s
```

Outputs:

```
    outputVolume: (an existing file name)
            Required: name of output NRRD file containing the resampled
            transformed anisotropy image.
```

113.19 gtractResampleB0

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputAnatomicalVolume: (an existing file name)
            Required: input file containing the anatomical image defining the
            origin, spacing and size of the resampled image (template)
            flag: --inputAnatomicalVolume %s
    inputTransform: (an existing file name)
            Required: input Rigid OR Bspline transform file name
            flag: --inputTransform %s
    inputVolume: (an existing file name)
            Required: input file containing the 4D image
            flag: --inputVolume %s
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputVolume: (a boolean or a file name)
            Required: name of output NRRD file containing the resampled input
            image.
            flag: --outputVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    transformType: ('Rigid' or 'B-Spline')
```

```
        Transform type: Rigid, B-Spline
        flag: --transformType %s
vectorIndex: (an integer (int or long))
        Index in the diffusion weighted image set for the B0 image
        flag: --vectorIndex %d
```

Outputs:

```
outputVolume: (an existing file name)
        Required: name of output NRRD file containing the resampled input
        image.
```

113.20 gtractResampleCodeImage

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputCodeVolume: (an existing file name)
        Required: input file containing the code image
        flag: --inputCodeVolume %s
inputReferenceVolume: (an existing file name)
        Required: input file containing the standard image to clone the
        characteristics of.
        flag: --inputReferenceVolume %s
inputTransform: (an existing file name)
        Required: input Rigid or Inverse-B-Spline transform file name
        flag: --inputTransform %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputVolume: (a boolean or a file name)
        Required: name of output NRRD file containing the resampled code
```

```
        image in acquisition space.
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transformType: ('Rigid' or 'Affine' or 'B-Spline' or
         'Inverse-B-Spline' or 'None')
        Transform type: Rigid or Inverse-B-Spline
        flag: --transformType %s
```

Outputs:

```
outputVolume: (an existing file name)
        Required: name of output NRRD file containing the resampled code
        image in acquisition space.
```

113.21 gtractResampleDWIInPlace

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
debugLevel: (an integer (int or long))
        Display debug messages, and produce debug intermediate results.
        0=OFF, 1=Minimal, 10=Maximum debugging.
        flag: --debugLevel %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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.
        flag: --imageOutputSize %s
inputTransform: (an existing file name)
        Required: transform file derived from rigid registration of b0 image
        to reference structural image.
        flag: --inputTransform %s
```

```
    inputVolume: (an existing file name)
            Required: input image is a 4D NRRD image.
            flag: --inputVolume %s
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputResampledB0: (a boolean or a file name)
            Convenience function for extracting the first index location
            (assumed to be the B0)
            flag: --outputResampledB0 %s
    outputVolume: (a boolean or a file name)
            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.
            flag: --outputVolume %s
    referenceVolume: (an existing file name)
            If provided, resample to the final space of the referenceVolume 3D
            data set.
            flag: --referenceVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    warpDWITransform: (an existing file name)
            Optional: transform file to warp gradient volumes.
            flag: --warpDWITransform %s
```

Outputs:

```
    outputResampledB0: (an existing file name)
            Convenience function for extracting the first index location
            (assumed to be the B0)
    outputVolume: (an existing file name)
            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.
```

113.22 gtractResampleFibers

Link to code

Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
```

```
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputForwardDeformationFieldVolume: (an existing file name)
        Required: input forward deformation field image file name
        flag: --inputForwardDeformationFieldVolume %s
inputReverseDeformationFieldVolume: (an existing file name)
        Required: input reverse deformation field image file name
        flag: --inputReverseDeformationFieldVolume %s
inputTract: (an existing file name)
        Required: name of input vtkPolydata file containing tract lines.
        flag: --inputTract %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputTract: (a boolean or a file name)
        Required: name of output vtkPolydata file containing tract lines and
        the point data collected along them.
        flag: --outputTract %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
writeXMLPolyDataFile: (a boolean)
        Flag to make use of the XML format for vtkPolyData fiber tracts.
        flag: --writeXMLPolyDataFile
```

Outputs:

```
outputTract: (an existing file name)
        Required: name of output vtkPolydata file containing tract lines and
        the point data collected along them.
```

113.23 gtractTensor

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
applyMeasurementFrame: (a boolean)
        Flag to apply the measurement frame to the gradient directions
        flag: --applyMeasurementFrame
args: (a string)
        Additional parameters to the command
        flag: %s
b0Index: (an integer (int or long))
        Index in input vector index to extract
        flag: --b0Index %d
backgroundSuppressingThreshold: (an integer (int or long))
        Image threshold to suppress background. This sets a threshold used
        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.
        flag: --backgroundSuppressingThreshold %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignoreIndex: (a list of items which are an integer (int or long))
        Ignore diffusion gradient index. Used to remove specific gradient
        directions with artifacts.
        flag: --ignoreIndex %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        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.
        flag: --inputVolume %s
maskProcessingMode: ('NOMASK' or 'ROIAUTO' or 'ROI')
        ROIAUTO: mask is implicitly defined using a otsu forground 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
        flag: --maskProcessingMode %s
maskVolume: (an existing file name)
        Mask Image, if maskProcessingMode is ROI
        flag: --maskVolume %s
medianFilterSize: (a list of items which are an integer (int or
         long))
        Median filter radius in all 3 directions
        flag: --medianFilterSize %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputVolume: (a boolean or a file name)
        Required: name of output NRRD file containing the Tensor vector
```

```
        image
        flag: --outputVolume %s
resampleIsotropic: (a boolean)
        Flag to resample to isotropic voxels. Enabling this feature is
        recommended if fiber tracking will be performed.
        flag: --resampleIsotropic
size: (a float)
        Isotropic voxel size to resample to
        flag: --size %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Required: name of output NRRD file containing the Tensor vector
        image
```

113.24 gtractTransformToDisplacementField

Link to code

Wraps 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 Ingalhalikar, and Greg Harris
acknowledgements: Funding for this version of the GTRACT program was provided by NIH/NINDS R01NS050568-01A2S1
Inputs:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputReferenceVolume: (an existing file name)
        Required: input image file name to exemplify the anatomical space
        over which to vcl_express the transform as a displacement field.
        flag: --inputReferenceVolume %s
inputTransform: (an existing file name)
        Input Transform File Name
        flag: --inputTransform %s
numberOfThreads: (an integer (int or long))
```

```
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputDeformationFieldVolume: (a boolean or a file name)
        Output deformation field
        flag: --outputDeformationFieldVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputDeformationFieldVolume: (an existing file name)
        Output deformation field
```

interfaces.semtools.diffusion.maxcurvature

114.1 maxcurvature

Link to code
Wraps command ** maxcurvature **
title: MaxCurvature-Hessian (DTIProcess)
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/DTIProcess

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 DTIProcess compatible with Slicer execution, and simplified the stand-alone build requirements by removing the dependancies on boost and a fortran compiler.
Inputs:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    image: (an existing file name)
            FA Image
            flag: --image %s
    output: (a boolean or a file name)
            Output File
            flag: --output %s
    sigma: (a float)
```

```
        Scale of Gradients
        flag: --sigma %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        produce verbose output
        flag: --verbose
```

Outputs:

```
output: (an existing file name)
        Output File
```

interfaces.semtools.diffusion.tractography.commandlineonly

115.1 fiberstats

Link to code
Wraps command ** fiberstats **
title: FiberStats (DTIProcess)
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/DTIProcess

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 DTIProcess compatible with Slicer execution, and simplified the stand-alone build requirements by removing the dependancies on boost and a fortran compiler.
Inputs:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fiber_file: (an existing file name)
        DTI Fiber File
        flag: --fiber_file %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        produce verbose output
        flag: --verbose
```

Outputs:

```
None
```

CHAPTER 116

interfaces.semtools.diffusion.tractography.fiberprocess

116.1 fiberprocess

Link to code
Wraps command ** fiberprocess **
title: FiberProcess (DTIProcess)
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/DTIProcess

contributor: Casey Goodlett
Inputs:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    displacement_field: (an existing file name)
            Displacement Field for warp and statistics lookup. If this option is
            used tensor-volume must also be specified.
```

```
        flag: --displacement_field %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
fiber_file: (an existing file name)
        DTI fiber file
        flag: --fiber_file %s
fiber_output: (a boolean or a file name)
        Output fiber file. May be warped or updated with new data depending
        on other options used.
        flag: --fiber_output %s
fiber_radius: (a float)
        set radius of all fibers to this value
        flag: --fiber_radius %f
h_field: (an existing file name)
        HField for warp and statistics lookup. If this option is used
        tensor-volume must also be specified.
        flag: --h_field %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
index_space: (a boolean)
        Use index-space for fiber output coordinates, otherwise us world
        space for fiber output coordinates (from tensor file).
        flag: --index_space
noDataChange: (a boolean)
        Do not change data ???
        flag: --noDataChange
no_warp: (a boolean)
        Do not warp the geometry of the tensors only obtain the new
        statistics.
        flag: --no_warp
saveProperties: (a boolean)
        save the tensor property as scalar data into the vtk (only works for
        vtk fiber files).
        flag: --saveProperties
tensor_volume: (an existing file name)
        Interpolate tensor values from the given field
        flag: --tensor_volume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        produce verbose output
        flag: --verbose
voxel_label: (an integer (int or long))
        Label for voxelized fiber
        flag: --voxel_label %d
voxelize: (a boolean or a file name)
        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
        flag: --voxelize %s
voxelize_count_fibers: (a boolean)
        Count number of fibers per-voxel instead of just setting to 1
```

```
        flag: --voxelize_count_fibers
```

Outputs:

```
fiber_output: (an existing file name)
        Output fiber file. May be warped or updated with new data depending
        on other options used.
voxelize: (an existing file name)
        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
```

CHAPTER 117

interfaces.semtools.diffusion.tractography.fibertrack

117.1 fibertrack

Link to code
Wraps command ** fibertrack **
title: FiberTrack (DTIProcess)
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 –fobidden_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/DTIProcess

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 DTIProcess compatible with Slicer execution, and simplified the stand-alone build requirements by removing the dependancies on boost and a fortran compiler.
Inputs:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
```

```
        Environment variables
forbidden_label: (an integer (int or long))
        Forbidden label
        flag: --forbidden_label %d
force: (a boolean)
        Ignore sanity checks.
        flag: --force
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
input_roi_file: (an existing file name)
        The filename of the image which contains the labels used for seeding
        and constraining the algorithm.
        flag: --input_roi_file %s
input_tensor_file: (an existing file name)
        Tensor Image
        flag: --input_tensor_file %s
max_angle: (a float)
        Maximum angle of change in radians
        flag: --max_angle %f
min_fa: (a float)
        The minimum FA threshold to continue tractography
        flag: --min_fa %f
output_fiber_file: (a boolean or a file name)
        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.
        flag: --output_fiber_file %s
really_verbose: (a boolean)
        Follow detail of fiber tracking algorithm
        flag: --really_verbose
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
        flag: --source_label %d
step_size: (a float)
        Step size in mm for the tracking algorithm
        flag: --step_size %f
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.
        flag: --target_label %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        produce verbose output
        flag: --verbose
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
        flag: --whole_brain
```

Outputs:

```
    output_fiber_file: (an existing file name)
            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.
```

interfaces.semtools.diffusion.tractography.ukftractography

118.1 UKFTractography

Link to code
Wraps command ** UKFTractography **
title: UKF Tractography
category: Diffusion.Tractography
description: This module traces fibers in a DWI Volume using the multiple tensor unscented Kalman Filter methology. For more informations check the documentation.
version: 1.0
documentation-url: http://www.nitrc.org/plugins/mwiki/index.php/ukftractography:MainPage
contributor: Yogesh Rathi, 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 Rathi), R01 MH092862 (PIs Westin and Verma), U01 NS083223 (PI Westin), R01 MH074794 (PI Westin) and P41 EB015902 (PI Kikinis).
Inputs:

```
    [Mandatory]

    [Optional]
    Ql: (a float)
            Process noise for eigenvalues
            flag: --Ql %f
    Qm: (a float)
            Process noise for angles/direction
            flag: --Qm %f
    Qw: (a float)
            Process noise for free water weights, ignored if no free water
            estimation
            flag: --Qw %f
    Rs: (a float)
            Measurement noise
            flag: --Rs %f
    args: (a string)
            Additional parameters to the command
            flag: %s
    dwiFile: (an existing file name)
            Input DWI volume
            flag: --dwiFile %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
```

```
    freeWater: (a boolean)
            Adds a term for free water difusion to the model. (Note for experts:
            if checked, the 1T simple model is forced)
            flag: --freeWater
    fullTensorModel: (a boolean)
            Whether to use the full tensor model. If unchecked, use the default
            simple tensor model
            flag: --fullTensorModel
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    labels: (a list of items which are an integer (int or long))
            A vector of the ROI labels to be used
            flag: --labels %s
    maskFile: (an existing file name)
            Mask for diffusion tractography
            flag: --maskFile %s
    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 supressed when this maxBranchingAngle is set to 0.0
            flag: --maxBranchingAngle %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
            flag: --maxHalfFiberLength %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)
            flag: --minBranchingAngle %f
    minFA: (a float)
            Abort the tractography when the Fractional Anisotropy is less than
            this value
            flag: --minFA %f
    minGA: (a float)
            Abort the tractography when the Generalized Anisotropy is less than
            this value
            flag: --minGA %f
    numTensor: ('1' or '2')
            Number of tensors used
            flag: --numTensor %s
    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
            number of cores detected will be used.
            flag: --numThreads %d
    recordCovariance: (a boolean)
            Whether to store the covariance. Will generate field 'covariance' in
            fiber.
            flag: --recordCovariance
    recordFA: (a boolean)
            Whether to store FA. Attaches field 'FA', and 'FA2' for 2-tensor
            case to fiber.
            flag: --recordFA
    recordFreeWater: (a boolean)
```

```
        Whether to store the fraction of free water. Attaches field
        'FreeWater' to fiber.
        flag: --recordFreeWater
recordLength: (a float)
        Record length of tractography, in millimeters
        flag: --recordLength %f
recordNMSE: (a boolean)
        Whether to store NMSE. Attaches field 'NMSE' to fiber.
        flag: --recordNMSE
recordState: (a boolean)
        Whether to attach the states to the fiber. Will generate field
        'state'.
        flag: --recordState
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.
        flag: --recordTensors
recordTrace: (a boolean)
        Whether to store Trace. Attaches field 'Trace', and 'Trace2' for
        2-tensor case to fiber.
        flag: --recordTrace
seedFALimit: (a float)
        Seed points whose FA are below this value are excluded
        flag: --seedFALimit %f
seedsFile: (an existing file name)
        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
        flag: --seedsFile %s
seedsPerVoxel: (an integer (int or long))
         Each seed generates a fiber, thus using more seeds generates more
        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).,
        flag: --seedsPerVoxel %d
stepLength: (a float)
        Step length of tractography, in millimeters
        flag: --stepLength %f
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
        flag: --storeGlyphs
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tracts: (a boolean or a file name)
        Tracts generated, with first tensor output
        flag: --tracts %s
tractsWithSecondTensor: (a boolean or a file name)
        Tracts generated, with second tensor output (if there is one)
        flag: --tractsWithSecondTensor %s
writeAsciiTracts: (a boolean)
        Write tract file as a VTK binary data file
        flag: --writeAsciiTracts
writeUncompressedTracts: (a boolean)
```

```
            Write tract file as a VTK uncompressed data file
            flag: --writeUncompressedTracts
```

Outputs:

```
    tracts: (an existing file name)
            Tracts generated, with first tensor output
    tractsWithSecondTensor: (an existing file name)
            Tracts generated, with second tensor output (if there is one)
```

CHAPTER 119

interfaces.semtools.featurecreator

119.1 GenerateCsfClippedFromClassifiedImage

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputCassifiedVolume: (an existing file name)
        Required: input tissue label image
        flag: --inputCassifiedVolume %s
outputVolume: (a boolean or a file name)
        Required: output image
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Required: output image
```

CHAPTER 120

interfaces.semtools.filtering.denoising

120.1 UnbiasedNonLocalMeans

Link to code
Wraps 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 algor

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-Fenandez, 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    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
        flag: --hp %f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Input MRI volume.
        flag: %s, position: -2
outputVolume: (a boolean or a file name)
        Output (filtered) MRI volume.
        flag: %s, position: -1
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)
        flag: --ps %f
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
        flag: --rc %s
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).
        flag: --rs %s
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.
        flag: --sigma %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Output (filtered) MRI volume.
```

CHAPTER 121

interfaces.semtools.filtering.featuredetection

121.1 CannyEdge

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Required: input tissue label image
        flag: --inputVolume %s
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.
        flag: --lowerThreshold %f
outputVolume: (a boolean or a file name)
        Required: output image
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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.
        flag: --upperThreshold %f
variance: (a float)
        Variance and Maximum error are used in the Gaussian smoothing of the
        input image. See itkDiscreteGaussianImageFilter for information on
        these parameters.
        flag: --variance %f
```

Outputs:

```
outputVolume: (an existing file name)
        Required: output image
```

121.2 CannySegmentationLevelSetImageFilter

Link to code

Wraps 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/CannySegmentationLevelSetImage
(copyright) Insight Software Consortium. See http://wiki.na-mic.org/Wiki/index.php/Slicer3:Execution_Model_Documentation
for more detailed descriptions.
Inputs:

```
[Mandatory]

[Optional]
advectionWeight: (a float)
        Controls the smoothness of the resulting mask, small number are more
        smooth, large numbers allow more sharp corners.
        flag: --advectionWeight %f
args: (a string)
        Additional parameters to the command
        flag: %s
cannyThreshold: (a float)
        Canny Threshold Value
        flag: --cannyThreshold %f
cannyVariance: (a float)
        Canny variance
        flag: --cannyVariance %f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
initialModel: (an existing file name)
        flag: --initialModel %s
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
        use 127.5).
        flag: --initialModelIsovalue %f
inputVolume: (an existing file name)
        flag: --inputVolume %s
maxIterations: (an integer (int or long))
        The
        flag: --maxIterations %d
outputSpeedVolume: (a boolean or a file name)
        flag: --outputSpeedVolume %s
outputVolume: (a boolean or a file name)
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputSpeedVolume: (an existing file name)
outputVolume: (an existing file name)
```

121.3 DilateImage

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputMaskVolume: (an existing file name)
        Required: input brain mask image
        flag: --inputMaskVolume %s
inputRadius: (an integer (int or long))
        Required: input neighborhood radius
        flag: --inputRadius %d
inputVolume: (an existing file name)
        Required: input image
        flag: --inputVolume %s
```

```
    outputVolume: (a boolean or a file name)
            Required: output image
            flag: --outputVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputVolume: (an existing file name)
            Required: output image
```

121.4 DilateMask

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputBinaryVolume: (an existing file name)
            Required: input brain mask image
            flag: --inputBinaryVolume %s
    inputVolume: (an existing file name)
            Required: input image
            flag: --inputVolume %s
    lowerThreshold: (a float)
            Required: lowerThreshold value
            flag: --lowerThreshold %f
    outputVolume: (a boolean or a file name)
            Required: output image
            flag: --outputVolume %s
    sizeStructuralElement: (an integer (int or long))
            size of structural element. sizeStructuralElement=1 means that 3x3x3
            structuring element for 3D
            flag: --sizeStructuralElement %d
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
```

```
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Required: output image
```

121.5 DistanceMaps

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputLabelVolume: (an existing file name)
        Required: input tissue label image
        flag: --inputLabelVolume %s
inputMaskVolume: (an existing file name)
        Required: input brain mask image
        flag: --inputMaskVolume %s
inputTissueLabel: (an integer (int or long))
        Required: input integer value of tissue type used to calculate
        distance
        flag: --inputTissueLabel %d
outputVolume: (a boolean or a file name)
        Required: output image
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Required: output image
```

121.6 DumpBinaryTrainingVectors

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputHeaderFilename: (an existing file name)
        Required: input header file name
        flag: --inputHeaderFilename %s
inputVectorFilename: (an existing file name)
        Required: input vector filename
        flag: --inputVectorFilename %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
None
```

121.7 ErodeImage

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
```

```
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputMaskVolume: (an existing file name)
            Required: input brain mask image
            flag: --inputMaskVolume %s
    inputRadius: (an integer (int or long))
            Required: input neighborhood radius
            flag: --inputRadius %d
    inputVolume: (an existing file name)
            Required: input image
            flag: --inputVolume %s
    outputVolume: (a boolean or a file name)
            Required: output image
            flag: --outputVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputVolume: (an existing file name)
            Required: output image
```

121.8 FlippedDifference

Link to code

Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
```

```
        interface fails to run
inputMaskVolume: (an existing file name)
        Required: input brain mask image
        flag: --inputMaskVolume %s
inputVolume: (an existing file name)
        Required: input image
        flag: --inputVolume %s
outputVolume: (a boolean or a file name)
        Required: output image
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Required: output image
```

121.9 GenerateBrainClippedImage

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputImg: (an existing file name)
        input volume 1, usally t1 image
        flag: --inputImg %s
inputMsk: (an existing file name)
        input volume 2, usally t2 image
        flag: --inputMsk %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputFileName: (a boolean or a file name)
        (required) output file name
        flag: --outputFileName %s
```

```
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputFileName: (an existing file name)
        (required) output file name
```

121.10 GenerateSummedGradientImage

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
MaximumGradient: (a boolean)
        If set this flag, it will compute maximum gradient between two input
        volumes instead of sum of it.
        flag: --MaximumGradient
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume1: (an existing file name)
        input volume 1, usally t1 image
        flag: --inputVolume1 %s
inputVolume2: (an existing file name)
        input volume 2, usally t2 image
        flag: --inputVolume2 %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputFileName: (a boolean or a file name)
        (required) output file name
        flag: --outputFileName %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputFileName: (an existing file name)
            (required) output file name
```

121.11 GenerateTestImage

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
            input volume 1, usally t1 image
            flag: --inputVolume %s
    lowerBoundOfOutputVolume: (a float)
            flag: --lowerBoundOfOutputVolume %f
    outputVolume: (a boolean or a file name)
            (required) output file name
            flag: --outputVolume %s
    outputVolumeSize: (a float)
            output Volume Size
            flag: --outputVolumeSize %f
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    upperBoundOfOutputVolume: (a float)
            flag: --upperBoundOfOutputVolume %f
```

Outputs:

```
    outputVolume: (an existing file name)
            (required) output file name
```

121.12 GradientAnisotropicDiffusionImageFilter

Link to code
Wraps command ** GradientAnisotropicDiffusionImageFilter **
title: GradientAnisopropicDiffusionFilter

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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
conductance: (a float)
        Conductance for diffusion process
        flag: --conductance %f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Required: input image
        flag: --inputVolume %s
numberOfIterations: (an integer (int or long))
        Optional value for number of Iterations
        flag: --numberOfIterations %d
outputVolume: (a boolean or a file name)
        Required: output image
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
timeStep: (a float)
        Time step for diffusion process
        flag: --timeStep %f
```

Outputs:

```
outputVolume: (an existing file name)
        Required: output image
```

121.13 HammerAttributeCreator

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    Scale: (an integer (int or long))
            Determine Scale of Ball
            flag: --Scale %d
    Strength: (a float)
            Determine Strength of Edges
            flag: --Strength %f
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputCSFVolume: (an existing file name)
            Required: input CSF posterior image
            flag: --inputCSFVolume %s
    inputGMVolume: (an existing file name)
            Required: input grey matter posterior image
            flag: --inputGMVolume %s
    inputWMVolume: (an existing file name)
            Required: input white matter posterior image
            flag: --inputWMVolume %s
    outputVolumeBase: (a string)
            Required: output image base name to be appended for each feature
            vector.
            flag: --outputVolumeBase %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    None
```

121.14 NeighborhoodMean

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
```

```
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputMaskVolume: (an existing file name)
            Required: input brain mask image
            flag: --inputMaskVolume %s
    inputRadius: (an integer (int or long))
            Required: input neighborhood radius
            flag: --inputRadius %d
    inputVolume: (an existing file name)
            Required: input image
            flag: --inputVolume %s
    outputVolume: (a boolean or a file name)
            Required: output image
            flag: --outputVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputVolume: (an existing file name)
            Required: output image
```

121.15 NeighborhoodMedian

Link to code

Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
```

```
        interface fails to run
inputMaskVolume: (an existing file name)
        Required: input brain mask image
        flag: --inputMaskVolume %s
inputRadius: (an integer (int or long))
        Required: input neighborhood radius
        flag: --inputRadius %d
inputVolume: (an existing file name)
        Required: input image
        flag: --inputVolume %s
outputVolume: (a boolean or a file name)
        Required: output image
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Required: output image
```

121.16 STAPLEAnalysis

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputDimension: (an integer (int or long))
        Required: input image Dimension 2 or 3
        flag: --inputDimension %d
inputLabelVolume: (a list of items which are an existing file name)
        Required: input label volume
        flag: --inputLabelVolume %s...
outputVolume: (a boolean or a file name)
        Required: output image
```

```
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Required: output image
```

121.17 TextureFromNoiseImageFilter

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputRadius: (an integer (int or long))
        Required: input neighborhood radius
        flag: --inputRadius %d
inputVolume: (an existing file name)
        Required: input image
        flag: --inputVolume %s
outputVolume: (a boolean or a file name)
        Required: output image
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Required: output image
```

121.18 TextureMeasureFilter

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
distance: (an integer (int or long))
        flag: --distance %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputMaskVolume: (an existing file name)
        flag: --inputMaskVolume %s
inputVolume: (an existing file name)
        flag: --inputVolume %s
insideROIValue: (a float)
        flag: --insideROIValue %f
outputFilename: (a boolean or a file name)
        flag: --outputFilename %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputFilename: (an existing file name)
```

