fMRI Workshop

day 1 - preprocessing

NeuroSpin February 14th, 2023

Planning of the day 1

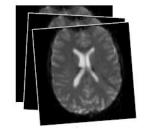
Morning - some theory
Afternoon - practice, exercises

- Introductory presentation of fMRI data and preprocessing
- Introduction to quality checks
- SPM12 demo
- bids organization
- fMRIPrep

What is a BOLD functional image?

Temporal series of 3D images:

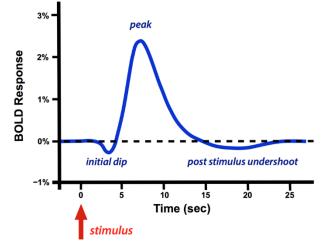
 $T_R \approx 1$ s to 4s (repetition time)



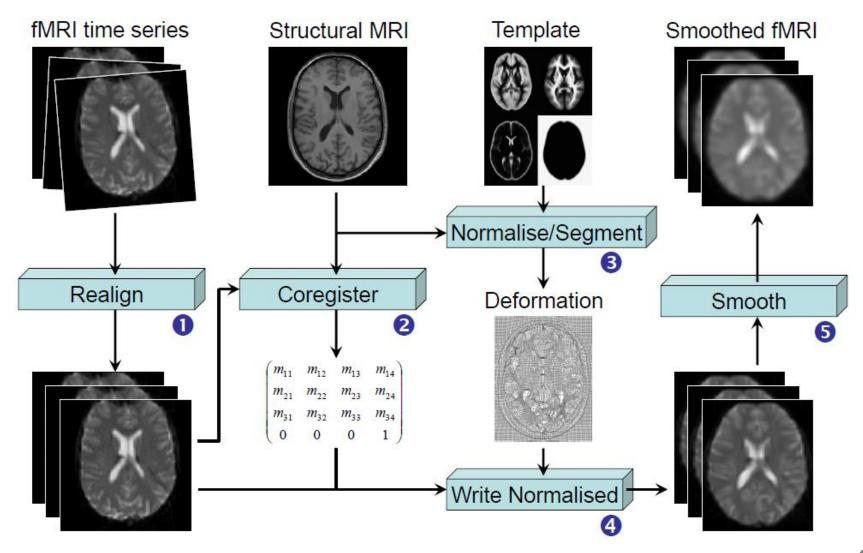
- Each 3D image = set of 2D slices acquired by an EPI sequence (echo-planar imaging)
- The slices are acquired sequentially or interleaved
- BOLD (*blood oxygen level dependent*) contrast: variation of T₂* due to the variation of iron concentration (oxyhemoglobin/deoxyhemoglobin)

