

LLN fMRI Workshop Tutorial

November 2019

Contributors:

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v0.0.1



Prerequisite (the things you need to install)

- Laptop
- Matlab
- [Install SPM12](#) (see [here](#) for more details for setup)
- Install the [atom text editor](#)
- Get data from [zenodo](#)
- Get the [analysis pipeline code](#)
- Install [MRIcron](#) and [MRIcroGL](#)
- Make sure you have at least 5 Go of free space on your computer
- Use this [invitation](#) to join the slack workspace of the workshop

Our agenda for today

- 1. How to design your fMRI experiment → START (9H00)
- 2. Look at the data
- 3. Preprocess
 - a. Slice timing
 - b. Realign & coregister
 - c. Normalize
 - d. Smooth→ BREAK (10H30 - 11H)
- 4. Subject level GLM
- 5. Group level GLM
- 6. Stats - correction
- 7. Looking at group level results
- 8. How to batch / script your analysis → BREAK (15H30 - 16H)
- END (18H00)

Format

We will try to alternate

1. Demos (that's for us):
 - a. Quick reminders of relevant “theoretical” points
 - b. Practical information for each “step”
2. Ask questions
3. Hands on (that's for you)
 - a. Follow instructions from the [google doc](#)
 - b. Ask for help when you get stuck

Glossary

Looking at your data

- Brain Imaging Data Structure
- Open MRI image
- Open metadata and tables

Looking at your data

- Brain Imaging Data Structure
 - What is it?
 - Standardized way to organize data AND metadata for MRI, fMRI, EEG, MEG

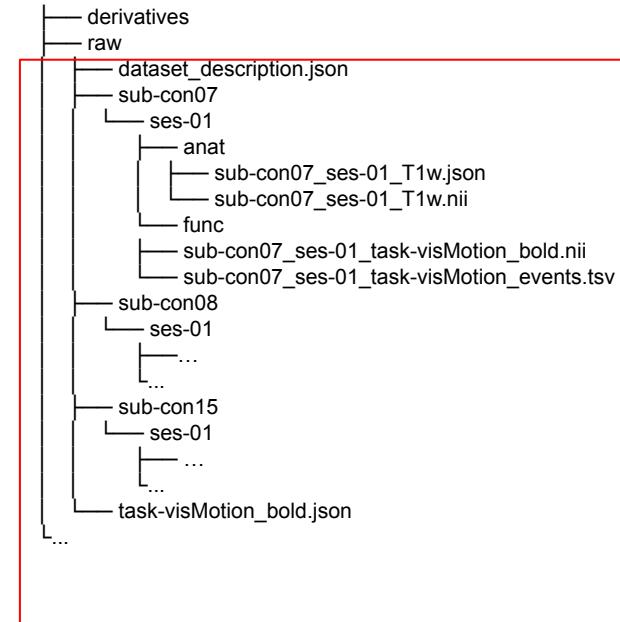


Looking at your data

- Brain Imaging Data Structure
 - What is it?
 - Standardized way to organize data AND metadata for MRI, fMRI, EEG, MEG
 - Why is it useful?
 - Facilitates data sharing between labs (e.g openneuro) and within labs
 - Facilitates creation of automated analysis pipelines (e.g fmriprep, MRIQC)

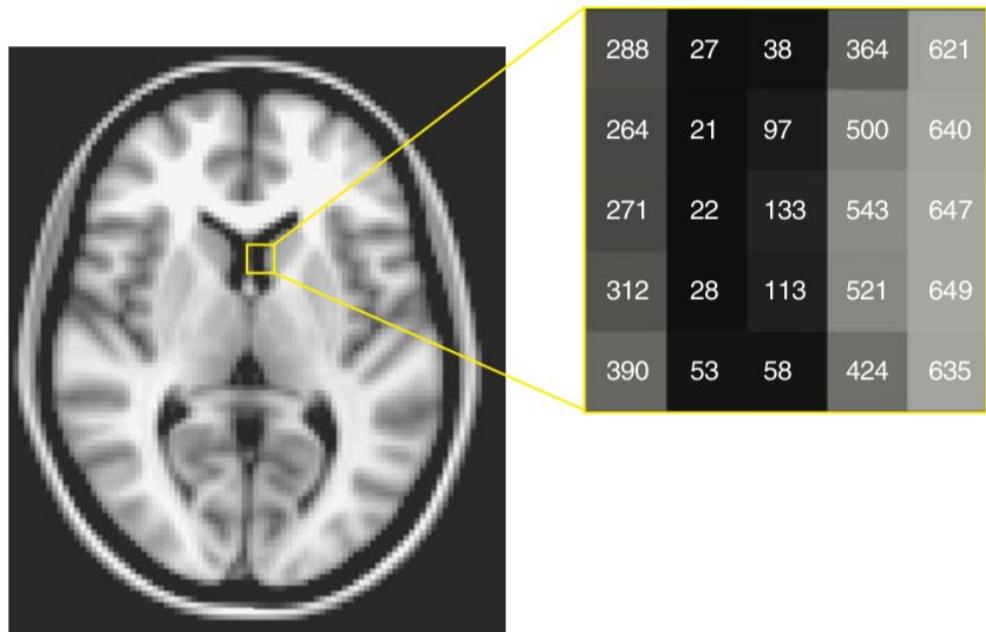
Looking at your data

- Brain Imaging Data Structure
 - Hierarchical folder structure:
 - Dataset
 - Subject
 - [Session]
 - MRI data: nifti images (.nii)
 - can be zipped (.nii.gz)
 - sub-XX[_ses-YY][_run-ZZ]_suffix.nii[.gz]
 - run
 - Tables: Tabulation Separated Values (.tsv)
 - e.g: *_events.tsv
 - Metadata: Java Script Object Notation (.json)
 - “side-car” to a .nii or .tsv file
 - Raw data VS Derivatives data
 - [BIDS validator](#)



Looking at your data

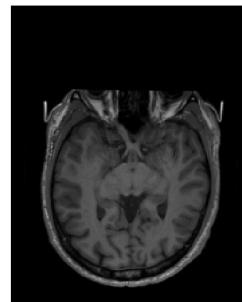
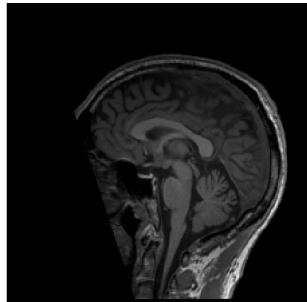
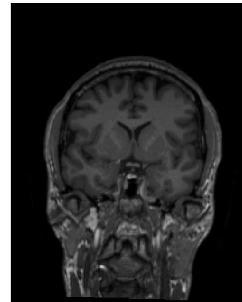
- Open MRI image
 - 3D Anatomical
 - Voxels
 - Slice
 - Volume
 - Image



Taken from *Handbook of Functional MRI Data Analysis*; Poldrack, Mumford, Nichols (2011)

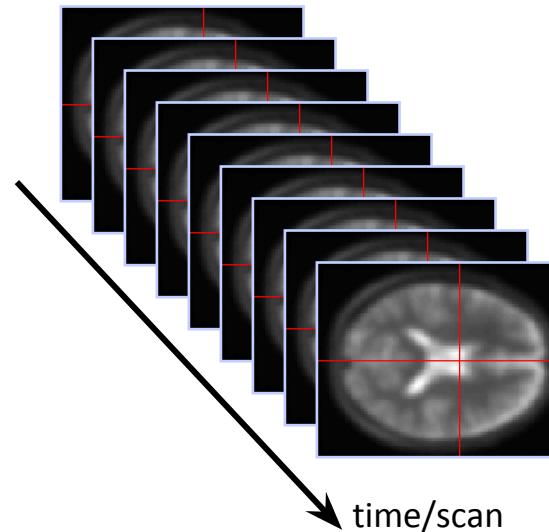
Looking at your data

- Open MRI image
 - 3D Anatomical
 - Original
 - Defaced



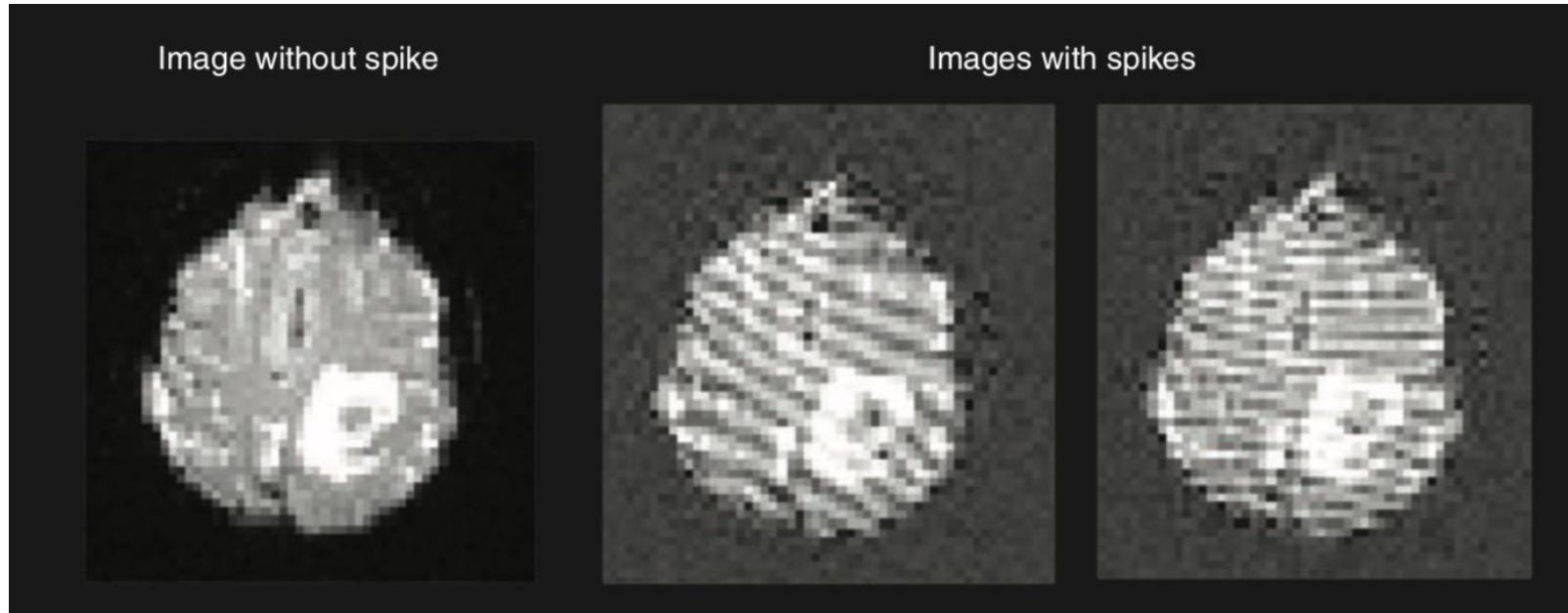
Looking at your data

- Open MRI image
 - 3D Anatomical
 - Original
 - Defaced
 - 4D Functional
 - One volume
 - All volumes as “movie”



Looking at your data

- Quality control



Taken from *Handbook of Functional MRI Data Analysis*; Poldrack, Mumford, Nichols (2011)

