

# rsfMRI denoising SOP

This SOP is written by Chun-Wei and checked by Josh in 2022/06/XX.

## Preprocessing

Note 1) This preprocessing SOP is specifically meant for those who are running experiments with **32-channel head coil** in **spm12**. For those running experiments with 64-channel, multi-band, or in other spm versions, some steps might require different set-up, and please do double-check the steps and parameters with Josh.

Note 2) Before doing this denoising step, please check the “**Functional Connectivity SOP**” created by Yi-Chung for preprocessing, including **coregister**, **realignment**, and **slice timing**. That is, your current data should be ready for 1<sup>st</sup> level analysis.

Note 3) The technique, anatomical CompCor (aCompCor) first presented by [Behzahi et al. \(2007\)](#) is used in this SOP. It is based on the observation that the BOLD signal in white matter (WM) and cerebrospinal fluid (CSF) is not neuronal in origin. Thus, the variation shared between gray matter and WM/CSF should be artifactual (e.g., due to motion, heartbeat, respiration, scanner drift). The aCompCor regresses the top few principal components (PCs) within WM and CSF to remove the noise.

Note 4) This SOP performs aCompCor in **PhysIO Toolbox** as part of **TAPAS software** (<https://github.com/translationalneuromodeling/tapas/tree/master/PhysIO>), which is integrated with the SPM Batch Editor. Please follow the instruction of the link to install PhysIO toolbox in the Matlab. After installing PhysIO toolbox in the Matlab, you can find **TAPAS PhysIO Toolbox** from **SPM > Tools** in the Batch Editor.

Note 5) The parameters not mentioned below are set to be default.

### 1. TAPAS PhysIO Toolbox

Note) Setting the log file names to empty values. The modules are ignored if no log\_files are specified.

1) > **save dir**: Apply the directory you wish the denoising result to be produced at.

2) > **scan timing > sqpar**

a) > **Nslices**: Number of slices (e.g., 38)

b) > **TR**: TR (e.g., 2)

c) > **Nscans**: Number of scans/volumes (e.g., 180)

d) > **onset slice**: Slice to which regressors are temporally aligned (e.g., 2)

Note) Please refer to the > **Reference slice** during slice timing

3) > **model**

a) > **output multiple regressors**: Output file name for physiological regressors (Default: multiple regressor.txt)

b) > **output physio**: Output mat-file name for physio-structure (Default:

- physio.mat)
- c) > **RETROICOR**: No
- d) > **Noise ROIs model**: Yes
  - i) **fMRI Time Series File(s)**: Apply ar\*.nii 4D image (i.e., images after realignment and slice timing)
  - ii) **Noise ROI Image File(s)**: Apply c2\*.nii (white matter mask) & c3\*.nii (CSF mask) in subject space
  - iii) **Force Coregister: Estimate & Reslice of the noise ROIs**: Yes
  - iv) **ROI thresholds**: 0.95
  - v) **Number of ROI pixels to be cropped**: 0
  - vi) **Number of principal components**: 5
- e) > **Movement**: Yes
  - i) **Realignment Parameter File**: Apply rp\*.txt (motion regressor produced during realignment)
  - ii) **order**: 12
  - iii) **Censoring Method for Thresholding**: none
- 4) > **verbose**
  - a) > **level**: 1
  - b) > **fig output file**: File name for regressor matrix figure (e.g., physio\_output\_figure.ps)

## 2. Specify 1<sup>st</sup>-level (fMRI model specification)

- 1) > **Directory**: Apply the directory you wish the denoising result to be produced at.
- 2) > **Timing Parameters**
  - a) > **Units for Design**: Seconds
  - b) > **Inter-scan interval**: TR (e.g., 2)
  - c) > **Microtime resolution**: Number of slices (e.g., 38)
  - d) > **Microtime onset**: 2

Note) Please refer to the > **Reference slice** during slice timing
- 3) > **Data & Design > Subject/Session**
  - a) Create sessions as many as the runs you have. And then for each session:
  - b) > **Scans**: Apply \*ar.nii images of each run to each session.
  - c) > **Multiple conditions**: Apply soa\*.mat of each run to each session.  
Note) if the conditions are not that complicated, manually apply the condition into > **Conditions**.
  - d) > **Regressors > Multiple regressors > Dependency**: Choose "TAPAS PhysIO Toolbox: physiological noise regressors file (Multiple Regressors)"

## 3. Estimate (Model estimation)

- 1) > **Select SPM.mat > Dependency**: Choose "fMRI model specification: SPM.mat File"
- 2) > **Write residuals**: Yes  
Note) After producing all the residuals, organize them into folders that only contain residuals of each run in order to run detrend and bandpass filter. Please check the "Functional Connectivity SOP" created by Yi-Chung for the rest of analysis.