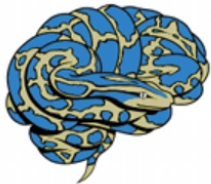


# Neuroimaging in python: Nipype

Foucalt@pycontw19



# **Nipype: Neuroimaging in Python Pipelines and Interfaces**

<https://nipype.readthedocs.io/en/latest/>

# Multimodal Brain Tumor Segmentation Challenge 2019



• Scope • Relevance • Tasks • Data • Evaluation • Participation Summary • Registration • Previous BrATS • People •


<http://braintumorsegmentation.org/>

The NIH Human Connectome Project

# Human Connectome Project

Enter search keyword

Home About Data Information Gallery Publications News



## The Human Connectome Project

Navigate the brain in a way that was never before possible. Fly through major brain pathways, compare essential circuits, zoom into a region to explore the cells that comprise it, and the functions that depend on it.

The Human Connectome Project aims to provide an unparalleled compilation of neural data, an interface to graphically navigate this data and the opportunity to achieve never before realized conclusions about the living human brain.

[Download Data](#)

*Laboratory of Brain Imaging*

### News

**NEO News**

**National Geographic features the Human Connectome Project**

New research from members of our HCP team suggests that brain circuitry is organized more like Manhattan's street grid than London's chaotic tangle of random roadways. Read the full article in the February 2014 issue of National Geographic.

**Director of NIH Proves the Human Connectome Project**

The Symphony Inside Your Brain By Dr. Francis Collins Ever wonder what it is that makes you, you? Depending on whom you ask, there are a lot of different answers, but Brain maps some of the world's top

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



## News

Keyword search

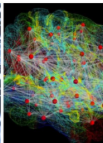
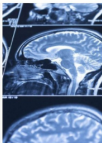
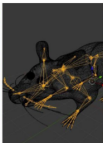
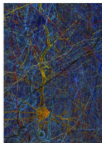
SEPT. 20, 2019

### Four CEols for HBP's Final Phase Opened

[FEATURED](#)

4 Calls for Expression of Interest (CEols) are now open for new projects to directly contribute to the development of the research Infrastructure (EBRAINS) and increase the scope of its application in terms of innovation, neuroscience and clinical research.

### Four CEols for HBP's Final Phase Opened



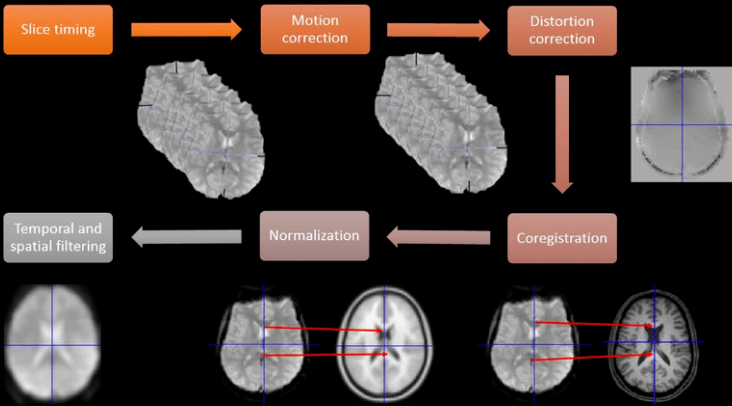
### Four New Calls

1. Validation and Inference
2. Brain atlas and simulation engine adapter construction
3. Whole brain multi-parametric imaging using invasive and non-invasive recordings
4. Rodent microcircuits

<https://www.humanbrainproject.eu/en/>

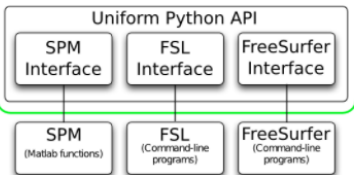








## Interfaces

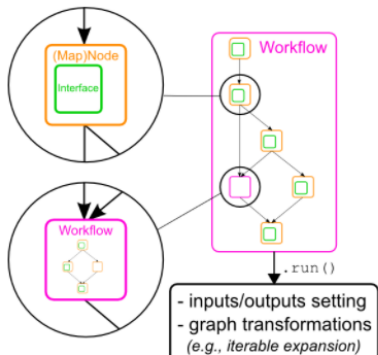


Idiosyncratic, Heterogeneous APIs

## Execution Plugins



## Workflow Engine



```
from nipype import Node, Workflow
```

```
from nipype.interfaces.fsl import SliceTimer, MCFLIRT, Smooth
```

*# Initiate a node to correct for slice wise acquisition*

```
slicetimer = Node(SliceTimer(index_dir=False,  
                             interleaved=True,  
                             time_repetition=2.5),  
                 name="slicetimer")
```

*# Initiate a node to correct for motion*

```
mcflirt = Node(MCFLIRT(mean_vol=True,  
                      save_plots=True),  
              name="mcflirt")
```

*# Initiate a node to smooth functional images*

```
smooth = Node(Smooth(fwhm=4), name="smooth")
```

```
preproc01 = Workflow(name='preproc01', base_dir='.')
```

```
preproc01.connect([(slicetimer, mcflirt, [('slice_time_corre  
cted_file', 'in_file')]),  
                    (mcflirt, smooth, [('out_file', 'in_fil  
e')])])
```

| IN | slicetimer | OUT                       |
|----|------------|---------------------------|
|    | fsl        |                           |
|    |            | slice_time_corrected_file |



| IN | mcflirt | OUT      |
|----|---------|----------|
|    | fsl     |          |
|    |         | out_file |



| IN | smooth | OUT |
|----|--------|-----|
|    | fsl    |     |
|    |        |     |

Running a workflow in parallel!

```
preproc02 = preproc01.clone('preproc02')
preproc03 = preproc01.clone('preproc03')
preproc04 = preproc01.clone('preproc04')
preproc05 = preproc01.clone('preproc05')
```

```
metaflow = Workflow(name='metaflow', base_dir='.')
```

```
metaflow.add_nodes([preproc01, preproc02, preproc03,
                    preproc04, preproc05])
```