SPM Course
Single Subject Analysis

Practical Session

Dr. Jakob Heinzle & Dr. Frederike Petzschner & Dr. Lionel Rigoux

Hands up:

- Who has programming experience with Matlab?
- Who has analyzed an fMRI experiment before?
- Who did the preparation for the practical session that was posted on the website?

Zurich SPM Course 2016
Practical session on 1st level analysis
Tutors: Frederike Petzschner, Liongel Rigoux, Jakob Heinzle

We assume that you have matlab installed and that you have downloaded the latest version of SPM (SPM12, release 6885).
SPM can be downloaded from http://www.fil.ion.ucl.ac.uk/spm/software/spm12/
Follow the instructions there.

Instructions for preparation to be performed prior to the session.

Step 1: Download the face-repetition data.
Goto http://www.fil.ion.ucl.ac.uk/spm/data/face_rep/
Download face_rep.zip
Download face_rep_spm12_batch.m
Download manual.pdf (for SPM 12, if you do not already have it).

Set up a directory on your computer that you will use for the tutorial.
Copy face_rep.zip to that directory. Unzip face_rep.zip into that directory and rename the directory face_rep as data. You should now have two folders (RawEPI and Structural) and two files (sots.mat and all_conditions.m) in the folder data.

Make an additional directory "scripts" within your tutorial folder and copy the face_rep_spm12_batch.m file in there.
Also, copy the file face_rep_spm12_prepare4session.m into the script folder. You should have gotten this file together with the instructions you are currently reading.

Open Matlab, add the scripts folder for your tutorial to the matlab path (and of course also SPM). Edit line 15 of face_rep_prepare4session.m so that it points to your!! tutorial folder. Then let the file run. This will do a complete preprocessing of the data and will take a bit of time.

Everything has worked, if the last three lines on your matlab command window read:
Running 'Smooth'
Done 'Smooth'
Done

Now you should be ready for the tutorial. See you there!

There was a bug:

open face_rep_prepare4session.m in Matlab

change

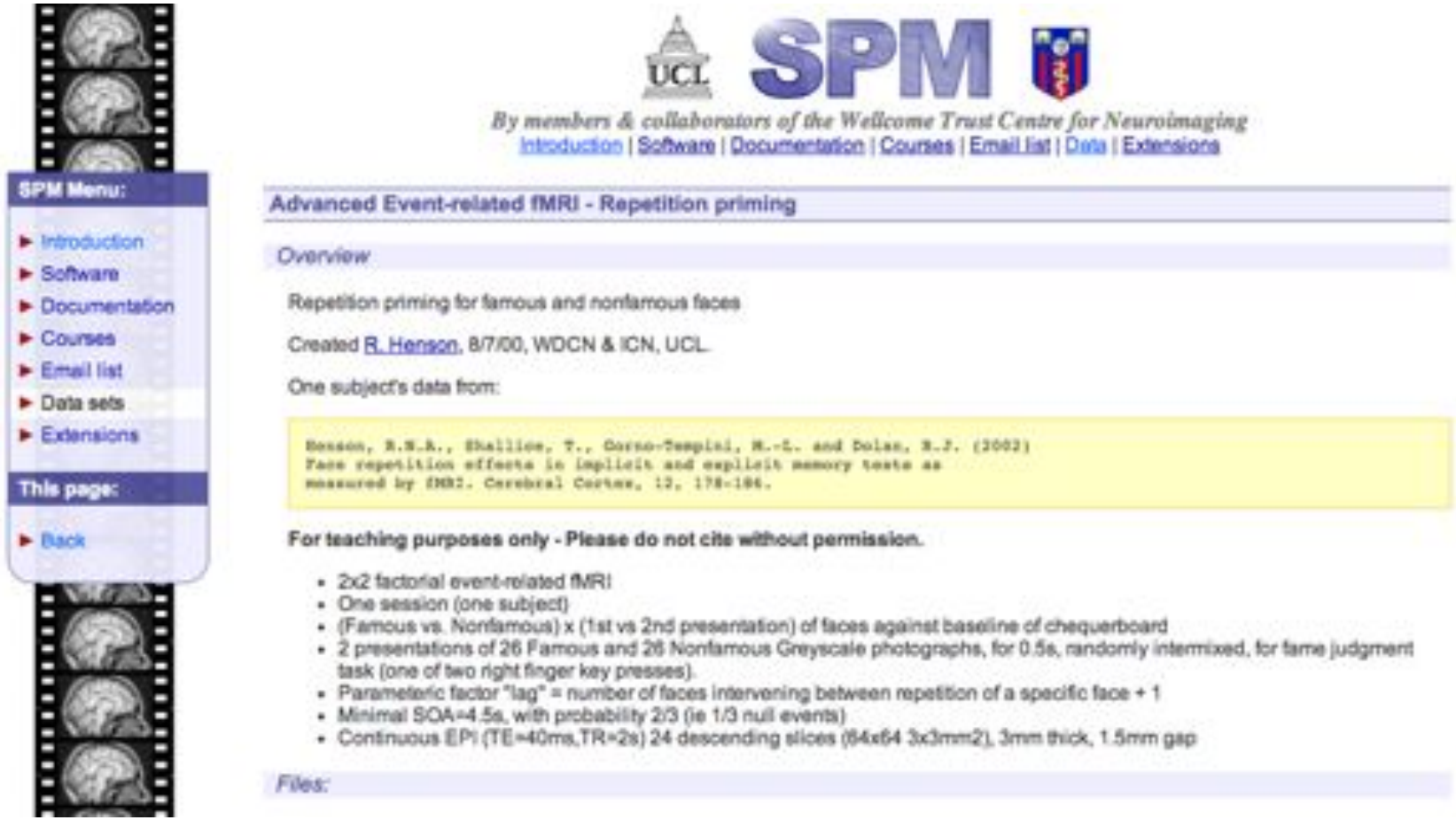
matlabbatch{2}.spm.spatial.realign.estwrite.data{1} = cellstr(spm_file(f(1,:),'prefix','a'));

to

matlabbatch{2}.spm.spatial.realign.estwrite.data{1} = cellstr(spm_file(f(:,:),'prefix','a'));

Download and install SPM

http://www.fil.ion.ucl.ac.uk/spm/data/face_rep/



Download and install SPM

Terminal

- cd /Users/login
- unzip spm12.zip
- unzip -o spm12_updates_rxxxx.zip -d spm
- Move spm12 to applications folder

Matlab

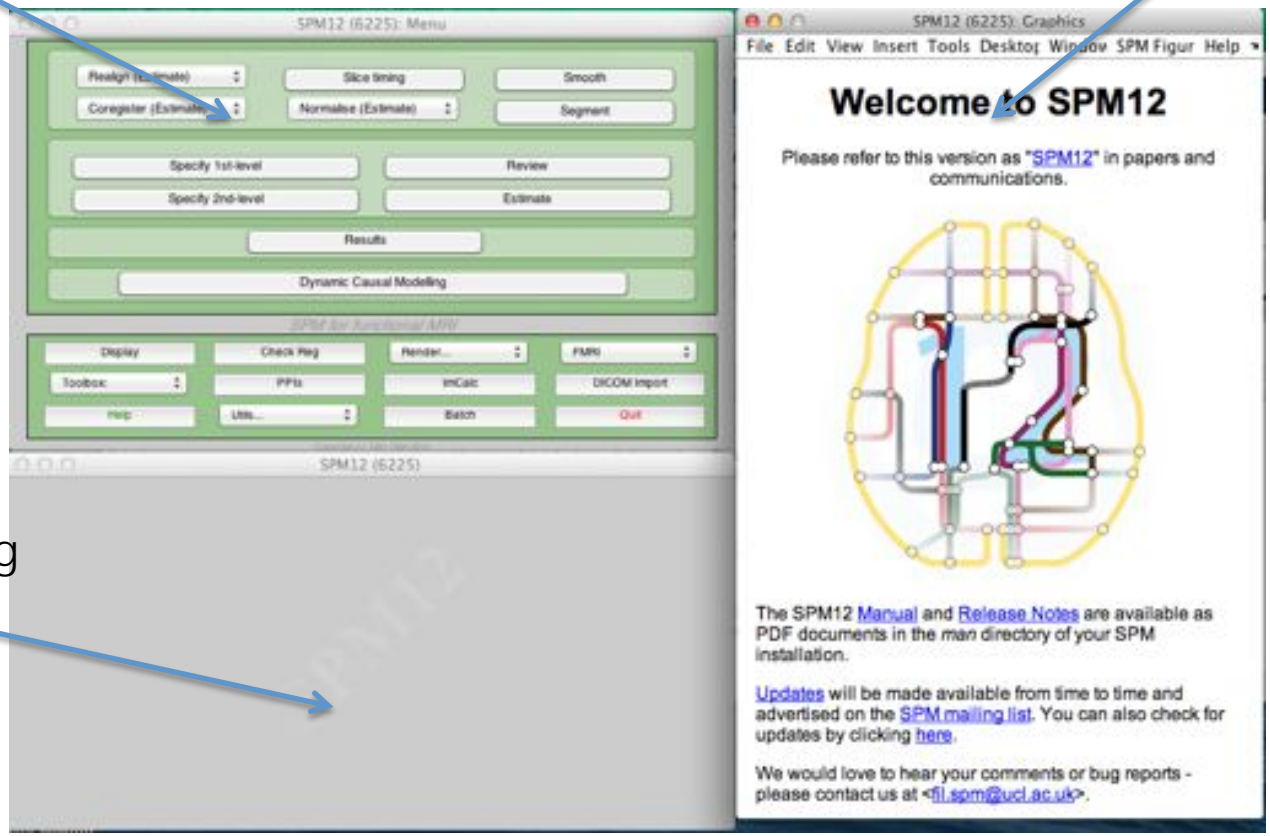
- Add path spm12 with subfolders
- Start SPM12: *spm fmri*