- The BOLD contrast is linked to the neural activity by the hemodynamic

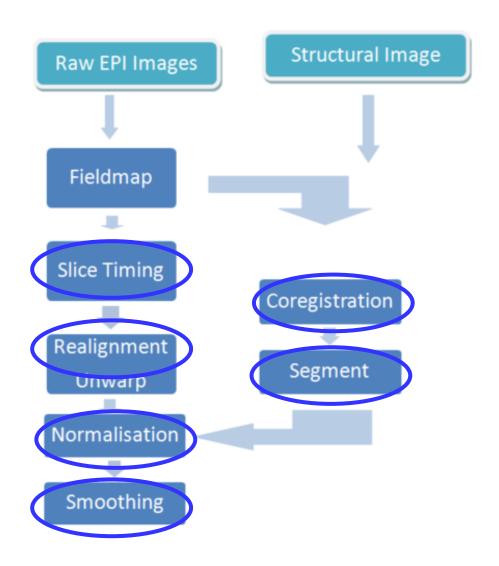
response function (H



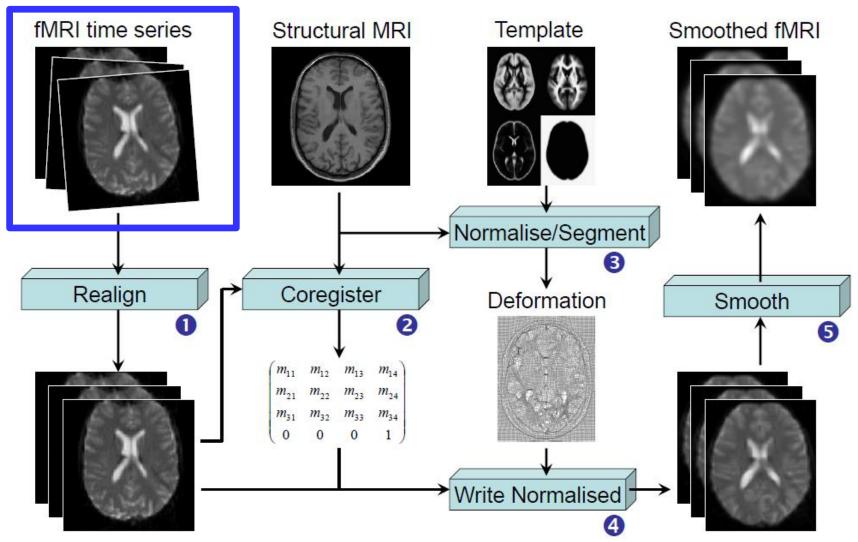
General steps of preprocessing



Some steps of preprocessing: slice timing, realignment, coregistration, segmentation + normalization, smoothing



Some steps of preprocessing: slice timing



Some steps of preprocessing: slice timing

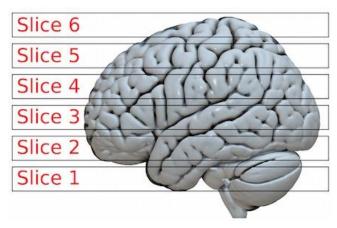
Used to correct (i.e., equalize) differences in the time when individual slices are recorded (the slices of a volume are not acquired simultaneously)

→ duration of the acquisition of a volume = T_R

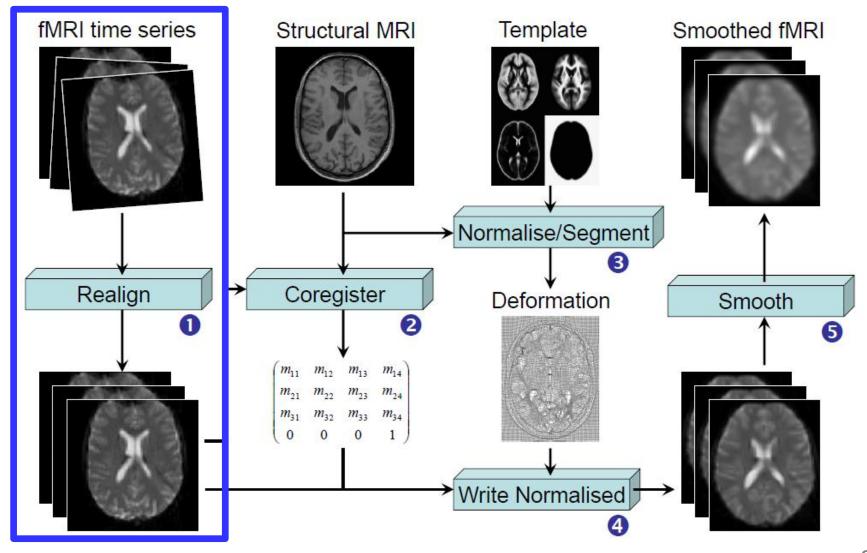
A functional volume (e.g. whole brain) is usually not covered at once but with a series of successively measured 2D slices. For example: for a functional volume of 30 slices and a T_R of 3 seconds, the data of the last slice is measured almost 3 seconds later than the data of the first slice.

Debate:

- Is slice timing necessary? Tip: this step is not necessary if the T_R is of the order of the second.
- Before or after movement correction?



Some steps of preprocessing: realignment (movement correction)



Some steps of preprocessing: realignment (movement correction)

Used to match spatially fMRI 3D images.

Corrects head movement in the scanner.

Relies on 3 translations (moving the image in X, Y, or Z direction) and 3 rotations (over the X, Y, and Z axis): 6 parameters (confounds) - rigid registration of each temporal step on a reference image

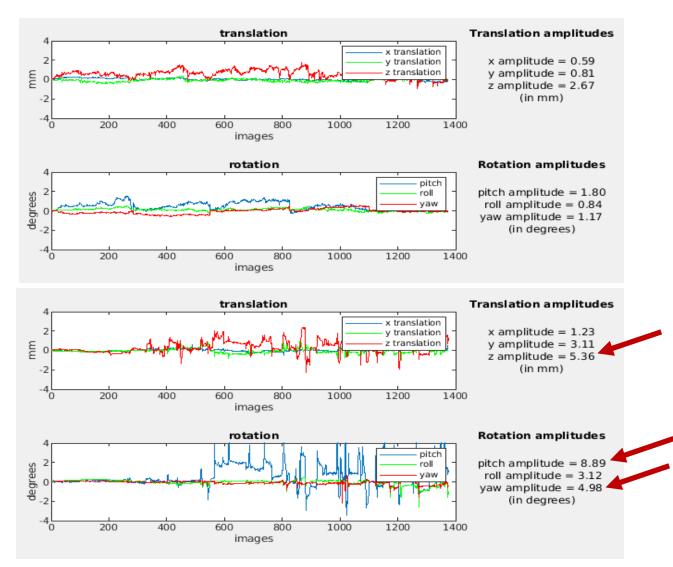
Tries to find the manipulation that minimizes the difference between two scans.