CHAPTER 122

interfaces.semtools.legacy.registration

122.1 scalartransform

Link to code
Wraps command ** scalartransform **
title: ScalarTransform (DTIProcess)
category: Legacy.Registration
version: 1.0.0
documentation-url: http://www.slicer.org/slicerWiki/index.php/Documentation/Nightly/Extensions/DTIProcess

contributor: Casey Goodlett
Inputs:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    deformation: (an existing file name)
            Deformation field.
            flag: --deformation %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    h_field: (a boolean)
            The deformation is an h-field.
            flag: --h_field
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    input_image: (an existing file name)
            Image to tranform
            flag: --input_image %s
    interpolation: ('nearestneighbor' or 'linear' or 'cubic')
            Interpolation type (nearestneighbor, linear, cubic)
            flag: --interpolation %s
    invert: (a boolean)
            Invert tranform before applying.
            flag: --invert
```

```
    output_image: (a boolean or a file name)
            The transformed image
            flag: --output_image %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    transformation: (a boolean or a file name)
            Output file for transformation parameters
            flag: --transformation %s
```

Outputs:

```
    output_image: (an existing file name)
            The transformed image
    transformation: (an existing file name)
            Output file for transformation parameters
```

interfaces.semtools.registration.brainsfit

123.1 BRAINSFit

Link to code
Wraps 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 avalable 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:

```
    [Mandatory]

    [Optional]
    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.
            flag: --ROIAutoClosingSize %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.
            flag: --ROIAutoDilateSize %f
    args: (a string)
            Additional parameters to the command
            flag: %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.
        flag: --backgroundFillValue %f
bsplineTransform: (a boolean or a file name)
        (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).
        flag: --bsplineTransform %s
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.,
        flag: --costFunctionConvergenceFactor %f
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)
        flag: --costMetric %s
debugLevel: (an integer (int or long))
        Display debug messages, and produce debug intermediate results.
        0=OFF, 1=Minimal, 10=Maximum debugging.
        flag: --debugLevel %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
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.
        flag: --failureExitCode %d
fixedBinaryVolume: (an existing file name)
        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.
        flag: --fixedBinaryVolume %s
fixedVolume: (an existing file name)
        Input fixed image (the moving image will be transformed into this
        image space).
        flag: --fixedVolume %s
fixedVolume2: (an existing file name)
        Input fixed image that will be used for multimodal registration.
        (the moving image will be transformed into this image space).
        flag: --fixedVolume2 %s
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.
        flag: --fixedVolumeTimeIndex %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.
        flag: --gui
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.
        flag: --histogramMatch
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
initialTransform: (an existing file name)
        Transform to be applied to the moving image to initialize the
        registration. This can only be used if Initialize Transform Mode is
        Off.
        flag: --initialTransform %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.
        flag: --initializeRegistrationByCurrentGenericTransform
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.
        flag: --initializeTransformMode %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, 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.
        flag: --interpolationMode %s
linearTransform: (a boolean or a file name)
        (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).
        flag: --linearTransform %s
logFileReport: (a boolean or a file name)
        A file to write out final information report in CSV file: MetricName
        ,MetricValue,FixedImageName,FixedMaskName,MovingImageName,MovingMask
        Name
        flag: --logFileReport %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.
        flag: --maskInferiorCutOffFromCenter %f
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.
        flag: --maskProcessingMode %s
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
        in computation time in the BSpline optimizer.,
        flag: --maxBSplineDisplacement %f
maximumNumberOfCorrections: (an integer (int or long))
        Maximum number of corrections in lbfgsb optimizer.
        flag: --maximumNumberOfCorrections %d
maximumNumberOfEvaluations: (an integer (int or long))
        Maximum number of evaluations for line search in lbfgsb optimizer.
        flag: --maximumNumberOfEvaluations %d
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.
        flag: --maximumStepLength %f
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).
        flag: --medianFilterSize %s
metricSamplingStrategy: ('Random')
        It defines the method that registration filter uses to sample the
        input fixed image. Only Random is supported for now.
        flag: --metricSamplingStrategy %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. Smaller values allows
        the optimizer to make smaller adjustments, but the registration time
        may increase.
        flag: --minimumStepLength %s
movingBinaryVolume: (an existing file name)
        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.
        flag: --movingBinaryVolume %s
movingVolume: (an existing file name)
        Input moving image (this image will be transformed into the fixed
        image space).
        flag: --movingVolume %s
movingVolume2: (an existing file name)
        Input moving image that will be used for multimodal
        registration(this image will be transformed into the fixed image
        space).
        flag: --movingVolume2 %s
```

```
    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
            flag: --movingVolumeTimeIndex %d
    numberOfHistogramBins: (an integer (int or long))
            The number of histogram levels used for mutual information metric
            estimation.
            flag: --numberOfHistogramBins %d
    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.
            flag: --numberOfIterations %s
    numberOfMatchPoints: (an integer (int or long))
            Number of histogram match points used for mutual information metric
            estimation.
            flag: --numberOfMatchPoints %d
    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.
            flag: --numberOfSamples %d
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use. (default is
            auto-detected)
            flag: --numberOfThreads %d
    outputFixedVolumeROI: (a boolean or a file name)
            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.
            flag: --outputFixedVolumeROI %s
    outputMovingVolumeROI: (a boolean or a file name)
            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.
            flag: --outputMovingVolumeROI %s
    outputTransform: (a boolean or a file name)
            (optional) Filename to which save the (optional) estimated
            transform. NOTE: You must select either the outputTransform or the
            outputVolume option.
            flag: --outputTransform %s
    outputVolume: (a boolean or a file name)
            (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).
            flag: --outputVolume %s
    outputVolumePixelType: ('float' or 'short' or 'ushort' or 'int' or
             'uint' or 'uchar')
            Data type for representing a voxel of the Output Volume.
            flag: --outputVolumePixelType %s
    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.,
        flag: --projectedGradientTolerance %f
promptUser: (a boolean)
        Prompt the user to hit enter each time an image is sent to the
        DebugImageViewer
        flag: --promptUser
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.
        flag: --relaxationFactor %f
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.
        flag: --removeIntensityOutliers %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
        flag: --reproportionScale %f
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.
        flag: --samplingPercentage %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.
        flag: --scaleOutputValues
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
        flag: --skewScale %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.
        flag: --splineGridSize %s
strippedOutputTransform: (a boolean or a file name)
        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.
        flag: --strippedOutputTransform %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transformType: (a list of items which are a 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.
        flag: --transformType %s
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.
        flag: --translationScale %f
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.
        flag: --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.
        flag: --useBSpline
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.
        flag: --useComposite
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.
        flag: --useROIBSpline
useRigid: (a boolean)
        Perform a rigid registration as part of the sequential registration
        steps. This family of options overrides the use of transformType if
        any of them are set.
        flag: --useRigid
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.
        flag: --useScaleSkewVersor3D
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.
        flag: --useScaleVersor3D
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.
        flag: --useSyN
```

```
    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.
            flag: --writeOutputTransformInFloat
    writeTransformOnFailure: (a boolean)
            Flag to save the final transform even if the numberOfIterations are
            reached without convergence. (Intended for use when
            --failureExitCode 0 )
            flag: --writeTransformOnFailure
```

Outputs:

```
    bsplineTransform: (an existing file name)
            (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).
    linearTransform: (an existing file name)
            (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).
    logFileReport: (an existing file name)
            A file to write out final information report in CSV file: MetricName
            ,MetricValue,FixedImageName,FixedMaskName,MovingImageName,MovingMask
            Name
    outputFixedVolumeROI: (an existing file name)
            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: (an existing file name)
            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.
    outputTransform: (an existing file name)
            (optional) Filename to which save the (optional) estimated
            transform. NOTE: You must select either the outputTransform or the
            outputVolume option.
    outputVolume: (an existing file name)
            (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).
    strippedOutputTransform: (an existing file name)
            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.
```

interfaces.semtools.registration.brainsresample

124.1 BRAINSResample

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    defaultValue: (a float)
            Default voxel value
            flag: --defaultValue %f
    deformationVolume: (an existing file name)
            Displacement Field to be used to warp the image (ITKv3 or earlier)
            flag: --deformationVolume %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    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
            makeing a 2D image of grid lines from the 3D space
            flag: --gridSpacing %s
    ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Image To Warp
        flag: --inputVolume %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
        flag: --interpolationMode %s
inverseTransform: (a boolean)
        True/False is to compute inverse of given transformation. Default is
        false
        flag: --inverseTransform
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputVolume: (a boolean or a file name)
        Resulting deformed image
        flag: --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.
        flag: --pixelType %s
referenceVolume: (an existing file name)
        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.
        flag: --referenceVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
warpTransform: (an existing file name)
        Filename for the BRAINSFit transform (ITKv3 or earlier) or composite
        transform file (ITKv4)
        flag: --warpTransform %s
```

Outputs:

```
outputVolume: (an existing file name)
        Resulting deformed image
```

interfaces.semtools.registration.brainsresize

125.1 BRAINSResize

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
            Image To Scale
            flag: --inputVolume %s
    outputVolume: (a boolean or a file name)
            Resulting scaled image
            flag: --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.
            flag: --pixelType %s
    scaleFactor: (a float)
```

```
        The scale factor for the image spacing.
        flag: --scaleFactor %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Resulting scaled image
```

interfaces.semtools.registration.specialized

126.1 BRAINSDemonWarp

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    arrayOfPyramidLevelIterations: (a list of items which are an integer
             (int or long))
            The number of iterations for each pyramid level
            flag: --arrayOfPyramidLevelIterations %s
    backgroundFillValue: (an integer (int or long))
            Replacement value to overwrite background when performing BOBF
            flag: --backgroundFillValue %d
    checkerboardPatternSubdivisions: (a list of items which are an
             integer (int or long))
            Number of Checkerboard subdivisions in all 3 directions
            flag: --checkerboardPatternSubdivisions %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    fixedBinaryVolume: (an existing file name)
            Mask filename for desired region of interest in the Fixed image.
            flag: --fixedBinaryVolume %s
```

```
    fixedVolume: (an existing file name)
            Required: input fixed (target) image
            flag: --fixedVolume %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)
            flag: --gradient_type %s
    gui: (a boolean)
            Display intermediate image volumes for debugging
            flag: --gui
    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.
            flag: --histogramMatch
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    initializeWithDisplacementField: (an existing file name)
            Initial deformation field vector image file name
            flag: --initializeWithDisplacementField %s
    initializeWithTransform: (an existing file name)
            Initial Transform filename
            flag: --initializeWithTransform %s
    inputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
            Input volumes will be typecast to this format:
            float|short|ushort|int|uchar
            flag: --inputPixelType %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
            flag: --interpolationMode %s
    lowerThresholdForBOBF: (an integer (int or long))
            Lower threshold for performing BOBF
            flag: --lowerThresholdForBOBF %d
    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
            forground 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.
            flag: --maskProcessingMode %s
    max_step_length: (a float)
            Maximum length of an update vector (0: no restriction)
            flag: --max_step_length %f
    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.
            flag: --medianFilterSize %s
    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)
        flag: --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)
        flag: --minimumMovingPyramid %s
movingBinaryVolume: (an existing file name)
        Mask filename for desired region of interest in the Moving image.
        flag: --movingBinaryVolume %s
movingVolume: (an existing file name)
        Required: input moving image
        flag: --movingVolume %s
neighborhoodForBOBF: (a list of items which are an integer (int or
     long))
        neighborhood in all 3 directions to be included when performing BOBF
        flag: --neighborhoodForBOBF %s
numberOfBCHApproximationTerms: (an integer (int or long))
        Number of terms in the BCH expansion
        flag: --numberOfBCHApproximationTerms %d
numberOfHistogramBins: (an integer (int or long))
        The number of histogram levels
        flag: --numberOfHistogramBins %d
numberOfMatchPoints: (an integer (int or long))
        The number of match points for histrogramMatch
        flag: --numberOfMatchPoints %d
numberOfPyramidLevels: (an integer (int or long))
        Number of image pyramid levels to use in the multi-resolution
        registration.
        flag: --numberOfPyramidLevels %d
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputCheckerboardVolume: (a boolean or a file name)
        Genete a checkerboard image volume between the fixedVolume and the
        deformed movingVolume.
        flag: --outputCheckerboardVolume %s
outputDebug: (a boolean)
        Flag to write debugging images after each step.
        flag: --outputDebug
outputDisplacementFieldPrefix: (a string)
        Displacement field filename prefix for writing separate x, y, and z
        component images
        flag: --outputDisplacementFieldPrefix %s
outputDisplacementFieldVolume: (a boolean or a file name)
        Output deformation field vector image (will have the same physical
        space as the fixedVolume).
        flag: --outputDisplacementFieldVolume %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.
        flag: --outputNormalized
outputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
        outputVolume will be typecast to this format:
        float|short|ushort|int|uchar
```

```
        flag: --outputPixelType %s
outputVolume: (a boolean or a file name)
        Required: output resampled moving image (will have the same physical
        space as the fixedVolume).
        flag: --outputVolume %s
promptUser: (a boolean)
        Prompt the user to hit enter each time an image is sent to the
        DebugImageViewer
        flag: --promptUser
registrationFilterType: ('Demons' or 'FastSymmetricForces' or
         'Diffeomorphic')
        Registration Filter Type: Demons|FastSymmetricForces|Diffeomorphic
        flag: --registrationFilterType %s
seedForBOBF: (a list of items which are an integer (int or long))
        coordinates in all 3 directions for Seed when performing BOBF
        flag: --seedForBOBF %s
smoothDisplacementFieldSigma: (a float)
        A gaussian smoothing value to be applied to the deformation feild at
        each iteration.
        flag: --smoothDisplacementFieldSigma %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
upFieldSmoothing: (a float)
        Smoothing sigma for the update field at each iteration
        flag: --upFieldSmoothing %f
upperThresholdForBOBF: (an integer (int or long))
        Upper threshold for performing BOBF
        flag: --upperThresholdForBOBF %d
use_vanilla_dem: (a boolean)
        Run vanilla demons algorithm
        flag: --use_vanilla_dem
```

Outputs:

```
outputCheckerboardVolume: (an existing file name)
        Genete a checkerboard image volume between the fixedVolume and the
        deformed movingVolume.
outputDisplacementFieldVolume: (an existing file name)
        Output deformation field vector image (will have the same physical
        space as the fixedVolume).
outputVolume: (an existing file name)
        Required: output resampled moving image (will have the same physical
        space as the fixedVolume).
```

126.2 BRAINSTransformFromFiducials

Link to code
Wraps 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
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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
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
        flag: --fixedLandmarks %s...
fixedLandmarksFile: (an existing file name)
        An fcsv formatted file with a list of landmark points.
        flag: --fixedLandmarksFile %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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
        flag: --movingLandmarks %s...
movingLandmarksFile: (an existing file name)
        An fcsv formatted file with a list of landmark points.
        flag: --movingLandmarksFile %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
saveTransform: (a boolean or a file name)
        Save the transform that results from registration
        flag: --saveTransform %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transformType: ('Translation' or 'Rigid' or 'Similarity')
        Type of transform to produce
        flag: --transformType %s
```

Outputs:

```
saveTransform: (an existing file name)
        Save the transform that results from registration
```

126.3 VBRAINSDemonWarp

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    arrayOfPyramidLevelIterations: (a list of items which are an integer
             (int or long))
            The number of iterations for each pyramid level
            flag: --arrayOfPyramidLevelIterations %s
    backgroundFillValue: (an integer (int or long))
            Replacement value to overwrite background when performing BOBF
            flag: --backgroundFillValue %d
    checkerboardPatternSubdivisions: (a list of items which are an
             integer (int or long))
            Number of Checkerboard subdivisions in all 3 directions
            flag: --checkerboardPatternSubdivisions %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    fixedBinaryVolume: (an existing file name)
            Mask filename for desired region of interest in the Fixed image.
            flag: --fixedBinaryVolume %s
    fixedVolume: (a list of items which are an existing file name)
            Required: input fixed (target) image
            flag: --fixedVolume %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)
            flag: --gradient_type %s
    gui: (a boolean)
            Display intermediate image volumes for debugging
            flag: --gui
    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.
            flag: --histogramMatch
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    initializeWithDisplacementField: (an existing file name)
            Initial deformation field vector image file name
            flag: --initializeWithDisplacementField %s
    initializeWithTransform: (an existing file name)
            Initial Transform filename
```

```
        flag: --initializeWithTransform %s
inputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
        Input volumes will be typecast to this format:
        float|short|ushort|int|uchar
        flag: --inputPixelType %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
        flag: --interpolationMode %s
lowerThresholdForBOBF: (an integer (int or long))
        Lower threshold for performing BOBF
        flag: --lowerThresholdForBOBF %d
makeBOBF: (a boolean)
        Flag to make Brain-Only Background-Filled versions of the input and
        target volumes.
        flag: --makeBOBF
max_step_length: (a float)
        Maximum length of an update vector (0: no restriction)
        flag: --max_step_length %f
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.
        flag: --medianFilterSize %s
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)
        flag: --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)
        flag: --minimumMovingPyramid %s
movingBinaryVolume: (an existing file name)
        Mask filename for desired region of interest in the Moving image.
        flag: --movingBinaryVolume %s
movingVolume: (a list of items which are an existing file name)
        Required: input moving image
        flag: --movingVolume %s...
neighborhoodForBOBF: (a list of items which are an integer (int or
         long))
        neighborhood in all 3 directions to be included when performing BOBF
        flag: --neighborhoodForBOBF %s
numberOfBCHApproximationTerms: (an integer (int or long))
        Number of terms in the BCH expansion
        flag: --numberOfBCHApproximationTerms %d
numberOfHistogramBins: (an integer (int or long))
        The number of histogram levels
        flag: --numberOfHistogramBins %d
numberOfMatchPoints: (an integer (int or long))
        The number of match points for histrogramMatch
        flag: --numberOfMatchPoints %d
```

```
    numberOfPyramidLevels: (an integer (int or long))
            Number of image pyramid levels to use in the multi-resolution
            registration.
            flag: --numberOfPyramidLevels %d
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputCheckerboardVolume: (a boolean or a file name)
            Genete a checkerboard image volume between the fixedVolume and the
            deformed movingVolume.
            flag: --outputCheckerboardVolume %s
    outputDebug: (a boolean)
            Flag to write debugging images after each step.
            flag: --outputDebug
    outputDisplacementFieldPrefix: (a string)
            Displacement field filename prefix for writing separate x, y, and z
            component images
            flag: --outputDisplacementFieldPrefix %s
    outputDisplacementFieldVolume: (a boolean or a file name)
            Output deformation field vector image (will have the same physical
            space as the fixedVolume).
            flag: --outputDisplacementFieldVolume %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.
            flag: --outputNormalized
    outputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
            outputVolume will be typecast to this format:
            float|short|ushort|int|uchar
            flag: --outputPixelType %s
    outputVolume: (a boolean or a file name)
            Required: output resampled moving image (will have the same physical
            space as the fixedVolume).
            flag: --outputVolume %s
    promptUser: (a boolean)
            Prompt the user to hit enter each time an image is sent to the
            DebugImageViewer
            flag: --promptUser
    registrationFilterType: ('Demons' or 'FastSymmetricForces' or
             'Diffeomorphic' or 'LogDemons' or 'SymmetricLogDemons')
            Registration Filter Type: Demons|FastSymmetricForces|Diffeomorphic|L
            ogDemons|SymmetricLogDemons
            flag: --registrationFilterType %s
    seedForBOBF: (a list of items which are an integer (int or long))
            coordinates in all 3 directions for Seed when performing BOBF
            flag: --seedForBOBF %s
    smoothDisplacementFieldSigma: (a float)
            A gaussian smoothing value to be applied to the deformation feild at
            each iteration.
            flag: --smoothDisplacementFieldSigma %f
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    upFieldSmoothing: (a float)
            Smoothing sigma for the update field at each iteration
            flag: --upFieldSmoothing %f
```

```
    upperThresholdForBOBF: (an integer (int or long))
            Upper threshold for performing BOBF
            flag: --upperThresholdForBOBF %d
    use_vanilla_dem: (a boolean)
            Run vanilla demons algorithm
            flag: --use_vanilla_dem
    weightFactors: (a list of items which are a float)
            Weight fatctors for each input images
            flag: --weightFactors %s
```

Outputs:

```
    outputCheckerboardVolume: (an existing file name)
            Genete a checkerboard image volume between the fixedVolume and the
            deformed movingVolume.
    outputDisplacementFieldVolume: (an existing file name)
            Output deformation field vector image (will have the same physical
            space as the fixedVolume).
    outputVolume: (an existing file name)
            Required: output resampled moving image (will have the same physical
            space as the fixedVolume).
```

interfaces.semtools.segmentation.specialized

127.1 BRAINSABC

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    atlasDefinition: (an existing file name)
            Contains all parameters for Atlas
            flag: --atlasDefinition %s
    atlasToSubjectInitialTransform: (a boolean or a file name)
            The initial transform from atlas to the subject
            flag: --atlasToSubjectInitialTransform %s
    atlasToSubjectTransform: (a boolean or a file name)
            The transform from atlas to the subject
            flag: --atlasToSubjectTransform %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.
            flag: --atlasToSubjectTransformType %s
    atlasWarpingOff: (a boolean)
            Deformable registration of atlas to subject
            flag: --atlasWarpingOff
    debuglevel: (an integer (int or long))
            Display debug messages, and produce debug intermediate results.
            0=OFF, 1=Minimal, 10=Maximum debugging.
            flag: --debuglevel %d
    defaultSuffix: (a string)
            flag: --defaultSuffix %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    filterIteration: (an integer (int or long))
```

```
        Filter iterations
        flag: --filterIteration %d
filterMethod: ('None' or 'CurvatureFlow' or
         'GradientAnisotropicDiffusion' or 'Median')
        Filter method for preprocessing of registration
        flag: --filterMethod %s
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.
        flag: --filterTimeStep %f
gridSize: (a list of items which are an integer (int or long))
        Grid size for atlas warping with BSplines
        flag: --gridSize %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
implicitOutputs: (a boolean or a list of items which are a file name)
        Outputs to be made available to NiPype. Needed because not all
        BRAINSABC outputs have command line arguments.
        flag: --implicitOutputs %s...
inputVolumeTypes: (a list of items which are a string)
        The list of input image types corresponding to the inputVolumes.
        flag: --inputVolumeTypes %s
inputVolumes: (a list of items which are an existing file name)
        The list of input image files to be segmented.
        flag: --inputVolumes %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.
        flag: --interpolationMode %s
maxBiasDegree: (an integer (int or long))
        Maximum bias degree
        flag: --maxBiasDegree %d
maxIterations: (an integer (int or long))
        Filter iterations
        flag: --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.
        flag: --medianFilterSize %s
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.
        flag: --numberOfSubSamplesInEachPlugArea %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputDir: (a boolean or a directory name)
        Ouput directory
        flag: --outputDir %s
```

```
    outputDirtyLabels: (a boolean or a file name)
            Output Dirty Label Image
            flag: --outputDirtyLabels %s
    outputFormat: ('NIFTI' or 'Meta' or 'Nrrd')
            Output format
            flag: --outputFormat %s
    outputLabels: (a boolean or a file name)
            Output Label Image
            flag: --outputLabels %s
    outputVolumes: (a boolean or a list of items which are a file name)
            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.
            flag: --outputVolumes %s...
    posteriorTemplate: (a string)
            filename template for Posterior output files
            flag: --posteriorTemplate %s
    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.
            flag: --purePlugsThreshold %f
    restoreState: (an existing file name)
            The initial state for the registration process
            flag: --restoreState %s
    saveState: (a boolean or a file name)
            (optional) Filename to which save the final state of the
            registration
            flag: --saveState %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.
            flag: --subjectIntermodeTransformType %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    useKNN: (a boolean)
            Use the KNN stage of estimating posteriors.
            flag: --useKNN
    writeLess: (a boolean)
            Does not write posteriors and filtered, bias corrected images
            flag: --writeLess
```

Outputs:

```
    atlasToSubjectInitialTransform: (an existing file name)
            The initial transform from atlas to the subject
    atlasToSubjectTransform: (an existing file name)
            The transform from atlas to the subject
    implicitOutputs: (a list of items which are an existing file name)
            Outputs to be made available to NiPype. Needed because not all
            BRAINSABC outputs have command line arguments.
    outputDir: (an existing directory name)
            Ouput directory
```

```
    outputDirtyLabels: (an existing file name)
            Output Dirty Label Image
    outputLabels: (an existing file name)
            Output Label Image
    outputVolumes: (a list of items which are an existing file name)
            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.
    saveState: (an existing file name)
            (optional) Filename to which save the final state of the
            registration
```

127.2 BRAINSConstellationDetector

Link to code

Wraps 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 extention 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:

```
    [Mandatory]

    [Optional]
    BackgroundFillValue: (a string)
            Fill the background of image with specified short int value. Enter
            number or use BIGNEG for a large negative number.
            flag: --BackgroundFillValue %s
    LLSModel: (an existing file name)
            Linear least squares model filename in HD5 format
            flag: --LLSModel %s
    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.,
            flag: --acLowerBound %f
    args: (a string)
            Additional parameters to the command
            flag: %s
    atlasLandmarkWeights: (an existing file name)
            Weights associated with atlas landmarks to be used for BRAINSFit
            registration initialization,
            flag: --atlasLandmarkWeights %s
    atlasLandmarks: (an existing file name)
```