Structure of SPM

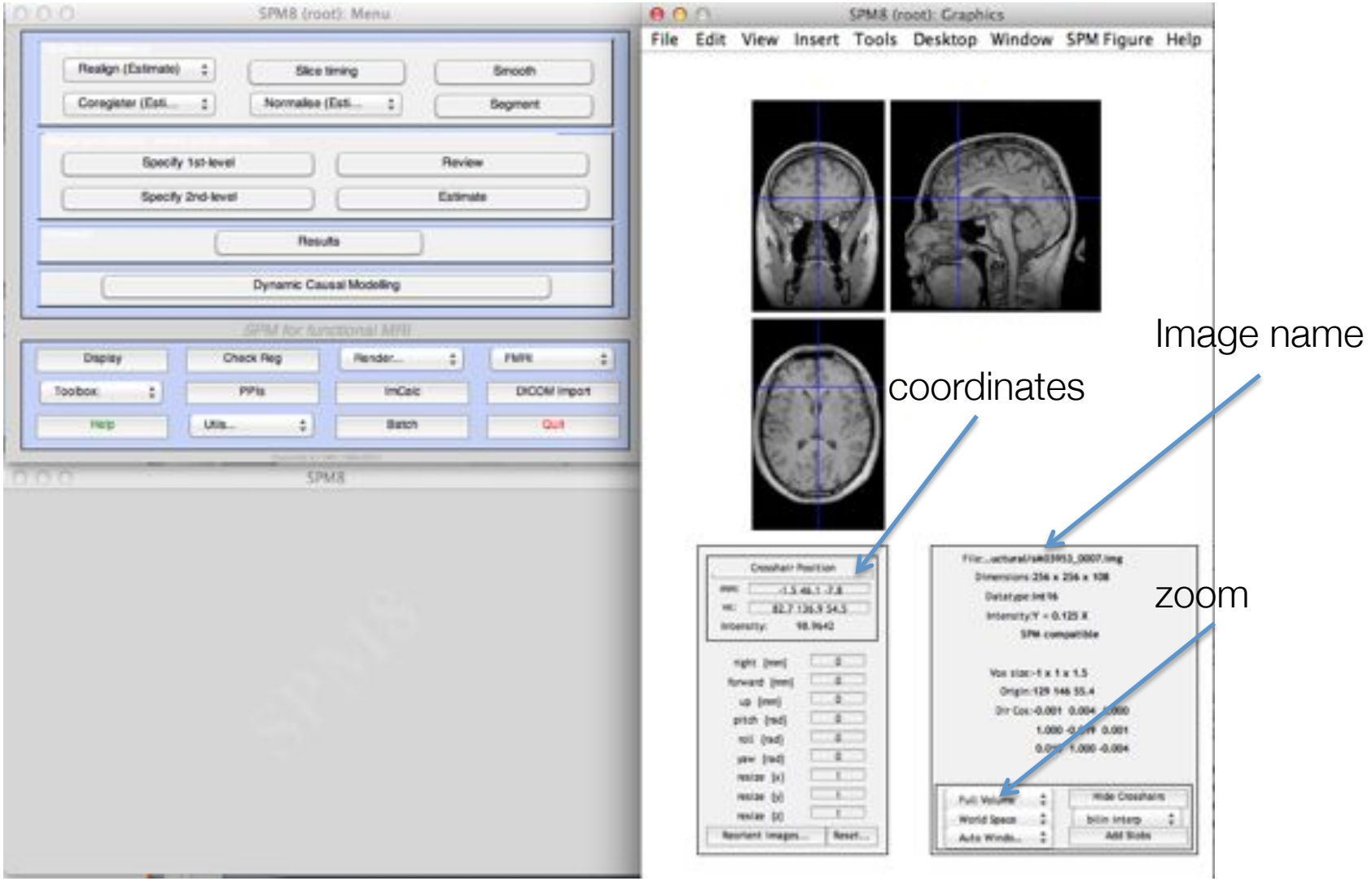
specification

display

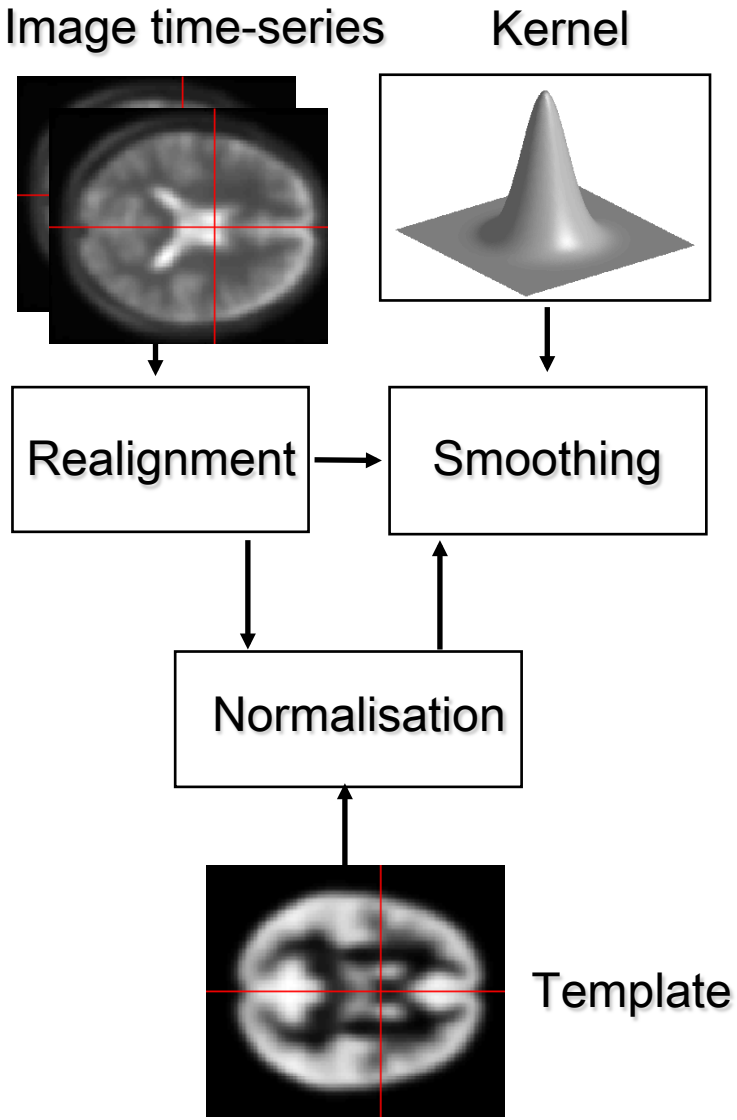
processing



Display

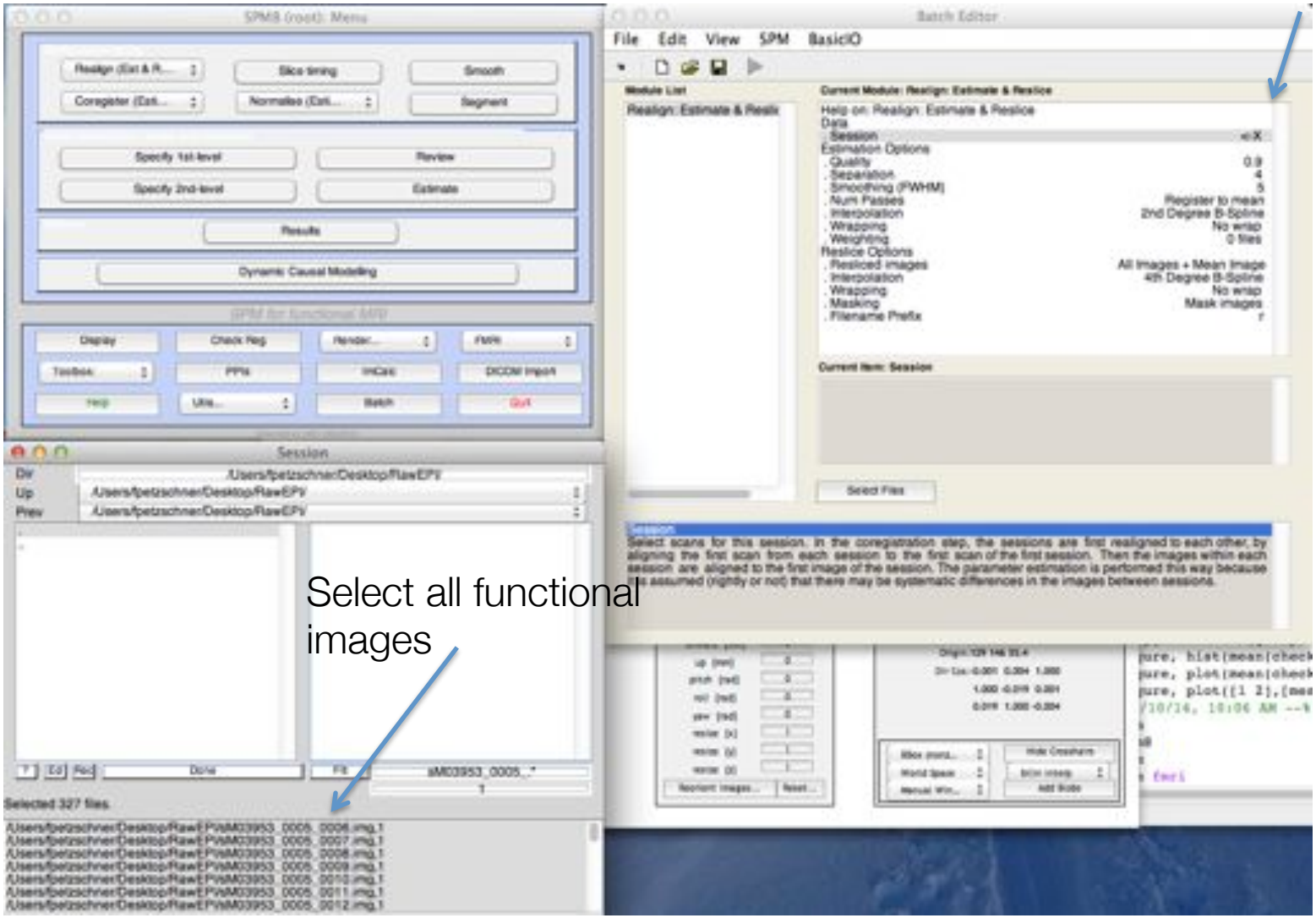

SPM8 (root): Menu
Realign (Estimate)
Slice timing
Smooth
Coregister (Esti...
Normalise (Esti...
Segment
Specify 1st-level
Review
Specify 2nd-level
Estimate
Results
Dynamic Causal Modelling
SPM for functional MRI
Display
Check Reg
Render...
Toolbox
PPIs
ImCalc
DICOM Import
Help
Utils...
Batch
Quit
SPM8
SPM8 (root): Graphics
File Edit View Insert Tools Desktop Window SPM Figure Help
coordinates
Image name
zoom

