

## Squirrel monkey Varian data pre-processing steps:

### Requirements:

1. Matlab18 above.
2. Install spm12 & FSL
3. Matlab machine learning toolbox
4. Install functional connectivity analysis tool (FCAnalysis(VUIIS)) an in-house software package compatible to SPM12 GUI. Folder contents vuTools and spm\_antimode.  
(These package runs on Mac, however, can be installed on Windows.)

### Instructions to run:

1. The code *readVarian\_data.m* convert Varian data (.fdf) to 4D nifty file. In case data is stored in 4D (.nii/.nii.gz). The pre-process data (post motion and slice time correction) is stored as *ring4D.nii*.
2. Run code *reg\_fnstSampleFSL4.m* to register fMRI and pre-process the data.
3. In case user need to regress out the muscle and CSF signal as confounding parameters draw mask o anatomic image. The sample data is provided to test the pre-processing of the fMRI data

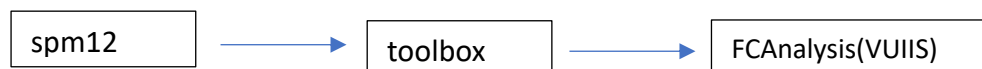
### Output files:

1. *.fdf/img4D.nii* – raw image
2. *ring4D.nii* – (stored image after deleting initial time points)
3. *prep\_img4D.nii*-(pre-processed image)
4. *snrRaw.nii* (raw SNR)
5. *snrReg.nii* (SNR post motion correction)
6. *snrLpf.nii* (SNR post low pass filtration)
7. *med\_img.nii* (median fMRI image)
8. *rmed\_img.nii* (preprocessed median image)

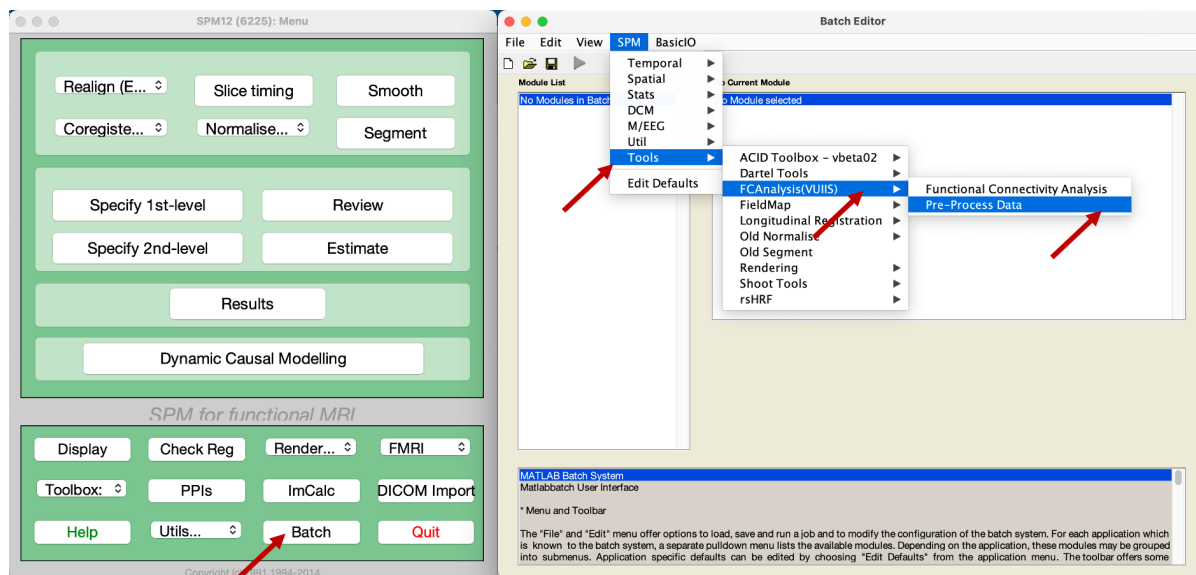
## Data process:

1. Code *reg\_fnstSampleFSL4.m* initiates data processing and registration in two stages. The toolbox needs to be installed before you run the code as two batch process are done before and after the median fMRI data is registered to the anatomic image using SPM12 and FSL from the command window. The batch files below does the stimulus and resting state connectivity analysis.
2. *prepS1sample.mat* (stimulus)
3. *prepS2sample.mat* (stimulus)
4. *prep1sample.mat* (resting)
5. *prep2sample.mat* (resting)
6. *restSample.mat*
7. *stimSample.mat*

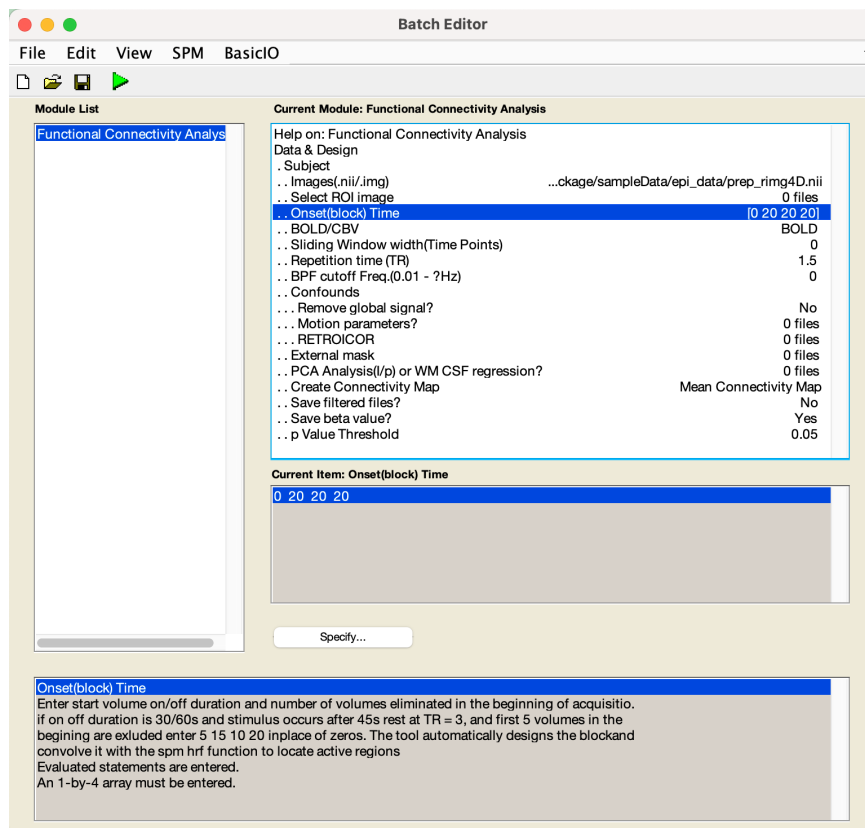
Unzip toolbox FCAnalysis(VUIIS) and save into SPM12



Type spm fmri in the command window and click on Batch



Click on arrows in a sequence (left to right) it will take you to data entry folder below. A short manual will appear in the window below describing type and requirement. The pre-processing of the data is crucial for both stimulus and resting data, which also include physiological signal correction done in the first step (physiological signal file-Gems.physiol). Below is the GUI for stimulus data analysis, user can also do part of pre-process here if the data is already registered to the anatomic image.



As described in the manuscript resting state data analysis should be performed following the stimulus analysis as the layer specific ROIs are needed to be defined beforehand. PSF dimensions in both cases are acquired of the t-map/beta maps (spmT\_0001/beta\_0001/Bstim/PsigC.nii) for stimulus data or correlation/zscore maps (MnCvt\_ar3b/ZMnCvt\_ar3b.nii) using code *defPSF\_parm.m*. This code outputs the major and minor axis of the gaussian fitted point spread function.

This code (*defPSF\_parm.m*) generates the PSF dimension in each layer for further statistical analysis along with contour plots. User interaction is needed to roughly identify the stimulated voxel/ROI in the resting state data.

*layerANOVA.m* performs the statistical analysis given the estimated parameters/output results stored in the .mat file.

*somAnalysis.m* Self organizing map-based classification of layers based on stimulus (2-layer) and resting (3-layer) PSF parameters.