

## Lesson 05: fMRI - Processing using SPM

### 1. Data organization:

1. Use the dataset given in lesson 05. The dataset includes scans of a single subject in .nii format in two folders:
  - a. An anatomical scan (a single volume)
  - b. two runs of a functional scan with the following scan parameters
    - i. TR = 2.5 sec
    - ii. Slices = 40
    - iii. Slice order = [ 2:2:40 , 1:2:40 ]
    - iv. In plane resolution 1.7188 x 1.7188 mm
    - v. Volumes in each run = 20
    - vi. Interslice times = 76ms
    - vii. Slice thickness 4mm , 0mm gap

### 2. SPM:

1. Add the SPM12 directory to your Matlab path using `addpath`
2. Run SPM by typing `spm_fmri` in the command line
3. Use the “Display” and “Check Reg” buttons to look at different NIfTI files (anatomical and functional)

### 3. Motion correction:

Perform motion correction for the functional dataset:

- a. Select option in SPM menu: Realign (Estimate & Reslice)
- b. Follow the instructions and fill in the different options
  - i. Select your data – add a new session and then specify for the session all volumes in the functional folder (files in \*.nii format)
  - ii. Keep most of the options on default
  - iii. Examine the ‘Num passes’ and ‘interpolation’ options
- c. In the file menu on top choose view → show .m code (or CTRL+S)
- d. Copy the code to a new matlab script in matlab editor window and save it under `motion_correction.m`
- e. Add the following command to the end of the script:

```
spm_jobman('run' , matlabbatch);
```
- f. Save and run the script. SPM will perform the motion correction
- g. Write a functions that gets a directory name and perform the motion correction step on all files within this directory with the same parameters as you ran in the previous step. Run your function to make sure it works!

- i. Use the given helper function `get_session_data.m` that returns a cell of strings of all file names in a given folder in a format suitable for the `data\volumes\images` part for the `matlabbatch` struct.

#### 4. Slice time correction:

Perform slice time correction for the functional dataset

- a. Select option in SPM menu: Slice timing
- b. Follow the instructions and fill in the different options
  - i. Select your data – add a new session and then specify for the session all volumes in the functional folder that went through realignment procedure (files in `r*.nii` format)
  - ii. Use the scan parameters on the first page to input the data here
  - iii. For slice order use the order as a formula (see scan settings)
  - iv. For reference slice (what we will align all slices to) use the first slice – (e.g. slice #2).
- c. In the file menu on top choose view → show .m code (or CTRL+S)
- d. Copy the code to a new matlab script in matlab editor window and save it under `slice_time_correction.m`
- e. Add the following command to the end of the script:
 

```
spm_jobman('run', matlabbatch);
```
- f. Save and run the script. SPM will perform the slice time correction
- g. Write a functions that gets a directory name and perform the motion correction step on all files within this directory with the same parameters as you ran in the previous step. Run your function to make sure it works!

#### 5. Coregister functional images to anatomical image:

Perform slice time correction for the functional dataset

- a. Select option in SPM menu: Coregister (Estimate & Reslice)
- b. As the reference image – choose the volume anatomical .nii
- c. As the source image choose the mean image created during realignment (starts with “mean”)
- d. Other – choose all the ‘`ar*.nii`’ images.
- e. Follow steps in previous sections to create a script for coregistration
- f. Run the coregistration script. SPM will reslice them by adding the prefix ‘`r`’ to existing ‘`ar`’ files (that have been already realigned and slice time corrected)

- g. Run 'check reg' as explained above and see how well the co-registration worked. Track anatomical landmarks such as the ventricles and the outline of the visual cortex– and make sure that the two images are aligned.
  - h. Write a functions that perform the motion correction step with the same parameters as you ran in the previous step. The function should be given the following variables:
    - i. Full path and name of the anatomical .nii file
    - ii. Full path and name of the mean functional .nii file
    - iii. A full path of the directory of all functional images
    - iv. The prefix of the functional images file names.
- Run your function to make sure it works!

## 6. Normalization

Perform Normalization of all images, including functional, mean and anatomical images

- a. Choose 'Normalize(Estimate & Write)'
  - b. Add a new subject
  - c. Enter the anatomical image as 'Image to align'
  - d. Enter all functional files that went through previous procedures (rar\*.nii) as 'Images to write'
  - e. Set all other options to the default value.
  - f. Create a script and run it to start normalization
  - g. Write a functions that perform the motion correction step with the same parameters as you ran in the previous step. The function should be given the following variables:
    - i. Full path and name of the anatomical .nii file
    - ii. Full path and name of the mean functional .nii file
    - iii. A full path of the directory of all functional images
    - iv. The prefix of the functional images file names.
- Run your function to make sure it works!

## 7. Smoothing

Perform Smoothing over of all functional images

- a. Choose 'Smooth'
- b. Enter files in 'Images to smooth' - all functional files that went through previous procedures (wrar\*.nii)
- c. Set FWHM to be [2 2 2]
- d. Set all other options to the default value.
- e. Create a script and run it to start smoothing

- f. Write a functions that gets a directory name and perform the motion correction step on all files within this directory with the same parameters as you ran in the previous step. Run your function to make sure it works!

## **8. Scripts**

Write a script that performs all preprocessing stages. The script should call the functions you wrote in the previous parts of your exercise.