

Practical 2: task-fMRI Preprocessings

Functional magnetic resonance imaging (fMRI) is a technique for measuring brain activity. It works by detecting the changes in blood oxygenation and blood flow that occur in response to neural activity.

This practical will guide you through key concepts for running and interpreting task fMRI preprocessings.

Part 1: You will learn how to preprocess your functional data using a volume-based approach.

Part 2: You will learn how to project your preprocessed data on the cortex to perform surface-based tfMRI analyses.

Exploring the Human Brain: tfMRI Hackathon
10 October 2018

Practical 2: task-fMRI Preprocessings

Before you start

An Ubuntu 16.04LTS container is available with all the practical required softwares installed. Please follow the **Setup: User Guide** tutorial to activate this container.

Part 1: Preprocessings your data

1. We will use the **pyprocess** (<https://github.com/neurospin/pyprocess>) package to preprocess the raw functional data.
2. This package provides common helper tools build over common softwares: FSL, SPM, ...
3. We will learn how to use this package using the provided notebook. Issue the following command line to start:

```
$ jupyter notebook $HOME/notebook/tfmri_spm_preproc.ipynb
```

Part 2: Toward the cortex

If you are working with large cohort this part may not be relevant for your study and you can directly refer to the volume-based first level analysis tutorial. Otherwise it may help to refine the analysis results.

Not mandatory but highly recommended is to run [FreeSurfer's recon-all](https://surfer.nmr.mgh.harvard.edu/fswiki/recon-all) process on the anatomical scans to retrieve the cortical information. recon-all is FreeSurfer's cortical reconstruction process that automatically creates a parcellation of cortical and a segmentation of subcortical regions. A more detailed description about the recon-all process can be found on the official homepage: <https://surfer.nmr.mgh.harvard.edu/fswiki/recon-all>.

Don't change the FreeSurfer's recon-all process output organization, because many of FreeSurfer's other algorithms will rely on this organization. The only negative point about recon-all is that it takes rather long to process a single subject. The average times are between 7-12h, but it is also possible that the process takes up to 48h.

The only thing that you need to keep in mind is to tell your system the path to the FreeSurfer folder by specifying the variable SUBJECTS_DIR.

Note

Depending of the input image resolution you may add the *highres* and *expert* command line arguments (<https://surfer.nmr.mgh.harvard.edu/fswiki/SubmillimeterRecon>).

Then using FreeSurfer other algorithms, it is possible to project the functional volume on the cortex, to smooth the functional time series on the surface, and finally to generate a subject vertex-to-vertex mapping useful during the group analysis. During the projection, we average the functional time series over the ribbon.

In the following Python notebook we will show you how to:

1. launch recon-all on all the subjects in parallel (you need to check if you have enough memory).
2. apply common FreeSurfer algorithms to retrieve a preprocessed function surface.

```
$ jupyter notebook $HOME/notebook/tfmri_freesurfer_surface.ipynb
```