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Rodent Whole-Brain fMRI Data Preprocessing Toolbox

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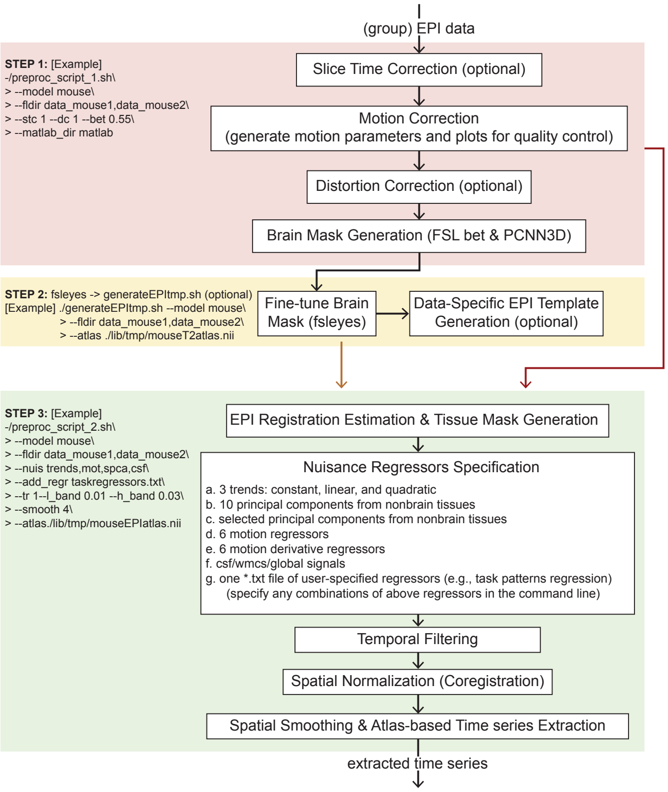
Rodent Whole-Brain fMRI Data Preprocessing Toolbox is a generally applicable and user-friendly functional magnetic resonance imaging (fMRI) preprocessing toolbox for whole-brain group datasets in rodents. Preprocessing of rodent fMRI data is challenging when using toolboxes designed for human data, so this toolbox contains procedures and parameters that are specific for mice and rats. It provides the standard preprocessing procedures for preprocessing rodent brains as described in Chuang et al. (1) and Lee et al. (2). It normalizes the group datasets to a standard template and then extracts time series based on an atlas. Different from the existing preprocessing pipelines, which are applicable only for a single animal model [e.g., either rats (3, 4) or mice (5)], this is the first software toolbox that is generalized for both mouse and rat group data. This is also the first software toolbox that allows a variety of combinations of preprocessing procedures and parameters that are specified by users depending on the applications. Moreover, a user-specified repressors file can be added for task pattern regressions in addition to the classical detrending, motion parameters, brain tissue or noise regressions, etc. (see Figure 1).

This software toolbox and a comprehensive user manual are available at https://github.com/GT-EmoryMINDlab/rodent-whole-brain-preprocessing-recipe. A Linux or Mac system with FSL5.0 (6), AFNI (7, 8), advanced neuroimaging tools (ANTs; 9, 10), and MATLAB (R.2018a or a later version) installed is required. For Windows systems, it is also possible to install these packages through a Windows Subsystem for Linux (WSL; see "SoftwareInstallation_fsl_afni_ants.txt" for more details), which is less preferable due to the lack of broad usages and support. Sample datasets for both



STEP 1: [Example]

```
-/preproc_script_1.sh\
> --model mouse\
> --fldir data_mouse1,data_mouse2\
> --stc 1 --dc 1 --bet 0.55\
> --matlab_dir matlab
```

STEP 2: fsleyes -> generateEPItmp.sh (optional)

```
[Example] ./generateEPItmp.sh --model mouse\
          > --fldir data_mouse1,data_mouse2\
          > --atlas ./lib/tmp/mouseT2atlas.nii
```

STEP 3: [Example]

```
-/preproc_script_2.sh\
> --model mouse\
> --fldir data_mouse1,data_mouse2\
> --nuis trends,mot,spca,csf\
> --add_regr taskregressors.txt\
> --tr 1--l_band 0.01 --h_band 0.03\
> --smooth 4\
> --atlas./lib/tmp/mouseEPIatlas.nii
```

Fig. 1. The pipeline for rodent brain fMRI group data processing.

rat and mouse and the frontier atlases, including a modified Allen Institute for Brain Science mouse atlas (11) and the SIGMA rat template (12), are provided in the library folder of the software package. A video tutorial for using this toolbox is also available at https://youtube.com/playlist?list=PLzI6IxEF9yCb3i0Coc5noXWzINKqWXTOd.