Preprocessing

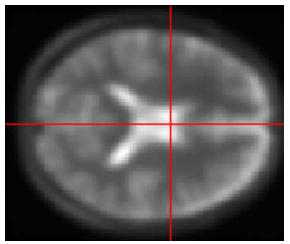


Realignment

Fill in everything with an X



Realignment

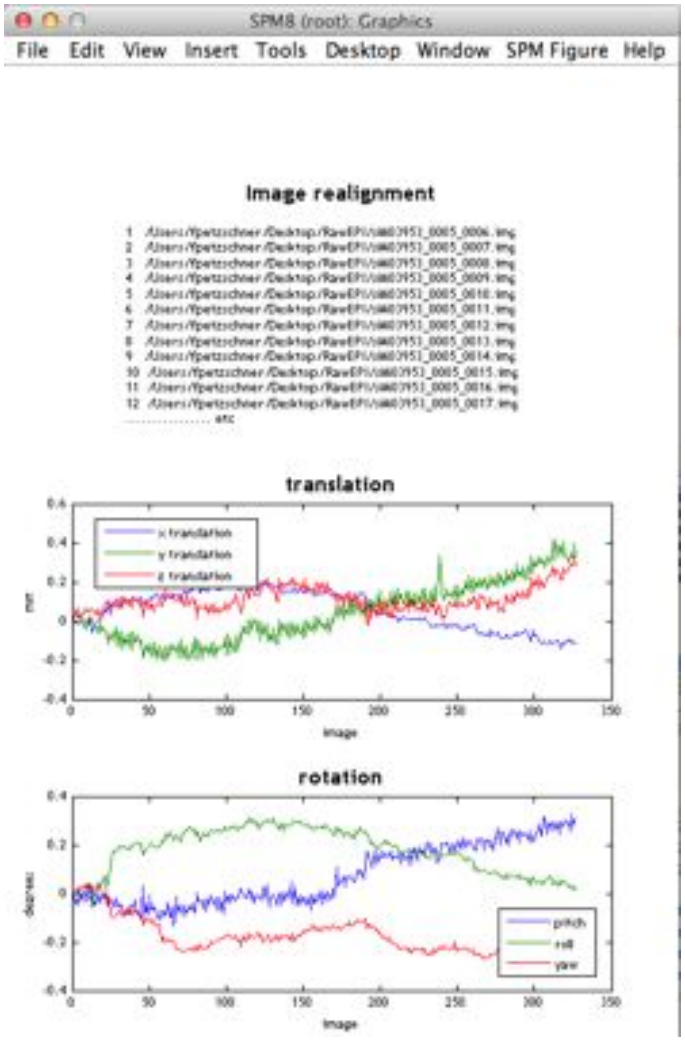


All images of a run will be aligned to the first image of the run

Images are then called **rp_sM……txt**

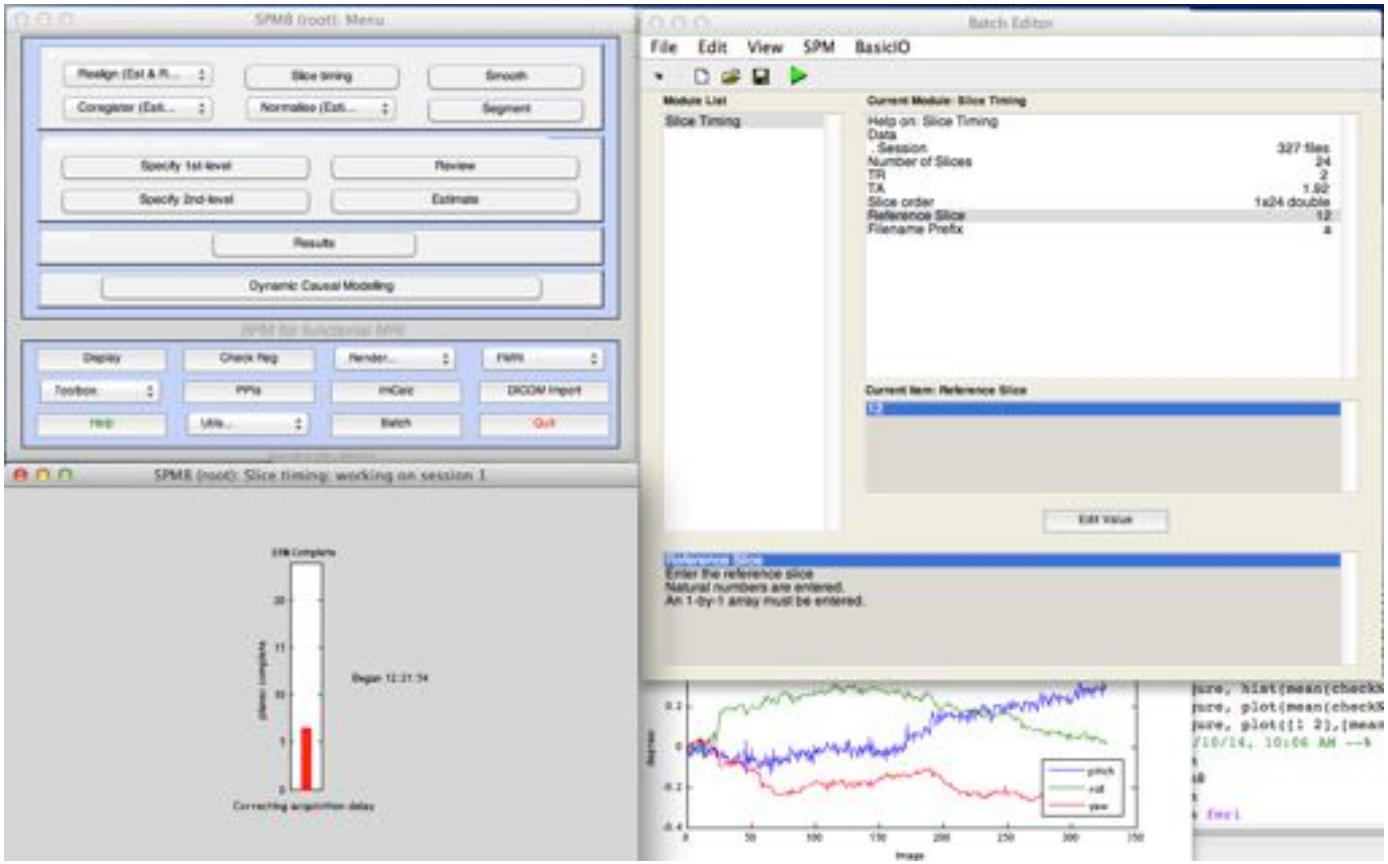
Returns the movement parameters:
Problematic if more than a voxels worth of motion!

Also creates a **meansM….img** that will used in the coregistration



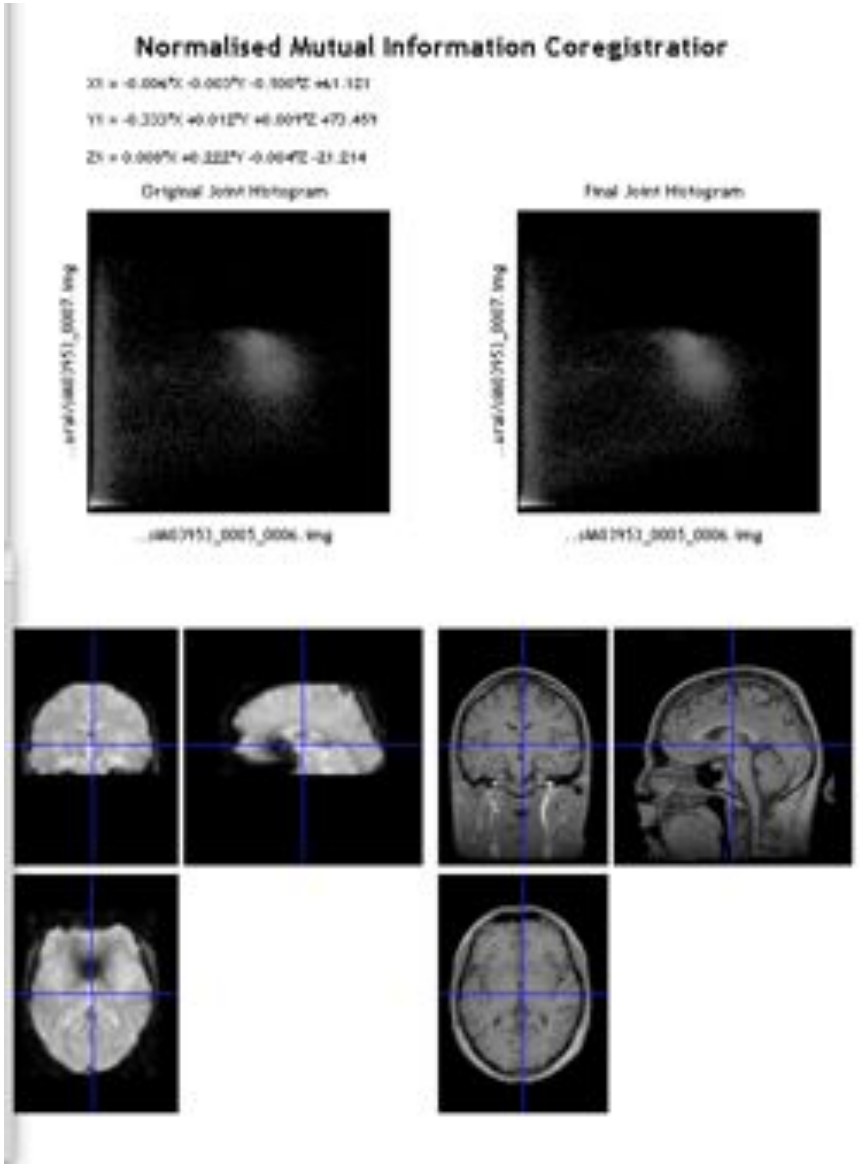
Slice Time Correction

TR = 2s
N = 24 slices
TA = TR – TR/N
Slice order: 24:-1:1
Reference Slice: 12
Use the **rp……txt**
And create **a……txt**



Coregistration

reference **means……img**
source: structural **s……img**



New in SPM 12

Segmentation

"Volumes" in "Data > Channels" and select the subjects coregistered anatomical image sM03953_0007.img.