```
        Atlas landmarks to be used for BRAINSFit registration
        initialization,
        flag: --atlasLandmarks %s
atlasVolume: (an existing file name)
        Atlas volume image to be used for BRAINSFit registration
        flag: --atlasVolume %s
cutOutHeadInOutputVolume: (a boolean)
        , Flag to cut out just the head tissue when producing an
        (un)transformed clipped volume.,
        flag: --cutOutHeadInOutputVolume
debug: (a boolean)
        , Show internal debugging information.,
        flag: --debug
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
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.,
        flag: --forceACPoint %s
forceHoughEyeDetectorReportFailure: (a boolean)
        , Flag indicates whether the Hough eye detector should report
        failure,
        flag: --forceHoughEyeDetectorReportFailure
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.,
        flag: --forcePCPoint %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.,
        flag: --forceRPPoint %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.,
        flag: --forceVN4Point %s
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.,
        flag: --houghEyeDetectorMode %d
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputLandmarksEMSP: (an existing file name)
        , 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.,
        flag: --inputLandmarksEMSP %s
inputTemplateModel: (an existing file name)
        User-specified template model.,
        flag: --inputTemplateModel %s
inputVolume: (an existing file name)
        Input image in which to find ACPC points
        flag: --inputVolume %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
        flag: --interpolationMode %s
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), NOTE: -1= Prealigned so no
        estimate!.,
        flag: --mspQualityLevel %d
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
otsuPercentileThreshold: (a float)
        , This is a parameter to FindLargestForegroundFilledMask, which is
        employed when acLowerBound is set and an
        outputUntransformedClippedVolume is requested.,
        flag: --otsuPercentileThreshold %f
outputLandmarksInACPCAlignedSpace: (a boolean or a file name)
        , 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.,
        flag: --outputLandmarksInACPCAlignedSpace %s
outputLandmarksInInputSpace: (a boolean or a file name)
        , 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.,
        flag: --outputLandmarksInInputSpace %s
outputMRML: (a boolean or a file name)
        , 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.,
        flag: --outputMRML %s
outputResampledVolume: (a boolean or a file name)
        ACPC-aligned output image in a resampled unifor space. Currently
        this is a 1mm, 256^3, Identity direction image.
        flag: --outputResampledVolume %s
outputTransform: (a boolean or a file name)
        The filename for the original space to ACPC alignment to be written
        (in .h5 format).,
        flag: --outputTransform %s
outputUntransformedClippedVolume: (a boolean or a file name)
        Output image in which to store neck-clipped input image, with the
        use of --acLowerBound and maybe --cutOutHeadInUntransformedVolume.
        flag: --outputUntransformedClippedVolume %s
outputVerificationScript: (a boolean or a file name)
        , 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.,
        flag: --outputVerificationScript %s
outputVolume: (a boolean or a file name)
```

```
        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-sagital plane is the plane where
        physical L/R coordinate is 0.0.
        flag: --outputVolume %s
rVN4: (a float)
        , Search radius for VN4 in unit of mm,
        flag: --rVN4 %f
rac: (a float)
        , Search radius for AC in unit of mm,
        flag: --rac %f
rescaleIntensities: (a boolean)
        , Flag to turn on rescaling image intensities on input.,
        flag: --rescaleIntensities
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.,
        flag: --rescaleIntensitiesOutputRange %s
resultsDir: (a boolean or a directory name)
        , The directory for the debuging images to be written.,
        flag: --resultsDir %s
rmpj: (a float)
        , Search radius for MPJ in unit of mm,
        flag: --rmpj %f
rpc: (a float)
        , Search radius for PC in unit of mm,
        flag: --rpc %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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.,
        flag: --trimRescaledIntensities %f
verbose: (a boolean)
        , Show more verbose output,
        flag: --verbose
writeBranded2DImage: (a boolean or a file name)
        , The filename for the 2D .png branded midline debugging image. This
        will happen only in conjunction with requesting an outputVolume.,
        flag: --writeBranded2DImage %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.,
        flag: --writedebuggingImagesLevel %d
```

Outputs:

```
outputLandmarksInACPCAlignedSpace: (an existing file name)
        , 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.,
```

```
    outputLandmarksInInputSpace: (an existing file name)
            , 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.,
    outputMRML: (an existing file name)
            , 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.,
    outputResampledVolume: (an existing file name)
            ACPC-aligned output image in a resampled unifor space. Currently
            this is a 1mm, 256^3, Identity direction image.
    outputTransform: (an existing file name)
            The filename for the original space to ACPC alignment to be written
            (in .h5 format).,
    outputUntransformedClippedVolume: (an existing file name)
            Output image in which to store neck-clipped input image, with the
            use of --acLowerBound and maybe --cutOutHeadInUntransformedVolume.
    outputVerificationScript: (an existing file name)
            , 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.,
    outputVolume: (an existing file name)
            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-sagital plane is the plane where
            physical L/R coordinate is 0.0.
    resultsDir: (an existing directory name)
            , The directory for the debuging images to be written.,
    writeBranded2DImage: (an existing file name)
            , The filename for the 2D .png branded midline debugging image. This
            will happen only in conjunction with requesting an outputVolume.,
```

127.3 BRAINSCreateLabelMapFromProbabilityMaps

Link to code

Wraps command ** BRAINSCreateLabelMapFromProbabilityMaps **
title: Create Label Map From Probability Maps (BRAINS)
category: Segmentation.Specialized
description: Given A list of Probability Maps, generate a LabelMap.
Inputs:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    cleanLabelVolume: (a boolean or a file name)
            the foreground labels volume
            flag: --cleanLabelVolume %s
    dirtyLabelVolume: (a boolean or a file name)
            the labels prior to cleaning
            flag: --dirtyLabelVolume %s
```

```
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    foregroundPriors: (a list of items which are an integer (int or
             long))
            A list: For each Prior Label, 1 if foreground, 0 if background
            flag: --foregroundPriors %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inclusionThreshold: (a float)
            tolerance for inclusion
            flag: --inclusionThreshold %f
    inputProbabilityVolume: (a list of items which are an existing file
             name)
            The list of proobabilityimages.
            flag: --inputProbabilityVolume %s...
    nonAirRegionMask: (an existing file name)
            a mask representing the 'NonAirRegion' -- Just force pixels in this
            region to zero
            flag: --nonAirRegionMask %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
            flag: --priorLabelCodes %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    cleanLabelVolume: (an existing file name)
            the foreground labels volume
    dirtyLabelVolume: (an existing file name)
            the labels prior to cleaning
```

127.4 BRAINSCut

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    NoTrainingVectorShuffling: (a boolean)
            If this flag is on, there will be no shuffling.
            flag: --NoTrainingVectorShuffling
    applyModel: (a boolean)
```

```
        apply the neural net
        flag: --applyModel
args: (a string)
        Additional parameters to the command
        flag: %s
computeSSEOn: (a boolean)
        compute Sum of Square Error (SSE) along the trained model until the
        number of iteration given in the modelConfigurationFilename file
        flag: --computeSSEOn
createVectors: (a boolean)
        create vectors for training neural net
        flag: --createVectors
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
generateProbability: (a boolean)
        Generate probability map
        flag: --generateProbability
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.
        flag: --histogramEqualization
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
method: ('RandomForest' or 'ANN')
        flag: --method %s
modelConfigurationFilename: (an existing file name)
        XML File defining BRAINSCut parameters
        flag: --modelConfigurationFilename %s
modelFilename: (a string)
         model file name given from user (not by xml configuration file)
        flag: --modelFilename %s
multiStructureThreshold: (a boolean)
        multiStructureThreshold module to deal with overlaping area
        flag: --multiStructureThreshold
netConfiguration: (an existing file name)
        XML File defining BRAINSCut parameters. OLD NAME. PLEASE USE
        modelConfigurationFilename instead.
        flag: --netConfiguration %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.
        flag: --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.
        flag: --randomTreeDepth %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
trainModel: (a boolean)
        train the neural net
        flag: --trainModel
trainModelStartIndex: (an integer (int or long))
```

```
        Starting iteration for training
        flag: --trainModelStartIndex %d
validate: (a boolean)
        validate data set.Just need for the first time run ( This is for
        validation of xml file and not working yet )
        flag: --validate
verbose: (an integer (int or long))
        print out some debugging information
        flag: --verbose %d
```

Outputs:

```
None
```

127.5 BRAINSMultiSTAPLE

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputCompositeT1Volume: (an existing file name)
        Composite T1, all label maps transofrmed into the space for this
        image.
        flag: --inputCompositeT1Volume %s
inputLabelVolume: (a list of items which are an existing file name)
        The list of proobabilityimages.
        flag: --inputLabelVolume %s...
inputTransform: (a list of items which are an existing file name)
        transforms to apply to label volumes
        flag: --inputTransform %s...
labelForUndecidedPixels: (an integer (int or long))
        Label for undecided pixels
        flag: --labelForUndecidedPixels %d
outputConfusionMatrix: (a boolean or a file name)
        Confusion Matrix
        flag: --outputConfusionMatrix %s
outputMultiSTAPLE: (a boolean or a file name)
        the MultiSTAPLE average of input label volumes
        flag: --outputMultiSTAPLE %s
resampledVolumePrefix: (a string)
        if given, write out resampled volumes with this prefix
        flag: --resampledVolumePrefix %s
```

```
    skipResampling: (a boolean)
            Omit resampling images into reference space
            flag: --skipResampling
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputConfusionMatrix: (an existing file name)
            Confusion Matrix
    outputMultiSTAPLE: (an existing file name)
            the MultiSTAPLE average of input label volumes
```

127.6 BRAINSROIAuto

Link to code
Wraps command ** BRAINSROIAuto **
title: Foreground masking (BRAINS)
category: Segmentation.Specialized
description: This program is used to create a mask over the most prominant forground 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:

```
    [Mandatory]

    [Optional]
    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.
            flag: --ROIAutoDilateSize %f
    args: (a string)
            Additional parameters to the command
            flag: %s
    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.
            flag: --closingSize %f
    cropOutput: (a boolean)
            The inputVolume cropped to the region of the ROI mask.
            flag: --cropOutput
    environ: (a dictionary with keys which are a value of type 'str' and
```

```
          with values which are a value of type 'str', nipype default value:
          {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        The input image for finding the largest region filled mask.
        flag: --inputVolume %s
maskOutput: (a boolean)
        The inputVolume multiplied by the ROI mask.
        flag: --maskOutput
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
otsuPercentileThreshold: (a float)
        Parameter to the Otsu threshold algorithm.
        flag: --otsuPercentileThreshold %f
outputROIMaskVolume: (a boolean or a file name)
        The ROI automatically found from the input image.
        flag: --outputROIMaskVolume %s
outputVolume: (a boolean or a file name)
        The inputVolume with optional [maskOutput|cropOutput] to the region
        of the brain mask.
        flag: --outputVolume %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.
        flag: --outputVolumePixelType %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
thresholdCorrectionFactor: (a float)
        A factor to scale the Otsu algorithm's result threshold, in case
        clipping mangles the image.
        flag: --thresholdCorrectionFactor %f
```

Outputs:

```
outputROIMaskVolume: (an existing file name)
        The ROI automatically found from the input image.
outputVolume: (an existing file name)
        The inputVolume with optional [maskOutput|cropOutput] to the region
        of the brain mask.
```

127.7 BinaryMaskEditorBasedOnLandmarks

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputBinaryVolume: (an existing file name)
            Input binary image in which to be edited
            flag: --inputBinaryVolume %s
    inputLandmarkNames: (a list of items which are a string)
             A target input landmark name to be edited. This should be listed in
            the inputLandmakrFilename Given.
            flag: --inputLandmarkNames %s
    inputLandmarkNamesForObliquePlane: (a list of items which are a
             string)
             Three subset landmark names of inputLandmarksFilename for a oblique
            plane computation. The plane computed for binary volume editing.
            flag: --inputLandmarkNamesForObliquePlane %s
    inputLandmarksFilename: (an existing file name)
             The filename for the landmark definition file in the same format
            produced by Slicer3 (.fcsv).
            flag: --inputLandmarksFilename %s
    outputBinaryVolume: (a boolean or a file name)
            Output binary image in which to be edited
            flag: --outputBinaryVolume %s
    setCutDirectionForLandmark: (a list of items which are a 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)
            flag: --setCutDirectionForLandmark %s
    setCutDirectionForObliquePlane: (a list of items which are a string)
            If this is true, the mask will be thresholded out to the direction
            of inferior, posterior, and/or left. Default behavrior is that
            cutting out to the direction of superior, anterior and/or right.
            flag: --setCutDirectionForObliquePlane %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputBinaryVolume: (an existing file name)
            Output binary image in which to be edited
```

127.8 ESLR

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
closingSize: (an integer (int or long))
        The closing size for hole filling.
        flag: --closingSize %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
high: (an integer (int or long))
        The higher bound of the labels to be used.
        flag: --high %d
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Input Label Volume
        flag: --inputVolume %s
low: (an integer (int or long))
        The lower bound of the labels to be used.
        flag: --low %d
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
openingSize: (an integer (int or long))
        The opening size for hole filling.
        flag: --openingSize %d
outputVolume: (a boolean or a file name)
        Output Label Volume
        flag: --outputVolume %s
preserveOutside: (a boolean)
        For values outside the specified range, preserve those values.
        flag: --preserveOutside
safetySize: (an integer (int or long))
        The safetySize size for the clipping region.
        flag: --safetySize %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Output Label Volume
```

CHAPTER 128

interfaces.semtools.utilities.brains

128.1 BRAINSAlignMSP

Link to code
Wraps command ** BRAINSAlignMSP **
title: Align Mid Saggital Brain (BRAINS)
category: Utilities.BRAINS
description: Resample an image into ACPC alignement ACPCDetect
Inputs:

```
[Mandatory]

[Optional]
BackgroundFillValue: (a string)
        Fill the background of image with specified short int value. Enter
        number or use BIGNEG for a large negative number.
        flag: --BackgroundFillValue %s
OutputresampleMSP: (a boolean or a file name)
        , The image to be output.,
        flag: --OutputresampleMSP %s
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        , The Image to be resampled,
        flag: --inputVolume %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
        flag: --interpolationMode %s
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).,
        flag: --mspQualityLevel %d
```

```
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    rescaleIntensities: (a boolean)
            , Flag to turn on rescaling image intensities on input.,
            flag: --rescaleIntensities
    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.,
            flag: --rescaleIntensitiesOutputRange %s
    resultsDir: (a boolean or a directory name)
            , The directory for the results to be written.,
            flag: --resultsDir %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    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.,
            flag: --trimRescaledIntensities %f
    verbose: (a boolean)
            , Show more verbose output,
            flag: --verbose
    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.,
            flag: --writedebuggingImagesLevel %d
```

Outputs:

```
    OutputresampleMSP: (an existing file name)
            , The image to be output.,
    resultsDir: (an existing directory name)
            , The directory for the results to be written.,
```

128.2 BRAINSClipInferior

Link to code

Wraps 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:

```
    [Mandatory]

    [Optional]
    BackgroundFillValue: (a string)
            Fill the background of image with specified short int value. Enter
```

```
        number or use BIGNEG for a large negative number.
        flag: --BackgroundFillValue %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.,
        flag: --acLowerBound %f
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Input image to make a clipped short int copy from.
        flag: --inputVolume %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputVolume: (a boolean or a file name)
        Output image, a short int copy of the upper portion of the input
        image, filled with BackgroundFillValue.
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Output image, a short int copy of the upper portion of the input
        image, filled with BackgroundFillValue.
```

128.3 BRAINSConstellationModeler

Link to code

Wraps command ** BRAINSConstellationModeler **
title: Generate Landmarks Model (BRAINS)
category: Utilities.BRAINS
description: Train up a model for BRAINSConstellationDetector
Inputs:

```
[Mandatory]

[Optional]
BackgroundFillValue: (a string)
        Fill the background of image with specified short int value. Enter
        number or use BIGNEG for a large negative number.
        flag: --BackgroundFillValue %s
args: (a string)
```

```
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputTrainingList: (an existing file name)
        , Setup file, giving all parameters for training up a template model
        for each landmark.,
        flag: --inputTrainingList %s
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).,
        flag: --mspQualityLevel %d
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
optimizedLandmarksFilenameExtender: (a 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.,
        flag: --optimizedLandmarksFilenameExtender %s
outputModel: (a boolean or a file name)
        , The full filename of the output model file.,
        flag: --outputModel %s
rescaleIntensities: (a boolean)
        , Flag to turn on rescaling image intensities on input.,
        flag: --rescaleIntensities
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.,
        flag: --rescaleIntensitiesOutputRange %s
resultsDir: (a boolean or a directory name)
        , The directory for the results to be written.,
        flag: --resultsDir %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.,
        flag: --saveOptimizedLandmarks
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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.,
        flag: --trimRescaledIntensities %f
verbose: (a boolean)
        , Show more verbose output,
        flag: --verbose
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.,
        flag: --writedebuggingImagesLevel %d
```

Outputs:

```
outputModel: (an existing file name)
        , The full filename of the output model file.,
resultsDir: (an existing directory name)
        , The directory for the results to be written.,
```

128.4 BRAINSEyeDetector

Link to code
Wraps command ** BRAINSEyeDetector **
title: Eye Detector (BRAINS)
category: Utilities.BRAINS
version: 1.0
documentation-url: http://www.nitrc.org/projects/brainscdetector/
Inputs:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
debugDir: (a string)
        A place for debug information
        flag: --debugDir %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        The input volume
        flag: --inputVolume %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputVolume: (a boolean or a file name)
        The output volume
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        The output volume
```

128.5 BRAINSInitializedControlPoints

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Input Volume
        flag: --inputVolume %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputLandmarksFile: (a string)
        Output filename
        flag: --outputLandmarksFile %s
outputVolume: (a boolean or a file name)
        Output Volume
        flag: --outputVolume %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)
        flag: --permuteOrder %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.
        flag: --splineGridSize %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
```

```
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Output Volume
```

128.6 BRAINSLandmarkInitializer

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputFixedLandmarkFilename: (an existing file name)
        input fixed landmark. *.fcsv
        flag: --inputFixedLandmarkFilename %s
inputMovingLandmarkFilename: (an existing file name)
        input moving landmark. *.fcsv
        flag: --inputMovingLandmarkFilename %s
inputWeightFilename: (an existing file name)
        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.
        flag: --inputWeightFilename %s
outputTransformFilename: (a boolean or a file name)
        output transform file name (ex: ./outputTransform.mat)
        flag: --outputTransformFilename %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputTransformFilename: (an existing file name)
        output transform file name (ex: ./outputTransform.mat)
```

128.7 BRAINSLinearModelerEPCA

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputTrainingList: (an existing file name)
        Input Training Landmark List Filename,
        flag: --inputTrainingList %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
None
```

128.8 BRAINSLmkTransform

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
```

```
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputFixedLandmarks: (an existing file name)
            Input Fixed Landmark list file in fcsv,
            flag: --inputFixedLandmarks %s
    inputMovingLandmarks: (an existing file name)
            Input Moving Landmark list file in fcsv,
            flag: --inputMovingLandmarks %s
    inputMovingVolume: (an existing file name)
            The filename of input moving volume
            flag: --inputMovingVolume %s
    inputReferenceVolume: (an existing file name)
            The filename of the reference volume
            flag: --inputReferenceVolume %s
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputAffineTransform: (a boolean or a file name)
            The filename for the estimated affine transform,
            flag: --outputAffineTransform %s
    outputResampledVolume: (a boolean or a file name)
            The filename of the output resampled volume
            flag: --outputResampledVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputAffineTransform: (an existing file name)
            The filename for the estimated affine transform,
    outputResampledVolume: (an existing file name)
            The filename of the output resampled volume
```

128.9 BRAINSMush

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
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
        flag: --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
        flag: --boundingBoxStart %s
desiredMean: (a float)
        Desired mean within the mask for weighted sum of both images.
        flag: --desiredMean %f
desiredVariance: (a float)
        Desired variance within the mask for weighted sum of both images.
        flag: --desiredVariance %f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputFirstVolume: (an existing file name)
        Input image (1) for mixture optimization
        flag: --inputFirstVolume %s
inputMaskVolume: (an existing file name)
        Input label image for mixture optimization
        flag: --inputMaskVolume %s
inputSecondVolume: (an existing file name)
        Input image (2) for mixture optimization
        flag: --inputSecondVolume %s
lowerThresholdFactor: (a float)
        Lower threshold factor for defining the brain mask
        flag: --lowerThresholdFactor %f
lowerThresholdFactorPre: (a float)
        Lower threshold factor for finding an initial brain mask
        flag: --lowerThresholdFactorPre %f
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
outputMask: (a boolean or a file name)
        The brain volume mask generated from the MUSH image
        flag: --outputMask %s
outputVolume: (a boolean or a file name)
        The MUSH image produced from the T1 and T2 weighted images
        flag: --outputVolume %s
outputWeightsFile: (a boolean or a file name)
        Output Weights File
        flag: --outputWeightsFile %s
seed: (a list of items which are an integer (int or long))
        Seed Point for Brain Region Filling
```

```
        flag: --seed %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
upperThresholdFactor: (a float)
        Upper threshold factor for defining the brain mask
        flag: --upperThresholdFactor %f
upperThresholdFactorPre: (a float)
        Upper threshold factor for finding an initial brain mask
        flag: --upperThresholdFactorPre %f
```

Outputs:

```
outputMask: (an existing file name)
        The brain volume mask generated from the MUSH image
outputVolume: (an existing file name)
        The MUSH image produced from the T1 and T2 weighted images
outputWeightsFile: (an existing file name)
        Output Weights File
```

128.10 BRAINSSnapShotWriter

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputBinaryVolumes: (a list of items which are an existing file name)
        Input mask (binary) volume list to be extracted as 2D image.
        Multiple input is possible.
        flag: --inputBinaryVolumes %s...
inputPlaneDirection: (a list of items which are an integer (int or
         long))
        Plane to display. In general, 0=saggital, 1=coronal, and 2=axial
        plane.
        flag: --inputPlaneDirection %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.
        flag: --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
        flag: --inputSliceToExtractInPercent %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.
        flag: --inputSliceToExtractInPhysicalPoint %s
inputVolumes: (a list of items which are an existing file name)
        Input image volume list to be extracted as 2D image. Multiple input
        is possible. At least one input is required.
        flag: --inputVolumes %s...
outputFilename: (a boolean or a file name)
        2D file name of input images. Required.
        flag: --outputFilename %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputFilename: (an existing file name)
        2D file name of input images. Required.
```

128.11 BRAINSTransformConvert

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
displacementVolume: (a boolean or a file name)
        flag: --displacementVolume %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
```

```
        interface fails to run
inputTransform: (an existing file name)
        flag: --inputTransform %s
outputPrecisionType: ('double' or 'float')
        Precision type of the output transform. It can be either single
        precision or double precision
        flag: --outputPrecisionType %s
outputTransform: (a boolean or a file name)
        flag: --outputTransform %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
        flag: --outputTransformType %s
referenceVolume: (an existing file name)
        flag: --referenceVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
displacementVolume: (an existing file name)
outputTransform: (an existing file name)
```

128.12 BRAINSTrimForegroundInDirection

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
BackgroundFillValue: (a string)
        Fill the background of image with specified short int value. Enter
        number or use BIGNEG for a large negative number.
        flag: --BackgroundFillValue %s
args: (a string)
        Additional parameters to the command
        flag: %s
closingSize: (an integer (int or long))
        , This is a parameter to FindLargestForegroundFilledMask,
        flag: --closingSize %d
directionCode: (an integer (int or long))
        , This flag chooses which dimension to compare. The sign lets you
        flip direction.,
        flag: --directionCode %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
```

```
        Environment variables
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.,
        flag: --headSizeLimit %f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Input image to trim off the neck (and also air-filling noise.)
        flag: --inputVolume %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
otsuPercentileThreshold: (a float)
        , This is a parameter to FindLargestForegroundFilledMask, which is
        employed to trim off air-filling noise.,
        flag: --otsuPercentileThreshold %f
outputVolume: (a boolean or a file name)
        Output image with neck and air-filling noise trimmed isotropic image
        with AC at center of image.
        flag: --outputVolume %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Output image with neck and air-filling noise trimmed isotropic image
        with AC at center of image.
```

128.13 CleanUpOverlapLabels

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputBinaryVolumes: (a list of items which are an existing file name)
        The list of binary images to be checked and cleaned up. Order is
        important. Binary volume given first always wins out.
        flag: --inputBinaryVolumes %s...
outputBinaryVolumes: (a boolean or a list of items which are a file
         name)
        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
        flag: --outputBinaryVolumes %s...
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputBinaryVolumes: (a list of items which are an existing file
         name)
        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
```

128.14 FindCenterOfBrain

Link to code
Wraps 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://wwww.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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
axis: (an integer (int or long))
        flag: --axis %d
backgroundValue: (an integer (int or long))
        flag: --backgroundValue %d
clippedImageMask: (a boolean or a file name)
        flag: --clippedImageMask %s
closingSize: (an integer (int or long))
        flag: --closingSize %d
debugAfterGridComputationsForegroundImage: (a boolean or a file name)
        flag: --debugAfterGridComputationsForegroundImage %s
debugClippedImageMask: (a boolean or a file name)
```

