This is a technical note for the analysis regarding the NeuroImage paper “The Subsystem Mechanism of Default Mode Network Underlying Rumination: a Reproducible Neuroimaging Study”. We have shared all the neuroimage data and behavioral data in this paper. This note is intended to help you reproduce our analysis.

Xiao Chen, Ph.D.

IPCAS

[chenxiaochina@hotmail.com](mailto:chenxiaochina@hotmail.com)

1. Preprocessing

This dataset contains 3 sites: IPCAS, PKUGE, PKUSIEMENS. Each site contains 2 sub-paths: rest and task.

The path “rest” consists of the resting state session and should be preprocessed as any typical resting state data. You may load the “DPARSFA\_IPCAS\_rest\_step1.mat”, “DPARSFA\_IPCAS\_rest\_step2.mat”and “DPARSFA\_IPCAS\_rest\_step3.mat” with DPARSFA sequentially to get the final results. Setp1 will preprocess the dataset with the default setting of DPARSFA. Setp2 will smooth the “FunImaARCWF” folder; Step3 will use the smoothed “FunImgARCWFS” to calculate the functional connectivity matrix. Note that:

1. The working directory should be changed accordingly;
2. The .mat file set the .mat files pre-loaded. You need to do the reorient yourself;
3. The ROI setting in step3 may not be compatible to your situation. You may need to load the 24 ROIs in the “DMN\_ROI” folder you downloaded from Github.

Similarly, the path “task” contains three .mat files. In addition, the “Event\_Regressor.txt” file is also needed in the task pipeline. You may need to change the path of “other covariates” in step1 according to your path of “Event\_Regressor.txt”.

For PKUSIEMENS, you should further copy the “SliceOrderInfo.tsv” and all “Sub\*\*\*SliceOrder.txt” files into your working memory. This was to deal with the multi-slice data. All the Sub\*\*\*SliceOrder.txt” files were generated with ~/scripts/ ReadSliceOrder.m

1. FC statistics

~/scripts/FC\_stats4Pub.m conducted all FC stats.

1. Questionnaire statistics

~/scripts/Questionnaire\_stats.m conducted all stats in terms of questionnaire scores.

\*Important note for reproducibility.

All analysis in the publication was conducted with DPABI\_V3.0 version. With this version, you should get the same results as we reported in the paper. However, due to the potential differences regarding operating system and software environment, the exact number may be slightly different.

You may wish to do all these analysis with the newest version of dpabi. Under this circumstance, the results may differ larger from the results we reported in the paper. Please note the impact of all the improvements in software and preprocessing guidelines as the field moving forward. For details on this issue, please refer to Carp (2012) and Esteban et al. (2019).

References:

Carp, J., 2012. The secret lives of experiments: Methods reporting in the fMRI literature. Neuroimage 63, 289-300.

Esteban, O., Markiewicz, C.J., Blair, R.W., Moodie, C.A., Isik, A.I., Erramuzpe, A., Kent, J.D., Goncalves, M., DuPre, E., Snyder, M., Oya, H., Ghosh, S.S., Wright, J., Durnez, J., Poldrack, R.A., Gorgolewski, K.J., 2019. fMRIPrep: a robust preprocessing pipeline for functional MRI. Nat Methods 16, 111-116.