Change "Save Bias Corrected" so that it contains "Save Bias Corrected" instead of "Save Nothing".

At the bottom of the list, select "Forward" in "Deformation Fields"

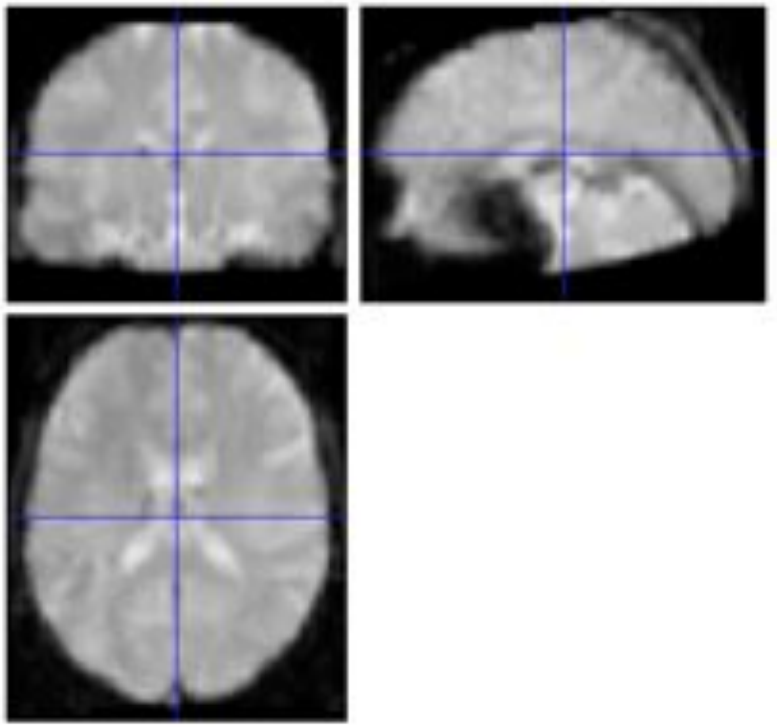
SPM will segment the structural image using the default tissue probability maps as priors. SPM will create, by default, gray and white matter images and bias-field corrected structral image. These can be viewed using the CheckReg

SPM will also write a spatial normalisation deformation field file eg. y_sM03953_0007.nii file in the original structural directory. This will be used in the next section to normalise the functional data.

New in SPM 12

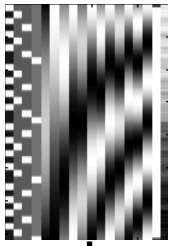
Normalise (Write)

Deformation field: **y……_.nii**
Images to write: realigned functional images **ars……img** and mean functional image **means……img**
Voxel size [2 2 2] → [3 3 3]
Create normalised files **w…..mat**

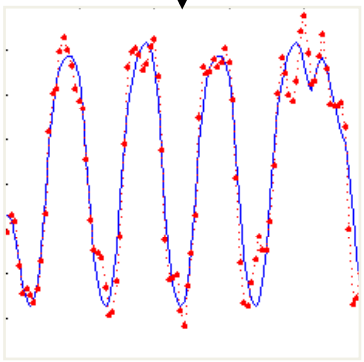


GLM

Design matrix



General linear model



Parameter estimates

The Task

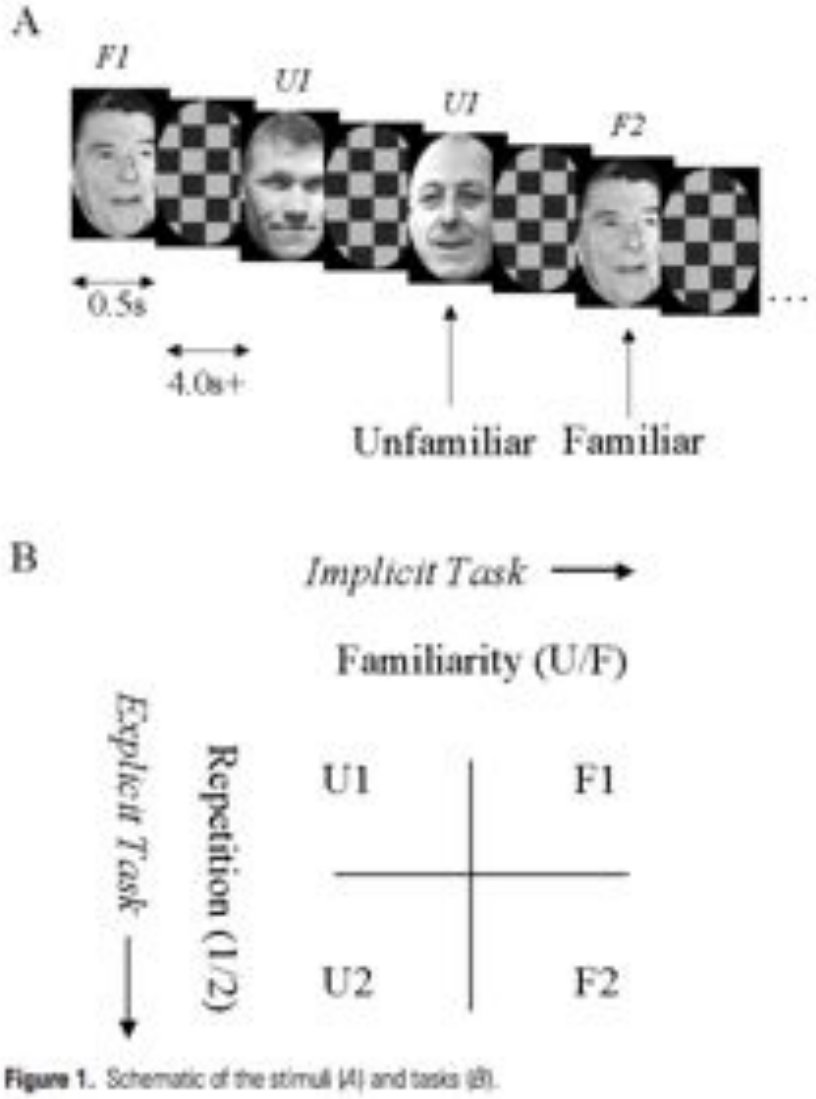
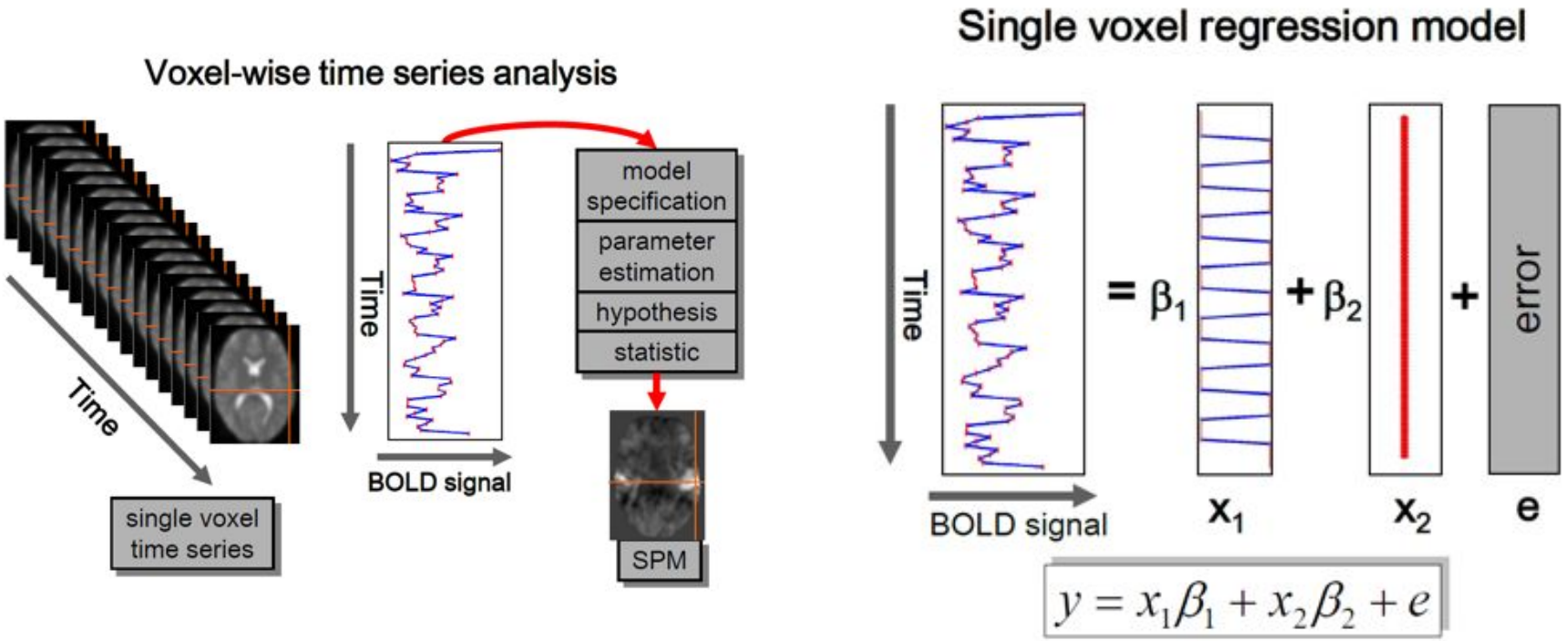


Figure 1. Schematic of the stimuli (A) and tasks (B).

