Tutorial: <http://surfer.nmr.mgh.harvard.edu/fswiki/FsFastTutorial>

Walkthrough: <http://surfer.nmr.mgh.harvard.edu/fswiki/FsFastFunctionalConnectivityWalkthrough>

[] Source the freesurfer environment:

export FREESURFER\_HOME=/Applications/freesurfer  
source $FREESURFER\_HOME/SetUpFreeSurfer.sh

export SUBJECTS\_DIR=/Users/caramazzalab/Desktop/Jess/Subjects

[] Set up the output type

export FSF\_OUTPUT\_FORMAT=nii.gz

[] Understanding the folder hierarchy <http://surfer.nmr.mgh.harvard.edu/fswiki/FsFastFunctionalConnectivityWalkthrough>



[] Setting up subject folder for RAW\_rest data

Initially

/Users/caramazzalab/Desktop/Jess/V1\_REST\_STUDY/dicomdir/S01/sample.dicom

Eventually:

/Users/caramazzalab/Desktop/Jess/V1\_REST\_STUDY/sessionS01/rest/ …

/Users/caramazzalab/Desktop/Jess/V1\_REST\_STUDY/sessionS02/rest/ …

/Users/caramazzalab/Desktop/Jess/V1\_REST\_STUDY/sessionS03/rest/ …

/Users/caramazzalab/Desktop/Jess/V1\_REST\_STUDY/sessionS04\_1/rest/ …

/Users/caramazzalab/Desktop/Jess/V1\_REST\_STUDY/sessionS04\_2/rest/ …

…

/Users/caramazzalab/Desktop/Jess/V1\_REST\_STUDY/sessionB01/rest/ …

/Users/caramazzalab/Desktop/Jess/V1\_REST\_STUDY/sessionB02/rest/ ...

[] Setting up the folder hierarchy

**Sample Code**:

dcmunpack -src dicomdir -targ sessionid -fsfast -run 3 bold nii.gz f.nii.gz -run 4 bold nii.gz f.nii.gz

**For you**:

cd /Users/caramazzalab/Desktop/Jess/V1\_REST\_STUDY/

dcmunpack -src dicomdir/B101 -targ sessionB101 -fsfast -run 1 rest nii.gz f.nii.gz

dcmunpack -src dicomdir/B101 -targ sessionB102 -fsfast -run 1 bold nii.gz f.nii.gz

Tried:

dcmunpack -src dicomdir/B101 -targ sessionB101 -fsfast

* Need input runs

dcmunpack -src dicomdir/B101 -targ sessionB101

* Need input runs

dcmunpack -src dicomdir/B102

**Step 3: preprocessing**

\*STEP 3: Pre-process your bold data using preproc-sess [preproc-sess](http://surfer.nmr.mgh.harvard.edu/fswiki/preproc-sess)

Sample command:

preproc-sess -s sessionid -fwhm 5 -surface fsaverage lhrh -mni305-2mm

For you:

preproc-sess -s sessionid -surface fsaverage lhrh -mni305-2mm

**More according to Ella’s directions**

<https://surfer.nmr.mgh.harvard.edu/fswiki/mkanalysis-sess.new>

mkanalysis-sess -polyfit 2 -hpf CutOffHz -mcextreg -nskip 2

More on the pipeline

\*STEP 4: Use fcseed-config to configure the parameters you wish to pass to your connectivity analysis.

Sample command: fcseed-config -segid 1010 -fcname L\_Posteriorcingulate.dat -fsd bold -mean -cfg mean.L\_Posteriorcingulate.config

This example will use the [FreeSurfer](http://surfer.nmr.mgh.harvard.edu/fswiki/FreeSurfer) cortical segmentation for the left posterior cingulate (segID: 1010, see $FREESURFER\_HOME/FreeSurferColorLUT.txt for more) as defined for this individual in aparc+aseg.mgz. For seed regions, we recommend generating the mean signal timecourse by using "-mean". Note that this does not perform any analysis, it just creates a text file with the configuration. You can include more -segid flags to include more regions (though it will create only one seed time course). NOTE: Once a config file is created it may be used for multiple sessions.

* V1 is #400

FULL DIRECTORY RESOURCE OF ALL COMMANDS:

<https://surfer.nmr.mgh.harvard.edu/fswiki/FsFast>

**Let’s go through the entire tutorial**

<http://surfer.nmr.mgh.harvard.edu/fswiki/FsFastTutorialV5.1/TutorialData>

/place/with/space = /Users/caramazzalab/Desktop/Jess/FsFast\_Tutorial

export TUTORIAL\_DATA=/Users/caramazzalab/Desktop/Jess/FsFast\_Tutorial

export FSF\_OUTPUT\_FORMAT=nii.gz

export SUBJECTS\_DIR=/Users/caramazzalab/Desktop/Jess/fsfast-tutorial.subjects

**To check information on timecourses**:

mri\_info --dim f.nii.gz  
mri\_info --res f.nii.gz

The first command results in '64 64 30 142'. This is the dimension of the functional data. Since it is functional, it has 4 dimensions: 3 spatial and one temporal (ie, 64 rows, 64 cols, 30 slices, and 142 time points or TRs or frames).

The second command results in '3.438 3.437 5.000 2000.000'. This is the resolution of the data, ie, each voxel is 3.438mm by 3.437mm by 5.000mm and the TR is 2000ms (2 sec).

* Of your dataL
  + 112 112 64 240
  + 2, 2, 2.2 2000
* TR: 2 seconds
* Voxel size: 2mm x 2mm x 2.2 mm
* Number of time points: 240

View the functional data with:

tkmedit -f f.nii.gz -t f.nii.gz

Click on a point to view the waveform at that point.

\*\*\* this actually worked!!

**To manually create .nii.gz from .dcm**

mri\_convert function … refer to dcm\_to\_nifti.sh in dicomdir/

**Finding data**

sess01/bold/001:

You will see many files there, but there are three important ones:

* fmcpr.up.sm5.fsaverage.lh.nii.gz - Left hemisphere of fsaverage
* fmcpr.up.sm5.fsaverage.rh.nii.gz = Right hemisphere of fsaverage
* fmcpr.sm5.mni305.2mm.nii.gz - Volume of fsaverage (MNI305 space) - for subcortical analyses

These are time series data, and their names indicate what has been performed on them:

* fmcpr - motion correction, per-run
* up - slice-timing correction using ascending
* sm5 - smoothed by 5mm FWHM (after resampling)
* fsaverage.lh - sampled on the surface of fsaverage left hemi
* fsaverage.rh - sampled on the surface of fsaverage right hemi
* mni305.2mm - sampled in the fsaverage (MNI305) volume at 2mm isotropic