```
        flag: --debugClippedImageMask %s
debugDistanceImage: (a boolean or a file name)
        flag: --debugDistanceImage %s
debugGridImage: (a boolean or a file name)
        flag: --debugGridImage %s
debugTrimmedImage: (a boolean or a file name)
        flag: --debugTrimmedImage %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
generateDebugImages: (a boolean)
        flag: --generateDebugImages
headSizeEstimate: (a float)
        flag: --headSizeEstimate %f
headSizeLimit: (a float)
        flag: --headSizeLimit %f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
imageMask: (an existing file name)
        flag: --imageMask %s
inputVolume: (an existing file name)
        The image in which to find the center.
        flag: --inputVolume %s
maximize: (a boolean)
        flag: --maximize
otsuPercentileThreshold: (a float)
        flag: --otsuPercentileThreshold %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
clippedImageMask: (an existing file name)
debugAfterGridComputationsForegroundImage: (an existing file name)
debugClippedImageMask: (an existing file name)
debugDistanceImage: (an existing file name)
debugGridImage: (an existing file name)
debugTrimmedImage: (an existing file name)
```

128.15 GenerateLabelMapFromProbabilityMap

Link to code

Wraps 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:

```
[Mandatory]
```

```
    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolumes: (a list of items which are an existing file name)
            The Input probaiblity images to be computed for lable maps
            flag: --inputVolumes %s...
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputLabelVolume: (a boolean or a file name)
            The Input binary image for region of interest
            flag: --outputLabelVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputLabelVolume: (an existing file name)
            The Input binary image for region of interest
```

128.16 ImageRegionPlotter

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputBinaryROIVolume: (an existing file name)
            The Input binary image for region of interest
            flag: --inputBinaryROIVolume %s
```

```
    inputLabelVolume: (an existing file name)
            The Label Image
            flag: --inputLabelVolume %s
    inputVolume1: (an existing file name)
            The Input image to be computed for statistics
            flag: --inputVolume1 %s
    inputVolume2: (an existing file name)
            The Input image to be computed for statistics
            flag: --inputVolume2 %s
    numberOfHistogramBins: (an integer (int or long))
             the number of histogram levels
            flag: --numberOfHistogramBins %d
    outputJointHistogramData: (a string)
             output data file name
            flag: --outputJointHistogramData %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    useIntensityForHistogram: (a boolean)
             Create Intensity Joint Histogram instead of Quantile Joint
            Histogram
            flag: --useIntensityForHistogram
    useROIAUTO: (a boolean)
             Use ROIAUTO to compute region of interest. This cannot be used with
            inputLabelVolume
            flag: --useROIAUTO
    verbose: (a boolean)
             print debugging information,
            flag: --verbose
```

Outputs:

```
    None
```

128.17 JointHistogram

Link to code

Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
```

```
        interface fails to run
inputMaskVolumeInXAxis: (an existing file name)
        Input mask volume for inputVolumeInXAxis. Histogram will be computed
        just for the masked region
        flag: --inputMaskVolumeInXAxis %s
inputMaskVolumeInYAxis: (an existing file name)
        Input mask volume for inputVolumeInYAxis. Histogram will be computed
        just for the masked region
        flag: --inputMaskVolumeInYAxis %s
inputVolumeInXAxis: (an existing file name)
        The Input image to be computed for statistics
        flag: --inputVolumeInXAxis %s
inputVolumeInYAxis: (an existing file name)
        The Input image to be computed for statistics
        flag: --inputVolumeInYAxis %s
outputJointHistogramImage: (a string)
         output joint histogram image file name. Histogram is usually 2D
        image.
        flag: --outputJointHistogramImage %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
         print debugging information,
        flag: --verbose
```

Outputs:

```
None
```

128.18 ShuffleVectorsModule

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVectorFileBaseName: (an existing file name)
```

```
        input vector file name prefix. Usually end with .txt and header file
        has prost fix of .txt.hdr
        flag: --inputVectorFileBaseName %s
outputVectorFileBaseName: (a boolean or a file name)
        output vector file name prefix. Usually end with .txt and header
        file has prost fix of .txt.hdr
        flag: --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.
        flag: --resampleProportion %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVectorFileBaseName: (an existing file name)
        output vector file name prefix. Usually end with .txt and header
        file has prost fix of .txt.hdr
```

128.19 fcsv_to_hdf5

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
landmarkGlobPattern: (a string)
        Glob pattern to select fcsv files
        flag: --landmarkGlobPattern %s
landmarkTypesList: (an existing file name)
        , file containing list of landmark types,
        flag: --landmarkTypesList %s
landmarksInformationFile: (a boolean or a file name)
        , name of HDF5 file to write matrices into,
        flag: --landmarksInformationFile %s
modelFile: (a boolean or a file name)
        , name of HDF5 file containing BRAINSConstellationDetector Model
        file (LLSMatrices, LLSMeans and LLSSearchRadii),
        flag: --modelFile %s
numberOfThreads: (an integer (int or long))
```

```
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
versionID: (a string)
        , Current version ID. It should be match with the version of BCD
        that will be using the output model file,
        flag: --versionID %s
```

Outputs:

```
landmarksInformationFile: (an existing file name)
        , name of HDF5 file to write matrices into,
modelFile: (an existing file name)
        , name of HDF5 file containing BRAINSConstellationDetector Model
        file (LLSMatrices, LLSMeans and LLSSearchRadii),
```

128.20 insertMidACPCpoint

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputLandmarkFile: (an existing file name)
        Input landmark file (.fcsv)
        flag: --inputLandmarkFile %s
outputLandmarkFile: (a boolean or a file name)
        Output landmark file (.fcsv)
        flag: --outputLandmarkFile %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputLandmarkFile: (an existing file name)
        Output landmark file (.fcsv)
```

128.21 landmarksConstellationAligner

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputLandmarksPaired: (an existing file name)
        Input landmark file (.fcsv)
        flag: --inputLandmarksPaired %s
outputLandmarksPaired: (a boolean or a file name)
        Output landmark file (.fcsv)
        flag: --outputLandmarksPaired %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputLandmarksPaired: (an existing file name)
        Output landmark file (.fcsv)
```

128.22 landmarksConstellationWeights

Link to code
Wraps command ** landmarksConstellationWeights **
title: Generate Landmarks Weights (BRAINS)
category: Utilities.BRAINS
description: Train up a list of Weights for the Landmarks in BRAINSConstellationDetector
Inputs:

```
[Mandatory]

[Optional]
LLSModel: (an existing file name)
        Linear least squares model filename in HD5 format
        flag: --LLSModel %s
args: (a string)
        Additional parameters to the command
        flag: %s
```

```
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputTemplateModel: (an existing file name)
            User-specified template model.,
            flag: --inputTemplateModel %s
    inputTrainingList: (an existing file name)
            , Setup file, giving all parameters for training up a Weight list
            for landmark.,
            flag: --inputTrainingList %s
    outputWeightsList: (a boolean or a file name)
            , The filename of a csv file which is a list of landmarks and their
            corresponding weights.,
            flag: --outputWeightsList %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputWeightsList: (an existing file name)
            , The filename of a csv file which is a list of landmarks and their
            corresponding weights.,
```

CHAPTER 129

interfaces.slicer.base

129.1 SlicerCommandLine

Link to code
Wraps command **None**
Inputs:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
None
```

CHAPTER 130

interfaces.slicer.converters

130.1 DicomToNrrdConverter

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputDicomDirectory: (an existing directory name)
            Directory holding Dicom series
            flag: --inputDicomDirectory %s
    outputDirectory: (a boolean or a directory name)
            Directory holding the output NRRD format
            flag: --outputDirectory %s
    outputVolume: (a string)
            Output filename (.nhdr or .nrrd)
```

```
        flag: --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.
        flag: --smallGradientThreshold %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
useBMatrixGradientDirections: (a boolean)
        Fill the nhdr header with the gradient directions and bvalues
        computed out of the BMatrix. Only changes behavior for Siemens data.
        flag: --useBMatrixGradientDirections
useIdentityMeaseurementFrame: (a boolean)
        Adjust all the gradients so that the measurement frame is an
        identity matrix.
        flag: --useIdentityMeaseurementFrame
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.
        flag: --writeProtocolGradientsFile
```

Outputs:

```
outputDirectory: (an existing directory name)
        Directory holding the output NRRD format
```

130.2 OrientScalarVolume

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
```

```
          with values which are a value of type 'str', nipype default value:
          {})
         Environment variables
ignore_exception: (a boolean, nipype default value: False)
         Print an error message instead of throwing an exception in case the
         interface fails to run
inputVolume1: (an existing file name)
         Input volume 1
         flag: %s, position: -2
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
         flag: --orientation %s
outputVolume: (a boolean or a file name)
         The oriented volume
         flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
         Control terminal output: `stream` - displays to terminal immediately
         (default), `allatonce` - waits till command is finished to display
         output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
         The oriented volume
```

interfaces.slicer.diffusion.diffusion

131.1 DTIexport

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputTensor: (an existing file name)
        Input DTI volume
        flag: %s, position: -2
outputFile: (a boolean or a file name)
        Output DTI file
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputFile: (an existing file name)
        Output DTI file
```

131.2 DTIimport

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputFile: (an existing file name)
        Input DTI file
        flag: %s, position: -2
outputTensor: (a boolean or a file name)
        Output DTI volume
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
testingmode: (a boolean)
        Enable testing mode. Sample helix file (helix-DTI.nhdr) will be
        loaded into Slicer and converted in Nifti.
        flag: --testingmode
```

Outputs:

```
outputTensor: (an existing file name)
        Output DTI volume
```

131.3 DWIJointRicianLMMSEFilter

Link to code
Wraps 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-diemensional 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
compressOutput: (a boolean)
        Compress the data of the compressed file using gzip
        flag: --compressOutput
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Input DWI volume.
        flag: %s, position: -2
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).
        flag: --ng %d
outputVolume: (a boolean or a file name)
        Output DWI volume.
        flag: %s, position: -1
re: (a list of items which are an integer (int or long))
        Estimation radius.
        flag: --re %s
rf: (a list of items which are an integer (int or long))
        Filtering radius.
        flag: --rf %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Output DWI volume.
```

131.4 DWIRicianLMMSEFilter

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
compressOutput: (a boolean)
        Compress the data of the compressed file using gzip
        flag: --compressOutput
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
hrf: (a float)
        How many histogram bins per unit interval.
        flag: --hrf %f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Input DWI volume.
        flag: %s, position: -2
iter: (an integer (int or long))
        Number of iterations for the noise removal filter.
        flag: --iter %d
maxnstd: (an integer (int or long))
        Maximum allowed noise standard deviation.
        flag: --maxnstd %d
minnstd: (an integer (int or long))
        Minimum allowed noise standard deviation.
        flag: --minnstd %d
mnve: (an integer (int or long))
        Minimum number of voxels in kernel used for estimation.
        flag: --mnve %d
mnvf: (an integer (int or long))
        Minimum number of voxels in kernel used for filtering.
```

```
        flag: --mnvf %d
outputVolume: (a boolean or a file name)
        Output DWI volume.
        flag: %s, position: -1
re: (a list of items which are an integer (int or long))
        Estimation radius.
        flag: --re %s
rf: (a list of items which are an integer (int or long))
        Filtering radius.
        flag: --rf %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
uav: (a boolean)
        Use absolute value in case of negative square.
        flag: --uav
```

Outputs:

```
outputVolume: (an existing file name)
        Output DWI volume.
```

131.5 DWIToDTIEstimation

Link to code

Wraps 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, weigthed 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
enumeration: ('LS' or 'WLS')
        LS: Least Squares, WLS: Weighted Least Squares
        flag: --enumeration %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Input DWI volume
        flag: %s, position: -3
mask: (an existing file name)
        Mask where the tensors will be computed
        flag: --mask %s
outputBaseline: (a boolean or a file name)
        Estimated baseline volume
        flag: %s, position: -1
outputTensor: (a boolean or a file name)
        Estimated DTI volume
        flag: %s, position: -2
shiftNeg: (a boolean)
        Shift eigenvalues so all are positive (accounts for bad tensors
        related to noise or acquisition error)
        flag: --shiftNeg
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputBaseline: (an existing file name)
        Estimated baseline volume
outputTensor: (an existing file name)
        Estimated DTI volume
```

131.6 DiffusionTensorScalarMeasurements

Link to code

Wraps 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 anistropic 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
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
        flag: --enumeration %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Input DTI volume
        flag: %s, position: -3
outputScalar: (a boolean or a file name)
        Scalar volume derived from tensor
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputScalar: (an existing file name)
        Scalar volume derived from tensor
```

131.7 DiffusionWeightedVolumeMasking

Link to code
Wraps command **DiffusionWeightedVolumeMasking **
title: Diffusion Weighted Volume Masking
category: Diffusion.Diffusion Weighted Images
description: Performs a mask calculation from a diffusion weighted (DW) image. 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.
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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

```
    inputVolume: (an existing file name)
            Input DWI volume
            flag: %s, position: -4
    otsuomegathreshold: (a float)
            Control the sharpness of the threshold in the Otsu computation. 0:
            lower threshold, 1: higher threhold
            flag: --otsuomegathreshold %f
    outputBaseline: (a boolean or a file name)
            Estimated baseline volume
            flag: %s, position: -2
    removeislands: (a boolean)
            Remove Islands in Threshold Mask?
            flag: --removeislands
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    thresholdMask: (a boolean or a file name)
            Otsu Threshold Mask
            flag: %s, position: -1
```

Outputs:

```
    outputBaseline: (an existing file name)
            Estimated baseline volume
    thresholdMask: (an existing file name)
            Otsu Threshold Mask
```

131.8 ResampleDTIVolume

Link to code

Wraps 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:

```
    [Mandatory]

    [Optional]
    Inverse_ITK_Transformation: (a boolean)
            Inverse the transformation before applying it from output image to
            input image (only for rigid and affine transforms)
            flag: --Inverse_ITK_Transformation
    Reference: (an existing file name)
```

```
        Reference Volume (spacing,size,orientation,origin)
        flag: --Reference %s
args: (a string)
        Additional parameters to the command
        flag: %s
centered_transform: (a boolean)
        Set the center of the transformation to the center of the input
        image (only for rigid and affine transforms)
        flag: --centered_transform
correction: ('zero' or 'none' or 'abs' or 'nearest')
        Correct the tensors if computed tensor is not semi-definite positive
        flag: --correction %s
defField: (an existing file name)
        File containing the deformation field (3D vector image containing
        vectors with 3 components)
        flag: --defField %s
default_pixel_value: (a float)
        Default pixel value for samples falling outside of the input region
        flag: --default_pixel_value %f
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)
        flag: --direction_matrix %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
hfieldtype: ('displacement' or 'h-Field')
        Set if the deformation field is an -Field
        flag: --hfieldtype %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
image_center: ('input' or 'output')
        Image to use to center the transform (used only if 'Centered
        Transform' is selected)
        flag: --image_center %s
inputVolume: (an existing file name)
        Input volume to be resampled
        flag: %s, position: -2
interpolation: ('linear' or 'nn' or 'ws' or 'bs')
        Sampling algorithm (linear , nn (nearest neighborhoor), ws
        (WindowedSinc), bs (BSpline) )
        flag: --interpolation %s
notbulk: (a boolean)
        The transform following the BSpline transform is not set as a bulk
        transform for the BSpline transform
        flag: --notbulk
number_of_thread: (an integer (int or long))
        Number of thread used to compute the output image
        flag: --number_of_thread %d
origin: (a list of items which are any value)
        Origin of the output Image
        flag: --origin %s
outputVolume: (a boolean or a file name)
        Resampled Volume
        flag: %s, position: -1
rotation_point: (a list of items which are any value)
```

```
        Center of rotation (only for rigid and affine transforms)
        flag: --rotation_point %s
size: (a list of items which are a float)
        Size along each dimension (0 means use input size)
        flag: --size %s
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)
        flag: --spaceChange
spacing: (a list of items which are a float)
        Spacing along each dimension (0 means use input spacing)
        flag: --spacing %s
spline_order: (an integer (int or long))
        Spline Order (Spline order may be from 0 to 5)
        flag: --spline_order %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transform: ('rt' or 'a')
        Transform algorithm, rt = Rigid Transform, a = Affine Transform
        flag: --transform %s
transform_matrix: (a list of items which are a float)
        12 parameters of the transform matrix by rows ( --last 3 being
        translation-- )
        flag: --transform_matrix %s
transform_order: ('input-to-output' or 'output-to-input')
        Select in what order the transforms are read
        flag: --transform_order %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)
        flag: --transform_tensor_method %s
transformationFile: (an existing file name)
        flag: --transformationFile %s
window_function: ('h' or 'c' or 'w' or 'l' or 'b')
        Window Function , h = Hamming , c = Cosine , w = Welch , l = Lanczos
        , b = Blackman
        flag: --window_function %s
```

Outputs:

```
outputVolume: (an existing file name)
        Resampled Volume
```

131.9 TractographyLabelMapSeeding

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
InputVolume: (an existing file name)
        Input DTI volume
        flag: %s, position: -2
OutputFibers: (a boolean or a file name)
        Tractography result
        flag: %s, position: -1
args: (a string)
        Additional parameters to the command
        flag: %s
clthreshold: (a float)
        Minimum Linear Measure for the seeding to start.
        flag: --clthreshold %f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputroi: (an existing file name)
        Label map with seeding ROIs
        flag: --inputroi %s
integrationsteplength: (a float)
        Distance between points on the same fiber in mm
        flag: --integrationsteplength %f
label: (an integer (int or long))
        Label value that defines seeding region.
        flag: --label %d
maximumlength: (a float)
        Maximum length of fibers (in mm)
        flag: --maximumlength %f
minimumlength: (a float)
        Minimum length of the fibers (in mm)
        flag: --minimumlength %f
name: (a string)
        Name to use for fiber files
        flag: --name %s
outputdirectory: (a boolean or a directory name)
        Directory in which to save fiber(s)
        flag: --outputdirectory %s
randomgrid: (a boolean)
        Enable random placing of seeds
        flag: --randomgrid
seedspacing: (a float)
        Spacing (in mm) between seed points, only matters if use Use Index
        Space is off
        flag: --seedspacing %f
stoppingcurvature: (a float)
        Tractography will stop if radius of curvature becomes smaller than
```

```
        this number units are degrees per mm
        flag: --stoppingcurvature %f
stoppingmode: ('LinearMeasure' or 'FractionalAnisotropy')
        Tensor measurement used to stop the tractography
        flag: --stoppingmode %s
stoppingvalue: (a float)
        Tractography will stop when the stopping measurement drops below
        this value
        flag: --stoppingvalue %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
useindexspace: (a boolean)
        Seed at IJK voxel grid
        flag: --useindexspace
writetofile: (a boolean)
        Write fibers to disk or create in the scene?
        flag: --writetofile
```

Outputs:

```
OutputFibers: (an existing file name)
        Tractography result
outputdirectory: (an existing directory name)
        Directory in which to save fiber(s)
```

interfaces.slicer.filtering.arithmetic

132.1 AddScalarVolumes

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume1: (an existing file name)
            Input volume 1
            flag: %s, position: -3
    inputVolume2: (an existing file name)
            Input volume 2
            flag: %s, position: -2
    order: ('0' or '1' or '2' or '3')
            Interpolation order if two images are in different coordinate frames
            or have different sampling.
            flag: --order %s
    outputVolume: (a boolean or a file name)
            Volume1 + Volume2
            flag: %s, position: -1
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
```

```
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Volume1 + Volume2
```

132.2 CastScalarVolume

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
InputVolume: (an existing file name)
        Input volume, the volume to cast.
        flag: %s, position: -2
OutputVolume: (a boolean or a file name)
        Output volume, cast to the new type.
        flag: %s, position: -1
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
type: ('Char' or 'UnsignedChar' or 'Short' or 'UnsignedShort' or
         'Int' or 'UnsignedInt' or 'Float' or 'Double')
        Type for the new output volume.
        flag: --type %s
```

Outputs:

```
OutputVolume: (an existing file name)
        Output volume, cast to the new type.
```

132.3 MaskScalarVolume

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
InputVolume: (an existing file name)
        Input volume to be masked
        flag: %s, position: -3
MaskVolume: (an existing file name)
        Label volume containing the mask
        flag: %s, position: -2
OutputVolume: (a boolean or a file name)
        Output volume: Input Volume masked by label value from Mask Volume
        flag: %s, position: -1
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
label: (an integer (int or long))
        Label value in the Mask Volume to use as the mask
        flag: --label %d
replace: (an integer (int or long))
        Value to use for the output volume outside of the mask
        flag: --replace %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
OutputVolume: (an existing file name)
        Output volume: Input Volume masked by label value from Mask Volume
```

132.4 MultiplyScalarVolumes

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume1: (an existing file name)
        Input volume 1
        flag: %s, position: -3
inputVolume2: (an existing file name)
        Input volume 2
        flag: %s, position: -2
order: ('0' or '1' or '2' or '3')
        Interpolation order if two images are in different coordinate frames
        or have different sampling.
        flag: --order %s
outputVolume: (a boolean or a file name)
        Volume1 * Volume2
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Volume1 * Volume2
```

132.5 SubtractScalarVolumes

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume1: (an existing file name)
        Input volume 1
        flag: %s, position: -3
inputVolume2: (an existing file name)
        Input volume 2
        flag: %s, position: -2
order: ('0' or '1' or '2' or '3')
        Interpolation order if two images are in different coordinate frames
        or have different sampling.
        flag: --order %s
outputVolume: (a boolean or a file name)
        Volume1 - Volume2
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Volume1 - Volume2
```

interfaces.slicer.filtering.checkerboardfilter

133.1 CheckerBoardFilter

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    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.
            flag: --checkerPattern %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume1: (an existing file name)
            First Input volume
            flag: %s, position: -3
    inputVolume2: (an existing file name)
            Second Input volume
```

```
        flag: %s, position: -2
outputVolume: (a boolean or a file name)
        Output filtered
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Output filtered
```

CHAPTER 134

interfaces.slicer.filtering.denoising

134.1 CurvatureAnisotropicDiffusion

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    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.
            flag: --conductance %f
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
```

```
        Input volume to be filtered
        flag: %s, position: -2
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.
        flag: --iterations %d
outputVolume: (a boolean or a file name)
        Output filtered
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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.
        flag: --timeStep %f
```

Outputs:

```
outputVolume: (an existing file name)
        Output filtered
```

134.2 GaussianBlurImageFilter

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Input volume
        flag: %s, position: -2
outputVolume: (a boolean or a file name)
```

```
        Blurred Volume
        flag: %s, position: -1
sigma: (a float)
        Sigma value in physical units (e.g., mm) of the Gaussian kernel
        flag: --sigma %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Blurred Volume
```

134.3 GradientAnisotropicDiffusion

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
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.
        flag: --conductance %f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
```

```
        Input volume to be filtered
        flag: %s, position: -2
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.
        flag: --iterations %d
outputVolume: (a boolean or a file name)
        Output filtered
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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.
        flag: --timeStep %f
```

Outputs:

```
outputVolume: (an existing file name)
        Output filtered
```

134.4 MedianImageFilter

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
```

```
        Input volume to be filtered
        flag: %s, position: -2
neighborhood: (a list of items which are an integer (int or long))
        The size of the neighborhood in each dimension
        flag: --neighborhood %s
outputVolume: (a boolean or a file name)
        Output filtered
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Output filtered
```

interfaces.slicer.filtering.extractskeleton

135.1 ExtractSkeleton

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    InputImageFileName: (an existing file name)
            Input image
            flag: %s, position: -2
    OutputImageFileName: (a boolean or a file name)
            Skeleton of the input image
            flag: %s, position: -1
    args: (a string)
            Additional parameters to the command
            flag: %s
    dontPrune: (a boolean)
            Return the full skeleton, not just the maximal skeleton
            flag: --dontPrune
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    numPoints: (an integer (int or long))
            Number of points used to represent the skeleton
            flag: --numPoints %d
    pointsFile: (a string)
```

```
        Name of the file to store the coordinates of the central (1D)
        skeleton points
        flag: --pointsFile %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
type: ('1D' or '2D')
        Type of skeleton to create
        flag: --type %s
```

Outputs:

```
OutputImageFileName: (an existing file name)
        Skeleton of the input image
```

interfaces.slicer.filtering.histogrammatching

136.1 HistogramMatching

Link to code
Wraps 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 orginally 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
            Input volume to be filtered
            flag: %s, position: -3
    numberOfHistogramLevels: (an integer (int or long))
            The number of hisogram levels to use
            flag: --numberOfHistogramLevels %d
    numberOfMatchPoints: (an integer (int or long))
```

```
        The number of match points to use
        flag: --numberOfMatchPoints %d
outputVolume: (a boolean or a file name)
        Output volume. This is the input volume with intensities matched to
        the reference volume.
        flag: %s, position: -1
referenceVolume: (an existing file name)
        Input volume whose histogram will be matched
        flag: %s, position: -2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
threshold: (a boolean)
        If on, only pixels above the mean in each volume are thresholded.
        flag: --threshold
```

Outputs:

```
outputVolume: (an existing file name)
        Output volume. This is the input volume with intensities matched to
        the reference volume.
```

interfaces.slicer.filtering.imagelabelcombine

137.1 ImageLabelCombine

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
InputLabelMap_A: (an existing file name)
        Label map image
        flag: %s, position: -3
InputLabelMap_B: (an existing file name)
        Label map image
        flag: %s, position: -2
OutputLabelMap: (a boolean or a file name)
        Resulting Label map image
        flag: %s, position: -1
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
first_overwrites: (a boolean)
        Use first or second label when both are present
        flag: --first_overwrites
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    OutputLabelMap: (an existing file name)
            Resulting Label map image
```

interfaces.slicer.filtering.morphology

138.1 GrayscaleFillHoleImageFilter

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
            Input volume to be filtered
            flag: %s, position: -2
```

