

fMRI univariate data analyses with SPM

C. Pallier

We follow closely chapters 30 to 32 of SPM12's manual.

First example: single subject auditory data set

If SPM12 is not installed on the computer, download it from <http://www.fil.ion.ucl.ac.uk/spm/software/spm12/> and unzip it.

Go to the page <https://www.fil.ion.ucl.ac.uk/spm/data/auditory/>, download the dataset <https://www.fil.ion.ucl.ac.uk/spm/download/data/MoAEpilot/MoAEpilot.zip> and unzip it in a working directory (e.g. Desktop)

Open SPM12 manual on Chapter 30 (starting on page 221)

1. Start Matlab and type:

```
addpath path-to-spm12-folder spm fmri
```
2. Click on **Display** and open the image `sM00223/sM00223_002.img`. Click on the sections to move in the brain
3. Click on **Display** and open `fM00223/fM00223_004.img`. This is an EPI (functional) image.

Instructor only: `fslview auditory-epi.nii.gz`

5. Follow the instructions from Chapter 30 of SPM12 manual
 - delete scans 4 to 15 (“dummy scans”) from `fM00223` folder
 - perform preprocessing:
 - spatial realignment of functional images
 - coregistration of anatomy to mean functional image
 - segmentation of the anatomy in gray and white matter
 - spatial normalisation of (1) functional images (2) anatomy
 - smoothing of functional images
 - perform statistical analysis
 - specify first level model
 - estimate model
 - results
 - * Create contrast listening with value ‘1’

- * Use FWE .05 threshold.
- * Use overlay/sections to project on normalized anatomy wmsM00223_002.nii
- * Press 'Whole Brain' to get statistics.
- * go to an activated voxel, press plot/fitted response/adjusted response/against scan or time
- * Change the threshold to $p < 0.01$ uncorrected, $p < 0.001$ uncorrected and the $p < 0.05$ FWE

Second Example: face repetition fMRI data single subject

We are going to analyse to data set face_rep.zip from http://www.fil.ion.ucl.ac.uk/spm/data/face_rep/

Briefly, greyscale photographs of 52 famous and 52 nonfamous face were presented for 0.5s for fame judgment task. Each photograph was presented twice during the experiment. The author is interested in comparing the effect of repetition on famous and nonfamous faces.

The full data analysis is described in chapter 31 of SPM12's manual (page 243).

1. I have already performed the preprocessing; You can download the obtained files from http://www.pallier.org/ressources/Brain-imaging-methods-MBC-UPF-2017/SPM/face_rep_preprocessed.zip
2. Use the button "check reg" to display the normalized anatomy (wmsM03953_0007.nii) and one of the smoothed functional scan.
3. create a `categorical`` subfolder in theface_rep' folder.
4. Go to section 31.2 p.253 of the SPM12 manual and follow the instructions to create the categorical model BUT choose 'canonical (no derivative)' in Basis Functions.
5. Use Results and inspect the following contrasts in face_rep/categorical/SPM.mat
 - '1 1 1 1' (positive response of stimulation)
 - '1 -1 1 -1' (repetition effect: N2 F2 > N1 F1)
 - '1 1 -1 -1' (unknown > famous)
 - '-1 -1 1 1' (famous > unknown)
 - '-1 1 1 -1' (interaction: repeton for famous > repetition for unknown)
 - '1 -1 -1 1' (interaction: repeton for famous < repetition for unknown)
6. (Optional) Redo the analysis proposed in the manual (include derivative and dispersion in the basis functions)

Third example: face fMRI data on 12 subjects

We are going to perform the analysis of face data on 12 subjects. See chapter 32 of SPM12 manual.

The dataset http://www.pallier.org/ressources/Brain-imaging-methods-MBC-UPF-2017/SPM/face_rfx/cons_can/

provides the individual contrast map ‘Faces > Baseline’ for 12 participants.

To see which area is significantly activated at the group level, Create one sample t-test model inputting all the contrasts in face_rep/cons_can (section 32.3 p. 272 of the manual).

Create and visualize the contrast ‘1’ to average individual contrasts.