Images interpolation for correcting the position of measures.

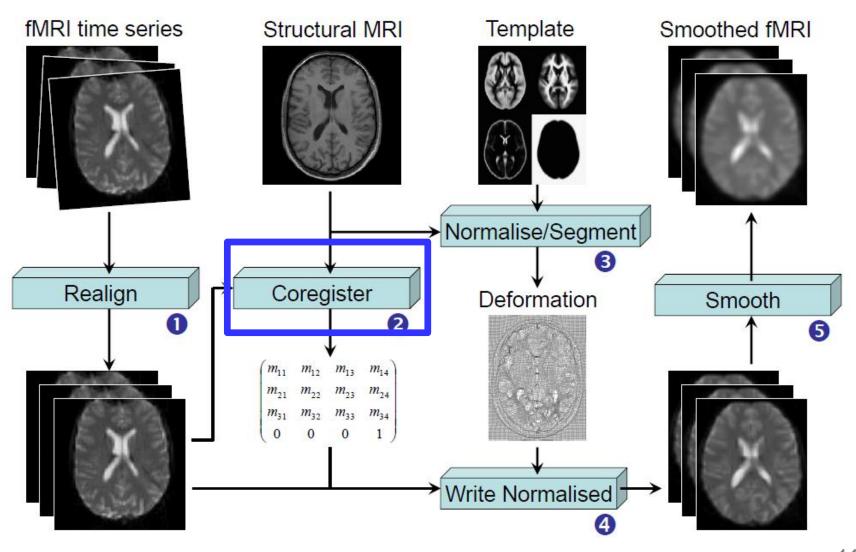
BUT movement has an effect on the signal value (*spin history effect*)

! Exclusion of data: if movement is too important

Some steps of preprocessing: **realignment (movement correction)**Examples of movement curves:



Some steps of preprocessing: coregister



Some steps of preprocessing: coregister

The Coregister function is used to match scans of different modalities, for instance, anatomical (T1) and functional (EPI) images.

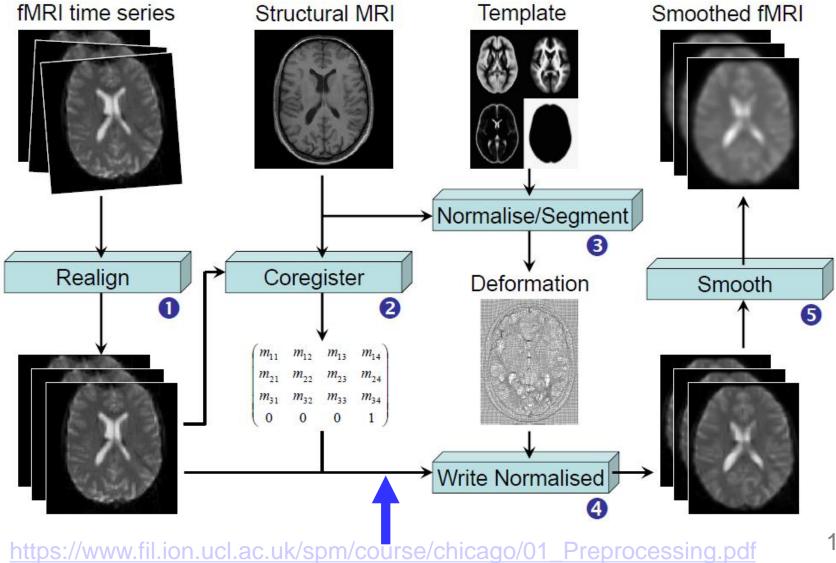
Cost function used: Mutual Information

Even when acquired in the same session, the functional and structural scans need to be coregistered. Subjects indeed often move quite a lot between runs. This is a within-subject (rigid-body transform), between-modality (the images have inverted contrasts, amongst other differences) problem.