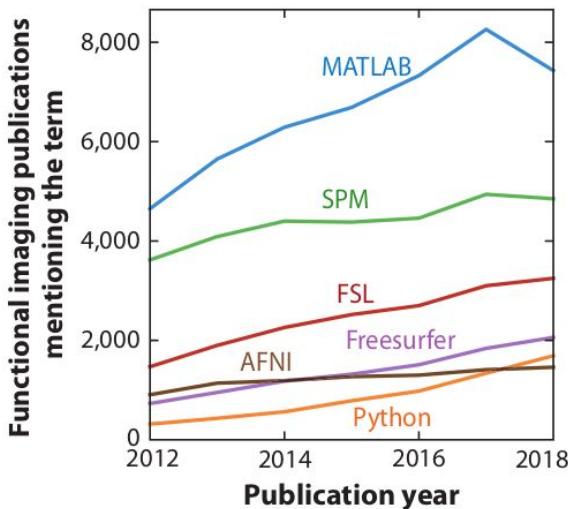
Looking at your data

- Open metadata and tables
 - Tables: Tabulation Separated Values (.tsv)
 - e.g: *sub-con07_ses-01_task-visMotion_events.tsv*
 - Metadata: Java Script Object Notation (.json)
 - e.g: *sub-con07_ses-01_task-visMotion_bold.json*

Things to know about the SPM

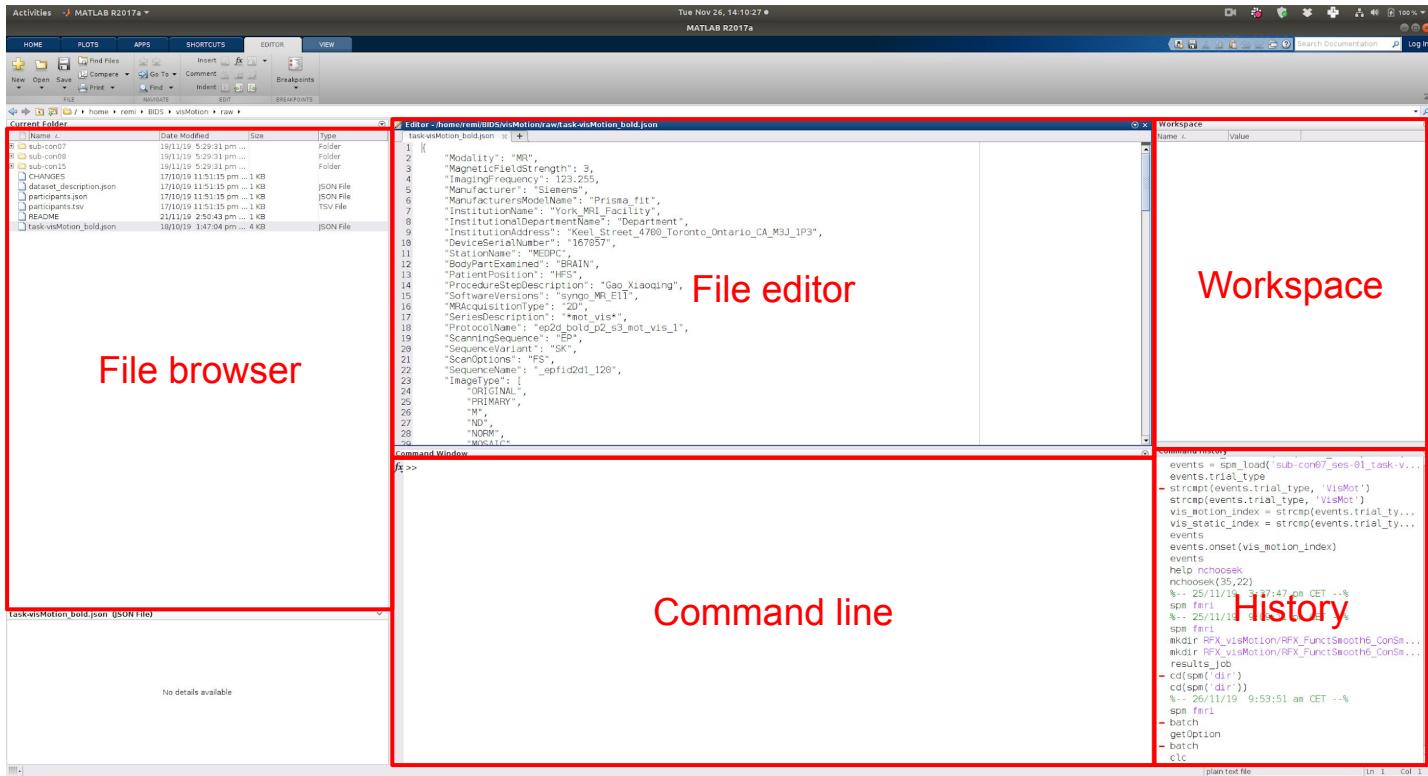
- One of several neuroimaging software

C Neuroimaging research usage
(Google Scholar)

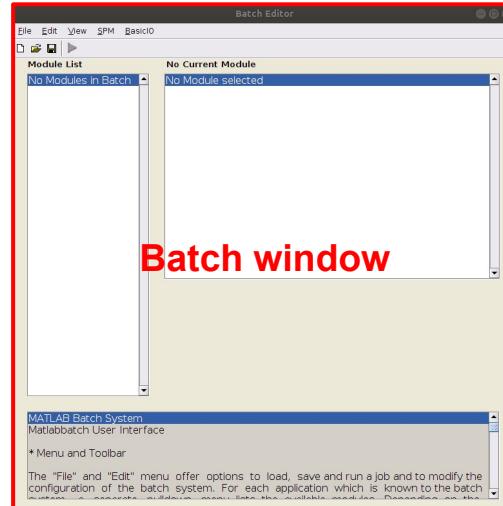
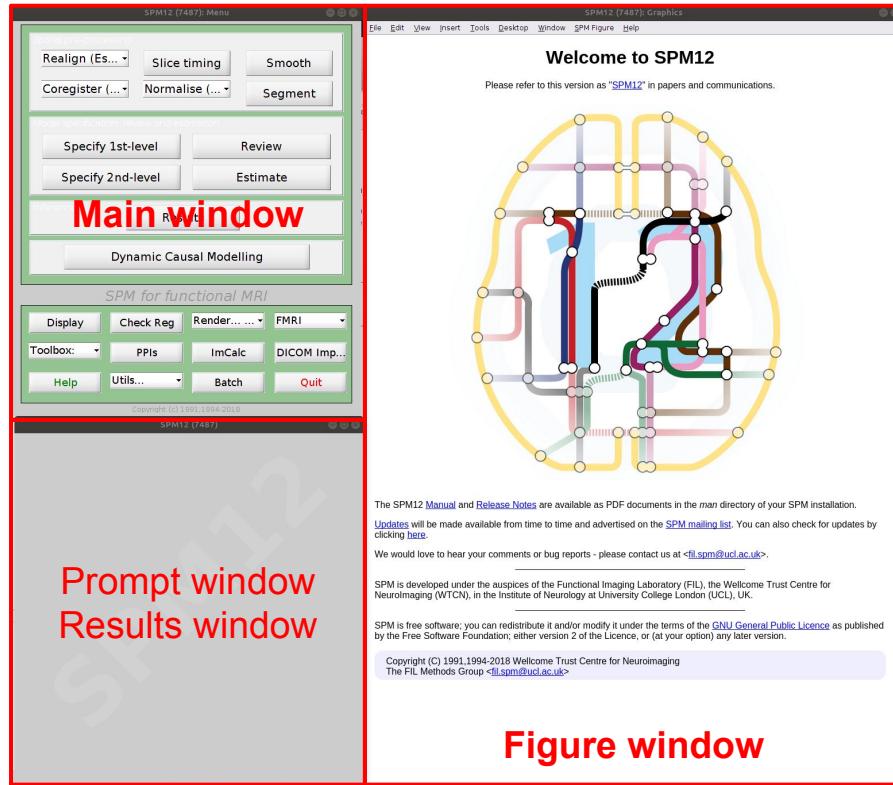


- Good reasons for choosing software X:
 - it offers useful tools for your problem
- OK reasons for choosing language X:
 - standard in your community – easier to get accepted
- Bad reasons for choosing language X:
 - it is the one you already know

Things to know about the MATLAB



Things to know about the SPM

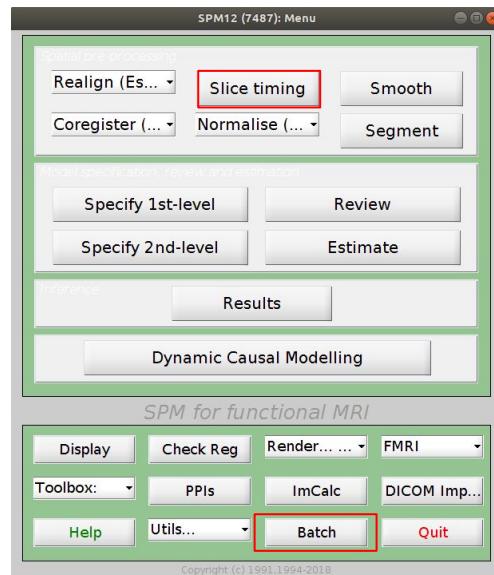


Things to know about the SPM

- No need to double click
- Adding and removing files in menus can be confusing
- A lot of “hidden” options / information by right-clicking
- SPM “session” = BIDS “run”