```
    outputVolume: (a boolean or a file name)
            Output filtered
            flag: %s, position: -1
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputVolume: (an existing file name)
            Output filtered
```

138.2 GrayscaleGrindPeakImageFilter

Link to code

Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
            Input volume to be filtered
```

```
        flag: %s, position: -2
outputVolume: (a boolean or a file name)
        Output filtered
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Output filtered
```

interfaces.slicer.filtering.n4itkbiasfieldcorrection

139.1 N4ITKBiasFieldCorrection

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    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.
            flag: --bsplineorder %d
    convergencethreshold: (a float)
            Stopping criterion for the iterative bias estimation. Larger values
            will lead to smaller execution time.
            flag: --convergencethreshold %f
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    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.
            flag: --histogramsharpening %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
```

```
    inputimage: (an existing file name)
            Input image where you observe signal inhomegeneity
            flag: --inputimage %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.
            flag: --iterations %s
    maskimage: (an existing file name)
            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.
            flag: --maskimage %s
    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)
            flag: --meshresolution %s
    outputbiasfield: (a boolean or a file name)
            Recovered bias field (OPTIONAL)
            flag: --outputbiasfield %s
    outputimage: (a boolean or a file name)
            Result of processing
            flag: --outputimage %s
    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.
            flag: --shrinkfactor %d
    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.
            flag: --splinedistance %f
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    weightimage: (an existing file name)
            Weight Image
            flag: --weightimage %s
```

Outputs:

```
    outputbiasfield: (an existing file name)
            Recovered bias field (OPTIONAL)
    outputimage: (an existing file name)
            Result of processing
```

interfaces.slicer.filtering.resamplescalarvectordwivolume

140.1 ResampleScalarVectorDWIVolume

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    Inverse_ITK_Transformation: (a boolean)
            Inverse the transformation before applying it from output image to
            input image
            flag: --Inverse_ITK_Transformation
    Reference: (an existing file name)
            Reference Volume (spacing,size,orientation,origin)
            flag: --Reference %s
    args: (a string)
            Additional parameters to the command
            flag: %s
    centered_transform: (a boolean)
            Set the center of the transformation to the center of the input
            image
            flag: --centered_transform
    defField: (an existing file name)
            File containing the deformation field (3D vector image containing
            vectors with 3 components)
            flag: --defField %s
```

```
    default_pixel_value: (a float)
            Default pixel value for samples falling outside of the input region
            flag: --default_pixel_value %f
    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)
            flag: --direction_matrix %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    hfieldtype: ('displacement' or 'h-Field')
            Set if the deformation field is an h-Field
            flag: --hfieldtype %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    image_center: ('input' or 'output')
            Image to use to center the transform (used only if 'Centered
            Transform' is selected)
            flag: --image_center %s
    inputVolume: (an existing file name)
            Input Volume to be resampled
            flag: %s, position: -2
    interpolation: ('linear' or 'nn' or 'ws' or 'bs')
            Sampling algorithm (linear or nn (nearest neighborhoor), ws
            (WindowedSinc), bs (BSpline) )
            flag: --interpolation %s
    notbulk: (a boolean)
            The transform following the BSpline transform is not set as a bulk
            transform for the BSpline transform
            flag: --notbulk
    number_of_thread: (an integer (int or long))
            Number of thread used to compute the output image
            flag: --number_of_thread %d
    origin: (a list of items which are any value)
            Origin of the output Image
            flag: --origin %s
    outputVolume: (a boolean or a file name)
            Resampled Volume
            flag: %s, position: -1
    rotation_point: (a list of items which are any value)
            Rotation Point in case of rotation around a point (otherwise
            useless)
            flag: --rotation_point %s
    size: (a list of items which are a float)
            Size along each dimension (0 means use input size)
            flag: --size %s
    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)
            flag: --spaceChange
    spacing: (a list of items which are a float)
            Spacing along each dimension (0 means use input spacing)
            flag: --spacing %s
    spline_order: (an integer (int or long))
            Spline Order
```

```
        flag: --spline_order %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transform: ('rt' or 'a')
        Transform algorithm, rt = Rigid Transform, a = Affine Transform
        flag: --transform %s
transform_matrix: (a list of items which are a float)
        12 parameters of the transform matrix by rows ( --last 3 being
        translation-- )
        flag: --transform_matrix %s
transform_order: ('input-to-output' or 'output-to-input')
        Select in what order the transforms are read
        flag: --transform_order %s
transformationFile: (an existing file name)
        flag: --transformationFile %s
window_function: ('h' or 'c' or 'w' or 'l' or 'b')
        Window Function , h = Hamming , c = Cosine , w = Welch , l = Lanczos
        , b = Blackman
        flag: --window_function %s
```

Outputs:

```
outputVolume: (an existing file name)
        Resampled Volume
```

interfaces.slicer.filtering.thresholdscalarvolume

141.1 ThresholdScalarVolume

Link to code
Wraps command **ThresholdScalarVolume **
title: Threshold Scalar Volume
category: Filtering
description: Threshold an image. Set image values to a user-specified outside value if they are below, above, or between simple threshold values. ThresholdAbove: The values greater than or equal to the threshold value are set to OutsideValue. ThresholdBelow: The values less than or equal to the threshold value are set to OutsideValue. ThresholdOutside: The values outside the range Lower-Upper are set to OutsideValue. Although all image types are supported on input, only signed types are produced.
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:

```
    [Mandatory]

    [Optional]
    InputVolume: (an existing file name)
            Input volume
            flag: %s, position: -2
    OutputVolume: (a boolean or a file name)
            Thresholded input volume
            flag: %s, position: -1
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    lower: (an integer (int or long))
            Lower threshold value
            flag: --lower %d
    outsidevalue: (an integer (int or long))
            Set the voxels to this value if they fall outside the threshold
```

```
            range
            flag: --outsidevalue %d
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    threshold: (an integer (int or long))
            Threshold value
            flag: --threshold %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.
            flag: --thresholdtype %s
    upper: (an integer (int or long))
            Upper threshold value
            flag: --upper %d
```

Outputs:

```
    OutputVolume: (an existing file name)
            Thresholded input volume
```

interfaces.slicer.filtering.votingbinaryholefillingimagefilter

142.1 VotingBinaryHoleFillingImageFilter

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    background: (an integer (int or long))
            The value associated with the background (not object)
            flag: --background %d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    foreground: (an integer (int or long))
            The value associated with the foreground (object)
            flag: --foreground %d
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
            Input volume to be filtered
            flag: %s, position: -2
    majorityThreshold: (an integer (int or long))
            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.
        flag: --majorityThreshold %d
outputVolume: (a boolean or a file name)
        Output filtered
        flag: %s, position: -1
radius: (a list of items which are an integer (int or long))
        The radius of a hole to be filled
        flag: --radius %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Output filtered
```

interfaces.slicer.legacy.converters

143.1 BSplineToDeformationField

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
defImage: (a boolean or a file name)
        flag: --defImage %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
refImage: (an existing file name)
        flag: --refImage %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
tfm: (an existing file name)
        flag: --tfm %s
```

Outputs:

```
defImage: (an existing file name)
```

interfaces.slicer.legacy.diffusion.denoising

144.1 DWIUnbiasedNonLocalMeansFilter

Link to code
Wraps 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/UnbiasedNonLocalMeansFilterForDW
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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    hp: (a float)
            This parameter is related to noise; the larger the parameter, the
            more agressive the filtering. Should be near 1, and only values
            between 0.8 and 1.2 are allowed
            flag: --hp %f
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
```

```
        Input DWI volume.
        flag: %s, position: -2
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).
        flag: --ng %d
outputVolume: (a boolean or a file name)
        Output DWI volume.
        flag: %s, position: -1
rc: (a list of items which are an integer (int or long))
        Similarity between blocks is measured using windows of this size.
        flag: --rc %s
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.
        flag: --re %s
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).
        flag: --rs %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Output DWI volume.
```

interfaces.slicer.legacy.filtering

145.1 OtsuThresholdImageFilter

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
            Input volume to be filtered
            flag: %s, position: -2
    insideValue: (an integer (int or long))
            The value assigned to pixels that are inside the computed threshold
            flag: --insideValue %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.
        flag: --numberOfBins %d
outputVolume: (a boolean or a file name)
        Output filtered
        flag: %s, position: -1
outsideValue: (an integer (int or long))
        The value assigned to pixels that are outside the computed threshold
        flag: --outsideValue %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Output filtered
```

145.2 ResampleScalarVolume

Link to code

Wraps 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 volumnes, 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:

```
[Mandatory]

[Optional]
InputVolume: (an existing file name)
        Input volume to be resampled
        flag: %s, position: -2
OutputVolume: (a boolean or a file name)
        Resampled Volume
        flag: %s, position: -1
args: (a string)
        Additional parameters to the command
        flag: %s
```

```
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    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;
            flag: --interpolation %s
    spacing: (a list of items which are a float)
            Spacing along each dimension (0 means use input spacing)
            flag: --spacing %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    OutputVolume: (an existing file name)
            Resampled Volume
```

interfaces.slicer.legacy.registration

146.1 AffineRegistration

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    FixedImageFileName: (an existing file name)
            Fixed image to which to register
            flag: %s, position: -2
    MovingImageFileName: (an existing file name)
            Moving image
            flag: %s, position: -1
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    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.
            flag: --fixedsmoothingfactor %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.
        flag: --histogrambins %d
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
initialtransform: (an existing file name)
        Initial transform for aligning the fixed and moving image. Maps
        positions in the fixed coordinate frame to positions in the moving
        coordinate frame. Optional.
        flag: --initialtransform %s
iterations: (an integer (int or long))
        Number of iterations
        flag: --iterations %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.
        flag: --movingsmoothingfactor %d
outputtransform: (a boolean or a file name)
        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).
        flag: --outputtransform %s
resampledmovingfilename: (a boolean or a file name)
        Resampled moving image to the fixed image coordinate frame. Optional
        (specify an output transform or an output volume or both).
        flag: --resampledmovingfilename %s
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.
        flag: --spatialsamples %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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.
        flag: --translationscale %f
```

Outputs:

```
outputtransform: (an existing file name)
        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: (an existing file name)
        Resampled moving image to the fixed image coordinate frame. Optional
        (specify an output transform or an output volume or both).
```

146.2 BSplineDeformableRegistration

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    FixedImageFileName: (an existing file name)
            Fixed image to which to register
            flag: %s, position: -2
    MovingImageFileName: (an existing file name)
            Moving image
            flag: %s, position: -1
    args: (a string)
            Additional parameters to the command
            flag: %s
    constrain: (a boolean)
            Constrain the deformation to the amount specified in Maximum
            Deformation
            flag: --constrain
    default: (an integer (int or long))
            Default pixel value used if resampling a pixel outside of the
            volume.
            flag: --default %d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    gridSize: (an integer (int or long))
            Number of grid points on interior of the fixed image. Larger grid
            sizes allow for finer registrations.
            flag: --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
            impulses and will inhibit reliable registration estimation.
            flag: --histogrambins %d
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    initialtransform: (an existing file name)
            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 an a bulk transform for the BSpline. Optional.
            flag: --initialtransform %s
    iterations: (an integer (int or long))
```

```
        Number of iterations
        flag: --iterations %d
maximumDeformation: (a float)
        If Constrain Deformation is checked, limit the deformation to this
        amount.
        flag: --maximumDeformation %f
outputtransform: (a boolean or a file name)
        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).
        flag: --outputtransform %s
outputwarp: (a boolean or a file name)
        Vector field that applies an equivalent warp as the BSpline. Maps
        positions from the fixed coordinate frame to the moving coordinate
        frame. Optional.
        flag: --outputwarp %s
resampledmovingfilename: (a boolean or a file name)
        Resampled moving image to fixed image coordinate frame. Optional
        (specify an output transform or an output volume or both).
        flag: --resampledmovingfilename %s
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.
        flag: --spatialsamples %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputtransform: (an existing file name)
        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: (an existing file name)
        Vector field that applies an equivalent warp as the BSpline. Maps
        positions from the fixed coordinate frame to the moving coordinate
        frame. Optional.
resampledmovingfilename: (an existing file name)
        Resampled moving image to fixed image coordinate frame. Optional
        (specify an output transform or an output volume or both).
```

146.3 ExpertAutomatedRegistration

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    affineMaxIterations: (an integer (int or long))
            Maximum number of affine optimization iterations
            flag: --affineMaxIterations %d
    affineSamplingRatio: (a float)
            Portion of the image to use in computing the metric during affine
            registration
            flag: --affineSamplingRatio %f
    args: (a string)
            Additional parameters to the command
            flag: %s
    bsplineMaxIterations: (an integer (int or long))
            Maximum number of bspline optimization iterations
            flag: --bsplineMaxIterations %d
    bsplineSamplingRatio: (a float)
            Portion of the image to use in computing the metric during BSpline
            registration
            flag: --bsplineSamplingRatio %f
    controlPointSpacing: (an integer (int or long))
            Number of pixels between control points
            flag: --controlPointSpacing %d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    expectedOffset: (a float)
            Expected misalignment after initialization
            flag: --expectedOffset %f
    expectedRotation: (a float)
            Expected misalignment after initialization
            flag: --expectedRotation %f
    expectedScale: (a float)
            Expected misalignment after initialization
            flag: --expectedScale %f
    expectedSkew: (a float)
            Expected misalignment after initialization
            flag: --expectedSkew %f
    fixedImage: (an existing file name)
            Image which defines the space into which the moving image is
            registered
            flag: %s, position: -2
    fixedImageMask: (an existing file name)
            Image which defines a mask for the fixed image
            flag: --fixedImageMask %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
            flag: --fixedLandmarks %s...
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    initialization: ('None' or 'Landmarks' or 'ImageCenters' or
             'CentersOfMass' or 'SecondMoments')
            Method to prime the registration process
```

```
        flag: --initialization %s
interpolation: ('NearestNeighbor' or 'Linear' or 'BSpline')
        Method for interpolation within the optimization process
        flag: --interpolation %s
loadTransform: (an existing file name)
        Load a transform that is immediately applied to the moving image
        flag: --loadTransform %s
metric: ('MattesMI' or 'NormCorr' or 'MeanSqrd')
        Method to quantify image match
        flag: --metric %s
minimizeMemory: (a boolean)
        Reduce the amount of memory required at the cost of increased
        computation time
        flag: --minimizeMemory
movingImage: (an existing file name)
        The transform goes from the fixed image's space into the moving
        image's space
        flag: %s, position: -1
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
        flag: --movingLandmarks %s...
numberOfThreads: (an integer (int or long))
        Number of CPU threads to use
        flag: --numberOfThreads %d
randomNumberSeed: (an integer (int or long))
        Seed to generate a consistent random number sequence
        flag: --randomNumberSeed %d
registration: ('None' or 'Initial' or 'Rigid' or 'Affine' or
         'BSpline' or 'PipelineRigid' or 'PipelineAffine' or
         'PipelineBSpline')
        Method for the registration process
        flag: --registration %s
resampledImage: (a boolean or a file name)
        Registration results
        flag: --resampledImage %s
rigidMaxIterations: (an integer (int or long))
        Maximum number of rigid optimization iterations
        flag: --rigidMaxIterations %d
rigidSamplingRatio: (a float)
        Portion of the image to use in computing the metric during rigid
        registration
        flag: --rigidSamplingRatio %f
sampleFromOverlap: (a boolean)
        Limit metric evaluation to the fixed image region overlapped by the
        moving image
        flag: --sampleFromOverlap
saveTransform: (a boolean or a file name)
        Save the transform that results from registration
        flag: --saveTransform %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbosityLevel: ('Silent' or 'Standard' or 'Verbose')
        Level of detail of reporting progress
        flag: --verbosityLevel %s
```

Outputs:

```
    resampledImage: (an existing file name)
            Registration results
    saveTransform: (an existing file name)
            Save the transform that results from registration
```

146.4 LinearRegistration

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    FixedImageFileName: (an existing file name)
            Fixed image to which to register
            flag: %s, position: -2
    MovingImageFileName: (an existing file name)
            Moving image
            flag: %s, position: -1
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    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.
            flag: --fixedsmoothingfactor %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.
            flag: --histogrambins %d
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    initialtransform: (an existing file name)
            Initial transform for aligning the fixed and moving image. Maps
            positions in the fixed coordinate frame to positions in the moving
            coordinate frame. Optional.
            flag: --initialtransform %s
    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.
        flag: --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.
        flag: --learningrate %s
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.
        flag: --movingsmoothingfactor %d
outputtransform: (a boolean or a file name)
        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).
        flag: --outputtransform %s
resampledmovingfilename: (a boolean or a file name)
        Resampled moving image to the fixed image coordinate frame. Optional
        (specify an output transform or an output volume or both).
        flag: --resampledmovingfilename %s
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.
        flag: --spatialsamples %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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.
        flag: --translationscale %f
```

Outputs:

```
outputtransform: (an existing file name)
        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: (an existing file name)
        Resampled moving image to the fixed image coordinate frame. Optional
        (specify an output transform or an output volume or both).
```

146.5 MultiResolutionAffineRegistration

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    fixedImage: (an existing file name)
            Image which defines the space into which the moving image is
            registered
            flag: %s, position: -2
    fixedImageMask: (an existing file name)
            Label image which defines a mask of interest for the fixed image
            flag: --fixedImageMask %s
    fixedImageROI: (a list of items which are any value)
            Label image which defines a ROI of interest for the fixed image
            flag: --fixedImageROI %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    metricTolerance: (a float)
            flag: --metricTolerance %f
    movingImage: (an existing file name)
            The transform goes from the fixed image's space into the moving
            image's space
            flag: %s, position: -1
    numIterations: (an integer (int or long))
            Number of iterations to run at each resolution level.
            flag: --numIterations %d
    numLineIterations: (an integer (int or long))
            Number of iterations to run at each resolution level.
            flag: --numLineIterations %d
    resampledImage: (a boolean or a file name)
            Registration results
            flag: --resampledImage %s
    saveTransform: (a boolean or a file name)
            Save the output transform from the registration
            flag: --saveTransform %s
    stepSize: (a float)
            The maximum step size of the optimizer in voxels
            flag: --stepSize %f
```

```
    stepTolerance: (a float)
            The maximum step size of the optimizer in voxels
            flag: --stepTolerance %f
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    resampledImage: (an existing file name)
            Registration results
    saveTransform: (an existing file name)
            Save the output transform from the registration
```

146.6 RigidRegistration

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    FixedImageFileName: (an existing file name)
            Fixed image to which to register
            flag: %s, position: -2
    MovingImageFileName: (an existing file name)
            Moving image
            flag: %s, position: -1
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    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.
        flag: --fixedsmoothingfactor %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.
        flag: --histogrambins %d
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
initialtransform: (an existing file name)
        Initial transform for aligning the fixed and moving image. Maps
        positions in the fixed coordinate frame to positions in the moving
        coordinate frame. Optional.
        flag: --initialtransform %s
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.
        flag: --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.
        flag: --learningrate %s
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.
        flag: --movingsmoothingfactor %d
outputtransform: (a boolean or a file name)
        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).
        flag: --outputtransform %s
resampledmovingfilename: (a boolean or a file name)
        Resampled moving image to the fixed image coordinate frame. Optional
        (specify an output transform or an output volume or both).
        flag: --resampledmovingfilename %s
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.
        flag: --spatialsamples %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
```

```
        output, `file` - writes output to file, `none` - output is ignored
    testingmode: (a boolean)
        Enable testing mode. Input transform will be used to construct
        floating image. The floating image will be ignored if passed.
        flag: --testingmode
    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.
        flag: --translationscale %f
```

Outputs:

```
    outputtransform: (an existing file name)
        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: (an existing file name)
        Resampled moving image to the fixed image coordinate frame. Optional
        (specify an output transform or an output volume or both).
```

interfaces.slicer.legacy.segmentation

147.1 OtsuThresholdSegmentation

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    brightObjects: (a boolean)
            Segmenting bright objects on a dark background or dark objects on a
            bright background.
            flag: --brightObjects
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    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.
            flag: --faceConnected
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
            Input volume to be segmented
            flag: %s, position: -2
```

```
    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.
            flag: --minimumObjectSize %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.
            flag: --numberOfBins %d
    outputVolume: (a boolean or a file name)
            Output filtered
            flag: %s, position: -1
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    outputVolume: (an existing file name)
            Output filtered
```

interfaces.slicer.quantification.changequantification

148.1 IntensityDifferenceMetric

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    baselineSegmentationVolume: (an existing file name)
            Label volume that contains segmentation of the structure of interest
            in the baseline volume.
            flag: %s, position: -3
    baselineVolume: (an existing file name)
            Baseline volume to be compared to
            flag: %s, position: -4
    changingBandSize: (an integer (int or long))
            How far (in mm) from the boundary of the segmentation should the
            intensity changes be considered.
            flag: --changingBandSize %d
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    followupVolume: (an existing file name)
            Followup volume to be compare to the baseline
            flag: %s, position: -2
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    outputVolume: (a boolean or a file name)
            Output volume to keep the results of change quantification.
            flag: %s, position: -1
    reportFileName: (a boolean or a file name)
```

```
        Report file name
        flag: --reportFileName %s
sensitivityThreshold: (a float)
        This parameter should be between 0 and 1, and defines how sensitive
        the metric should be to the intensity changes.
        flag: --sensitivityThreshold %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Output volume to keep the results of change quantification.
reportFileName: (an existing file name)
        Report file name
```

interfaces.slicer.quantification.petstandarduptakevaluecomputation

149.1 PETStandardUptakeValueComputation

Link to code
Wraps 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/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:

```
    [Mandatory]

    [Optional]
    OutputLabel: (a string)
            List of labels for which SUV values were computed
            flag: --OutputLabel %s
    OutputLabelValue: (a string)
            List of label values for which SUV values were computed
            flag: --OutputLabelValue %s
    SUVMax: (a string)
            SUV max for each label
            flag: --SUVMax %s
    SUVMean: (a string)
            SUV mean for each label
            flag: --SUVMean %s
    SUVMin: (a string)
            SUV minimum for each label
            flag: --SUVMin %s
    args: (a string)
            Additional parameters to the command
            flag: %s
    color: (an existing file name)
            Color table to to map labels to colors and names
            flag: --color %s
```

```
    csvFile: (a boolean or a file name)
            A file holding the output SUV values in comma separated lines, one
            per label. Optional.
            flag: --csvFile %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    labelMap: (an existing file name)
            Input label volume containing the volumes of interest
            flag: --labelMap %s
    petDICOMPath: (an existing directory name)
            Input path to a directory containing a PET volume containing DICOM
            header information for SUV computation
            flag: --petDICOMPath %s
    petVolume: (an existing file name)
            Input PET volume for SUVbw computation (must be the same volume as
            pointed to by the DICOM path!).
            flag: --petVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    csvFile: (an existing file name)
            A file holding the output SUV values in comma separated lines, one
            per label. Optional.
```

interfaces.slicer.registration.brainsfit

150.1 BRAINSFit

Link to code
Wraps 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://wwww.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:

```
    [Mandatory]

    [Optional]
    NEVER_USE_THIS_FLAG_IT_IS_OUTDATED_00: (a boolean)
            DO NOT USE THIS FLAG
            flag: --NEVER_USE_THIS_FLAG_IT_IS_OUTDATED_00
    NEVER_USE_THIS_FLAG_IT_IS_OUTDATED_01: (a boolean)
            DO NOT USE THIS FLAG
            flag: --NEVER_USE_THIS_FLAG_IT_IS_OUTDATED_01
    NEVER_USE_THIS_FLAG_IT_IS_OUTDATED_02: (a boolean)
            DO NOT USE THIS FLAG
            flag: --NEVER_USE_THIS_FLAG_IT_IS_OUTDATED_02
    ROIAutoClosingSize: (a float)
            This flag is only relavent 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.
            flag: --ROIAutoClosingSize %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.
        flag: --ROIAutoDilateSize %f
args: (a string)
        Additional parameters to the command
        flag: %s
backgroundFillValue: (a float)
        Background fill value for output image.
        flag: --backgroundFillValue %f
bsplineTransform: (a boolean or a file name)
        (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
        flag: --bsplineTransform %s
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.,
        flag: --costFunctionConvergenceFactor %f
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)
        flag: --costMetric %s
debugLevel: (an integer (int or long))
        Display debug messages, and produce debug intermediate results.
        0=OFF, 1=Minimal, 10=Maximum debugging.
        flag: --debugLevel %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
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.
        flag: --failureExitCode %d
fixedBinaryVolume: (an existing file name)
        Fixed Image binary mask volume, ONLY FOR MANUAL ROI mode.
        flag: --fixedBinaryVolume %s
fixedVolume: (an existing file name)
        The fixed image for registration by mutual information optimization.
        flag: --fixedVolume %s
fixedVolumeTimeIndex: (an integer (int or long))
        The index in the time series for the 3D fixed image to fit, if
        4-dimensional.
        flag: --fixedVolumeTimeIndex %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 my arise!
        flag: --forceMINumberOfThreads %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.
```

```
        flag: --gui
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 modailties.
        flag: --histogramMatch
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
initialTransform: (an existing file name)
        Filename of transform used to initialize the registration. This CAN
        NOT be used with either CenterOfHeadLAlign, MomentsAlign,
        GeometryAlign, or initialTransform file.
        flag: --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.
        flag: --initializeTransformMode %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, 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.
        flag: --interpolationMode %s
linearTransform: (a boolean or a file name)
        (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
        flag: --linearTransform %s
maskInferiorCutOffFromCenter: (a float)
        For use with --useCenterOfHeadAlign (and --maskProcessingMode
        ROIAUTO): the cut-off below the image centers, in millimeters,
        flag: --maskInferiorCutOffFromCenter %f
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.
        flag: --maskProcessingMode %s
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.,
        flag: --maxBSplineDisplacement %f
maximumStepLength: (a float)
        Internal debugging parameter, and should probably never be used from
        the command line. This will be removed in the future.
        flag: --maximumStepLength %f
medianFilterSize: (a list of items which are an integer (int or
         long))
        The radius for the optional MedianImageFilter preprocessing in all 3
        directions.
        flag: --medianFilterSize %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.
        flag: --minimumStepLength %s
movingBinaryVolume: (an existing file name)
        Moving Image binary mask volume, ONLY FOR MANUAL ROI mode.
        flag: --movingBinaryVolume %s
movingVolume: (an existing file name)
        The moving image for registration by mutual information
        optimization.
        flag: --movingVolume %s
movingVolumeTimeIndex: (an integer (int or long))
        The index in the time series for the 3D moving image to fit, if
        4-dimensional.
        flag: --movingVolumeTimeIndex %d
numberOfHistogramBins: (an integer (int or long))
        The number of histogram levels
        flag: --numberOfHistogramBins %d
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
        flag: --numberOfIterations %s
numberOfMatchPoints: (an integer (int or long))
        the number of match points
        flag: --numberOfMatchPoints %d
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.
        flag: --numberOfSamples %d
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use. (default is
        auto-detected)
        flag: --numberOfThreads %d
outputFixedVolumeROI: (a boolean or a file name)
        The ROI automatically found in fixed image, ONLY FOR ROIAUTO mode.
        flag: --outputFixedVolumeROI %s
outputMovingVolumeROI: (a boolean or a file name)
        The ROI automatically found in moving image, ONLY FOR ROIAUTO mode.
        flag: --outputMovingVolumeROI %s
outputTransform: (a boolean or a file name)
        (optional) Filename to which save the (optional) estimated
        transform. NOTE: You must select either the outputTransform or the
        outputVolume option.
```

```
        flag: --outputTransform %s
outputVolume: (a boolean or a file name)
        (optional) Output image for registration. NOTE: You must select
        either the outputTransform or the outputVolume option.
        flag: --outputVolume %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.
        flag: --outputVolumePixelType %s
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.
        flag: --permitParameterVariation %s
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.,
        flag: --projectedGradientTolerance %f
promptUser: (a boolean)
        Prompt the user to hit enter each time an image is sent to the
        DebugImageViewer
        flag: --promptUser
relaxationFactor: (a float)
        Internal debugging parameter, and should probably never be used from
        the command line. This will be removed in the future.
        flag: --relaxationFactor %f
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.
        flag: --removeIntensityOutliers %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
        flag: --reproportionScale %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.
        flag: --scaleOutputValues
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
        flag: --skewScale %f
```

```
    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.
            flag: --splineGridSize %s
    strippedOutputTransform: (a boolean or a file name)
            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.
            flag: --strippedOutputTransform %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    transformType: (a list of items which are a 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.
            flag: --transformType %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.
            flag: --translationScale %f
    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.
            flag: --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.
            flag: --useBSpline
    useCachingOfBSplineWeightsMode: ('ON' or 'OFF')
            This is a 5x speed advantage at the expense of requiring much more
            memory. Only relevant when transformType is BSpline.
            flag: --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.
            flag: --useExplicitPDFDerivativesMode %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.
            flag: --useRigid
    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.
            flag: --useScaleSkewVersor3D
    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.
        flag: --useScaleVersor3D
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.
        flag: --writeOutputTransformInFloat
writeTransformOnFailure: (a boolean)
        Flag to save the final transform even if the numberOfIterations are
        reached without convergence. (Intended for use when
        --failureExitCode 0 )
        flag: --writeTransformOnFailure
```

