pipe.py offers a range of capabilities for preprocessing and analysis of fMRI data. The following provides a quick start guide to the most common application, i.e. running a preprocessing pipeline on a set of data. If you are looking for a pipeline to preprocess your fMRI data this is what you need. For more advanced/detailed functionality see the User Guide.

Syntax

The following runs a preprocessing pipeline on the data for all the subjects listed in the 'subjects file'.

pipe.py --subjects <subjects file> --pipeline <pipeline file>

<subjects file> is a text file, which lists the path to data files for all the subjects to be preprocessed. The file lists all the required data in a simple format. For a list of all data fields refer to the User Guide.

<pipeline file> is a text file listing the preprocessing steps to be run as part of the preprocessing pipeline, in a simple format. For a list of the available preprocessing steps refer to the User Guide.

Example

```
pipe.py --subjects mySubjects.txt --pipeline myPipeline.txt
```

myPipeline.txt

```
slicetimer --odd
mcflirt
brainExtractAFNI
ssmooth -fwhm 5
3dFourier -highpass 0.01 -ignore 0
retroicor -ignore 10
```

mySubjects.txt

```
--bold '/data/experiment1/nii/subject1_bold.nii.gz' --structural
'/data/experiment1/nii/subject1_struct.nii.gz' --structuralbrainmask
'/data/experiment1/nii/subject1_struct_brainmask.nii.gz' --opath '/data/experiment1/processed'
--bold '/data/experiment1/nii/subject2_bold.nii.gz' --structural
'/data/experiment1/nii/subject2_struct.nii.gz' --structuralbrainmask
'/data/experiment1/nii/subject2_struct_brainmask.nii.gz' --opath '/data/experiment1/processed'
```

Getting help

To get help, type the following in the terminal:

```
pipe.py --help
```