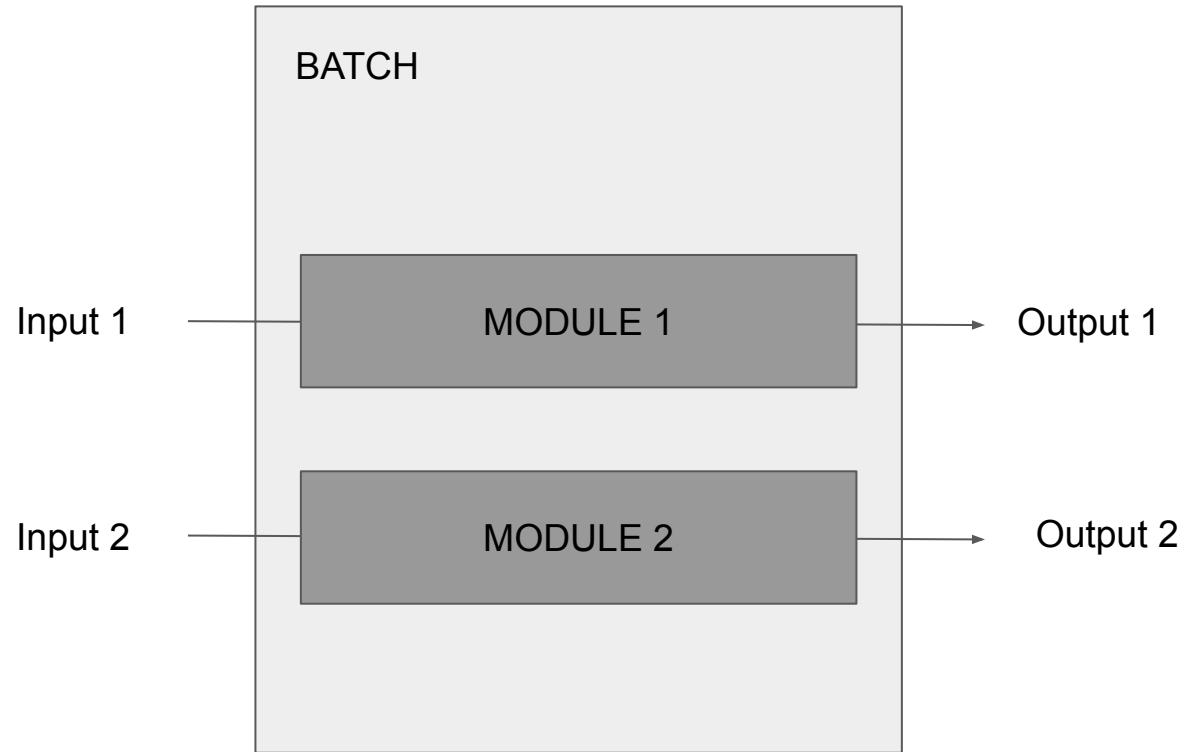
Things to know about the SPM

- Matlab batch:
 - Access



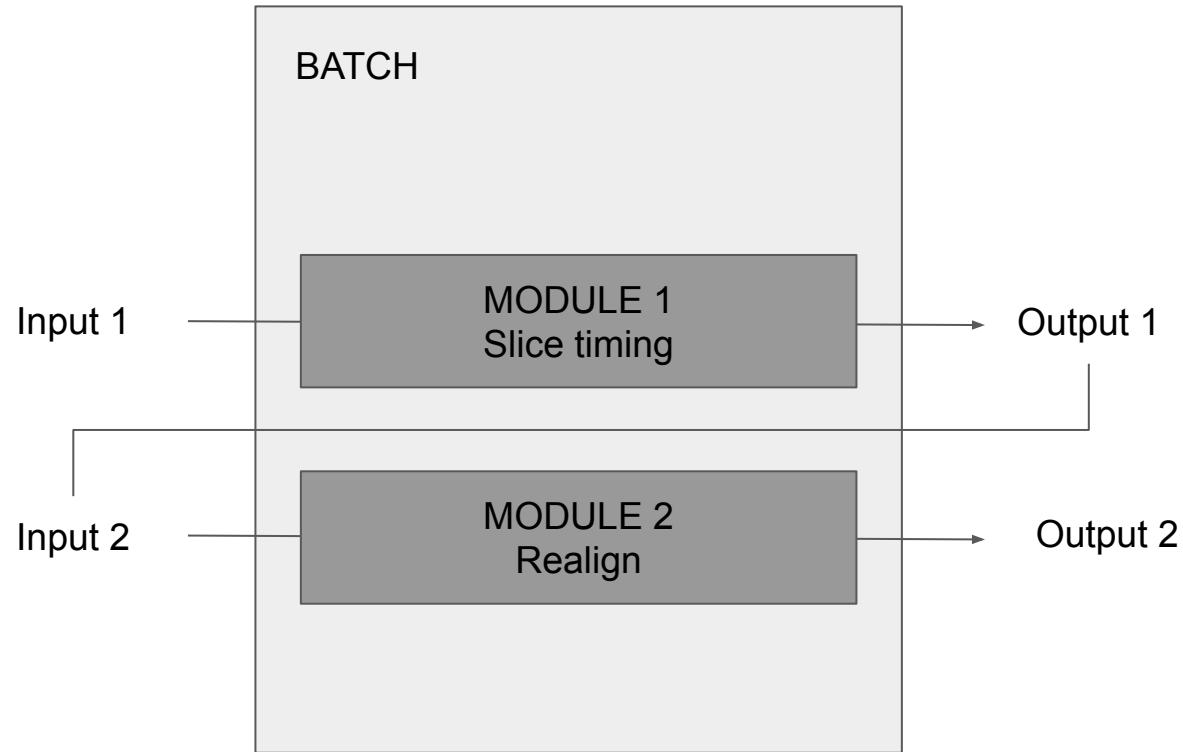
Things to know about the SPM

- Matlab batch:
 - Access
 - **Modules**



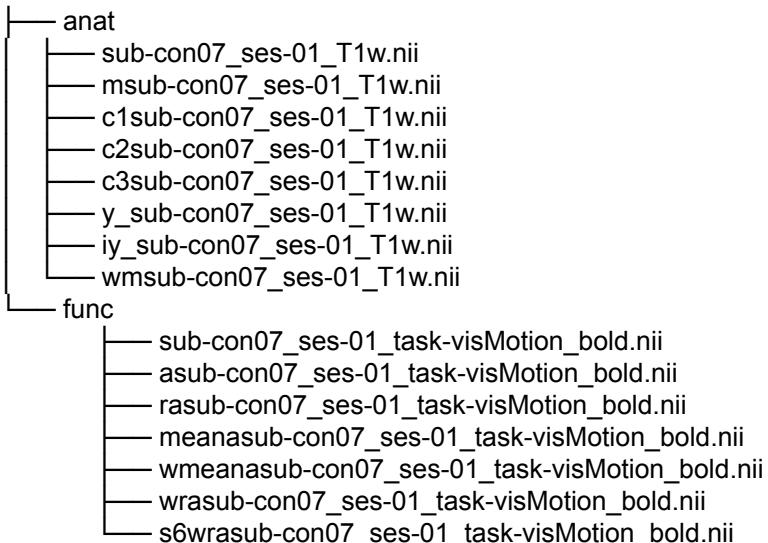
Things to know about the SPM

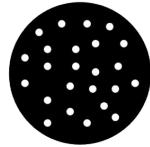
- Matlab batch:
 - Access
 - Modules
 - **Dependencies**



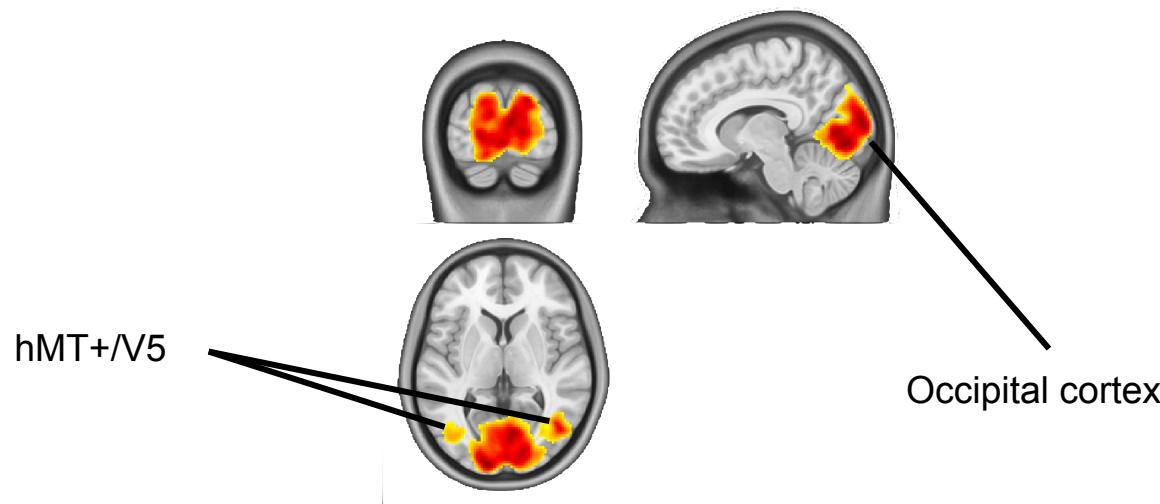
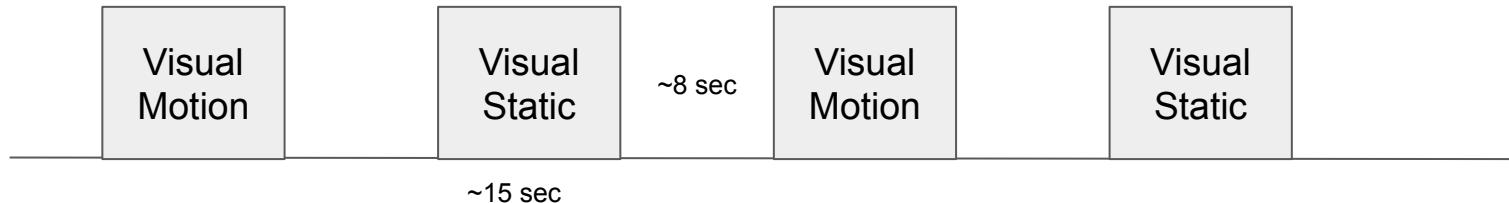
Things to know about the SPM

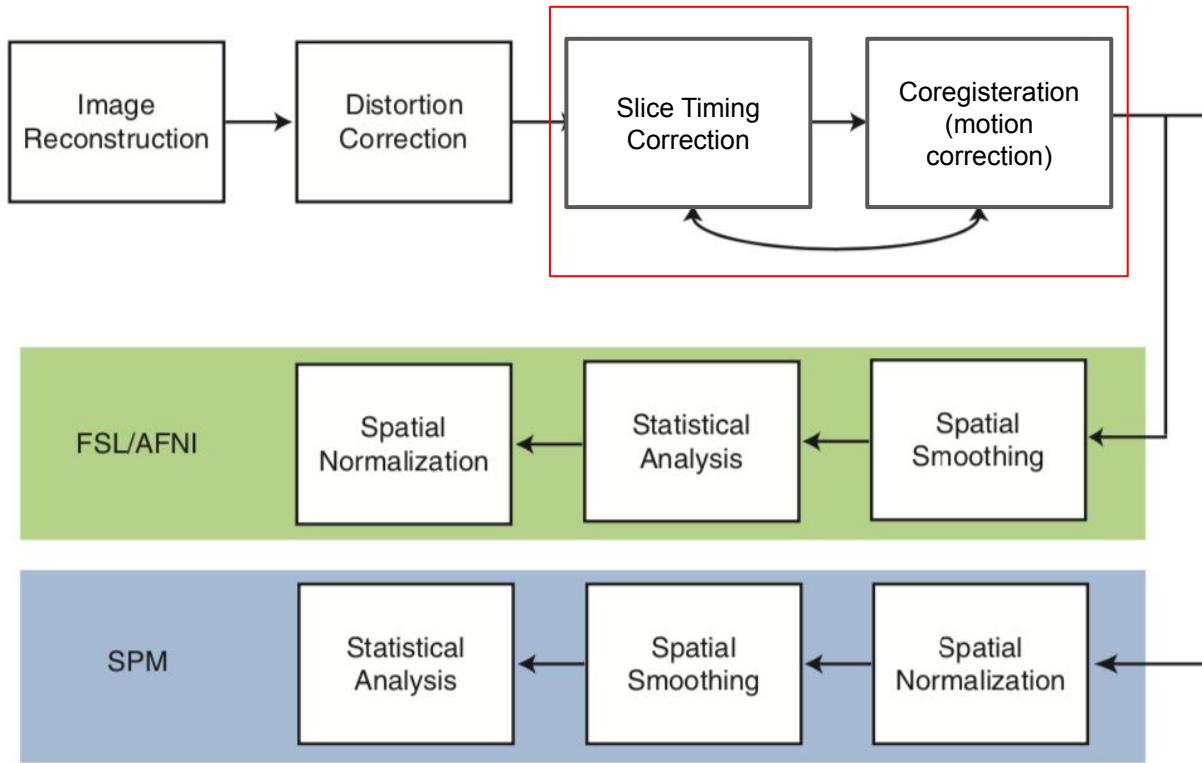
- Some of the SPM prefixes
 - a - slice time corrected
 - r - resliced
 - w - normalized (warped)
 - s - smoothed
 - mean - mean functional image
 - c# - tissue probability map
 - m - bias corrected
 - y_ forward deformation field
 - iy_ inverse deformation field