Transformation:

BOLD fMRI images → anatomy T₁

Some steps of preprocessing: distortion correction



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Some steps of preprocessing: distortion correction

- Cause of the distortions: inhomogeneities in the magnetic field due to interfaces of magnetic susceptibility (air-filled cavities, auditory conducts)

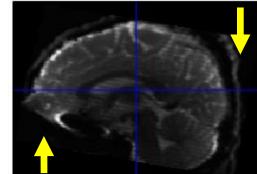
- Geometrical compression/expansion on the phase encoding direction

(AP = Anterior-Posterior, PA = Posterior-Anterior)

Possible correction methods:

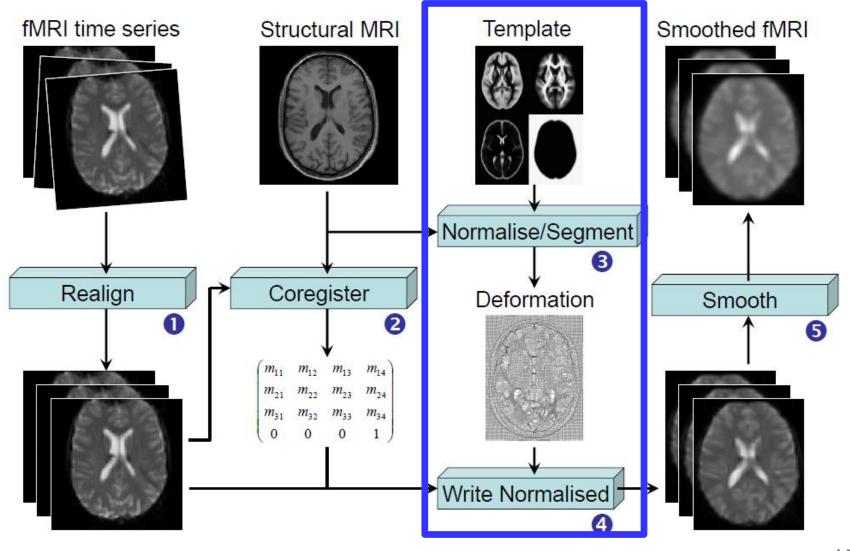
- B0 map
- TOPUP: 2 acquisitions with opposing polarities of the phase
- Non-linear registration on the anatomy
- No correction (pediatrics)

AP



PA

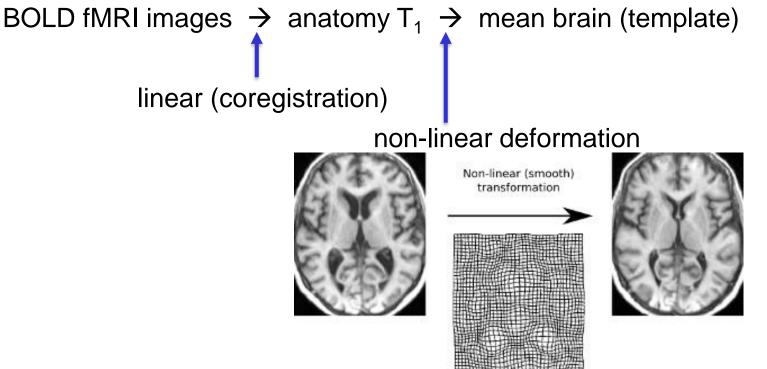
Some steps of preprocessing: **segmentation + normalization**



Some steps of preprocessing: **segmentation + normalization**

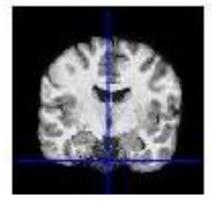
Spatial normalization: allows group analyses (different subjects must be spatially aligned)

Transformations:



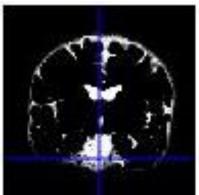
Some steps of preprocessing: **segmentation + normalization**

Segment is used to separate cerebral tissues: Grey Matter (GM), White Matter (WM), CerebroSpinal Fluid (CSF), etc. in T1 anatomical image.