- Parameteric factor "lag" = number of faces intervening between repetition of a specific face + 1
- Continuous EPI (TE=40ms,TR=2s) 24 descending slices (64x64 3x3mm2), 3mm thick, 1.5mm gap

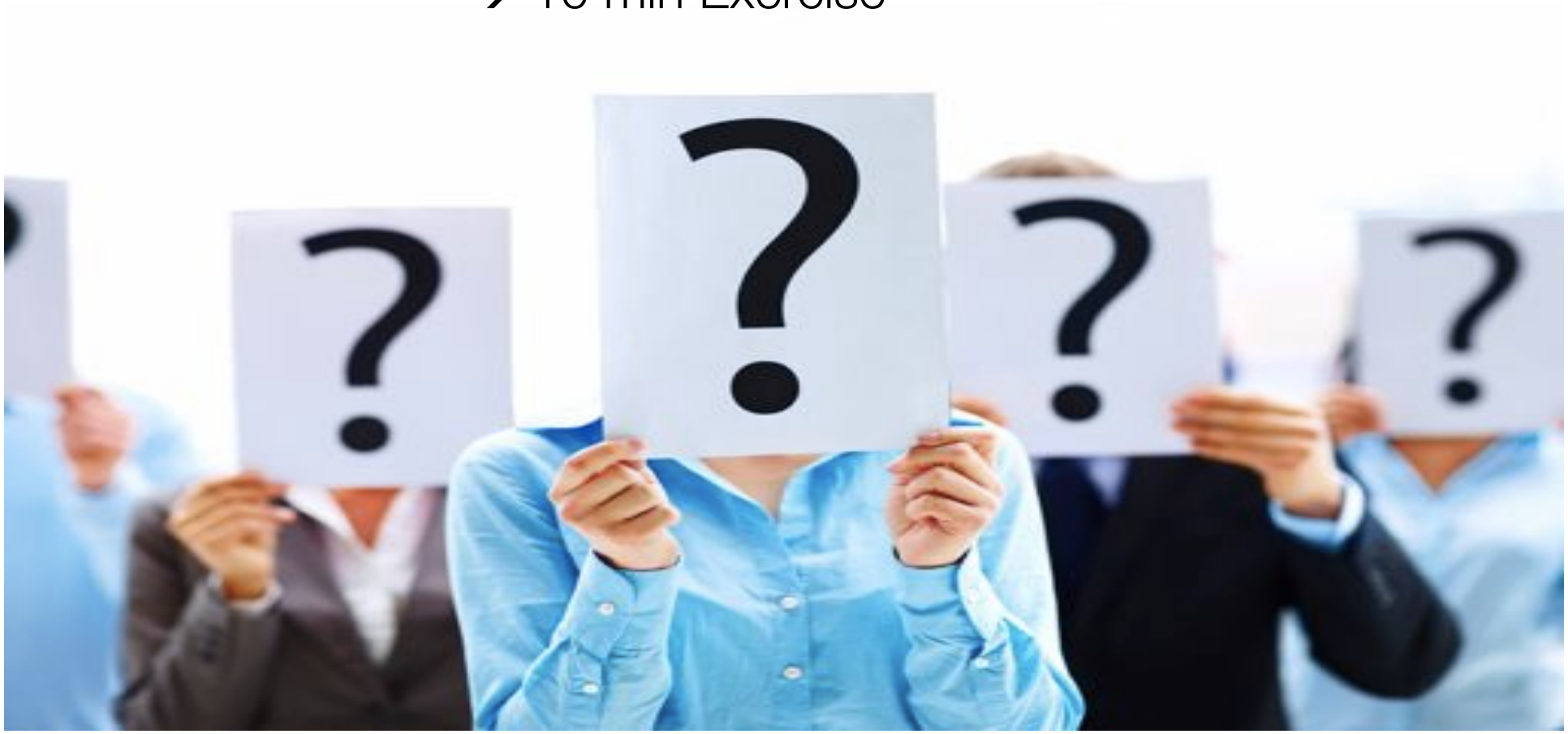
Henson, R.N.A., Shallice, T., Gorno-Tempini, M.-L. and Dolan, R.J. (2002) Face repetition effects in implicit and explicit memory tests as measured by fMRI. Cerebral Cortex, 12, 178-186.

Model Specification:



- What questions can we answer with this data set?
- How would your GLM look like?

→ 10 min Exercise

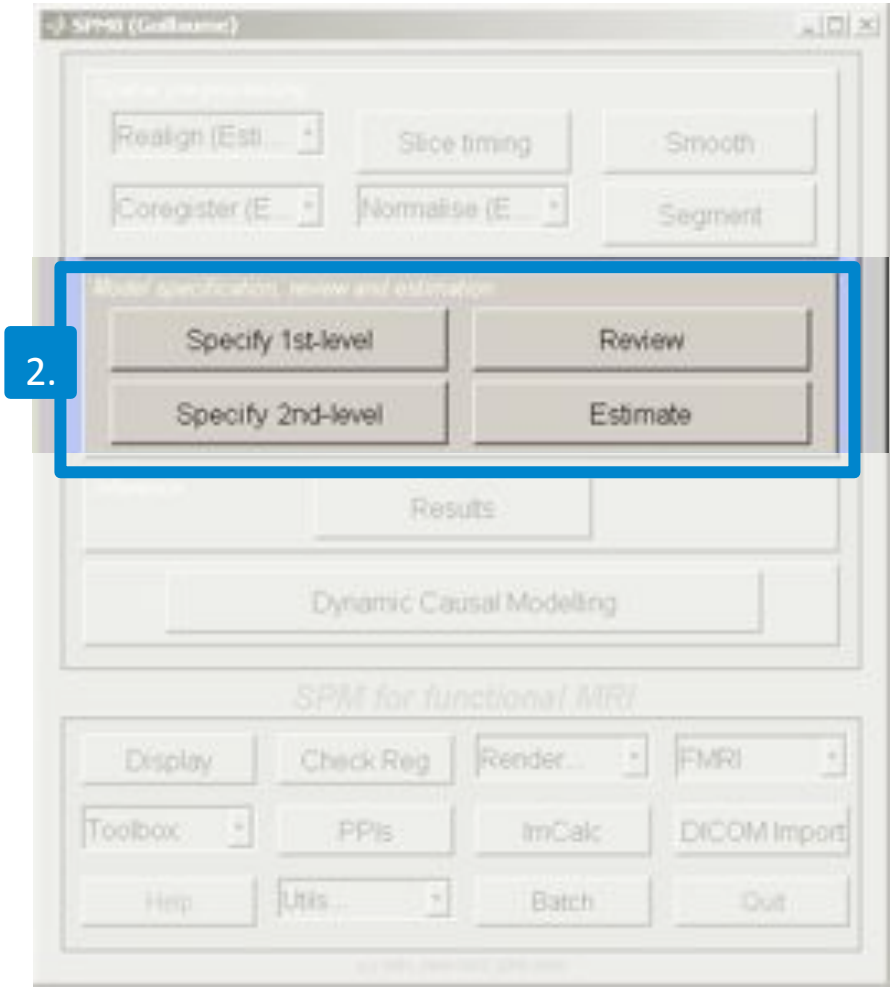


- What questions can we answer with this data set?

  → Difference between familiar and unfamiliar faces
  → Difference between repetition 1 and repetition 2
  → Difference between a repetition of a familiar face versus and unfamiliar one

- How would your GLM look like?
  - Regressors for familiar and unfamiliar and repetition 1 and 2
  - Regressors for motion

The SPM Graphical User Interface (GUI)

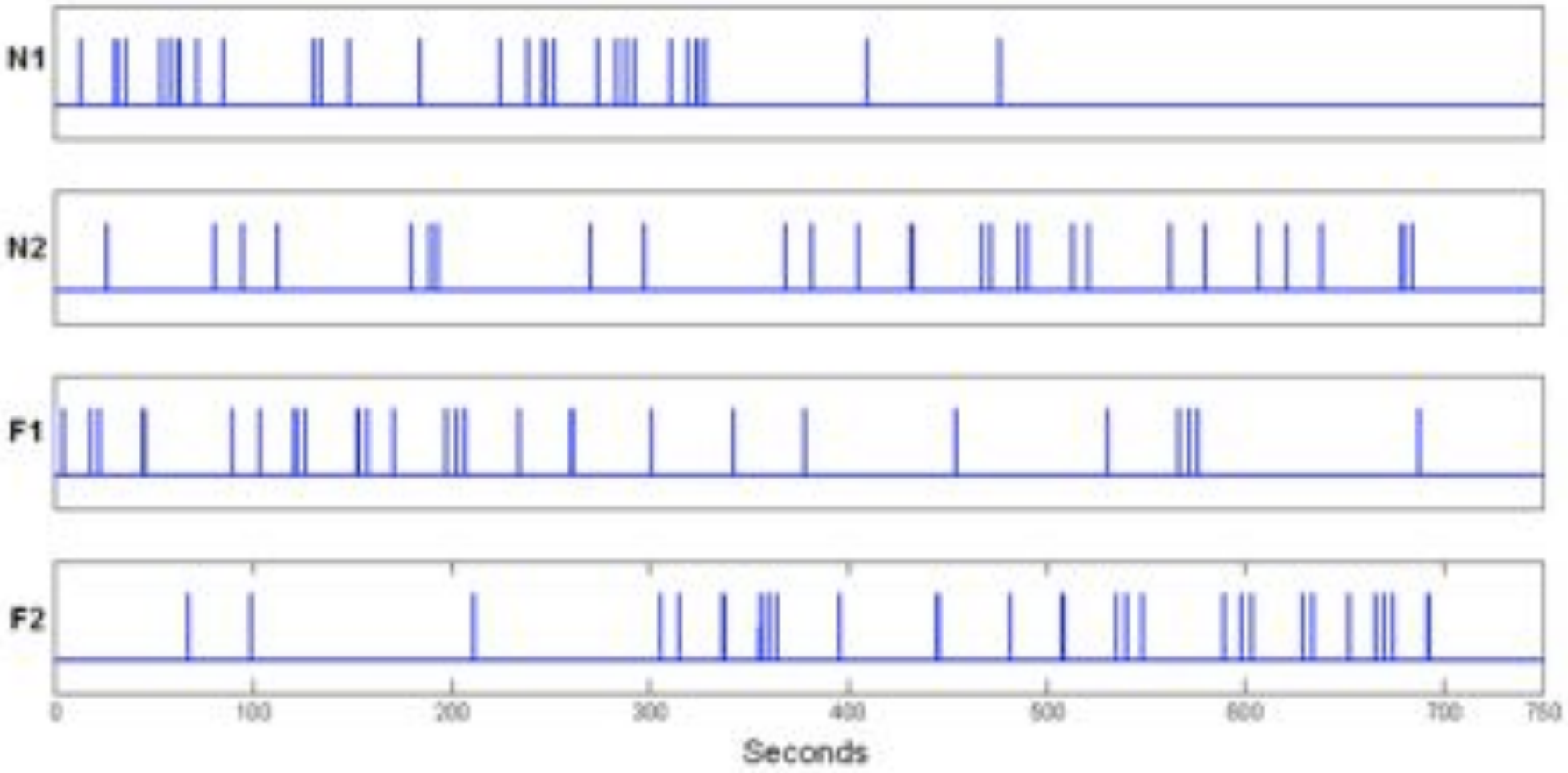


2.