Experimental design

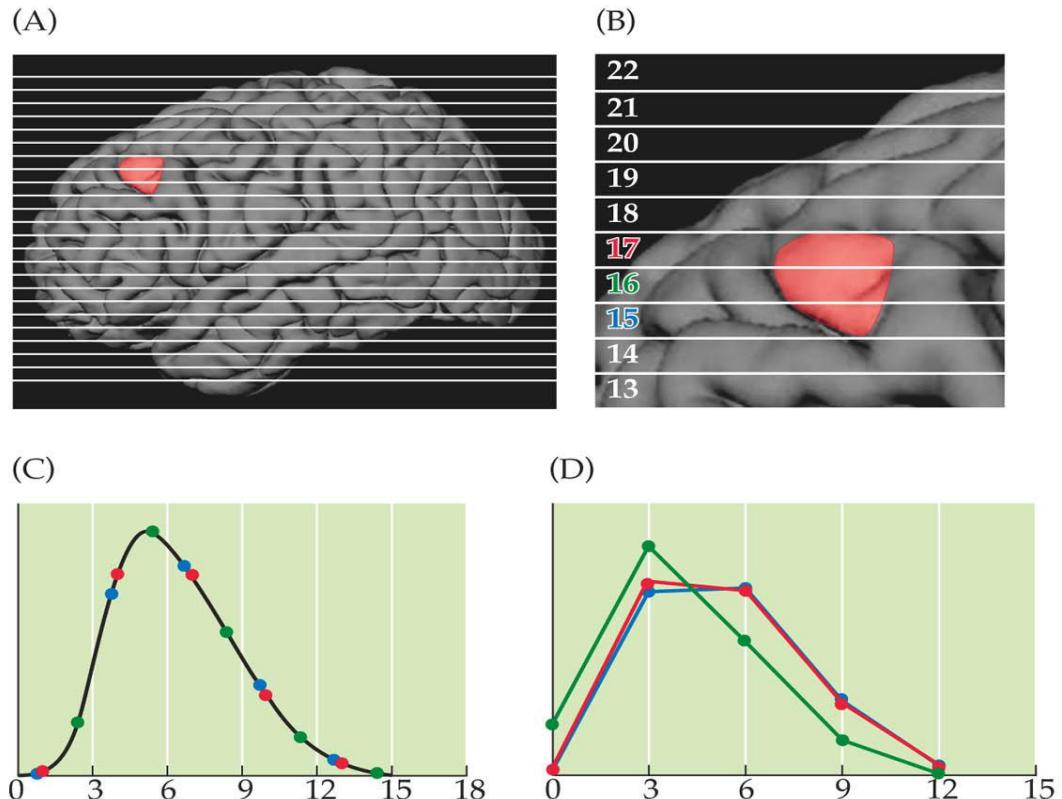




Slice timing

sub-con07_ses-01_T1w.nii

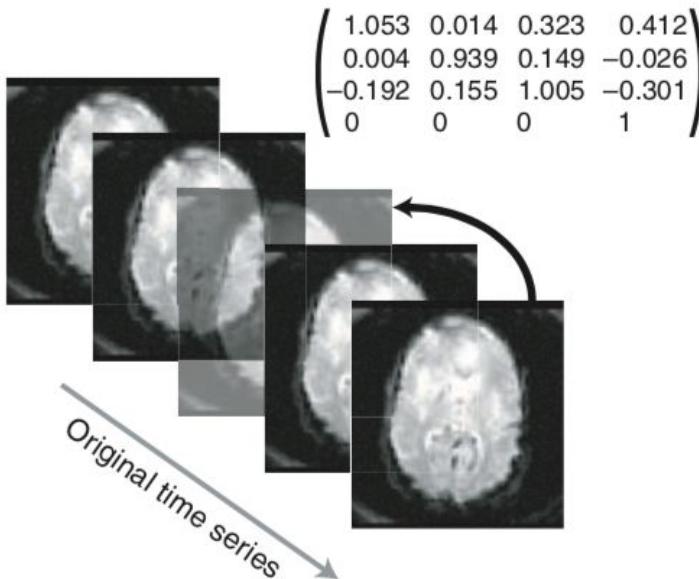
asub-con07_ses-01_T1w.nii



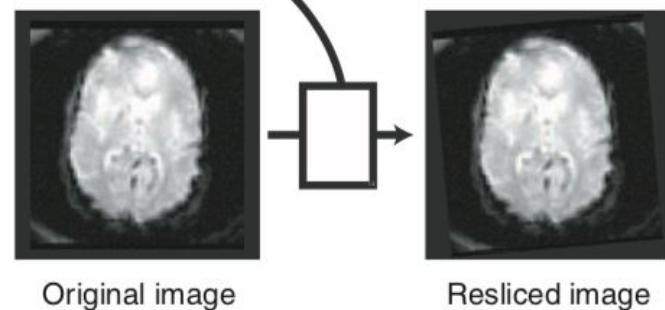
Modified from Source: Huettel S.A., Song A.W., McCarthy G.

Realign

Step 1: Estimate parameters

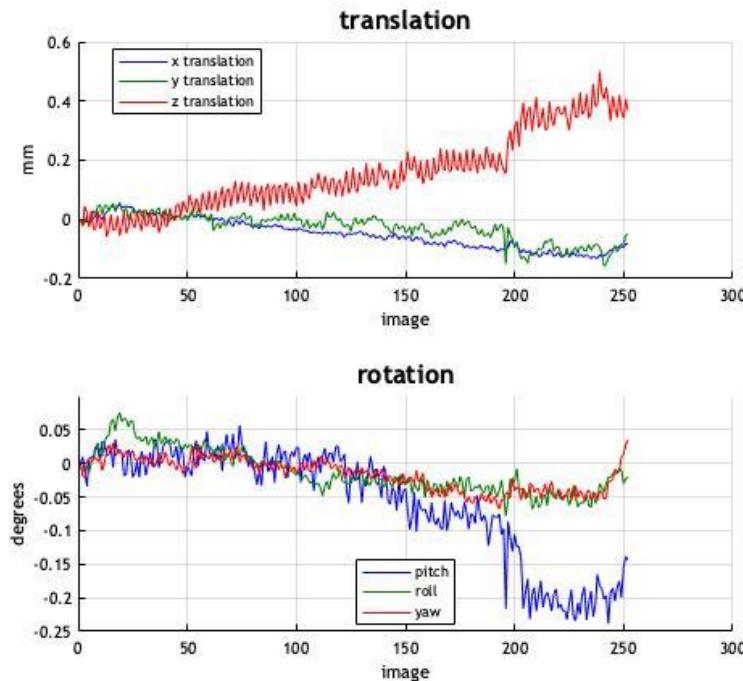


Step 2: Reslice images



Taken from *Handbook of Functional MRI Data Analysis*; Poldrack, Mumford, Nichols (2011)

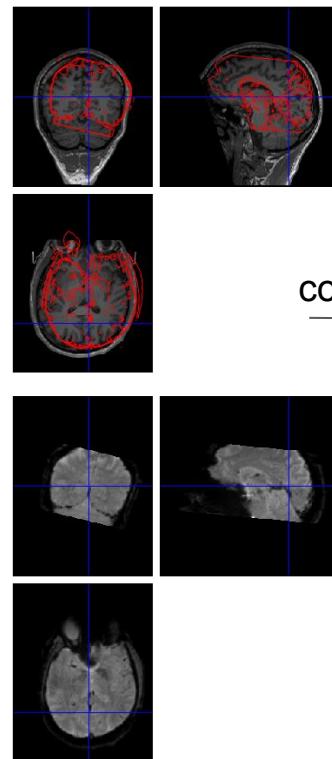
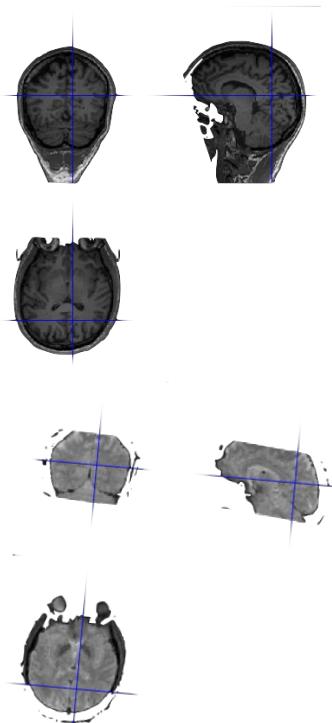
Realign



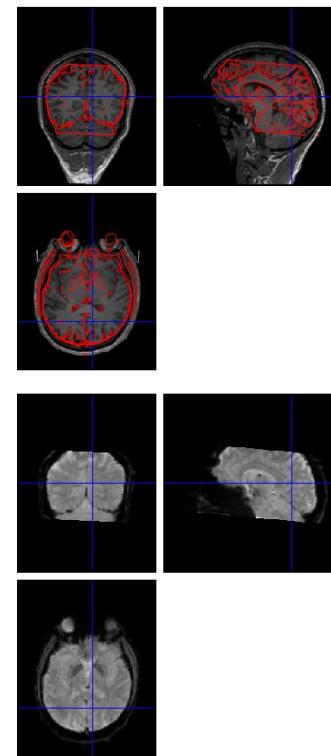
asub-con07_ses-01_task-visMotion_bold.nii

asub-con07_ses-01_task-visMotion_bold.nii
meanasub-con07_ses-01_task-visMotion_bold.nii