Outputs:

```
bsplineTransform: (an existing file name)
        (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
linearTransform: (an existing file name)
        (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
outputFixedVolumeROI: (an existing file name)
        The ROI automatically found in fixed image, ONLY FOR ROIAUTO mode.
outputMovingVolumeROI: (an existing file name)
        The ROI automatically found in moving image, ONLY FOR ROIAUTO mode.
outputTransform: (an existing file name)
        (optional) Filename to which save the (optional) estimated
        transform. NOTE: You must select either the outputTransform or the
        outputVolume option.
outputVolume: (an existing file name)
        (optional) Output image for registration. NOTE: You must select
        either the outputTransform or the outputVolume option.
strippedOutputTransform: (an existing file name)
        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.
```

interfaces.slicer.registration.brainsresample

151.1 BRAINSResample

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    defaultValue: (a float)
            Default voxel value
            flag: --defaultValue %f
    deformationVolume: (an existing file name)
            Displacement Field to be used to warp the image
            flag: --deformationVolume %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    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
            makeing a 2D image of grid lines from the 3D space
            flag: --gridSpacing %s
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
```

```
    inputVolume: (an existing file name)
            Image To Warp
            flag: --inputVolume %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
            flag: --interpolationMode %s
    inverseTransform: (a boolean)
            True/False is to compute inverse of given transformation. Default is
            false
            flag: --inverseTransform
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputVolume: (a boolean or a file name)
            Resulting deformed image
            flag: --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.
            flag: --pixelType %s
    referenceVolume: (an existing file name)
            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.
            flag: --referenceVolume %s
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    warpTransform: (an existing file name)
            Filename for the BRAINSFit transform used in place of the
            deformation field
            flag: --warpTransform %s
```

Outputs:

```
    outputVolume: (an existing file name)
            Resulting deformed image
```

interfaces.slicer.registration.specialized

152.1 ACPCTransform

Link to code
Wraps command **ACPCTransform **
title: ACPC Transform
category: Registration.Specialized
description: Calculate a transformation from two lists of fiducial points. 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. 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. Use the Filtering moduleResample Scalar/Vector/DWI Volumeto apply the transformation to a volume.
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:

```
    [Mandatory]

    [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.
            flag: --acpc %s...
    args: (a string)
            Additional parameters to the command
            flag: %s
    debugSwitch: (a boolean)
            Click if wish to see debugging output
            flag: --debugSwitch
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    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).
        flag: --midline %s...
outputTransform: (a boolean or a file name)
        A transform filled in from the ACPC and Midline registration
        calculation
        flag: --outputTransform %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputTransform: (an existing file name)
        A transform filled in from the ACPC and Midline registration
        calculation
```

152.2 BRAINSDemonWarp

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
arrayOfPyramidLevelIterations: (a list of items which are an integer
         (int or long))
        The number of iterations for each pyramid level
        flag: --arrayOfPyramidLevelIterations %s
backgroundFillValue: (an integer (int or long))
        Replacement value to overwrite background when performing BOBF
        flag: --backgroundFillValue %d
checkerboardPatternSubdivisions: (a list of items which are an
         integer (int or long))
        Number of Checkerboard subdivisions in all 3 directions
        flag: --checkerboardPatternSubdivisions %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
```

```
        Environment variables
fixedBinaryVolume: (an existing file name)
        Mask filename for desired region of interest in the Fixed image.
        flag: --fixedBinaryVolume %s
fixedVolume: (an existing file name)
        Required: input fixed (target) image
        flag: --fixedVolume %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)
        flag: --gradient_type %s
gui: (a boolean)
        Display intermediate image volumes for debugging
        flag: --gui
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.
        flag: --histogramMatch
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
initializeWithDisplacementField: (an existing file name)
        Initial deformation field vector image file name
        flag: --initializeWithDisplacementField %s
initializeWithTransform: (an existing file name)
        Initial Transform filename
        flag: --initializeWithTransform %s
inputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
        Input volumes will be typecast to this format:
        float|short|ushort|int|uchar
        flag: --inputPixelType %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
        flag: --interpolationMode %s
lowerThresholdForBOBF: (an integer (int or long))
        Lower threshold for performing BOBF
        flag: --lowerThresholdForBOBF %d
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
        forground 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.
        flag: --maskProcessingMode %s
max_step_length: (a float)
        Maximum length of an update vector (0: no restriction)
        flag: --max_step_length %f
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.
```

```
        flag: --medianFilterSize %s
    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)
        flag: --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)
        flag: --minimumMovingPyramid %s
    movingBinaryVolume: (an existing file name)
        Mask filename for desired region of interest in the Moving image.
        flag: --movingBinaryVolume %s
    movingVolume: (an existing file name)
        Required: input moving image
        flag: --movingVolume %s
    neighborhoodForBOBF: (a list of items which are an integer (int or
         long))
        neighborhood in all 3 directions to be included when performing BOBF
        flag: --neighborhoodForBOBF %s
    numberOfBCHApproximationTerms: (an integer (int or long))
        Number of terms in the BCH expansion
        flag: --numberOfBCHApproximationTerms %d
    numberOfHistogramBins: (an integer (int or long))
        The number of histogram levels
        flag: --numberOfHistogramBins %d
    numberOfMatchPoints: (an integer (int or long))
        The number of match points for histrogramMatch
        flag: --numberOfMatchPoints %d
    numberOfPyramidLevels: (an integer (int or long))
        Number of image pyramid levels to use in the multi-resolution
        registration.
        flag: --numberOfPyramidLevels %d
    numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
    outputCheckerboardVolume: (a boolean or a file name)
        Genete a checkerboard image volume between the fixedVolume and the
        deformed movingVolume.
        flag: --outputCheckerboardVolume %s
    outputDebug: (a boolean)
        Flag to write debugging images after each step.
        flag: --outputDebug
    outputDisplacementFieldPrefix: (a string)
        Displacement field filename prefix for writing separate x, y, and z
        component images
        flag: --outputDisplacementFieldPrefix %s
    outputDisplacementFieldVolume: (a boolean or a file name)
        Output deformation field vector image (will have the same physical
        space as the fixedVolume).
        flag: --outputDisplacementFieldVolume %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.
```

```
        flag: --outputNormalized
outputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
        outputVolume will be typecast to this format:
        float|short|ushort|int|uchar
        flag: --outputPixelType %s
outputVolume: (a boolean or a file name)
        Required: output resampled moving image (will have the same physical
        space as the fixedVolume).
        flag: --outputVolume %s
promptUser: (a boolean)
        Prompt the user to hit enter each time an image is sent to the
        DebugImageViewer
        flag: --promptUser
registrationFilterType: ('Demons' or 'FastSymmetricForces' or
         'Diffeomorphic')
        Registration Filter Type: Demons|FastSymmetricForces|Diffeomorphic
        flag: --registrationFilterType %s
seedForBOBF: (a list of items which are an integer (int or long))
        coordinates in all 3 directions for Seed when performing BOBF
        flag: --seedForBOBF %s
smoothDisplacementFieldSigma: (a float)
        A gaussian smoothing value to be applied to the deformation feild at
        each iteration.
        flag: --smoothDisplacementFieldSigma %f
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
upFieldSmoothing: (a float)
        Smoothing sigma for the update field at each iteration
        flag: --upFieldSmoothing %f
upperThresholdForBOBF: (an integer (int or long))
        Upper threshold for performing BOBF
        flag: --upperThresholdForBOBF %d
use_vanilla_dem: (a boolean)
        Run vanilla demons algorithm
        flag: --use_vanilla_dem
```

Outputs:

```
outputCheckerboardVolume: (an existing file name)
        Genete a checkerboard image volume between the fixedVolume and the
        deformed movingVolume.
outputDisplacementFieldVolume: (an existing file name)
        Output deformation field vector image (will have the same physical
        space as the fixedVolume).
outputVolume: (an existing file name)
        Required: output resampled moving image (will have the same physical
        space as the fixedVolume).
```

152.3 FiducialRegistration

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
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
        flag: --fixedLandmarks %s...
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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
        flag: --movingLandmarks %s...
outputMessage: (a string)
        Provides more information on the output
        flag: --outputMessage %s
rms: (a float)
        Display RMS Error.
        flag: --rms %f
saveTransform: (a boolean or a file name)
        Save the transform that results from registration
        flag: --saveTransform %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
transformType: ('Translation' or 'Rigid' or 'Similarity')
        Type of transform to produce
        flag: --transformType %s
```

Outputs:

```
saveTransform: (an existing file name)
        Save the transform that results from registration
```

152.4 VBRAINSDemonWarp

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    arrayOfPyramidLevelIterations: (a list of items which are an integer
             (int or long))
            The number of iterations for each pyramid level
            flag: --arrayOfPyramidLevelIterations %s
    backgroundFillValue: (an integer (int or long))
            Replacement value to overwrite background when performing BOBF
            flag: --backgroundFillValue %d
    checkerboardPatternSubdivisions: (a list of items which are an
             integer (int or long))
            Number of Checkerboard subdivisions in all 3 directions
            flag: --checkerboardPatternSubdivisions %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    fixedBinaryVolume: (an existing file name)
            Mask filename for desired region of interest in the Fixed image.
            flag: --fixedBinaryVolume %s
    fixedVolume: (a list of items which are an existing file name)
            Required: input fixed (target) image
            flag: --fixedVolume %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)
            flag: --gradient_type %s
    gui: (a boolean)
            Display intermediate image volumes for debugging
            flag: --gui
    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.
            flag: --histogramMatch
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    initializeWithDisplacementField: (an existing file name)
            Initial deformation field vector image file name
            flag: --initializeWithDisplacementField %s
    initializeWithTransform: (an existing file name)
            Initial Transform filename
```

```
        flag: --initializeWithTransform %s
inputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
        Input volumes will be typecast to this format:
        float|short|ushort|int|uchar
        flag: --inputPixelType %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
        flag: --interpolationMode %s
lowerThresholdForBOBF: (an integer (int or long))
        Lower threshold for performing BOBF
        flag: --lowerThresholdForBOBF %d
makeBOBF: (a boolean)
        Flag to make Brain-Only Background-Filled versions of the input and
        target volumes.
        flag: --makeBOBF
max_step_length: (a float)
        Maximum length of an update vector (0: no restriction)
        flag: --max_step_length %f
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.
        flag: --medianFilterSize %s
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)
        flag: --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)
        flag: --minimumMovingPyramid %s
movingBinaryVolume: (an existing file name)
        Mask filename for desired region of interest in the Moving image.
        flag: --movingBinaryVolume %s
movingVolume: (a list of items which are an existing file name)
        Required: input moving image
        flag: --movingVolume %s...
neighborhoodForBOBF: (a list of items which are an integer (int or
         long))
        neighborhood in all 3 directions to be included when performing BOBF
        flag: --neighborhoodForBOBF %s
numberOfBCHApproximationTerms: (an integer (int or long))
        Number of terms in the BCH expansion
        flag: --numberOfBCHApproximationTerms %d
numberOfHistogramBins: (an integer (int or long))
        The number of histogram levels
        flag: --numberOfHistogramBins %d
numberOfMatchPoints: (an integer (int or long))
        The number of match points for histrogramMatch
        flag: --numberOfMatchPoints %d
```

```
    numberOfPyramidLevels: (an integer (int or long))
            Number of image pyramid levels to use in the multi-resolution
            registration.
            flag: --numberOfPyramidLevels %d
    numberOfThreads: (an integer (int or long))
            Explicitly specify the maximum number of threads to use.
            flag: --numberOfThreads %d
    outputCheckerboardVolume: (a boolean or a file name)
            Genete a checkerboard image volume between the fixedVolume and the
            deformed movingVolume.
            flag: --outputCheckerboardVolume %s
    outputDebug: (a boolean)
            Flag to write debugging images after each step.
            flag: --outputDebug
    outputDisplacementFieldPrefix: (a string)
            Displacement field filename prefix for writing separate x, y, and z
            component images
            flag: --outputDisplacementFieldPrefix %s
    outputDisplacementFieldVolume: (a boolean or a file name)
            Output deformation field vector image (will have the same physical
            space as the fixedVolume).
            flag: --outputDisplacementFieldVolume %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.
            flag: --outputNormalized
    outputPixelType: ('float' or 'short' or 'ushort' or 'int' or 'uchar')
            outputVolume will be typecast to this format:
            float|short|ushort|int|uchar
            flag: --outputPixelType %s
    outputVolume: (a boolean or a file name)
            Required: output resampled moving image (will have the same physical
            space as the fixedVolume).
            flag: --outputVolume %s
    promptUser: (a boolean)
            Prompt the user to hit enter each time an image is sent to the
            DebugImageViewer
            flag: --promptUser
    registrationFilterType: ('Demons' or 'FastSymmetricForces' or
             'Diffeomorphic' or 'LogDemons' or 'SymmetricLogDemons')
            Registration Filter Type: Demons|FastSymmetricForces|Diffeomorphic|L
            ogDemons|SymmetricLogDemons
            flag: --registrationFilterType %s
    seedForBOBF: (a list of items which are an integer (int or long))
            coordinates in all 3 directions for Seed when performing BOBF
            flag: --seedForBOBF %s
    smoothDisplacementFieldSigma: (a float)
            A gaussian smoothing value to be applied to the deformation feild at
            each iteration.
            flag: --smoothDisplacementFieldSigma %f
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
    upFieldSmoothing: (a float)
            Smoothing sigma for the update field at each iteration
            flag: --upFieldSmoothing %f
```

```
    upperThresholdForBOBF: (an integer (int or long))
            Upper threshold for performing BOBF
            flag: --upperThresholdForBOBF %d
    use_vanilla_dem: (a boolean)
            Run vanilla demons algorithm
            flag: --use_vanilla_dem
    weightFactors: (a list of items which are a float)
            Weight fatctors for each input images
            flag: --weightFactors %s
```

Outputs:

```
    outputCheckerboardVolume: (an existing file name)
            Genete a checkerboard image volume between the fixedVolume and the
            deformed movingVolume.
    outputDisplacementFieldVolume: (an existing file name)
            Output deformation field vector image (will have the same physical
            space as the fixedVolume).
    outputVolume: (an existing file name)
            Required: output resampled moving image (will have the same physical
            space as the fixedVolume).
```

interfaces.slicer.segmentation.simpleregiongrowingsegmentation

153.1 SimpleRegionGrowingSegmentation

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    inputVolume: (an existing file name)
            Input volume to be filtered
            flag: %s, position: -2
    iterations: (an integer (int or long))
            Number of iterations of region growing
            flag: --iterations %d
    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
            flag: --labelvalue %d
    multiplier: (a float)
            Number of standard deviations to include in intensity model
```

```
        flag: --multiplier %f
neighborhood: (an integer (int or long))
        The radius of the neighborhood over which to calculate intensity
        model
        flag: --neighborhood %d
outputVolume: (a boolean or a file name)
        Output filtered
        flag: %s, position: -1
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
        flag: --seed %s...
smoothingIterations: (an integer (int or long))
        Number of smoothing iterations
        flag: --smoothingIterations %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
timestep: (a float)
        Timestep for curvature flow
        flag: --timestep %f
```

Outputs:

```
outputVolume: (an existing file name)
        Output filtered
```

interfaces.slicer.segmentation.specialized

154.1 BRAINSROIAuto

Link to code
Wraps 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 prominant 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://wwww.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:

```
    [Mandatory]

    [Optional]
    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.
            flag: --ROIAutoDilateSize %f
    args: (a string)
            Additional parameters to the command
            flag: %s
    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.
            flag: --closingSize %f
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
```

```
        interface fails to run
inputVolume: (an existing file name)
        The input image for finding the largest region filled mask.
        flag: --inputVolume %s
numberOfThreads: (an integer (int or long))
        Explicitly specify the maximum number of threads to use.
        flag: --numberOfThreads %d
otsuPercentileThreshold: (a float)
        Parameter to the Otsu threshold algorithm.
        flag: --otsuPercentileThreshold %f
outputClippedVolumeROI: (a boolean or a file name)
        The inputVolume clipped to the region of the brain mask.
        flag: --outputClippedVolumeROI %s
outputROIMaskVolume: (a boolean or a file name)
        The ROI automatically found from the input image.
        flag: --outputROIMaskVolume %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.
        flag: --outputVolumePixelType %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
thresholdCorrectionFactor: (a float)
        A factor to scale the Otsu algorithm's result threshold, in case
        clipping mangles the image.
        flag: --thresholdCorrectionFactor %f
```

Outputs:

```
outputClippedVolumeROI: (an existing file name)
        The inputVolume clipped to the region of the brain mask.
outputROIMaskVolume: (an existing file name)
        The ROI automatically found from the input image.
```

154.2 EMSegmentCommandLine

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
```

```
        flag: %s
atlasVolumeFileNames: (a list of items which are an existing file
         name)
        Use an alternative atlas to the one that is specified by the mrml
        file - note the order matters !
        flag: --atlasVolumeFileNames %s...
disableCompression: (a boolean)
        Don't use compression when writing result image to disk.
        flag: --disableCompression
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.
        flag: --disableMultithreading %d
dontUpdateIntermediateData: (an integer (int or long))
        Disable update of intermediate results. -1: Do not overwrite default
        value. 0: Disable. 1: Enable.
        flag: --dontUpdateIntermediateData %d
dontWriteResults: (a boolean)
        Used for testing. Don't actually write the resulting labelmap to
        disk.
        flag: --dontWriteResults
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
generateEmptyMRMLSceneAndQuit: (a boolean or a file name)
        Used for testing. Only write a scene with default mrml parameters.
        flag: --generateEmptyMRMLSceneAndQuit %s
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
intermediateResultsDirectory: (an existing directory name)
        Directory where EMSegmenter will write intermediate data (e.g.,
        aligned atlas data).
        flag: --intermediateResultsDirectory %s
keepTempFiles: (a boolean)
        If flag is set then at the end of command the temporary files are
        not removed
        flag: --keepTempFiles
loadAtlasNonCentered: (a boolean)
        Read atlas files non-centered.
        flag: --loadAtlasNonCentered
loadTargetCentered: (a boolean)
        Read target files centered.
        flag: --loadTargetCentered
mrmlSceneFileName: (an existing file name)
        Active MRML scene that contains EMSegment algorithm parameters.
        flag: --mrmlSceneFileName %s
parametersMRMLNodeName: (a string)
        The name of the EMSegment parameters node within the active MRML
        scene. Leave blank for default.
        flag: --parametersMRMLNodeName %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
        flag: --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
        flag: --registrationDeformableType %d
registrationPackage: (a string)
        specify the registration package for preprocessing (CMTK or BRAINS
        or PLASTIMATCH or DEMONS)
        flag: --registrationPackage %s
resultMRMLSceneFileName: (a boolean or a file name)
        Write out the MRML scene after command line substitutions have been
        made.
        flag: --resultMRMLSceneFileName %s
resultStandardVolumeFileName: (an existing file name)
        Used for testing. Compare segmentation results to this image and
        return EXIT_FAILURE if they do not match.
        flag: --resultStandardVolumeFileName %s
resultVolumeFileName: (a boolean or a file name)
        The file name that the segmentation result volume will be written
        to.
        flag: --resultVolumeFileName %s
targetVolumeFileNames: (a list of items which are an existing file
         name)
        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.
        flag: --targetVolumeFileNames %s...
taskPreProcessingSetting: (a string)
        Specifies the different task parameter. Leave blank for default.
        flag: --taskPreProcessingSetting %s
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
verbose: (a boolean)
        Enable verbose output.
        flag: --verbose
```

Outputs:

```
generateEmptyMRMLSceneAndQuit: (an existing file name)
        Used for testing. Only write a scene with default mrml parameters.
resultMRMLSceneFileName: (an existing file name)
        Write out the MRML scene after command line substitutions have been
        made.
resultVolumeFileName: (an existing file name)
        The file name that the segmentation result volume will be written
        to.
```

154.3 RobustStatisticsSegmenter

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
curvatureWeight: (a float)
        Given sphere 1.0 score and extreme rough bounday/surface 0 score,
        what is the expected smoothness of the object?
        flag: --curvatureWeight %f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
expectedVolume: (a float)
        The approximate volume of the object, in mL.
        flag: --expectedVolume %f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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.
        flag: --intensityHomogeneity %f
labelImageFileName: (an existing file name)
        Label image for initialization
        flag: %s, position: -2
labelValue: (an integer (int or long))
        Label value of the output image
        flag: --labelValue %d
maxRunningTime: (a float)
        The program will stop if this time is reached.
        flag: --maxRunningTime %f
originalImageFileName: (an existing file name)
        Original image to be segmented
        flag: %s, position: -3
segmentedImageFileName: (a boolean or a file name)
        Segmented image
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
segmentedImageFileName: (an existing file name)
        Segmented image
```

interfaces.slicer.surface

155.1 GrayscaleModelMaker

Link to code
Wraps 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:

```
    [Mandatory]

    [Optional]
    InputVolume: (an existing file name)
            Volume containing the input grayscale data.
            flag: %s, position: -2
    OutputGeometry: (a boolean or a file name)
            Output that contains geometry model.
            flag: %s, position: -1
    args: (a string)
            Additional parameters to the command
            flag: %s
    decimate: (a float)
            Target reduction during decimation, as a decimal percentage
            reduction in the number of polygons. If 0, no decimation will be
            done.
            flag: --decimate %f
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    name: (a string)
```

```
        Name to use for this model.
        flag: --name %s
pointnormals: (a boolean)
        Calculate the point normals? Calculated point normals make the
        surface appear smooth. Without point normals, the surface will
        appear faceted.
        flag: --pointnormals
smooth: (an integer (int or long))
        Number of smoothing iterations. If 0, no smoothing will be done.
        flag: --smooth %d
splitnormals: (a boolean)
        Splitting normals is useful for visualizing sharp features. However
        it creates holes in surfaces which affect measurements
        flag: --splitnormals
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
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.
        flag: --threshold %f
```

Outputs:

```
OutputGeometry: (an existing file name)
        Output that contains geometry model.
```

155.2 LabelMapSmoothing

Link to code
Wraps 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-alising 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:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
gaussianSigma: (a float)
        The standard deviation of the Gaussian kernel
```

```
        flag: --gaussianSigma %f
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputVolume: (an existing file name)
        Input label map to smooth
        flag: %s, position: -2
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.
        flag: --labelToSmooth %d
maxRMSError: (a float)
        The maximum RMS error.
        flag: --maxRMSError %f
numberOfIterations: (an integer (int or long))
        The number of iterations of the level set AntiAliasing algorithm
        flag: --numberOfIterations %d
outputVolume: (a boolean or a file name)
        Smoothed label map
        flag: %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputVolume: (an existing file name)
        Smoothed label map
```

155.3 MergeModels

Link to code
Wraps 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:

```
[Mandatory]

[Optional]
Model1: (an existing file name)
        Model
        flag: %s, position: -3
Model2: (an existing file name)
        Model
        flag: %s, position: -2
ModelOutput: (a boolean or a file name)
        Model
```

```
        flag: %s, position: -1
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
ModelOutput: (an existing file name)
        Model
```

155.4 ModelMaker

Link to code

Wraps command **ModelMaker **
title: Model Maker
category: Surface Models
description: Create 3D surface models from segmented data. 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). Create Multiple: If you specify a list of Labels, it will over ride any start/end label settings. If you clickGenerate Allit will over ride the list of lables and any start/end label settings. Model Maker Settings: 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:
slicer.modules.modelmaker.cliModuleLogic().DeleteTemporaryFilesOff()
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:

```
[Mandatory]

[Optional]
InputVolume: (an existing file name)
        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.
        flag: %s, position: -1
args: (a string)
        Additional parameters to the command
```

```
        flag: %s
color: (an existing file name)
        Color table to make labels to colors and objects
        flag: --color %s
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)
        flag: --debug
decimate: (a float)
        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.
        flag: --decimate %f
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.
        flag: --end %d
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
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.
        flag: --filtertype %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.
        flag: --generateAll
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
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.
        flag: --jointsmooth
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.
        flag: --labels %s
modelSceneFile: (a boolean or a list of items which are a file name)
        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.
        flag: --modelSceneFile %s...
name: (a 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.
        flag: --name %s
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.
        flag: --pad
pointnormals: (a boolean)
        Turn this flag on if you wish to calculate the normal vectors for
        the points.
        flag: --pointnormals
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().
        flag: --saveIntermediateModels
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.
        flag: --skipUnNamed
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.
        flag: --smooth %d
splitnormals: (a boolean)
        Splitting normals is useful for visualizing sharp features. However
        it creates holes in surfaces which affects measurements.
        flag: --splitnormals
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).
        flag: --start %d
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
modelSceneFile: (a list of items which are an existing file name)
        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.
```

155.5 ModelToLabelMap

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
InputVolume: (an existing file name)
        Input volume
        flag: %s, position: -3
OutputVolume: (a boolean or a file name)
        The label volume
        flag: %s, position: -1
args: (a string)
        Additional parameters to the command
        flag: %s
distance: (a float)
        Sample distance
        flag: --distance %f
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
surface: (an existing file name)
        Model
        flag: %s, position: -2
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
OutputVolume: (an existing file name)
        The label volume
```

155.6 ProbeVolumeWithModel

Link to code

Wraps 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:

```
[Mandatory]

[Optional]
InputModel: (an existing file name)
        Input model
        flag: %s, position: -2
InputVolume: (an existing file name)
        Volume to use to 'paint' the model
        flag: %s, position: -3
OutputModel: (a boolean or a file name)
        Output 'painted' model
        flag: %s, position: -1
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
OutputModel: (an existing file name)
        Output 'painted' model
```

interfaces.slicer.utilities

156.1 EMSegmentTransformToNewFormat

Link to code
Wraps command **EMSegmentTransformToNewFormat **
title: Transform MRML Files to New EMSegmenter Standard
category: Utilities
description: Transform MRML Files to New EMSegmenter Standard
Inputs:

```
[Mandatory]

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
inputMRMLFileName: (an existing file name)
        Active MRML scene that contains EMSegment algorithm parameters in
        the format before 3.6.3 - please include absolute file name in path.
        flag: --inputMRMLFileName %s
outputMRMLFileName: (a boolean or a file name)
        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
        flag: --outputMRMLFileName %s
templateFlag: (a boolean)
        Set to true if the transformed mrml file should be used as template
        file
        flag: --templateFlag
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
outputMRMLFileName: (an existing file name)
        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
```

CHAPTER 157

interfaces.spm.model

157.1 EstimateContrast

Link to code
use spm_contrasts to estimate contrasts of interest

157.1.1 Examples

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
beta_images: (a list of items which are an existing file name)
        Parameter estimates of the design matrix
contrasts: (a list of items which are a tuple of the form: (a string,
         'T', a list of items which are a string, a list of items which are
         a float) or a tuple of the form: (a string, 'T', a list of items
         which are a string, a list of items which are a float, a list of
         items which are a float) or a tuple of the form: (a string, 'F', a
         list of items which are a tuple of the form: (a string, 'T', a list
         of items which are a string, a list of items which are a float) or
         a tuple of the form: (a string, 'T', a list of items which are a
         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.
residual_image: (an existing file name)
        Mean-squared image of the residuals
spm_mat_file: (an existing file name)
        Absolute path to SPM.mat

[Optional]
group_contrast: (a boolean)
```

```
        higher level contrast
        mutually_exclusive: use_derivs
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
use_derivs: (a boolean)
        use derivatives for estimation
        mutually_exclusive: group_contrast
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
con_images: (a list of items which are an existing file name)
        contrast images from a t-contrast
ess_images: (a list of items which are an existing file name)
        contrast images from an F-contrast
spmF_images: (a list of items which are an existing file name)
        stat images from an F-contrast
spmT_images: (a list of items which are an existing file name)
        stat images from a t-contrast
spm_mat_file: (an existing file name)
        Updated SPM mat file
```

157.2 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

157.2.1 Examples

```
>>> est = EstimateModel()
>>> est.inputs.spm_mat_file = 'SPM.mat'
>>> est.run()
```

Inputs:

```
[Mandatory]
estimation_method: (a dictionary with keys which are 'Classical' or
         'Bayesian2' or 'Bayesian' and with values which are any value)
        Classical, Bayesian2, Bayesian (dict)
spm_mat_file: (an existing file name)
        absolute path to SPM.mat

[Optional]
flags: (a string)
        optional arguments (opt)
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
```

```
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
RPVimage: (an existing file name)
        Resels per voxel image
beta_images: (a list of items which are an existing file name)
        design parameter estimates
mask_image: (an existing file name)
        binary mask to constrain estimation
residual_image: (an existing file name)
        Mean-squared image of the residuals
spm_mat_file: (an existing file name)
        Updated SPM mat file
```

157.3 FactorialDesign

Link to code

Base class for factorial designs

http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=77

Inputs:

```
[Mandatory]

[Optional]
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}
explicit_mask_file: (a file name)
        use an implicit mask file to threshold
global_calc_mean: (a boolean)
        use mean for global calculation
        mutually_exclusive: global_calc_omit, global_calc_values
global_calc_omit: (a boolean)
        omit global calculation
        mutually_exclusive: global_calc_mean, 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
global_normalization: (1 or 2 or 3)
        global normalization None-1, Proportional-2, ANCOVA-3
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
```

```
        Run m-code using m-file
no_grand_mean_scaling: (a boolean)
        do not perform grand mean scaling
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
spm_mat_dir: (an existing directory name)
        directory to store SPM.mat file (opt)
threshold_mask_absolute: (a float)
        use an absolute threshold
        mutually_exclusive: threshold_mask_none, threshold_mask_relative
threshold_mask_none: (a boolean)
        do not use threshold masking
        mutually_exclusive: threshold_mask_absolute, 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
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
spm_mat_file: (an existing file name)
        SPM mat file
```

157.4 Level1Design

Link to code
Generate an SPM design matrix
http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=59

157.4.1 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.run()
```

Inputs:

```
[Mandatory]
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
         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
    interscan_interval: (a float)
            Interscan interval in secs
    session_info: (any value)
            Session specific information generated by ``modelgen.SpecifyModel``
    timing_units: ('secs' or 'scans')
            units for specification of onsets

    [Optional]
    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)
    global_intensity_normalization: ('none' or 'scaling')
            Global intensity normalization - scaling or none
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    mask_image: (an existing file name)
            Image for explicitly masking the analysis
    mask_threshold: ('-Inf' or a float, nipype default value: -Inf)
            Thresholding for the mask
    matlab_cmd: (a string)
            matlab command to use
    mfile: (a boolean, nipype default value: True)
            Run m-code using m-file
    microtime_onset: (a float)
            The onset/time-bin in seconds for alignment (opt)
    microtime_resolution: (an integer (int or long))
            Number of time-bins per scan in secs (opt)
    model_serial_correlations: ('AR(1)' or 'FAST' or 'none')
            Model serial correlations AR(1), FAST or none. FAST is available in
            SPM12
    paths: (a list of items which are a directory name)
            Paths to add to matlabpath
    spm_mat_dir: (an existing directory name)
            directory to store SPM.mat file (opt)
    use_mcr: (a boolean)
            Run m-code using SPM MCR
    use_v8struct: (a boolean, nipype default value: True)
            Generate SPM8 and higher compatible jobs
    volterra_expansion_order: (1 or 2)
            Model interactions - yes:1, no:2
```

Outputs:

```
    spm_mat_file: (an existing file name)
            SPM mat file
```

157.5 MultipleRegressionDesign

Link to code

Create SPM design for multiple regression

157.5.1 Examples

```
>>> mreg = MultipleRegressionDesign()
>>> mreg.inputs.in_files = ['cont1.nii','cont2.nii']
>>> mreg.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of at least 2 items which are an existing file
          name)
         List of files

[Optional]
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}
explicit_mask_file: (a file name)
         use an implicit mask file to threshold
global_calc_mean: (a boolean)
         use mean for global calculation
         mutually_exclusive: global_calc_omit, global_calc_values
global_calc_omit: (a boolean)
         omit global calculation
         mutually_exclusive: global_calc_mean, 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
global_normalization: (1 or 2 or 3)
         global normalization None-1, Proportional-2, ANCOVA-3
ignore_exception: (a boolean, nipype default value: False)
         Print an error message instead of throwing an exception in case the
         interface fails to run
include_intercept: (a boolean, nipype default value: True)
         Include intercept in design
matlab_cmd: (a string)
         matlab command to use
mfile: (a boolean, nipype default value: True)
         Run m-code using m-file
no_grand_mean_scaling: (a boolean)
         do not perform grand mean scaling
paths: (a list of items which are a directory name)
         Paths to add to matlabpath
spm_mat_dir: (an existing directory name)
         directory to store SPM.mat file (opt)
threshold_mask_absolute: (a float)
         use an absolute threshold
         mutually_exclusive: threshold_mask_none, threshold_mask_relative
threshold_mask_none: (a boolean)
         do not use threshold masking
         mutually_exclusive: threshold_mask_absolute, 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
use_mcr: (a boolean)
         Run m-code using SPM MCR
```

```
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
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}
```

Outputs:

```
spm_mat_file: (an existing file name)
        SPM mat file
```

157.6 OneSampleTTestDesign

Link to code

Create SPM design for one sample t-test

157.6.1 Examples

```
>>> ttest = OneSampleTTestDesign()
>>> ttest.inputs.in_files = ['cont1.nii', 'cont2.nii']
>>> ttest.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of at least 2 items which are an existing file
         name)
        input files

[Optional]
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}
explicit_mask_file: (a file name)
        use an implicit mask file to threshold
global_calc_mean: (a boolean)
        use mean for global calculation
        mutually_exclusive: global_calc_omit, global_calc_values
global_calc_omit: (a boolean)
        omit global calculation
        mutually_exclusive: global_calc_mean, 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
global_normalization: (1 or 2 or 3)
        global normalization None-1, Proportional-2, ANCOVA-3
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
no_grand_mean_scaling: (a boolean)
        do not perform grand mean scaling
paths: (a list of items which are a directory name)
```

```
        Paths to add to matlabpath
spm_mat_dir: (an existing directory name)
        directory to store SPM.mat file (opt)
threshold_mask_absolute: (a float)
        use an absolute threshold
        mutually_exclusive: threshold_mask_none, threshold_mask_relative
threshold_mask_none: (a boolean)
        do not use threshold masking
        mutually_exclusive: threshold_mask_absolute, 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
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
spm_mat_file: (an existing file name)
        SPM mat file
```

157.7 PairedTTestDesign

Link to code

Create SPM design for paired t-test

157.7.1 Examples

```
>>> pttest = PairedTTestDesign()
>>> pttest.inputs.paired_files = [['cont1.nii','cont1a.nii'],['cont2.nii','cont2a.nii']]
>>> pttest.run()
```

Inputs:

```
[Mandatory]
paired_files: (a list of at least 2 items which are a list of from 2
         to 2 items which are an existing file name)
        List of paired files

[Optional]
ancova: (a boolean)
        Specify ancova-by-factor regressors
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}
explicit_mask_file: (a file name)
        use an implicit mask file to threshold
global_calc_mean: (a boolean)
        use mean for global calculation
        mutually_exclusive: global_calc_omit, global_calc_values
global_calc_omit: (a boolean)
        omit global calculation
        mutually_exclusive: global_calc_mean, 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
global_normalization: (1 or 2 or 3)
        global normalization None-1, Proportional-2, ANCOVA-3
grand_mean_scaling: (a boolean)
        Perform grand mean scaling
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
no_grand_mean_scaling: (a boolean)
        do not perform grand mean scaling
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
spm_mat_dir: (an existing directory name)
        directory to store SPM.mat file (opt)
threshold_mask_absolute: (a float)
        use an absolute threshold
        mutually_exclusive: threshold_mask_none, threshold_mask_relative
threshold_mask_none: (a boolean)
        do not use threshold masking
        mutually_exclusive: threshold_mask_absolute, 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
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
spm_mat_file: (an existing file name)
        SPM mat file
```

157.8 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.

157.8.1 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()
```

Inputs:

```
    [Mandatory]
    contrast_index: (an integer (int or long))
            which contrast in the SPM.mat to use
    spm_mat_file: (an existing file name)
            absolute path to SPM.mat
    stat_image: (an existing file name)
            stat image

    [Optional]
    extent_fdr_p_threshold: (a float, nipype default value: 0.05)
            p threshold on FDR corrected cluster size probabilities
    extent_threshold: (an integer (int or long), nipype default value: 0)
            Minimum cluster size in voxels
    force_activation: (a boolean, nipype default value: False)
            In case no clusters survive the topological inference step this will
            pick a culster with the highes sum of t-values. Use with care.
    height_threshold: (a float, nipype default value: 0.05)
            value for initial thresholding (defining clusters)
    height_threshold_type: ('p-value' or 'stat', nipype default value:
             p-value)
            Is the cluster forming threshold a stat value or p-value?
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    matlab_cmd: (a string)
            matlab command to use
    mfile: (a boolean, nipype default value: True)
            Run m-code using m-file
    paths: (a list of items which are a directory name)
            Paths to add to matlabpath
    use_fwe_correction: (a boolean, nipype default value: True)
            whether to use FWE (Bonferroni) correction for initial threshold
            (height_threshold_type has to be set to p-value)
    use_mcr: (a boolean)
            Run m-code using SPM MCR
    use_topo_fdr: (a boolean, nipype default value: True)
            whether to use FDR over cluster extent probabilities
    use_v8struct: (a boolean, nipype default value: True)
            Generate SPM8 and higher compatible jobs
```

Outputs:

```
    activation_forced: (a boolean)
    cluster_forming_thr: (a float)
    n_clusters: (an integer (int or long))
    pre_topo_fdr_map: (an existing file name)
    pre_topo_n_clusters: (an integer (int or long))
    thresholded_map: (an existing file name)
```

157.9 ThresholdStatistics

Link to code

Given height and cluster size threshold calculate theoretical probabilities concerning false positives

157.9.1 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()
```

Inputs:

```
[Mandatory]
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)
spm_mat_file: (an existing file name)
        absolute path to SPM.mat
stat_image: (an existing file name)
        stat image

[Optional]
extent_threshold: (an integer (int or long), nipype default value: 0)
        Minimum cluster size in voxels
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
clusterwise_P_FDR: (a float)
clusterwise_P_RF: (a float)
voxelwise_P_Bonf: (a float)
voxelwise_P_FDR: (a float)
voxelwise_P_RF: (a float)
voxelwise_P_uncor: (a float)
```

157.10 TwoSampleTTestDesign

Link to code
Create SPM design for two sample t-test

157.10.1 Examples

```
>>> ttest = TwoSampleTTestDesign()
>>> ttest.inputs.group1_files = ['cont1.nii', 'cont2.nii']
>>> ttest.inputs.group2_files = ['cont1a.nii', 'cont2a.nii']
>>> ttest.run()
```

Inputs:

```
[Mandatory]
group1_files: (a list of at least 2 items which are an existing file
         name)
        Group 1 input files
group2_files: (a list of at least 2 items which are an existing file
         name)
        Group 2 input files

[Optional]
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}
dependent: (a boolean)
        Are the measurements dependent between levels
explicit_mask_file: (a file name)
        use an implicit mask file to threshold
global_calc_mean: (a boolean)
        use mean for global calculation
        mutually_exclusive: global_calc_omit, global_calc_values
global_calc_omit: (a boolean)
        omit global calculation
        mutually_exclusive: global_calc_mean, 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
global_normalization: (1 or 2 or 3)
        global normalization None-1, Proportional-2, ANCOVA-3
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
no_grand_mean_scaling: (a boolean)
        do not perform grand mean scaling
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
spm_mat_dir: (an existing directory name)
        directory to store SPM.mat file (opt)
threshold_mask_absolute: (a float)
        use an absolute threshold
        mutually_exclusive: threshold_mask_none, threshold_mask_relative
threshold_mask_none: (a boolean)
        do not use threshold masking
        mutually_exclusive: threshold_mask_absolute, threshold_mask_relative
threshold_mask_relative: (a float)
        threshold using a proportion of the global value
        mutually_exclusive: threshold_mask_absolute, threshold_mask_none
unequal_variance: (a boolean)
        Are the variances equal or unequal between groups
use_implicit_threshold: (a boolean)
        use implicit mask NaNs or zeros to threshold
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
```

```
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
spm_mat_file: (an existing file name)
        SPM mat file
```

CHAPTER 158

interfaces.spm.preprocess

158.1 ApplyDeformations

Link to code
Inputs:

```
[Mandatory]
deformation_field: (an existing file name)
in_files: (a list of items which are an existing file name)
reference_volume: (an existing file name)

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interp: (0 <= an integer <= 7)
        degree of b-spline used for interpolation
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
out_files: (a list of items which are an existing file name)
```

158.2 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

158.2.1 Examples

```
>>> import nipype.interfaces.spm as spm
>>> coreg = spm.Coregister()
>>> coreg.inputs.target = 'functional.nii'
```

```
>>> coreg.inputs.source = 'structural.nii'
>>> coreg.run()
```

Inputs:

```
[Mandatory]
source: (a list of items which are an existing file name)
        file to register to target
target: (an existing file name)
        reference file to register to

[Optional]
apply_to_files: (a list of items which are an existing file name)
        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)
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
jobtype: ('estwrite' or 'estimate' or 'write', nipype default value:
         estwrite)
        one of: estimate, write, estwrite
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
out_prefix: (a string, nipype default value: r)
        coregistered output prefix
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
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
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
write_interp: (0 <= an integer <= 7)
        degree of b-spline used for interpolation
write_mask: (a boolean)
        True/False mask output image
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]
```

Outputs:

```
coregistered_files: (a list of items which are an existing file name)
        Coregistered other files
coregistered_source: (a list of items which are an existing file
         name)
        Coregistered source files
```

158.3 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

158.3.1 Examples

```
>>> import nipype.interfaces.spm as spm
>>> create_warped = spm.CreateWarped()
>>> create_warped.inputs.image_files = ['rc1s1.nii', 'rc1s2.nii']
>>> create_warped.inputs.flowfield_files = ['u_rc1s1_Template.nii', 'u_rc1s2_Template.nii']
>>> create_warped.run()
```

Inputs:

```
[Mandatory]
flowfield_files: (a list of items which are an existing file name)
        DARTEL flow fields u_rc1*
image_files: (a list of items which are an existing file name)
        A list of files to be warped

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interp: (0 <= an integer <= 7)
        degree of b-spline used for interpolation
iterations: (0 <= an integer <= 9)
        The number of iterations: log2(number of time steps)
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
modulate: (a boolean)
        Modulate images
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
warped_files: (a list of items which are an existing file name)
```

158.4 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

158.4.1 Examples

```
>>> import nipype.interfaces.spm as spm
>>> dartel = spm.DARTEL()
>>> dartel.inputs.image_files = [['rc1s1.nii','rc1s2.nii'],['rc2s1.nii', 'rc2s2.nii']]
>>> dartel.run()
```

Inputs:

```
[Mandatory]
image_files: (a list of items which are a list of items which are an
         existing file name)
        A list of files to be segmented

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
iteration_parameters: (a list of from 3 to 12 items which are a tuple
         of the form: (1 <= an 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
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
optimization_parameters: (a tuple of the form: (a float, 1 <= an
         integer <= 8, 1 <= an integer <= 8))
        Optimization settings a tuple
         - LM regularization
         - cycles of multigrid solver
         - relaxation iterations
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
regularization_form: ('Linear' or 'Membrane' or 'Bending')
        Form of regularization energy term
template_prefix: (a string, nipype default value: Template)
        Prefix for template
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
dartel_flow_fields: (a list of items which are an existing file name)
        DARTEL flow fields
final_template_file: (an existing file name)
        final DARTEL template
template_files: (a list of items which are an existing file name)
        Templates from different stages of iteration
```

158.5 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

158.5.1 Examples

```
>>> import nipype.interfaces.spm as spm
>>> nm = spm.DARTELNorm2MNI()
>>> nm.inputs.template_file = 'Template_6.nii'
>>> nm.inputs.flowfield_files = ['u_rc1s1_Template.nii', 'u_rc1s3_Template.nii']
>>> nm.inputs.apply_to_files = ['c1s1.nii', 'c1s3.nii']
>>> nm.inputs.modulate = True
>>> nm.run()
```

Inputs:

```
[Mandatory]
apply_to_files: (a list of items which are an existing file name)
        Files to apply the transform to
flowfield_files: (a list of items which are an existing file name)
        DARTEL flow fields u_rc1*
template_file: (an existing file name)
        DARTEL template

[Optional]
bounding_box: (a tuple of the form: (a float, a float, a float, a
         float, a float, a float))
        Voxel sizes for output file
fwhm: (a list of from 3 to 3 items which are a float or a float)
        3-list of fwhm for each dimension
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
modulate: (a boolean)
        Modulate out images - no modulation preserves concentrations
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
voxel_size: (a tuple of the form: (a float, a float, a float))
        Voxel sizes for output file
```

Outputs:

```
normalization_parameter_file: (an existing file name)
        Transform parameters to MNI space
normalized_files: (a list of items which are an existing file name)
        Normalized files in MNI space
```

158.6 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

158.6.1 Examples

```
>>> import nipype.interfaces.spm as spm
>>> seg = spm.NewSegment()
>>> seg.inputs.channel_files = 'structural.nii'
>>> seg.inputs.channel_info = (0.0001, 60, (True, True))
>>> seg.run()
```

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()
```

Inputs:

```
[Mandatory]
channel_files: (a list of items which are an existing file name)
        A list of files to be segmented

[Optional]
affine_regularization: ('mni' or 'eastern' or 'subj' or 'none')
        mni, eastern, subj, none
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 reguralisation (0-10)
         - FWHM of Gaussian smoothness of bias
         - which maps to save (Corrected, Field) - a tuple of two boolean
        values
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
sampling_distance: (a float)
        Sampling distance on data for parameter estimation
tissues: (a list of items which are a tuple of the form: (a tuple of
         the form: (an existing file name, 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
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
warping_regularization: (a float)
        Aproximate distance between sampling points.
write_deformation_fields: (a list of from 2 to 2 items which are a
         boolean)
        Which deformation fields to write:[Inverse, Forward]
```

Outputs:

```
bias_corrected_images: (a list of items which are an existing file
         name)
        bias corrected images
bias_field_images: (a list of items which are an existing file name)
        bias field images
dartel_input_images: (a list of items which are a list of items which
         are an existing file name)
        dartel imported class images
forward_deformation_field: (a list of items which are an existing
         file name)
inverse_deformation_field: (a list of items which are an existing
         file name)
modulated_class_images: (a list of items which are a list of items
         which are an existing file name)
        modulated+normalized class images
native_class_images: (a list of items which are a list of items which
         are an existing file name)
        native space probability maps
normalized_class_images: (a list of items which are a list of items
         which are an existing file name)
        normalized class images
transformation_mat: (a list of items which are an existing file name)
        Normalization transformation
```

158.7 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

158.7.1 Examples

```
>>> import nipype.interfaces.spm as spm
>>> norm = spm.Normalize()
>>> norm.inputs.source = 'functional.nii'
>>> norm.run()
```

