Pipeline file

The pipeline file is a text file listing all the preprocessing steps in the pipeline. Each step should be entered in a separate line with no empty lines in between. The steps are listed in order.

The available steps are listed in the following table:

Preprocessing step	Description	Arguments	Notes
mcflirt	FSL's mcflirt motion correction		Updates --motpar field in the subjects data
ssmooth	Spatial smoothing using AFNI's 3dmerge	[-fwhm <fwhm=5>]	
retroicor	RETROICOR correction using AFNI's 3dretroicor	[-ignore <# initial frames to ignore = 0> -threshold < Threshold for detection of R-wave peaks in input> -order <order of Fourier series expansion = 2> -cardphase: handle to save cardiac phase in a text file -respphase: handle to save respiratory phase in a text file]	Need to provide --card and --resp fields in the subjects file.
brainExtractAFNI	Skull strip using AFNI's 3dAutomask		Updates --brainmask field in the subjects data
brainExtractFSL	Skull strip using FSL's bet2		Updates --brainmask field in the subjects data
3dFourier	Temporal filtering using AFNI's 3dFourier	3dFourier arguments	Refer to AFNI 3dFourier documentation
motreg	Regression of motion parameters		Requires the --motpar field of the subjects data to be non-empty, or this step must be preceded by mcflirt.
slicetimer	Slice timing correction using FSL's slicetimer	slicetimer arguments	Refer to FSL slicetimer documentation
tcompcor	tCompCor using Nipype impelementaion	[-ignore <# initial frames to ignore = 0>]	Saves components in a text file with suffix __components.txt
acompcor	aCompCor using Nipype impelementaion	-mask <select one from the following: csf, wm, csfwm> [-ignore <# initial frames to ignore = 0>]	Parcellates the input image if needed. Saves components in a text file with suffix __components.txt.
fsl_motion_outliers	Motion censoring	[--refrms: use RMS intensity difference to reference volume as metric (default metric) --dvars: use DVARS as metric --refmse: Mean Square Error version of --refrms (used in original version of fsl_motion_outliers) --fd: use FD (framewise displacement) as metric --fdrms: use FD with RMS matrix calculation as metric]	
lpf	Low-pass filtering	< f_{stop}>	
hpf	High-pass filtering	< f_{stop}>	
bpf	Band-pass filtering	<f_{stop1}> <f_{stop2}>	
globalsigreg	Global signal regression		Requires the --brainmask field of the subjects data to be non-empty, or this step must be preceded by brain extraction.
csfreg	Mean CSF signal regression		If mean CSF time-series not available, it will be calculated
wmreg	Mean WM signal regression		If mean WM time-series not available, it will be calculated
csfwmreg	Mean CSF and WM signal regression		If mean CSF and/or WM time-series not available, it will be calculated
3dDetrend	AFNI's 3dDetrend	3dDetrend arguments	Refer to AFNI 3dDetrend documentation

3dBlurToFWHM	AFNI's 3dBlurToFWHM	3dBlurToFWHM arguments	Refer to AFNI 3dBlurToFWHM documentation

List of the available preprocessing steps. Default values shown following the equal sign '='. Optional arguments are denoted by square brackets '[]'.

Example

myPipeline.txt

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

Subjects file

The pipeline file is a text file listing all the data for every subject to be processed. Each subject should be entered in a separate line with no empty lines in between. The following table lists the available data fields for the subjects file.

Depending on the given preprocessing pipeline, different fields may be required. Some of the data field can be assigned a value or updated during the preprocessing. For example, --brainmask will assigned a value or updated if the pipeline includes a brain extraction step.

Field	Description	
--subjectID	Subject ID	
--sessionID	Session ID	
--sequence	Sequence name	
--bold	BOLD file in NIFTI format	
--structural	Structural file in NIFTI format	
--structuralbrainmask	Structural brain mask in NIFTI format	
--card	1D cardiac file used for RETROICOR	
--resp	1D respiratory file used for RETROICOR	
--opath	Output path- where all pipeline output will be saved	
--connseed	Connectivity seed- should be a binary mask in NIFTI format	
--motpar	Motion parameters- text file	
--brainmask	Functional brain mask in NIFTI format	
--motglm	GLM parameter estimates (GLM betas) for motion regression- text file	
--fsrecondir	Freesurfer recon directory	
--aseg	Freesurfer aseg file (used for segmentation)	
--regintermed		
--func2struct	Functional to structural transformation matrix (FSL FLIRT)	
--struct2func	Structural to functional transformation matrix (FSL FLIRT)	
--struct2mni	Structural to template transformation matrix (FSL FLIRT)	
--mni2struct	Template to structural transformation matrix (FSL FLIRT)	
--func2mni	Functional to template transformation matrix (FSL FLIRT)	
--mni2func	Template to functional transformation matrix (FSL FLIRT)	
--structuralcsf	Structural image CSF segmentation- binary mask in NIFTI format	
--structuralgm	Structural image GM segmentation- binary mask in NIFTI format	
--structuralwm	Structural image WM segmentation- binary mask in NIFTI format	
--boldgm	Functional image GM segmentation- binary mask in NIFTI format	
--boldwm	Functional image WM segmentation- binary mask in NIFTI format	
--boldcsf	Functional image CSF segmentation- binary mask in NIFTI format	
--boldcsfwm	Functional image CSF and WM segmentation- binary mask in NIFTI format	
--meants	Global mean time series- text file	
--meantsgm	GM mean time series- text file	
--meantswm	WM mean time series- text file	
--meantscsf	CSF mean time series- text file	

--meantscsfwm	CSF and WM mean time series- text file	

Example

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'
```