Coregistration



coregistration

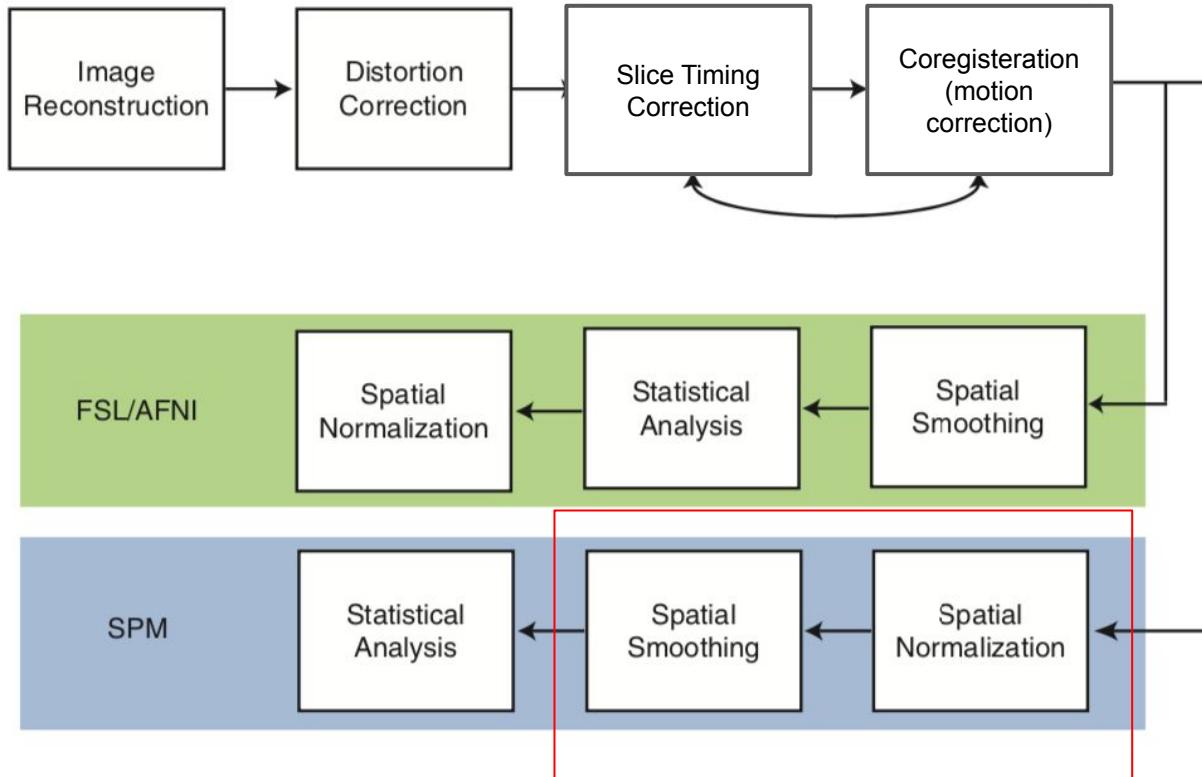


Practical session

Data exploration

Slice time correction

Realign & Coregistration



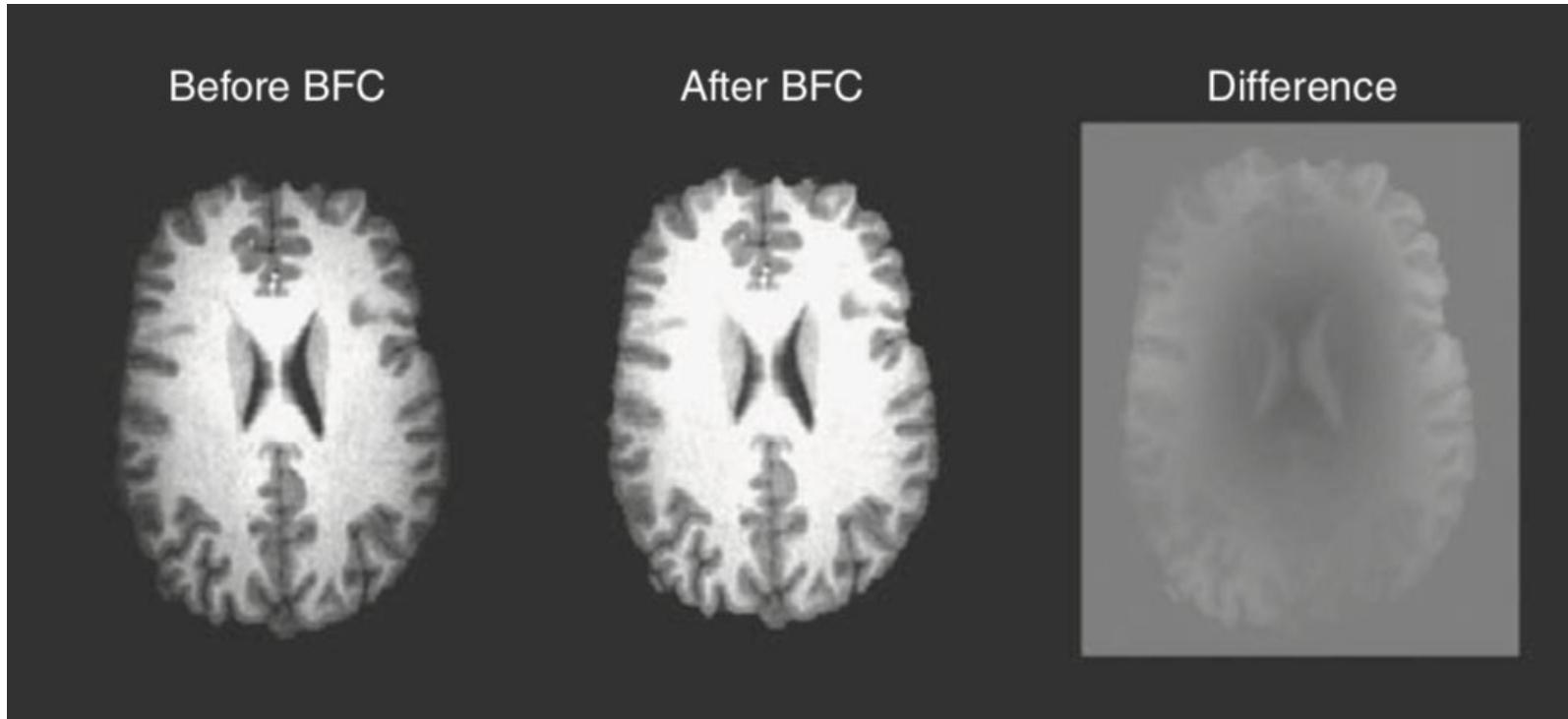
Normalize

- Brains of different subjects vary in shape and size
 - Need to bring them all into a common anatomical space (MNI)
 - In SPM, alignment is achieved by matching:
 - Subject grey matter with MNI grey matter
 - Subject white matter with MNI white matter
 - Need to correct for field bias first
- 
- Need to segment

Bias correction

sub-con07_ses-01_T1w.nii

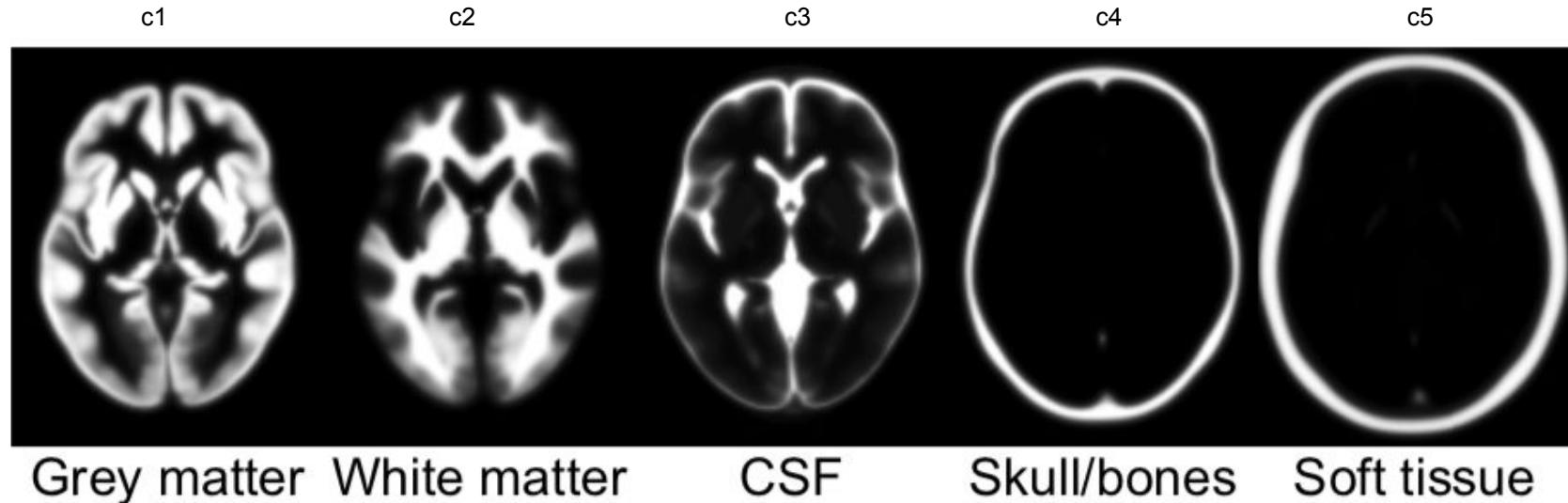
msub-con07_ses-01_T1w.nii



Taken from *Handbook of Functional MRI Data Analysis*; Poldrack, Mumford, Nichols (2011)

Segmentation

c#sub-con07_ses-01_T1w.nii

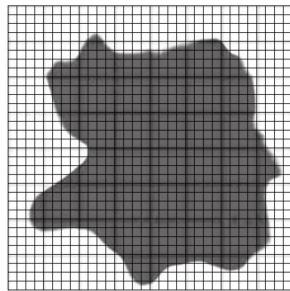
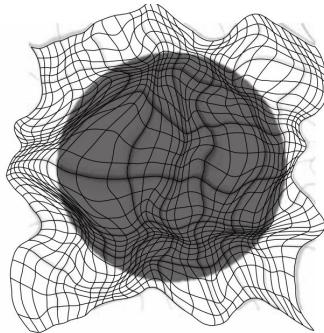


Taken from *Handbook of Functional MRI Data Analysis*; Poldrack, Mumford, Nichols (2011)

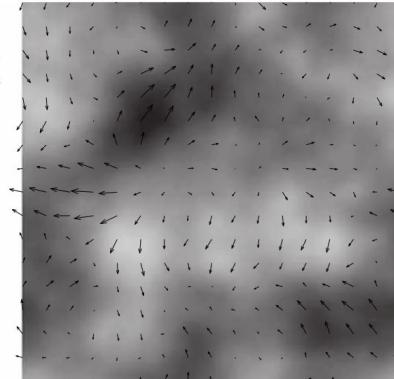
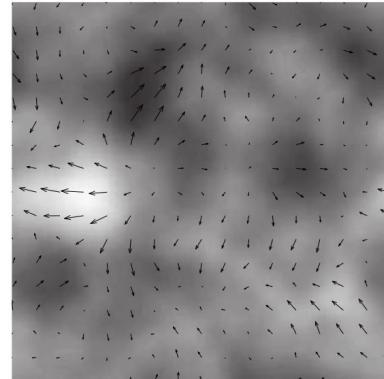
Note: in SPM the tissue probability maps are in a 4D image in *spm12/tpm/TPM.nii*