This preprocessing toolbox enables the group analysis of rodent brains, which is critical for understanding the general brain dynamics of rodents. Notably, a variety of combinations of signal regression options have been compared and discussed in detail for rodent brains (1). Following the preprocessing procedures recommended in Chuang et al. (1), this preprocessing toolbox has been tested on 5 different fMRI group datasets of rodent whole brains with different imaging and experimental settings, including 3 rats groups (13–15) and 2 mice groups (2, 16). Decent functional connectivity maps and quasiperiodic dynamic patterns (17) were successfully obtained in our postanalysis using the preprocessed time series as illustrated in Figure 2.

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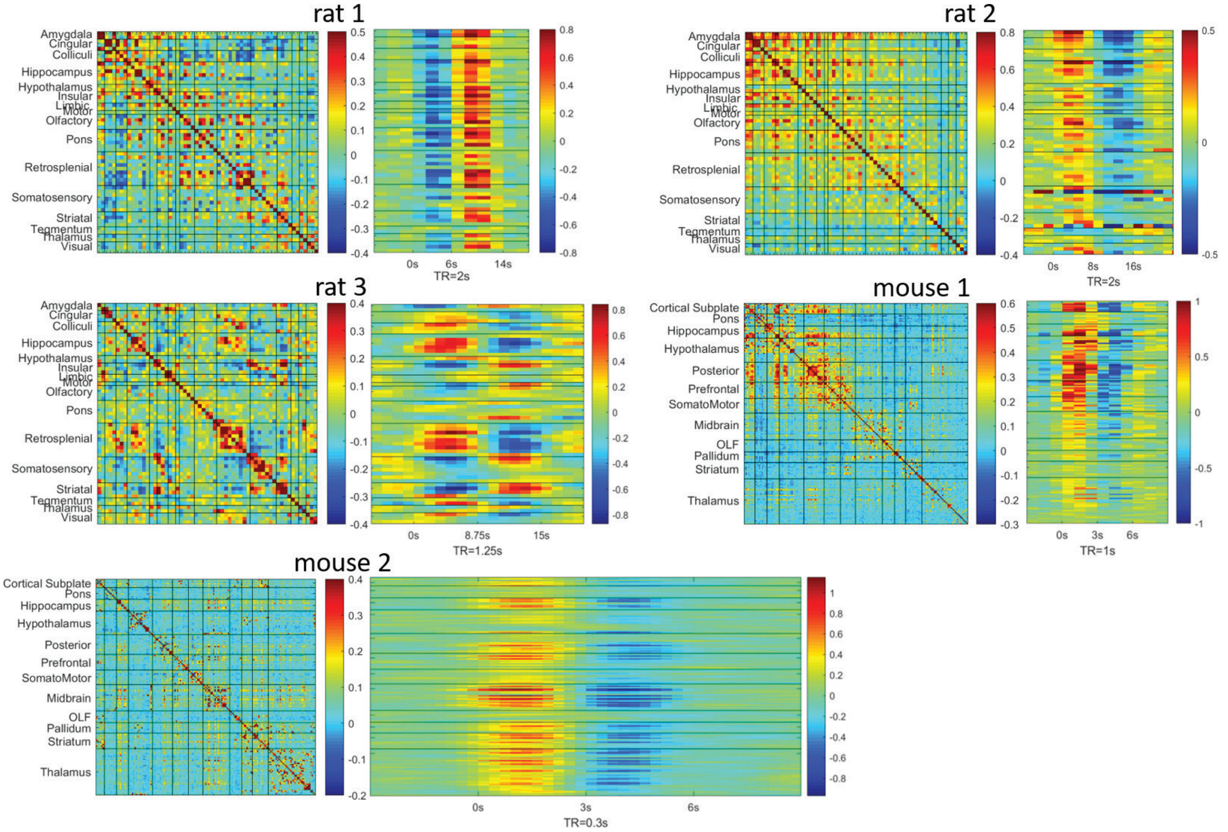

Fig. 2. Functional connectivity maps (left) and quasiperiodic dynamic patterns (right) obtained from the preprocessed rodent brains for 5 rodent datasets. Three rat groups include a dataset of 8 rats (rat 1) recorded in Pan et al. (14, 15), a dataset of 1 rat scan (rat 2) provided by Dr. Annabelle Singer's laboratory at the joint Georgia Tech/Emory University Biomedical Engineering Department, and a dataset of 3 rat scans (rat 3) presented in Anumba et al. (13). Two groups include a dataset of 3 mouse scans (mouse 1) randomly selected from the open dataset published in Grandjean et al. (16), and a dataset of 8 mice (mouse 2) recorded in Lee et al. (2). Fully covered brain parcels were selected and reorganized into the functional systems for generating the functional connectivity maps and quasiperiodic dynamic patterns. Note that the window length of the quasiperiodic dynamic patterns (in secs) is similar across different datasets of the same animal model. However, due to the different TR values, the quasiperiodic dynamic pattern of different datasets may have different timepoints. For example, a dataset with a small TR such as mouse 2 has more timepoints in its quasiperiodic dynamic pattern.

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