Inputs:

```
    [Mandatory]
    parameter_file: (a file name)
            normalization parameter file*_sn.mat
            mutually_exclusive: source, template
    source: (a list of items which are an existing file name)
            file to normalize to template
            mutually_exclusive: parameter_file
    template: (an existing file name)
            template file to normalize to
            mutually_exclusive: parameter_file

    [Optional]
    DCT_period_cutoff: (a float)
            Cutoff of for DCT bases
    affine_regularization_type: ('mni' or 'size' or 'none')
            mni, size, none
    apply_to_files: (a list of items which are an existing file name or a
             list of items which are an existing file name)
            files to apply transformation to
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    jobtype: ('estwrite' or 'est' or 'write', nipype default value:
             estwrite)
            Estimate, Write or do both
    matlab_cmd: (a string)
            matlab command to use
    mfile: (a boolean, nipype default value: True)
            Run m-code using m-file
    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
    out_prefix: (a string, nipype default value: w)
            normalized output prefix
    paths: (a list of items which are a directory name)
            Paths to add to matlabpath
    source_image_smoothing: (a float)
            source smoothing
    source_weight: (a file name)
            name of weighting image for source
    template_image_smoothing: (a float)
            template smoothing
    template_weight: (a file name)
            name of weighting image for template
    use_mcr: (a boolean)
            Run m-code using SPM MCR
    use_v8struct: (a boolean, nipype default value: True)
            Generate SPM8 and higher compatible jobs
    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_interp: (0 <= an integer <= 7)
            degree of b-spline used for interpolation
    write_preserve: (a boolean)
            True/False warped images are modulated
    write_voxel_sizes: (a list of from 3 to 3 items which are a float)
```

```
        3-element list
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
```

Outputs:

```
normalization_parameters: (a list of items which are an existing file
         name)
        MAT files containing the normalization parameters
normalized_files: (a list of items which are an existing file name)
        Normalized other files
normalized_source: (a list of items which are an existing file name)
        Normalized source files
```

158.8 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 cass in SPM8.
http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=49

158.8.1 Examples

```
>>> import nipype.interfaces.spm as spm
>>> norm12 = spm.Normalize12()
>>> norm12.inputs.image_to_align = 'structural.nii'
>>> norm12.inputs.apply_to_files = 'functional.nii'
>>> norm12.run()
```

Inputs:

```
[Mandatory]
deformation_file: (a file name)
        file y_*.nii containing 3 deformation fields for the deformation in
        x, y and z dimension
        mutually_exclusive: image_to_align, tpm
image_to_align: (an existing file name)
        file to estimate normalization parameters with
        mutually_exclusive: deformation_file

[Optional]
affine_regularization_type: ('mni' or 'size' or 'none')
        mni, size, none
apply_to_files: (a list of items which are an existing file name or a
         list of items which are an existing file name)
        files to apply transformation to
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
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)
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
jobtype: ('estwrite' or 'est' or 'write', nipype default value:
```

```
          estwrite)
        Estimate, Write or do Both
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
sampling_distance: (a float)
        Sampling distance on data for parameter estimation
smoothness: (a float)
        value (in mm) to smooth the data before normalization
tpm: (an existing file name)
        template in form of tissue probablitiy maps to normalize to
        mutually_exclusive: deformation_file
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
warping_regularization: (a list of from 5 to 5 items which are a
         float)
        controls balance between parameters and data
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_interp: (0 <= an integer <= 7)
        degree of b-spline used for interpolation
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
```

Outputs:

```
deformation_field: (a list of items which are an existing file name)
        NIfTI file containing 3 deformation fields for the deformation in x,
        y and z dimension
normalized_files: (a list of items which are an existing file name)
        Normalized other files
normalized_image: (a list of items which are an existing file name)
        Normalized file that needed to be aligned
```

158.9 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

158.9.1 Examples

```
>>> import nipype.interfaces.spm as spm
>>> realign = spm.Realign()
>>> realign.inputs.in_files = 'functional.nii'
>>> realign.inputs.register_to_mean = True
>>> realign.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a list of items which are an
          existing file name or an existing file name)
         list of filenames to realign

[Optional]
fwhm: (a floating point number >= 0.0)
        gaussian smoothing kernel width
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interp: (0 <= an integer <= 7)
        degree of b-spline used for interpolation
jobtype: ('estwrite' or 'estimate' or 'write', nipype default value:
          estwrite)
        one of: estimate, write, estwrite
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
out_prefix: (a string, nipype default value: r)
        realigned output prefix
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
quality: (0.0 <= a floating point number <= 1.0)
        0.1 = fast, 1.0 = precise
register_to_mean: (a boolean)
        Indicate whether realignment is done to the mean image
separation: (a floating point number >= 0.0)
        sampling separation in mm
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
weight_img: (an existing file name)
        filename of weighting image
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_interp: (0 <= an integer <= 7)
        degree of b-spline used for interpolation
write_mask: (a boolean)
        True/False mask output image
write_which: (a list of items which are a value of type 'int', nipype
         default value: [2, 1])
        determines which images to reslice
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]
```

Outputs:

```
mean_image: (an existing file name)
        Mean image file from the realignment
modified_in_files: (a list of items which are a list of items which
         are an existing file name or an existing file name)
        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
         an existing file name or an existing file name)
        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 an existing file
         name)
        Estimated translation and rotation parameters
```

158.10 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

158.10.1 Examples

```
>>> import nipype.interfaces.spm as spm
>>> seg = spm.Segment()
>>> seg.inputs.data = 'structural.nii'
>>> seg.run()
```

Inputs:

```
[Mandatory]
data: (a list of items which are an existing file name)
        one scan per subject

[Optional]
affine_regularization: ('mni' or 'eastern' or 'subj' or 'none' or '')
        Possible options: "mni", "eastern", "subj", "none" (no
        reguralisation), "" (no affine registration)
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
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)
clean_masks: ('no' or 'light' or 'thorough')
        clean using estimated brain mask ('no','light','thorough')
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]
gaussians_per_class: (a list of items which are an integer (int or
         long))
        num Gaussians capture intensity distribution
gm_output_type: (a list of from 3 to 3 items which are a boolean)
        Options to produce grey matter images: c1*.img, wc1*.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]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
mask_image: (an existing file name)
        Binary image to restrict parameter estimation
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
sampling_distance: (a float)
        Sampling distance on data for parameter estimation
save_bias_corrected: (a boolean)
        True/False produce a bias corrected image
tissue_prob_maps: (a list of items which are an existing file name)
        list of gray, white & csf prob. (opt,)
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
warp_frequency_cutoff: (a float)
        Cutoff of DCT bases
warping_regularization: (a float)
        Controls balance between parameters and data
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]
```

Outputs:

```
bias_corrected_image: (a file name)
        bias-corrected version of input image
inverse_transformation_mat: (an existing file name)
        Inverse normalization info
modulated_csf_image: (a file name)
        modulated, normalized csf probability map
modulated_gm_image: (a file name)
        modulated, normalized grey probability map
modulated_input_image: (a file name)
        bias-corrected version of input image
modulated_wm_image: (a file name)
        modulated, normalized white probability map
native_csf_image: (a file name)
```

```
        native space csf probability map
native_gm_image: (a file name)
        native space grey probability map
native_wm_image: (a file name)
        native space white probability map
normalized_csf_image: (a file name)
        normalized csf probability map
normalized_gm_image: (a file name)
        normalized grey probability map
normalized_wm_image: (a file name)
        normalized white probability map
transformation_mat: (an existing file name)
        Normalization transformation
```

158.11 SliceTiming

Link to code
Use spm to perform slice timing correction.
http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf#page=19

158.11.1 Examples

```
>>> from nipype.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()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are a list of items which are an
          existing file name or an existing file name)
        list of filenames to apply slice timing
num_slices: (an integer (int or long))
        number of slices in a volume
ref_slice: (an integer (int or long))
        1-based Number of the reference slice
slice_order: (a list of items which are an integer (int or long))
        1-based order in which slices are acquired
time_acquisition: (a float)
        time of volume acquisition. usuallycalculated as TR-(TR/num_slices)
time_repetition: (a float)
        time between volume acquisitions(start to start time)

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
```

```
out_prefix: (a string, nipype default value: a)
        slicetimed output prefix
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
timecorrected_files: (a list of items which are a list of items which
         are an existing file name or an existing file name)
        slice time corrected files
```

158.12 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

158.12.1 Examples

```
>>> import nipype.interfaces.spm as spm
>>> smooth = spm.Smooth()
>>> smooth.inputs.in_files = 'functional.nii'
>>> smooth.inputs.fwhm = [4, 4, 4]
>>> smooth.run()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        list of files to smooth

[Optional]
data_type: (an integer (int or long))
        Data type of the output images
fwhm: (a list of from 3 to 3 items which are a float or a float)
        3-list of fwhm for each dimension
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
implicit_masking: (a boolean)
        A mask implied by a particularvoxel value
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
out_prefix: (a string, nipype default value: s)
        smoothed output prefix
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
smoothed_files: (a list of items which are an existing file name)
        smoothed files
```

158.13 VBMSegment

Link to code
Use VBM8 toolbox to separate structural images into different tissue classes.

158.13.1 Example

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        A list of files to be segmented

[Optional]
bias_corrected_affine: (a boolean, nipype default value: False)
bias_corrected_native: (a boolean, nipype default value: False)
bias_corrected_normalized: (a boolean, nipype default value: True)
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', nipype default value: 60)
        FWHM of Gaussian smoothness of bias
bias_regularization: (0 or 1e-05 or 0.0001 or 0.001 or 0.01 or 0.1 or
         1 or 10, nipype default value: 0.0001)
        no(0) - extremely heavy (10)
cleanup_partitions: (an integer (int or long), nipype default value:
         1)
        0=None,1=light,2=thorough
csf_dartel: (0 <= an integer <= 2, nipype default value: 0)
        0=None,1=rigid(SPM8 default),2=affine
csf_modulated_normalized: (0 <= an integer <= 2, nipype default
         value: 2)
        0=none,1=affine+non-linear(SPM8 default),2=non-linear only
csf_native: (a boolean, nipype default value: False)
csf_normalized: (a boolean, nipype default value: False)
dartel_template: (an existing file name)
deformation_field: (a tuple of the form: (a boolean, a boolean),
         nipype default value: (0, 0))
        forward and inverse field
display_results: (a boolean, nipype default value: True)
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)),
         nipype default value: (2, 2, 2, 3, 4, 2))
        number of gaussians for each tissue class
gm_dartel: (0 <= an integer <= 2, nipype default value: 0)
        0=None,1=rigid(SPM8 default),2=affine
gm_modulated_normalized: (0 <= an integer <= 2, nipype default value:
         2)
        0=none,1=affine+non-linear(SPM8 default),2=non-linear only
gm_native: (a boolean, nipype default value: False)
gm_normalized: (a boolean, nipype default value: False)
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
jacobian_determinant: (a boolean, nipype default value: False)
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
mrf_weighting: (a float, nipype default value: 0.15)
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
pve_label_dartel: (0 <= an integer <= 2, nipype default value: 0)
        0=None,1=rigid(SPM8 default),2=affine
pve_label_native: (a boolean, nipype default value: False)
pve_label_normalized: (a boolean, nipype default value: False)
sampling_distance: (a float, nipype default value: 3)
        Sampling distance on data for parameter estimation
spatial_normalization: ('high' or 'low', nipype default value: high)
tissues: (an existing file name)
        tissue probability map
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_sanlm_denoising_filter: (0 <= an integer <= 2, nipype default
         value: 2)
        0=No denoising, 1=denoising,2=denoising multi-threaded
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
warping_regularization: (a float, nipype default value: 4)
        Controls balance between parameters and data
wm_dartel: (0 <= an integer <= 2, nipype default value: 0)
        0=None,1=rigid(SPM8 default),2=affine
wm_modulated_normalized: (0 <= an integer <= 2, nipype default value:
         2)
        0=none,1=affine+non-linear(SPM8 default),2=non-linear only
wm_native: (a boolean, nipype default value: False)
wm_normalized: (a boolean, nipype default value: False)
```

Outputs:

```
bias_corrected_images: (a list of items which are an existing file
         name)
        bias corrected images
dartel_input_images: (a list of items which are a list of items which
         are an existing file name)
        dartel imported class images
forward_deformation_field: (a list of items which are an existing
         file name)
inverse_deformation_field: (a list of items which are an existing
         file name)
```

```
    jacobian_determinant_images: (a list of items which are an existing
             file name)
    modulated_class_images: (a list of items which are a list of items
             which are an existing file name)
            modulated+normalized class images
    native_class_images: (a list of items which are a list of items which
             are an existing file name)
            native space probability maps
    normalized_bias_corrected_images: (a list of items which are an
             existing file name)
            bias corrected images
    normalized_class_images: (a list of items which are a list of items
             which are an existing file name)
            normalized class images
    pve_label_native_images: (a list of items which are an existing file
             name)
    pve_label_normalized_images: (a list of items which are an existing
             file name)
    pve_label_registered_images: (a list of items which are an existing
             file name)
    transformation_mat: (a list of items which are an existing file name)
            Normalization transformation
```

CHAPTER 159

interfaces.spm.utils

159.1 Analyze2nii

Link to code
Inputs:

```
[Mandatory]
analyze_file: (an existing file name)

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
nifti_file: (an existing file name)
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

159.2 ApplyInverseDeformation

Link to code
Uses spm to apply inverse deformation stored in a .mat file or a deformation field to a given file

159.2.1 Examples

```
>>> import nipype.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()
```

Inputs:

```
[Mandatory]
in_files: (a list of items which are an existing file name)
        Files on which deformation is applied

[Optional]
bounding_box: (a list of from 6 to 6 items which are a float)
        6-element list (opt)
deformation: (an existing file name)
        SN SPM deformation file
        mutually_exclusive: deformation_field
deformation_field: (an existing file name)
        SN SPM deformation file
        mutually_exclusive: deformation
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interpolation: (0 <= an integer <= 7)
        degree of b-spline used for interpolation
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
target: (an existing file name)
        File defining target space
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
voxel_sizes: (a list of from 3 to 3 items which are a float)
        3-element list (opt)
```

Outputs:

```
out_files: (a list of items which are an existing file name)
        Transformed files
```

159.3 ApplyTransform

Link to code

Uses SPM to apply transform stored in a .mat file to given file

159.3.1 Examples

```
>>> import nipype.interfaces.spm.utils as spmu
>>> applymat = spmu.ApplyTransform()
>>> applymat.inputs.in_file = 'functional.nii'
>>> applymat.inputs.mat = 'func_to_struct.mat'
>>> applymat.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        file to apply transform to, (only updates header)
mat: (an existing file name)
        file holding transform to apply

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
out_file: (a file name)
        output file name for transformed data
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
out_file: (an existing file name)
        Transformed image file
```

159.4 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

159.4.1 Examples

```
>>> import nipype.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()
```

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]
    moving: (an existing file name)
            volume transform can be applied to register with target
    target: (an existing file name)
            target for generating affine transform

    [Optional]
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    invmat: (a file name)
            Filename used to store inverse affine matrix
    mat: (a file name)
            Filename used to store affine matrix
    matlab_cmd: (a string)
            matlab command to use
    mfile: (a boolean, nipype default value: True)
            Run m-code using m-file
    paths: (a list of items which are a directory name)
            Paths to add to matlabpath
    use_mcr: (a boolean)
            Run m-code using SPM MCR
    use_v8struct: (a boolean, nipype default value: True)
            Generate SPM8 and higher compatible jobs
```

Outputs:

```
    invmat: (a file name)
            Matlab file holding inverse transform
    mat: (an existing file name)
            Matlab file holding transform
```

159.5 DicomImport

Link to code

Uses spm to convert DICOM files to nii or img+hdr.

159.5.1 Examples

```
    >>> import nipype.interfaces.spm.utils as spmu
    >>> di = spmu.DicomImport()
    >>> di.inputs.in_files = ['functional_1.dcm', 'functional_2.dcm']
    >>> di.run()
```

Inputs:

```
    [Mandatory]
    in_files: (a list of items which are an existing file name)
            dicom files to be converted

    [Optional]
    format: ('nii' or 'img', nipype default value: nii)
            output format.
    icedims: (a boolean, nipype 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.
    ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
output_dir: (a string, nipype default value: ./converted_dicom)
        output directory.
output_dir_struct: ('flat' or 'series' or 'patname' or 'patid_date'
         or 'patid' or 'date_time', nipype default value: flat)
        directory structure for the output.
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
out_files: (a list of items which are an existing file name)
        converted files
```

159.6 Reslice

Link to code

uses spm_reslice to resample in_file into space of space_defining

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        file to apply transform to, (only updates header)
space_defining: (an existing file name)
        Volume defining space to slice in_file into

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
interp: (0 <= an integer <= 7, nipype default value: 0)
        degree of b-spline used for interpolation0 is nearest neighbor
        (default)
matlab_cmd: (a string)
        matlab command to use
mfile: (a boolean, nipype default value: True)
        Run m-code using m-file
out_file: (a file name)
        Optional file to save resliced volume
paths: (a list of items which are a directory name)
        Paths to add to matlabpath
use_mcr: (a boolean)
        Run m-code using SPM MCR
use_v8struct: (a boolean, nipype default value: True)
        Generate SPM8 and higher compatible jobs
```

Outputs:

```
    out_file: (an existing file name)
            resliced volume
```

159.7 ResliceToReference

Link to code

Uses spm to reslice a volume to a target image space or to a provided voxel size and bounding box

159.7.1 Examples

```
>>> import nipype.interfaces.spm.utils as spmu
>>> r2ref = spmu.ResliceToReference()
>>> r2ref.inputs.in_files = 'functional.nii'
>>> r2ref.inputs.target = 'structural.nii'
>>> r2ref.run()
```

Inputs:

```
    [Mandatory]
    in_files: (a list of items which are an existing file name)
            Files on which deformation is applied

    [Optional]
    bounding_box: (a list of from 6 to 6 items which are a float)
            6-element list (opt)
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    interpolation: (0 <= an integer <= 7)
            degree of b-spline used for interpolation
    matlab_cmd: (a string)
            matlab command to use
    mfile: (a boolean, nipype default value: True)
            Run m-code using m-file
    paths: (a list of items which are a directory name)
            Paths to add to matlabpath
    target: (an existing file name)
            File defining target space
    use_mcr: (a boolean)
            Run m-code using SPM MCR
    use_v8struct: (a boolean, nipype default value: True)
            Generate SPM8 and higher compatible jobs
    voxel_sizes: (a list of from 3 to 3 items which are a float)
            3-element list (opt)
```

Outputs:

```
    out_files: (a list of items which are an existing file name)
            Transformed files
```

CHAPTER 160

interfaces.utility

160.1 AssertEqual

Link to code
Inputs:

```
[Mandatory]
volume1: (an existing file name)
volume2: (an existing file name)

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
None
```

160.2 CSVReader

Link to code

160.2.1 Examples

```
>>> reader = CSVReader()
>>> reader.inputs.in_file = 'noHeader.csv'
>>> out = reader.run()
>>> out.outputs.column_0 == ['foo', 'bar', 'baz']
True
>>> out.outputs.column_1 == ['hello', 'world', 'goodbye']
True
>>> out.outputs.column_2 == ['300.1', '5', '0.3']
True
```

```
>>> reader = CSVReader()
>>> reader.inputs.in_file = 'header.csv'
>>> reader.inputs.header = True
>>> out = reader.run()
>>> out.outputs.files == ['foo', 'bar', 'baz']
True
>>> out.outputs.labels == ['hello', 'world', 'goodbye']
True
>>> out.outputs.erosion == ['300.1', '5', '0.3']
True
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        Input comma-seperated value (CSV) file

[Optional]
header: (a boolean, nipype default value: False)
        True if the first line is a column header
```

Outputs:

```
None
```

160.3 Function

Link to code
Runs arbitrary function as an interface

160.3.1 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 string)
        code for function

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
None
```

160.4 IdentityInterface

Link to code
Basic interface class generates identity mappings

160.4.1 Examples

```
>>> from nipype.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()
ValueError: IdentityInterface requires a value for input 'b' because it was listed in 'fields' I
```

Inputs:

```
None
```

Outputs:

```
None
```

160.5 Merge

Link to code

Basic interface class to merge inputs into a single list

160.5.1 Examples

```
>>> from nipype.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]
```

Inputs:

```
[Mandatory]

[Optional]
axis: ('vstack' or 'hstack', nipype default value: vstack)
        direction in which to merge, hstack requires same number of elements
        in each input
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
no_flatten: (a boolean, nipype default value: False)
        append to outlist instead of extending in vstack mode
```

Outputs:

```
out: (a list of items which are any value)
        Merged output
```

160.6 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.

160.6.1 Examples

```
>>> from nipype.interfaces.utility import Rename
>>> rename1 = Rename()
>>> rename1.inputs.in_file = "zstat1.nii.gz"
>>> rename1.inputs.format_string = "Faces-Scenes.nii.gz"
>>> res = rename1.run()
>>> res.outputs.out_file
'Faces-Scenes.nii.gz"
```

```
>>> rename2 = Rename(format_string="%(subject_id)s_func_run%(run)02d")
>>> rename2.inputs.in_file = "functional.nii"
>>> rename2.inputs.keep_ext = True
>>> rename2.inputs.subject_id = "subj_201"
>>> rename2.inputs.run = 2
>>> res = rename2.run()
>>> res.outputs.out_file
'subj_201_func_run02.nii'
```

```
>>> rename3 = Rename(format_string="%(subject_id)s_%(seq)s_run%(run)02d.nii")
>>> rename3.inputs.in_file = "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()
>>> res.outputs.out_file
'subj_201_epi_run02.nii'
```

Inputs:

```
[Mandatory]
format_string: (a string)
        Python formatting string for output template
in_file: (an existing file name)
        file to rename

[Optional]
keep_ext: (a boolean)
        Keep in_file extension, replace non-extension component of name
parse_string: (a string)
        Python regexp parse string to define replacement inputs
use_fullpath: (a boolean, nipype default value: False)
        Use full path as input to regex parser
```

Outputs:

```
out_file: (a file name)
        softlink to original file with new name
```

160.7 Select

Link to code

Basic interface class to select specific elements from a list

160.7.1 Examples

```
>>> from nipype.interfaces.utility import Select
>>> sl = Select()
>>> _ = sl.inputs.set(inlist=[1, 2, 3, 4, 5], index=[3])
>>> out = sl.run()
>>> out.outputs.out
~
```

```
>>> _ = sl.inputs.set(inlist=[1, 2, 3, 4, 5], index=[3, 4])
>>> out = sl.run()
>>> out.outputs.out
[4, 5]
```

Inputs:

```
[Mandatory]
index: (a list of items which are an integer (int or long))
        0-based indices of values to choose
inlist: (a list of items which are any value)
        list of values to choose from

[Optional]
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
```

Outputs:

```
out: (a list of items which are any value)
        list of selected values
```

160.8 Split

Link to code

Basic interface class to split lists into multiple outputs

160.8.1 Examples

```
>>> from nipype.interfaces.utility import Split
>>> sp = Split()
>>> _ = sp.inputs.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]
ignore_exception: (a boolean, nipype default value: False)
```

```
        Print an error message instead of throwing an exception in case the
        interface fails to run
squeeze: (a boolean, nipype default value: False)
        unfold one-element splits removing the list
```

Outputs:

```
None
```

CHAPTER 161

interfaces.vista.vista

161.1 Vnifti2Image

Link to code
Wraps command **vnifti2image**
Convert a nifti file into a vista file.

161.1.1 Example

```
>>> vimage = Vnifti2Image()
>>> vimage.inputs.in_file = 'image.nii'
>>> vimage.cmdline
'vnifti2image -in image.nii -out image.v'
>>> vimage.run()
```

Inputs:

```
[Mandatory]
in_file: (an existing file name)
        in file
        flag: -in %s, position: 1

[Optional]
args: (a string)
        Additional parameters to the command
        flag: %s
attributes: (an existing file name)
        attribute file
        flag: -attr %s, position: 2
environ: (a dictionary with keys which are a value of type 'str' and
         with values which are a value of type 'str', nipype default value:
         {})
        Environment variables
ignore_exception: (a boolean, nipype default value: False)
        Print an error message instead of throwing an exception in case the
        interface fails to run
out_file: (a file name)
        output data file
        flag: -out %s, position: -1
terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
        Control terminal output: `stream` - displays to terminal immediately
        (default), `allatonce` - waits till command is finished to display
        output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
            Output vista file
```

161.2 VtoMat

Link to code
Wraps command **vtomat**
Convert a nifti file into a vista file.

161.2.1 Example

```
>>> vimage = VtoMat()
>>> vimage.inputs.in_file = 'image.v'
>>> vimage.cmdline
'vtomat -in image.v -out image.mat'
>>> vimage.run()
```

Inputs:

```
    [Mandatory]
    in_file: (an existing file name)
            in file
            flag: -in %s, position: 1

    [Optional]
    args: (a string)
            Additional parameters to the command
            flag: %s
    environ: (a dictionary with keys which are a value of type 'str' and
             with values which are a value of type 'str', nipype default value:
             {})
            Environment variables
    ignore_exception: (a boolean, nipype default value: False)
            Print an error message instead of throwing an exception in case the
            interface fails to run
    out_file: (a file name)
            output mat file
            flag: -out %s, position: -1
    terminal_output: ('stream' or 'allatonce' or 'file' or 'none')
            Control terminal output: `stream` - displays to terminal immediately
            (default), `allatonce` - waits till command is finished to display
            output, `file` - writes output to file, `none` - output is ignored
```

Outputs:

```
    out_file: (an existing file name)
            Output mat file
```

CHAPTER 162

interfaces.vtkbase

162.1 configure_input_data()

Link to code
Configure the input data for vtk pipeline object obj. Copied from latest version of mayavi

162.2 vtk_old()

Link to code
Checks if VTK uses the old-style pipeline (VTK<6.0)

162.3 vtk_output()

Link to code
Configure the input data for vtk pipeline object obj.

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Symbols

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