- Model Specification
  - Specify 1st level
  - Review
  - Estimate

stimulus onset times

load sots.mat file



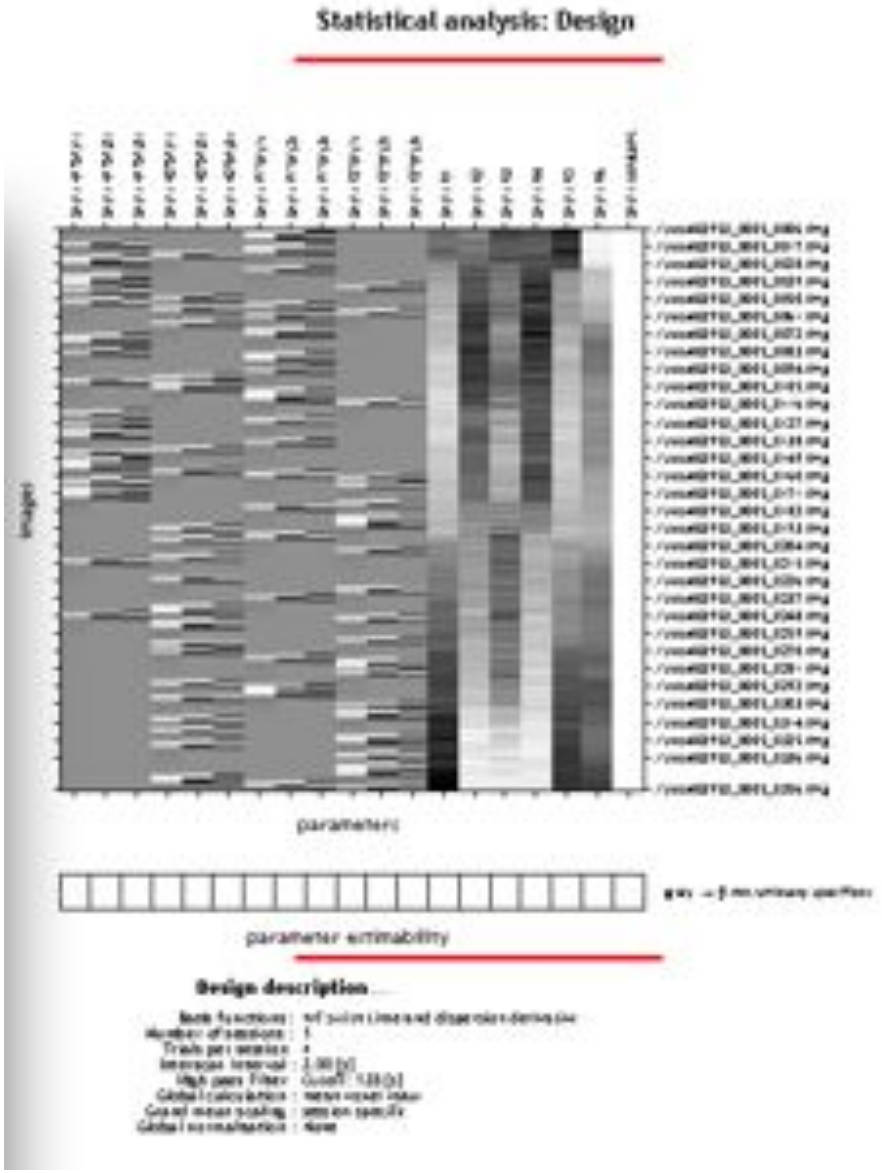
Modelling

Load **sots.ma**
Units of design: Scans
Interscan interval: 2
Microtime Resolution: 24
Mircotime Onset: 12

Use smoothed images: **swars…img**

Conditions: N1, N2, F1, F2
Multiple Regressors: realignment file rp_.txt
Factorial Design: Fam and Rep