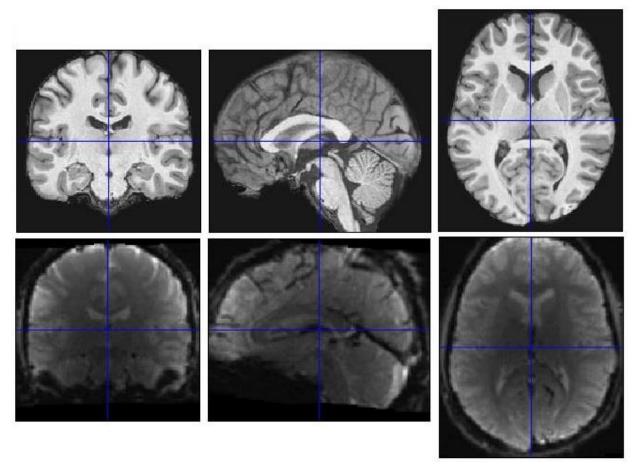


It produces a transformation matrix, that is to say a file containing normalization parameters (file ending with "*_seg8.mat") and also an image of field deformation (file beginning with "y_*.nii").

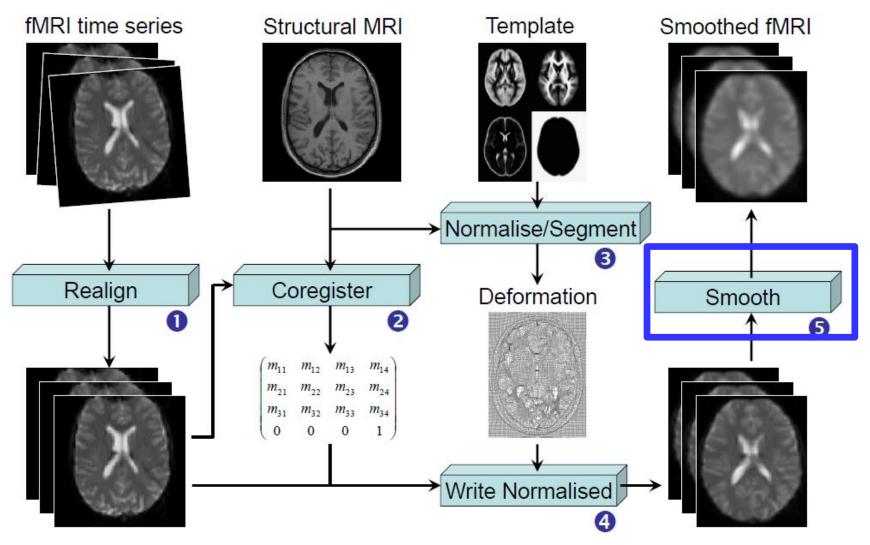
Some steps of preprocessing: **segmentation + normalization**

The Deformation field image is used to put all the fMRI scans (already registered with the anatomy) into standardized (MNI = "Montreal Neurological Institute) space.

This is called "normalization".



Some steps of preprocessing: smoothing



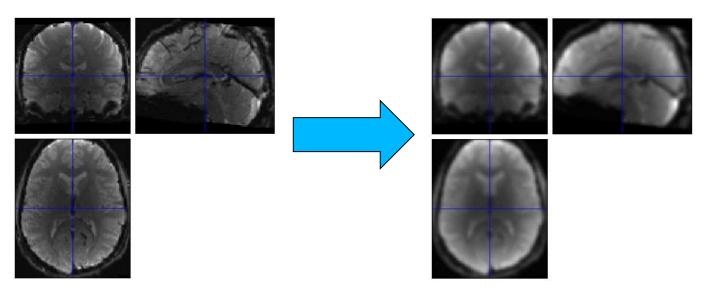
Some steps of preprocessing: smoothing

Used to correct for slight remaining functional anatomical variability between subjects and improve the signal-to-noise ratio.

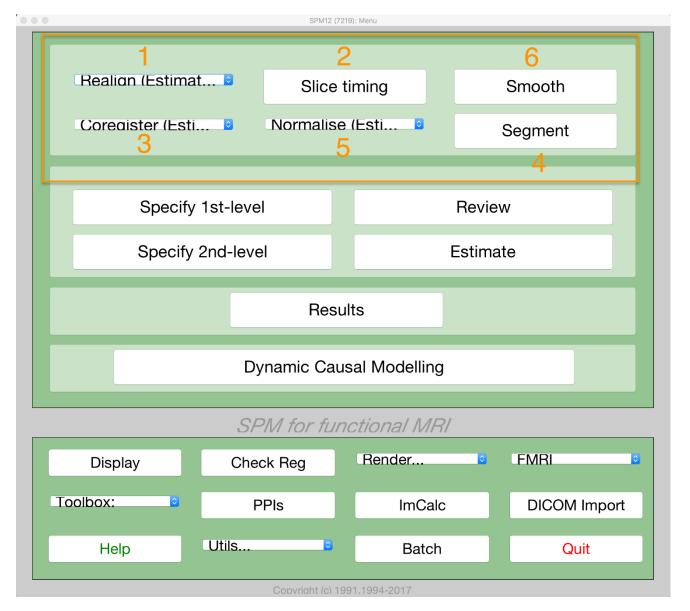
! There is a inverse relation between level of smoothing and accuracy of the spatial resolution

Smoothing is achieved by averaging every voxel with a weighted sum of its neighbors (defined by a Gaussian kernel which size is given by its Full Width at Half Maximum (FWHM) - typically twice the voxel size).