Deformation field

y_msub-con07_ses-01_T1w.nii

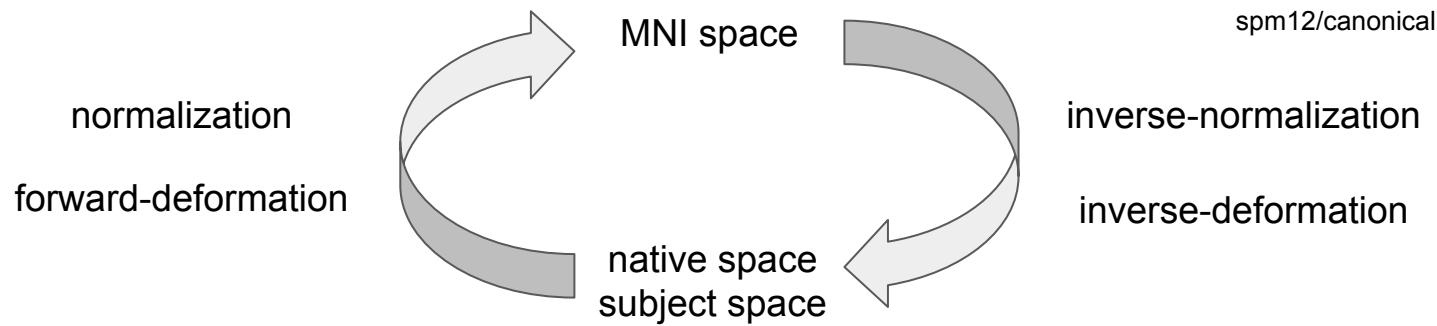
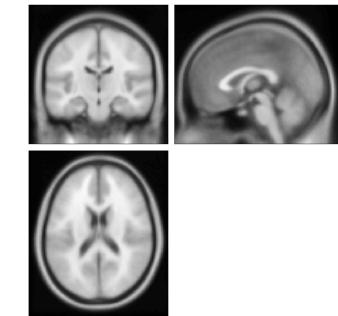
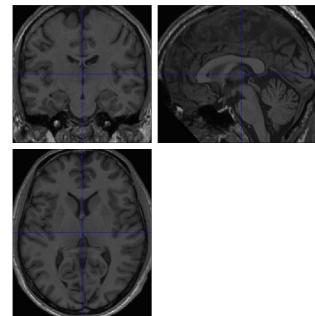


iy_msub-con07_ses-01_T1w.nii

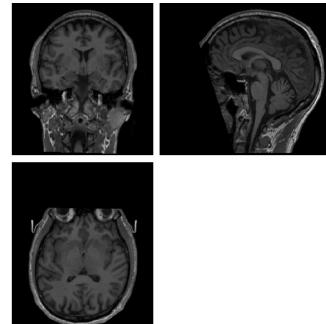


Normalize

wmsub-con07_ses-01_T1w.nii

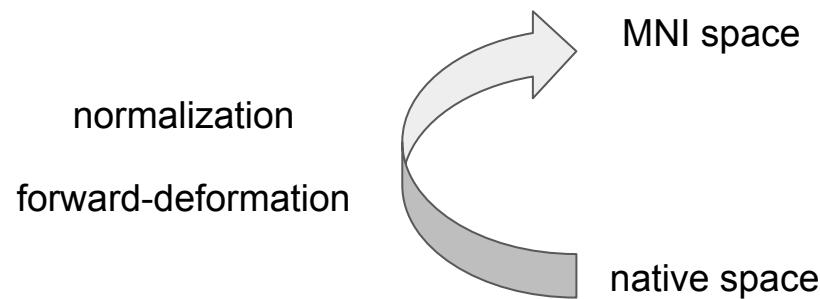
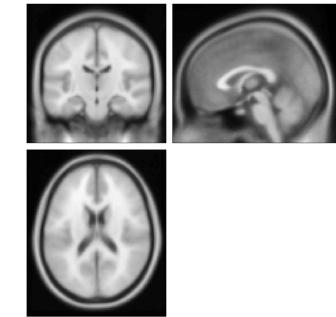
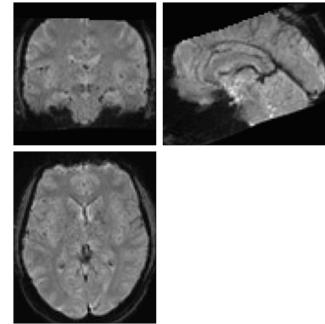


msub-con07_ses-01_T1w.nii

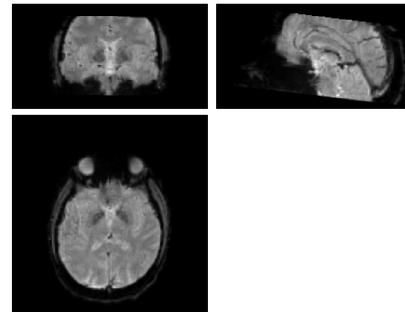


Normalize

wmeanasub-con07_ses-01_task-visMotion_bold.nii
wasub-con07_ses-01_task-visMotion_bold.nii



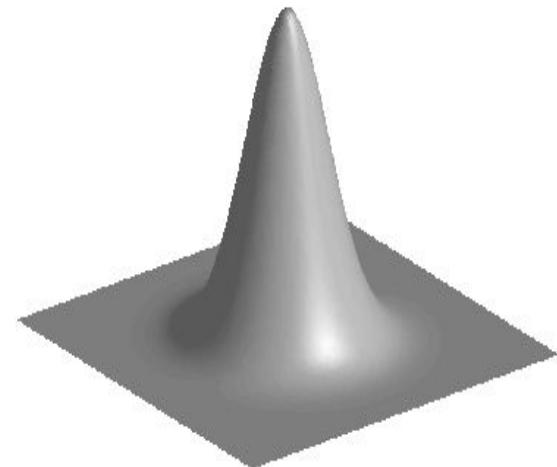
meanasub-con07_ses-01_task-visMotion_bold.nii
asub-con07_ses-01_task-visMotion_bold.nii



Smooth



Increased degrees of smoothing (FWHM)



Gaussian smoothing kernel

wasub-con07_ses-01_task-visMotion_bold.nii

s6wasub-con07_ses-01_task-visMotion_bold.nii

Practical session

Segmentation

Normalization

Smoothing

Subject level GLM (AKA FFX)

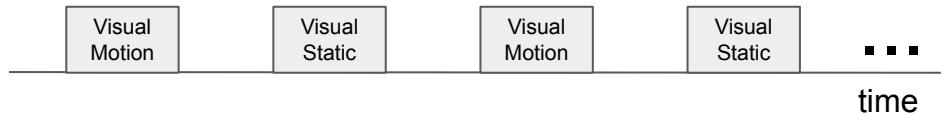
$$Y = X\beta + \varepsilon$$

Diagram illustrating the components of the Subject level GLM (AKA FFX) equation:

- fMRI signal**: Points to the X matrix.
- Different conditions (Design)**: Points to the X matrix.
- Beta estimates**: Points to the β vector.
- Error term**: Points to the ε term.

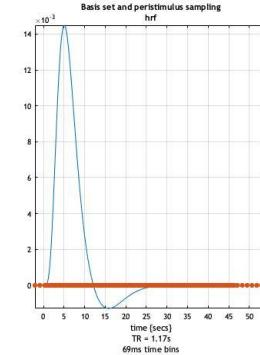
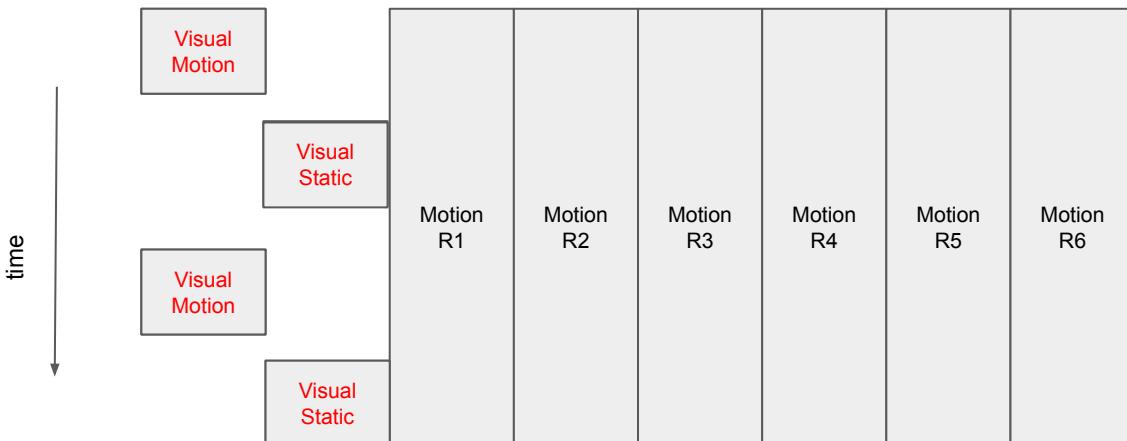
Subject level GLM (AKA FFX)

$$Y = X\beta + \epsilon$$



Motion Static

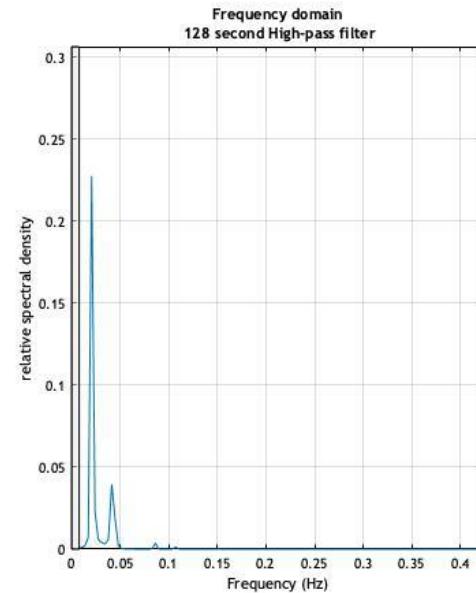
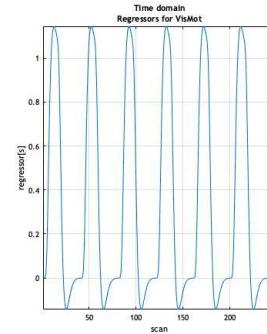
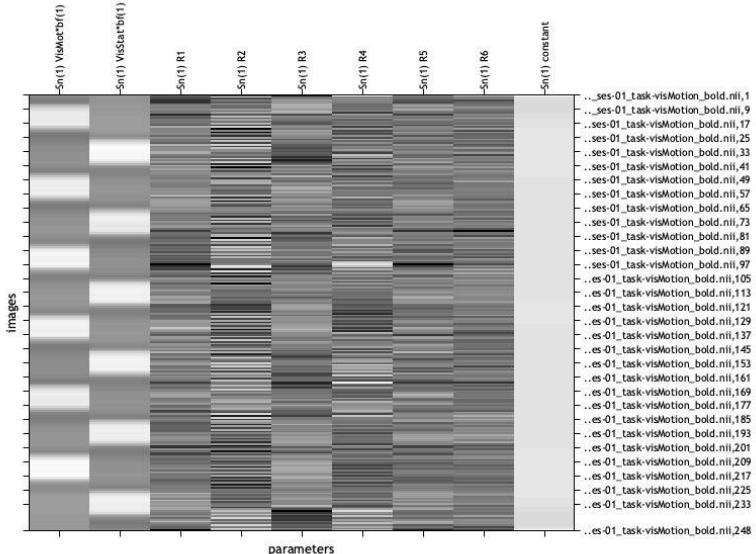
6 Motion regressors



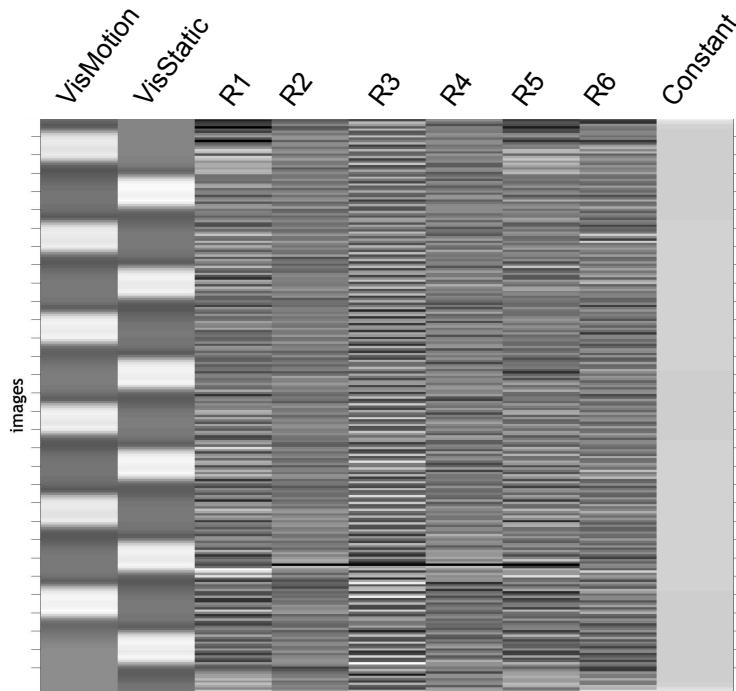
Subject level GLM (AKA FFX)

$$Y = X\beta + \varepsilon$$

Statistical analysis: Design



Contrast creation



Visual Motion:

[1 0 0 0 0 0 0 0 0]

Visual Static:

[0 1 0 0 0 0 0 0 0]

Visual Motion > Visual Static:

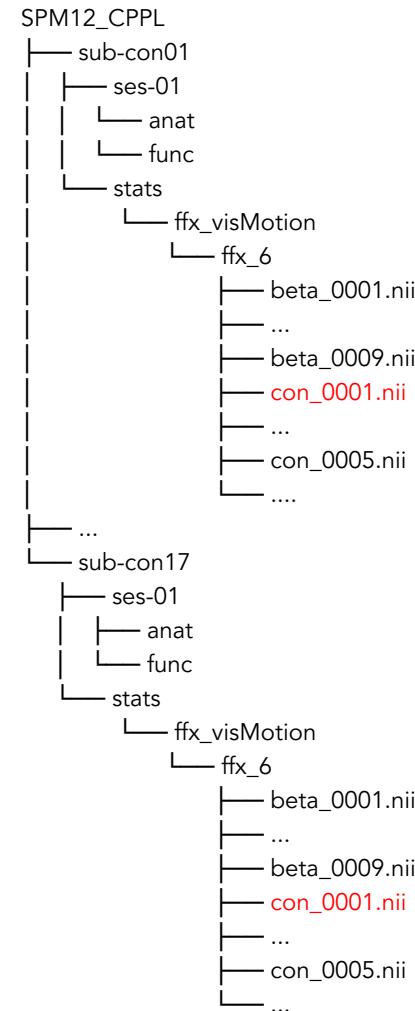
[1 -1 0 0 0 0 0 0 0]

Effect of subject movement:

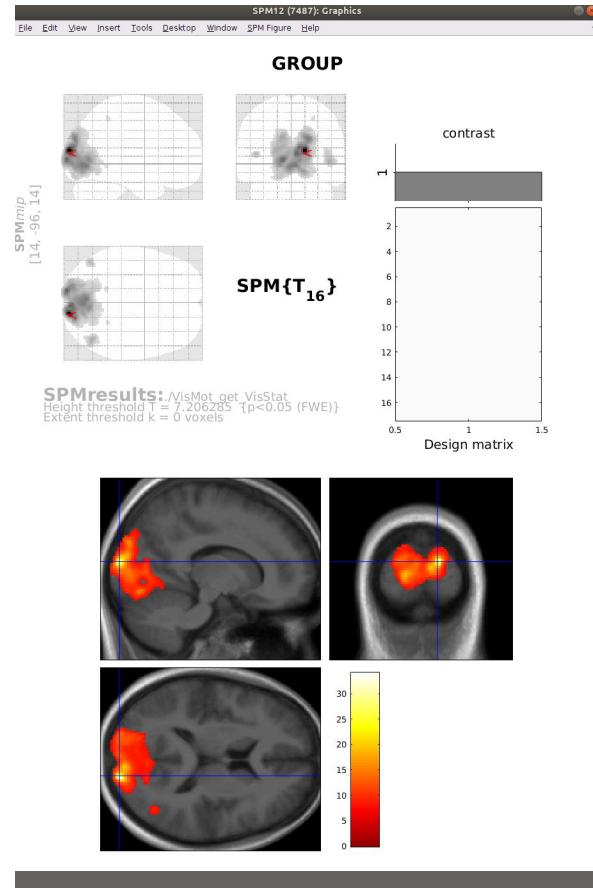
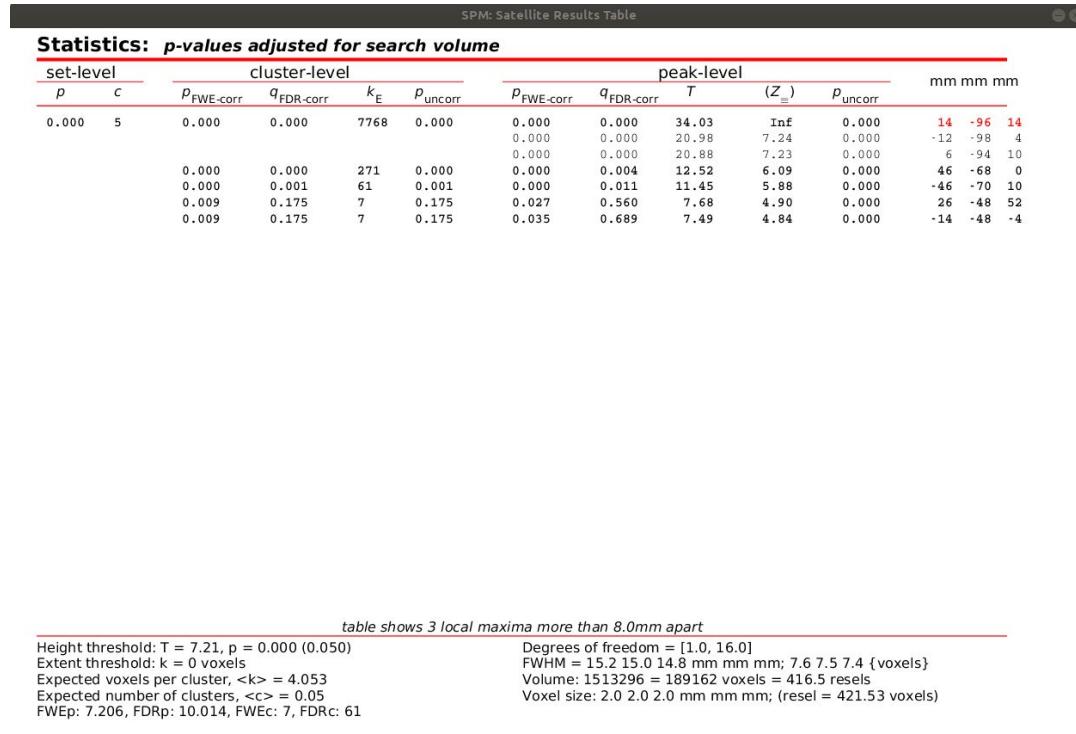
[0 0 1 0 0 0 0 0 0;
0 0 0 1 0 0 0 0 0;
0 0 0 0 1 0 0 0 0;
0 0 0 0 0 1 0 0 0;
0 0 0 0 0 0 1 0 0;
0 0 0 0 0 0 0 1 0]

Group level GLM (AKA RFX)

- Random effects analysis
- Summary statistics approach
 - Get an estimate for each subject
 - Only bring those at the group level

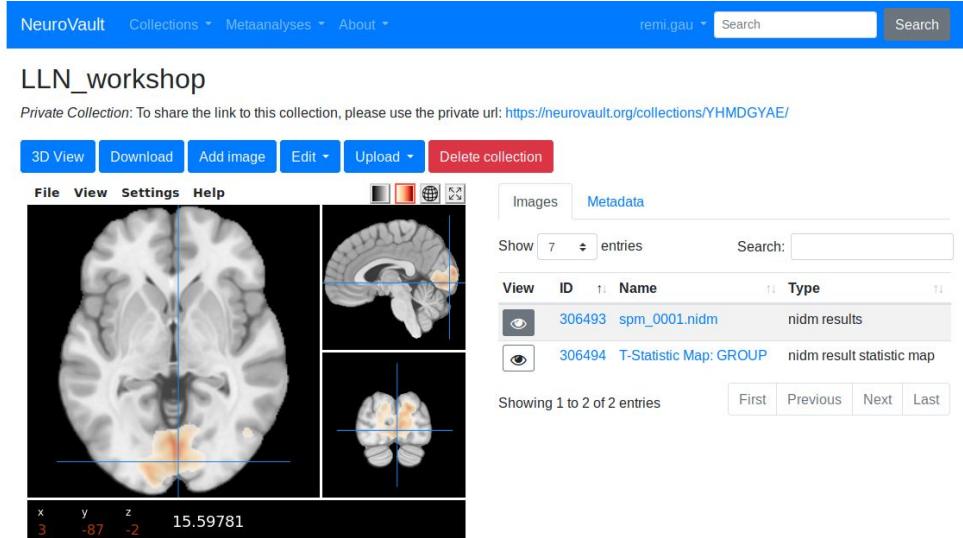


Statistical inferences



Sharing results

- Table for paper
- 2D image for paper
- 3D maps: [neurovault](#)



Practical session

First level analysis

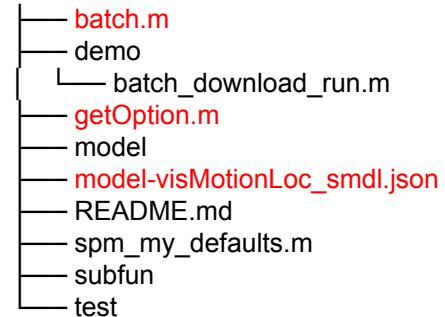
Second level analysis

Why you should script your analysis.

	Graphic user interface (GUI)	Scripting
Easy	+	
<u>Speed for simple things</u>	+	It gets better with practice.
<u>Speed for complex things</u>	-	+
Flexibility	Well... At least you get <i>reproducible</i> errors.	+
Risk of error	+	
Reproducibility	-	+

How to script your analysis

- CPP pipeline
 - Minimize the number of files to edit
 - **get.option.m**
 - What subject to analyze
 - What task to analyze
 - Where the data is
 - Where the model file is
 - **model-*_smdl.json**
 - What contrast to compute
 - **batch.m**
 - What steps to run



Feedback

Hot take survey:

https://etherpad.net/p/LLN_fMRI_workshop_2011_hot_take

Colder take survey:

<https://forms.gle/kpq1TAr3RYqdACvP7>

Coming soon

Open science in MRI research

Web site:

<https://openmrbenelux.github.io/>

Registration:

<https://openmrbenelux.github.io/page-registration/>

The image is a promotional graphic for the OpenMR Benelux 2020 conference. It features a dark blue background with abstract circular patterns in yellow, purple, and white. In the center, there is a stylized map of the Benelux region (Belgium, Netherlands, and Luxembourg) colored with the respective national flags. To the left of the map, the 'openMR' logo is displayed, consisting of a stylized 'e' icon followed by the word 'openMR'. To the right of the map, the word 'Benelux' is written in a large, bold, white font. Below the map, the text 'Towards inclusive, transparent, and reproducible science in Magnetic Resonance Imaging' is written in a smaller white font. At the bottom, the dates '21-23 January 2020' are shown. On the left side, under the heading 'What is it?', a brief description of the conference is provided: 'OpenMR Benelux 2020 is an exciting 3-day program lined up with talks, discussions, workshops, training sessions and hackathons concerning open MRI science!'. On the right side, under the heading 'Venue', the location 'Donders Institute for Cognition, Brain and Behaviour Nijmegen, The Netherlands' is mentioned. A QR code is located in the bottom right corner. Social media links for Twitter (@openmrbenelux) and email (openmrbenelux@gmail.com) are also present at the bottom.