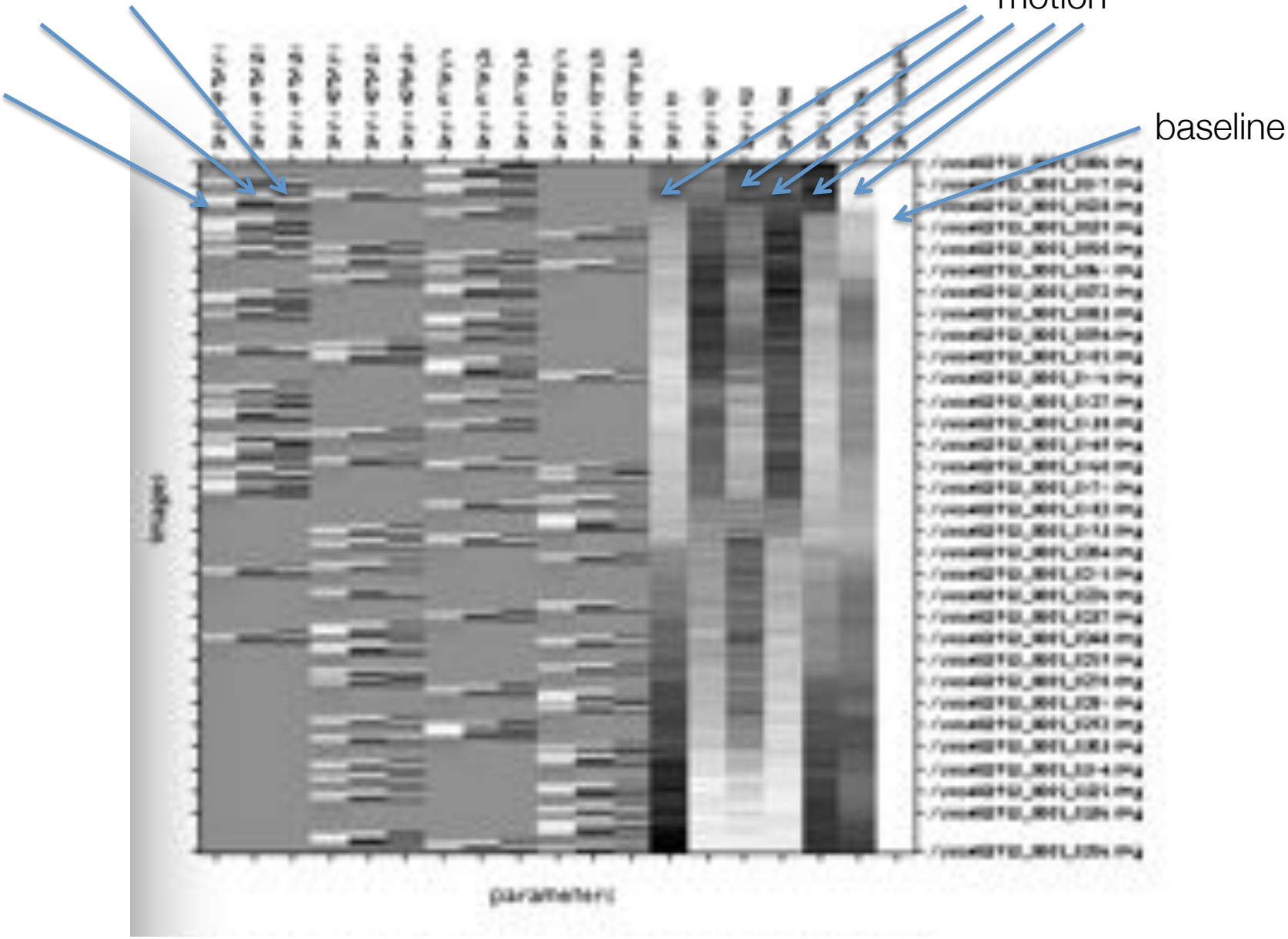
Canonical HRF: select all derivatives



HRF and derivatives

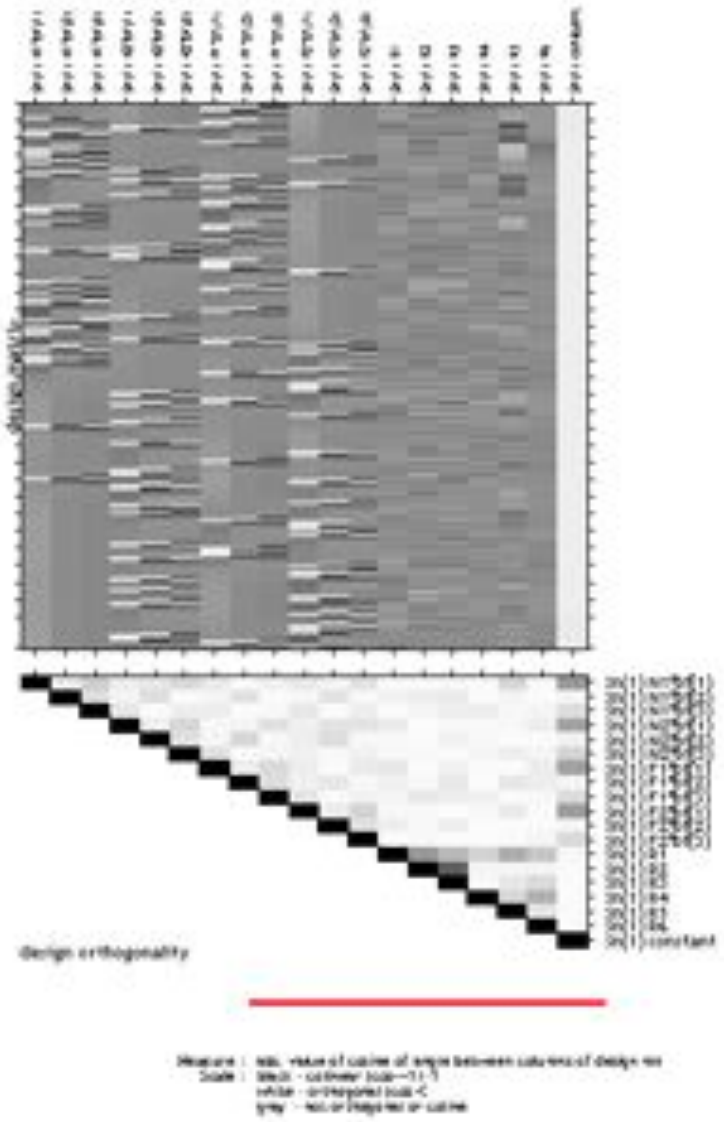
motion

baseline

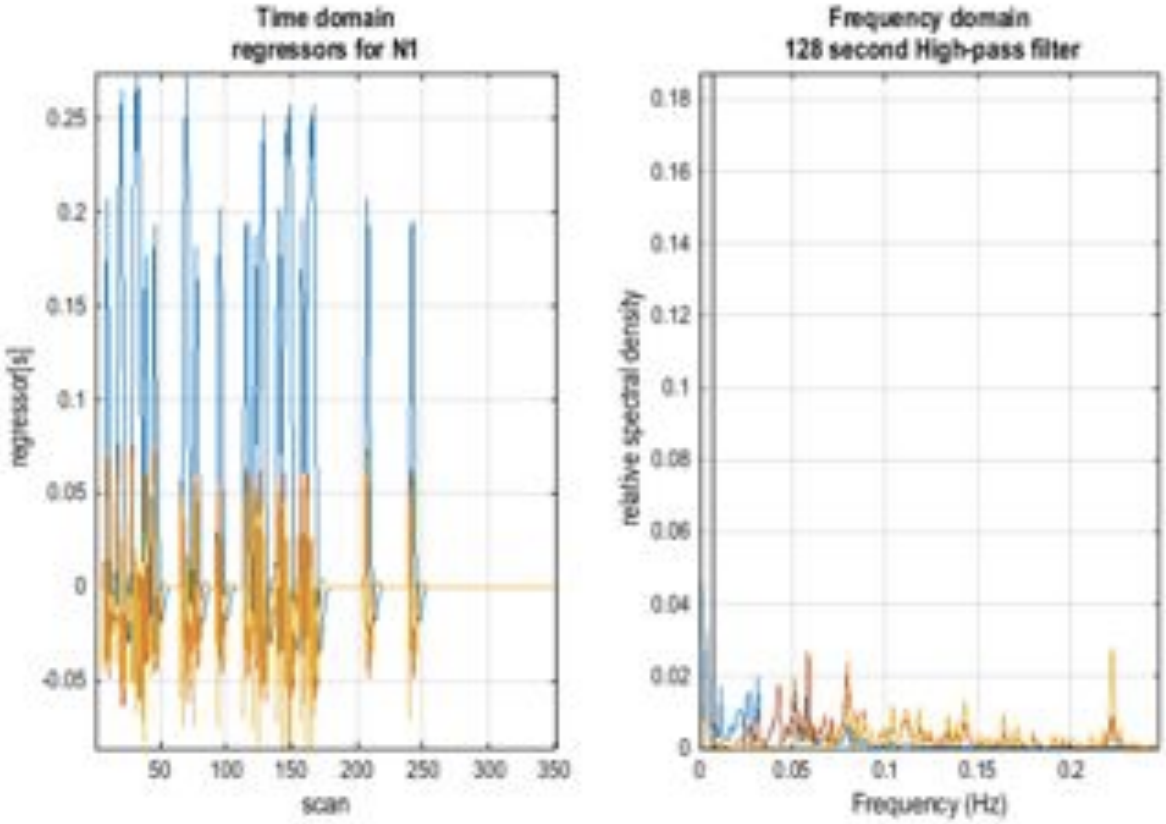


Orthogonality

Estimate **SPM.mat**

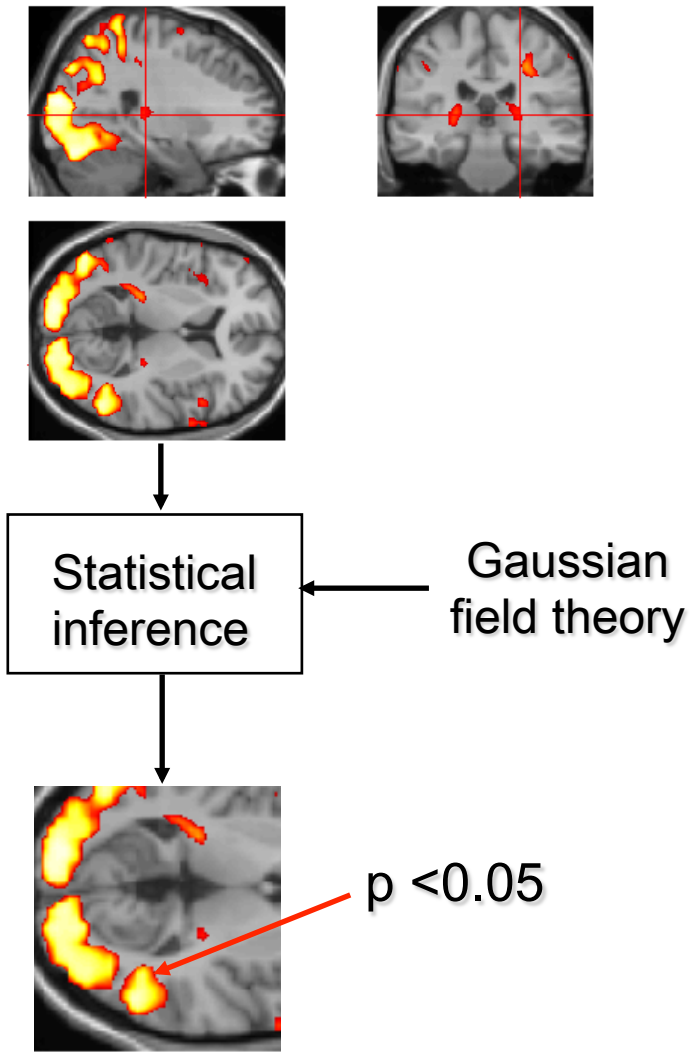


Regressors


Time domain
regressors for N1
regressor[s]
scan
Frequency domain
128 second High-pass filter
relative spectral density
Frequency (Hz)

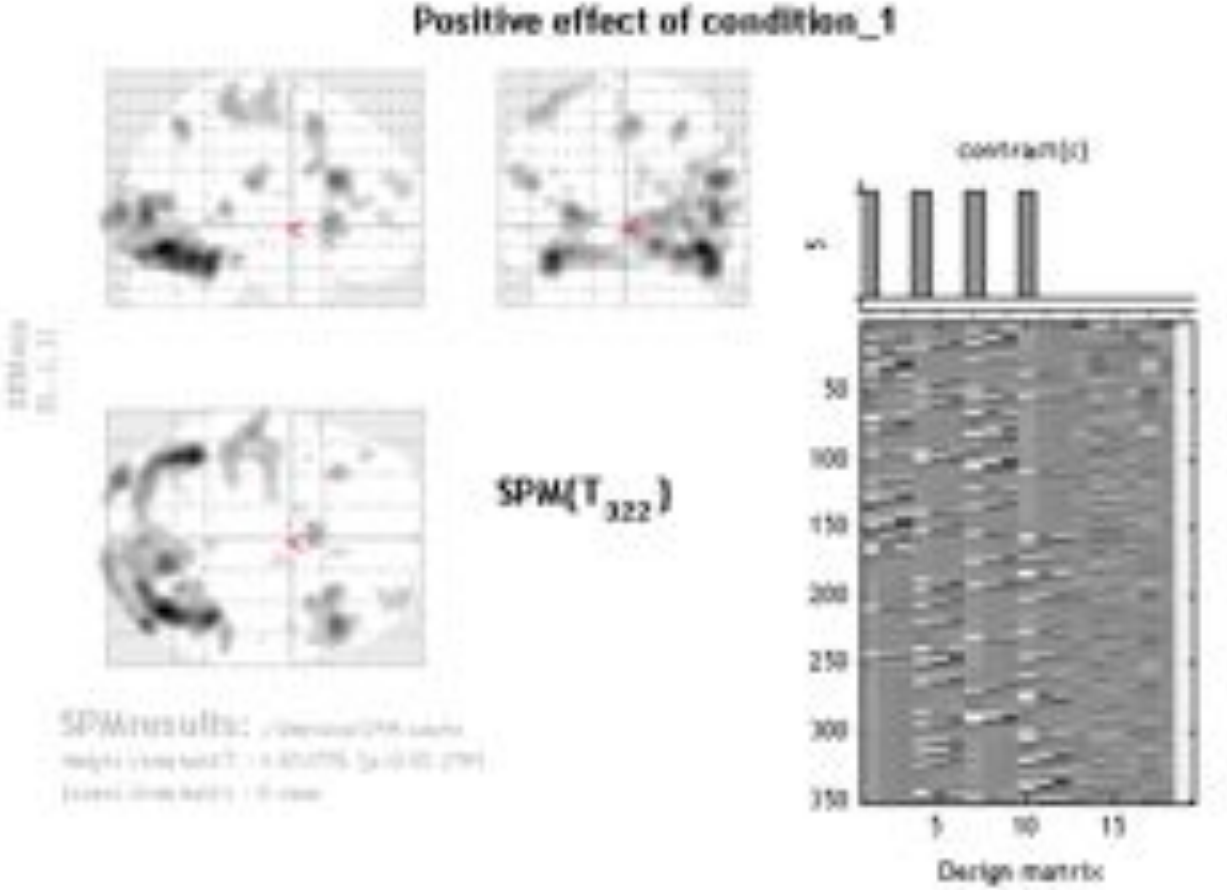
Statistics

Statistical parametric map (SPM)



T-Test

- Positive Effect of condition 1?