For instance, a FWHM of [6mm 6mm 6mm] is commonly used for a spatial resolution of [3mm 3mm 3mm].

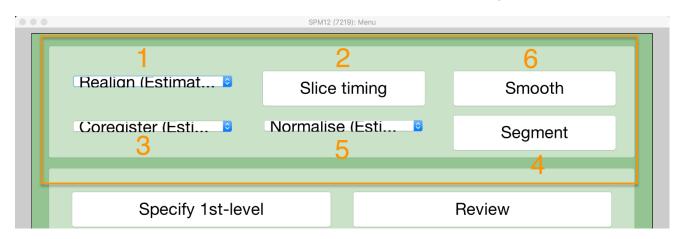


SPM12 interface



SPM12 interface – tips:

- Slice timing: previously extract slice timing info (dicom files)
 - ! Select ALL 3D images 1:1000 (for example)
- Realign: Estimate & Reslice
 - ! Select ALL 3D images 1:1000 (for example)
- Coregister: Estimate (ref: anat brain; source: realigned func)
- Segment: only anatomy
- Normalise: Write (Images to write: anatomy and ra* func)
 - ! Select ALL 3D images 1:1000 (for example)
- Smooth (filter ^wra.* and select ALL 3D images)



Show batch code alternative to button-pressing

```
% Actions to perform
% possible actions are:
    'slicetiming'
                                                            prefix 'a'
% 'realign' or 'unrwarp' (the latter requires B0 files) prefix 'r' and 'u' respectively
% 'topup' (requires AP/PA files)
                                                            prefix 't'
  'segmentnormalize'
                                                            prefix 'w'
  'smooth'
                                                            prefix 's'
    'run' to run the specified batch. Without 'run', the batch is simply saved (expect for topup)
% All these actions can be combined, e.g.: {'run', realign', 'segmentnormalize'}
% Because the batch works with any prefix defined by the user (see
% regexp fun below), one can start the batch at any processing step. For
% instance, the slice timing correction may have been already computed, and
% the batch {'run', realign', 'segmentnormalize'} can start from there by
% specifying regexp func = '^aepi.*\.nii';
% The order of arguments does not matter.
actions
               = { 'run', 'slicetiming', 'realign', 'topup', 'segmentnormalize', 'smooth' };
```

Used in NeuroSpin:

- fMRIPrep fmriprep.org/
- FSL fsl.fmrib.ox.ac.uk/
- SPM www.fil.ion.ucl.ac.uk/spm/
- pypreprocess (interface Python for SPM)
 qithub.com/neurospin/pypreprocess
- nilearn nilearn.github.io/
- BrainVoyager (logiciel payant) brainvoyager.com/

Other questions:

- References about slice timing
- SNR
- Physiological movements/corrections
- ...

Check on the NeuroSpin wiki:

References

Preprocessing with SPM

Resources on the NeuroSpin wiki: https://www.neurospin-wiki.org/pmwiki/Main/PreprocessingMRIData

En français: https://blricrex.hypotheses.org/ressources/fmri/preprocessing/spm12

In English: https://blricrex.hypotheses.org/ressources/fmri/preprocessing/spm12#English

SPM tutorial:

https://andysbrainbook.readthedocs.io/en/latest/SPM/SPM_Short_Course/SPM_04_Preprocessing.html

YouTube tutorial 4-a: https://www.youtube.com/watch?v=i39j-t7eRiY

YouTube tutorial 4-b: https://www.youtube.com/watch?v=zSqBoB1GrDk

Guillaume Flandin's presentation:

https://www.fil.ion.ucl.ac.uk/spm/course/chicago/01 Preprocessing.pdf

fMRIPrep: https://fmriprep.org

MRI Questions: https://mriquestions.com/index.html

NIAK fMRI preprocessing: https://niak.simexp-lab.org/build/html/PREPROCESSING.html