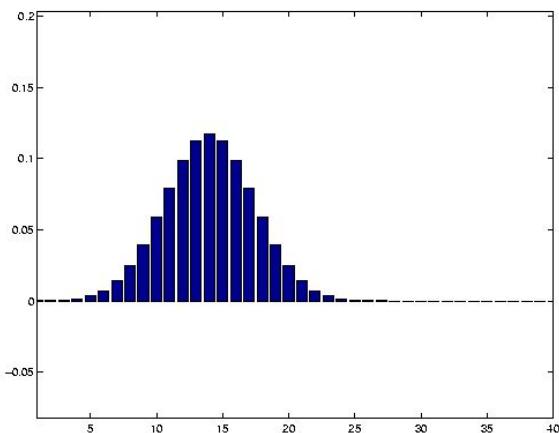
openmrbenelux.github.io/page-registration/

More info:

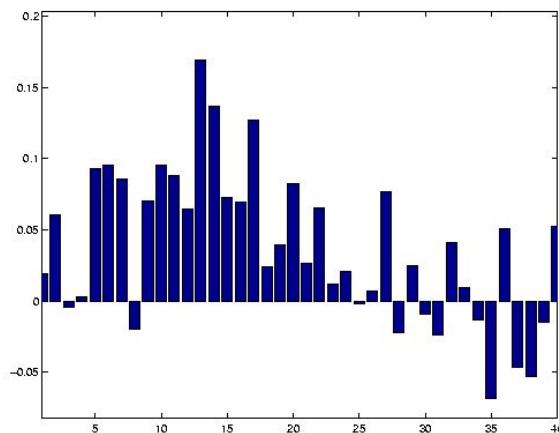
openmrbenelux.github.io @openmrbenelux openmrbenelux@gmail.com

Smooth

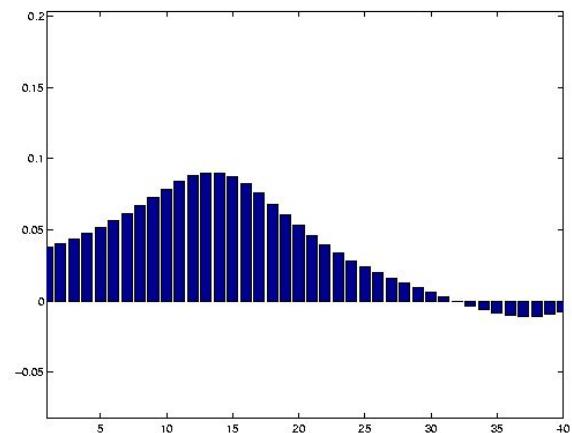
Signal



Signal + noise

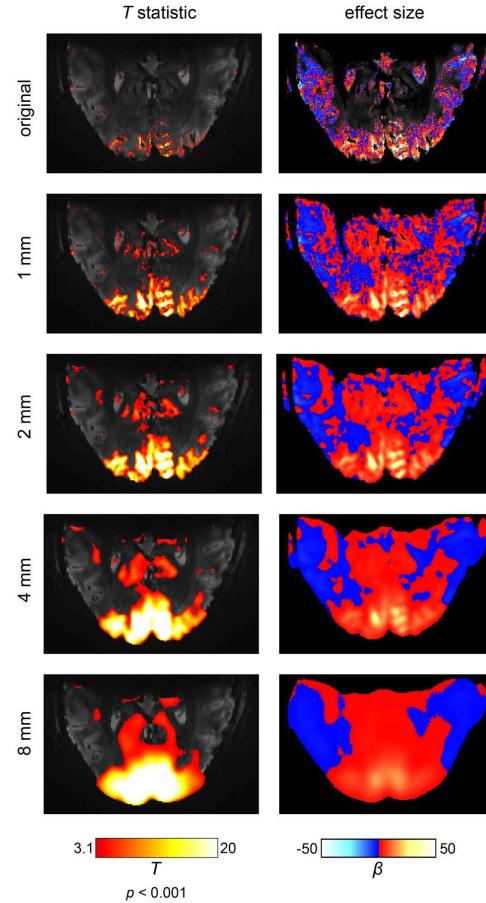


Signal + noise
smoothed with gaussian

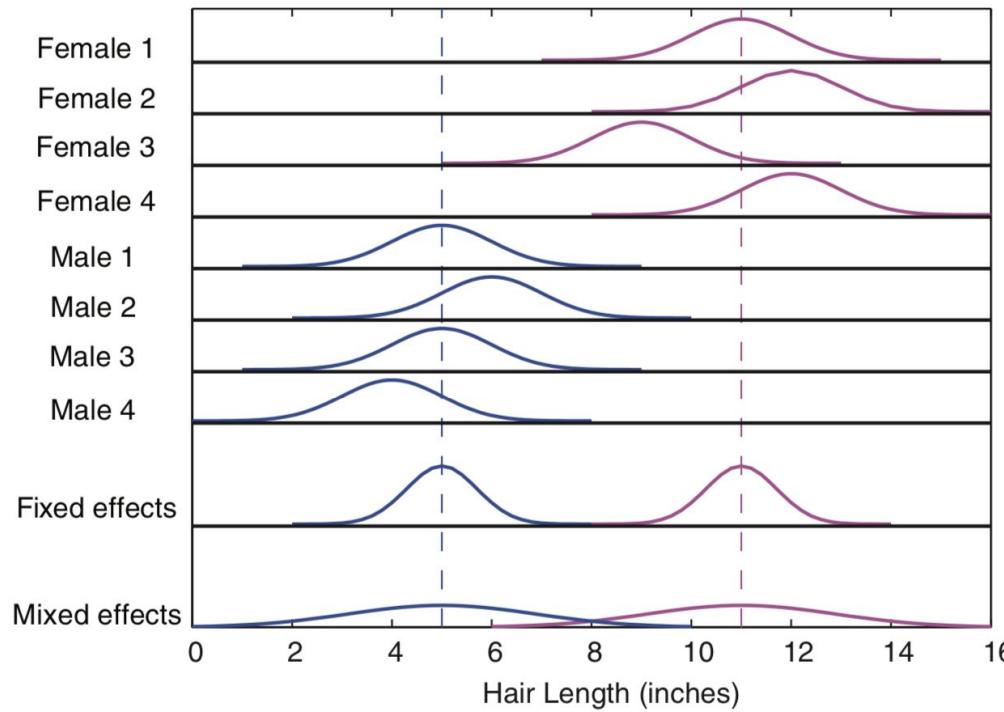


More info: [here](#) and [here](#)

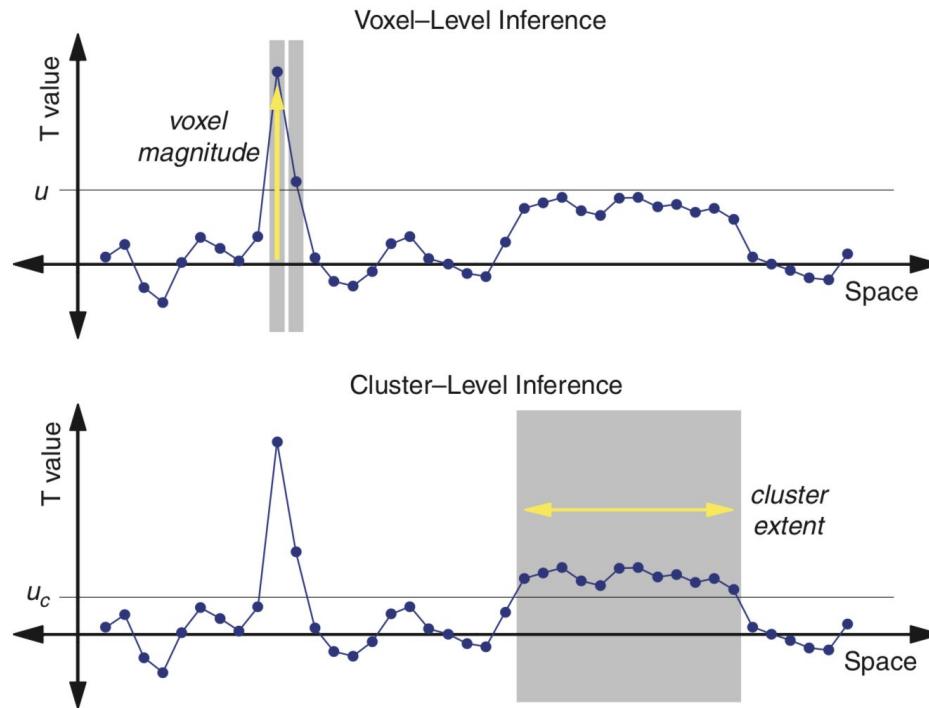
Smooth



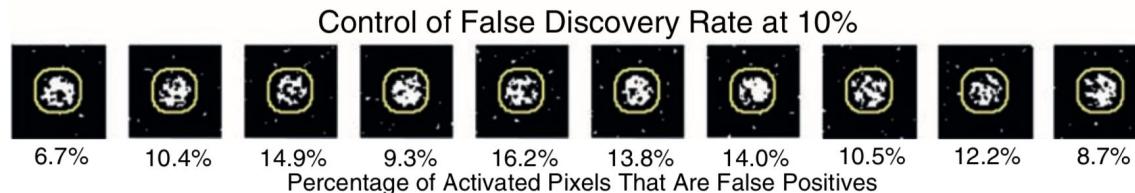
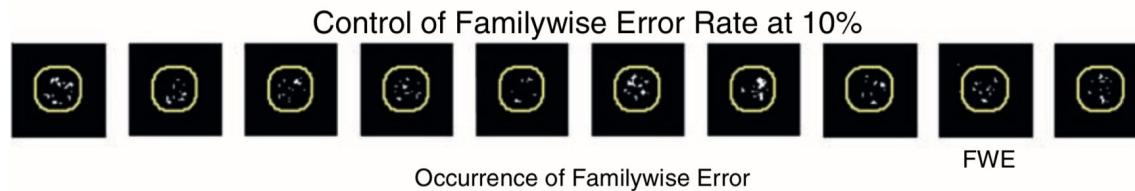
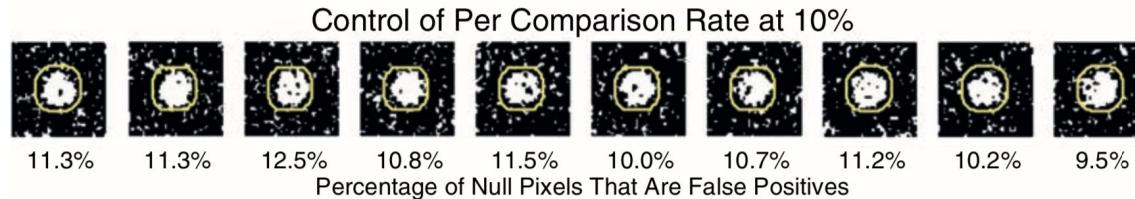
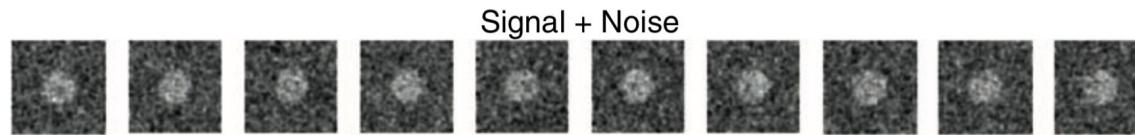
Statistical inferences



Statistical inferences



Statistical inferences



Subject level GLM (AKA FFX)

$$Y = X\beta + \epsilon$$