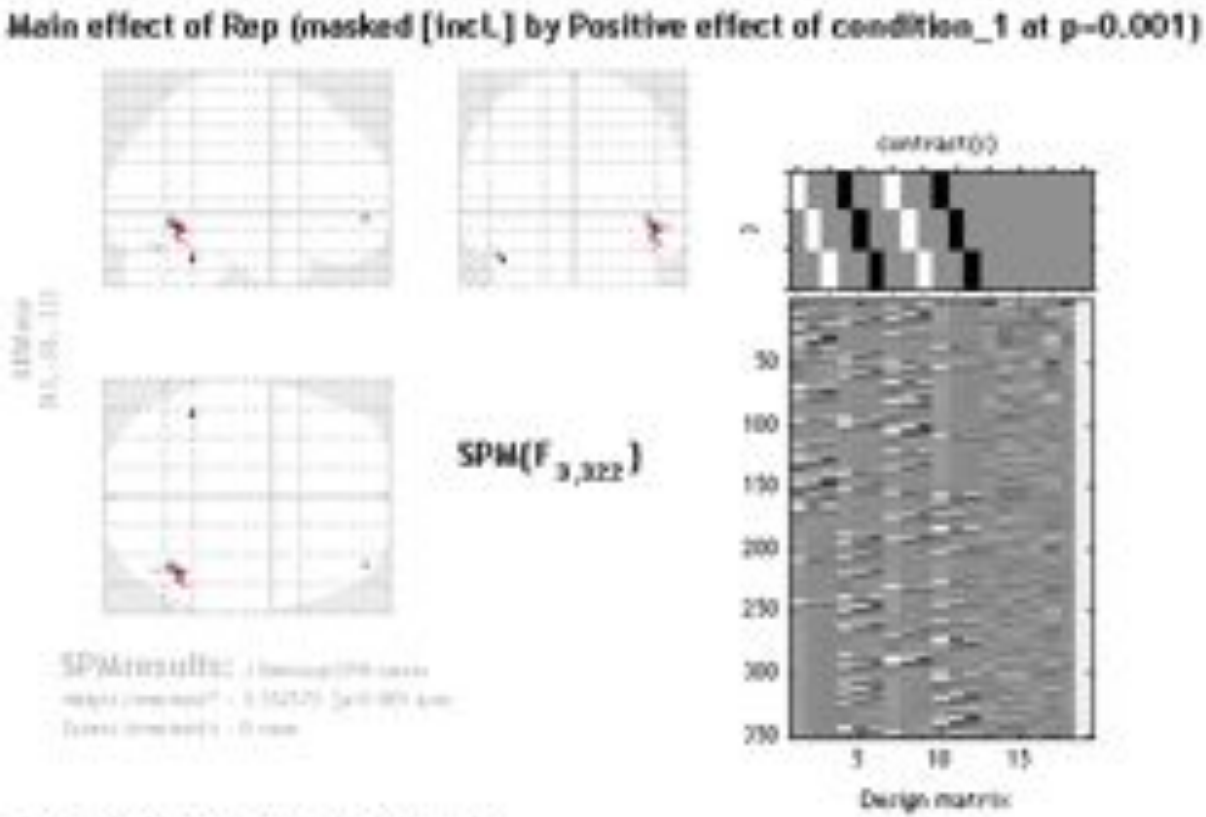
Levels

• peak-level: the chance (p) of finding (under the null hypothesis) a peak with this or a greater height (T- or Z-statistic), corrected (FWE or FDR)/ uncorrected for search volume.

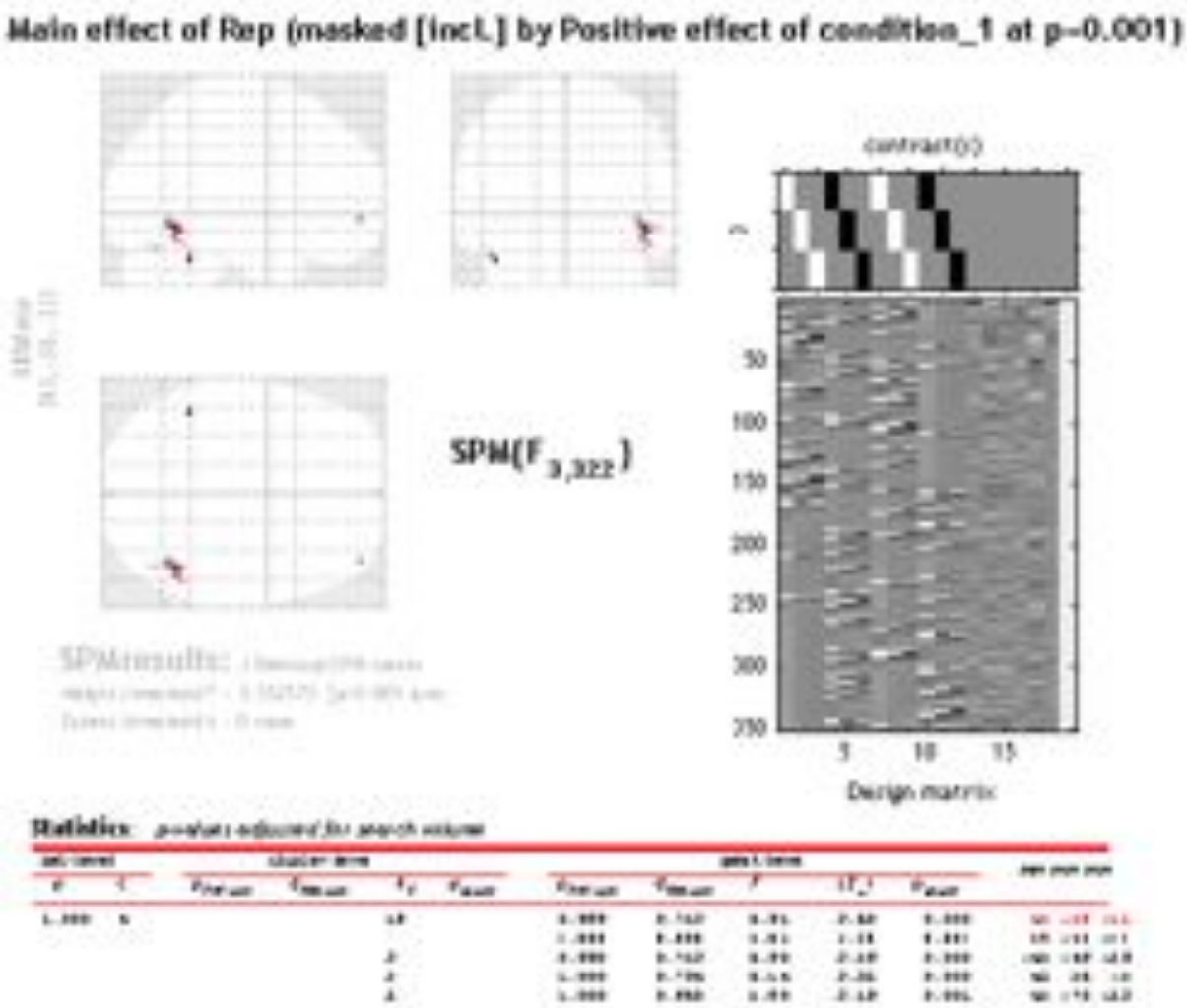
• cluster-level: the chance (p) of finding a cluster with this many(ke) or a greater number of voxels, corrected (FWE or FDR)/ uncorrected for search volume.

• set-level: the chance (p) of finding this (c) or a greater number of clusters in the search
volume.

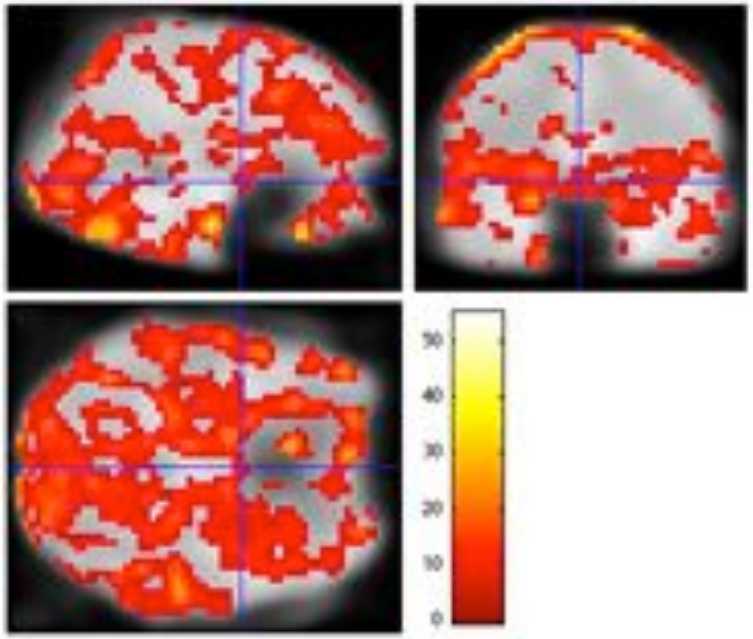
F-Test

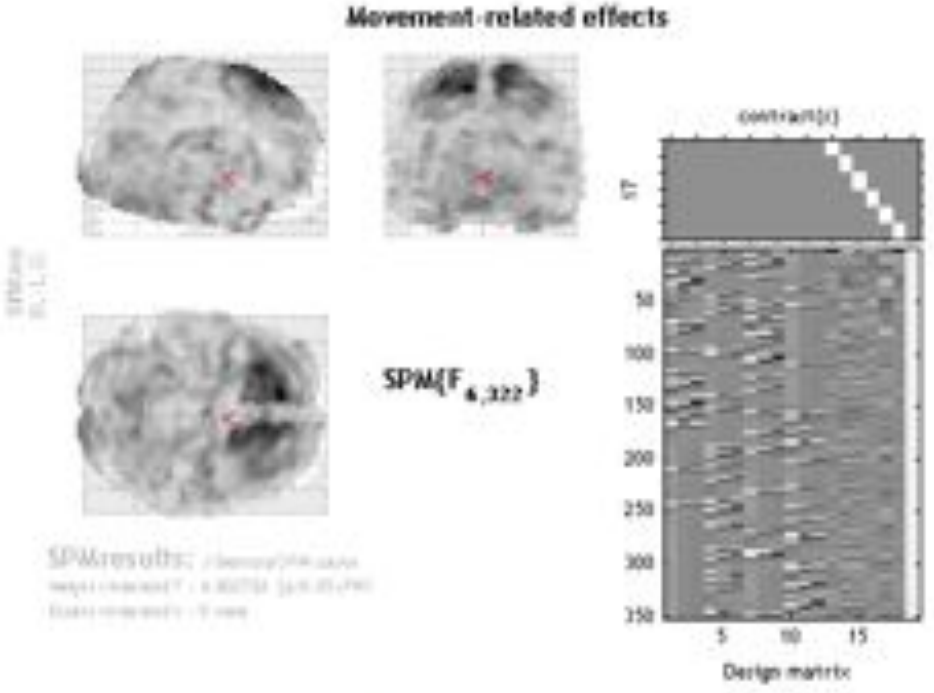

Main effect of Rep (masked [incl.] by Positive effect of condition_1 at p=0.001)
SPM(F 3,322)
contrast(s)
50
100
150
200
250
300
350
5
10
15
Design matrix

F-Test


Main effect of Rep (masked [incl.] by Positive effect of condition_1 at p=0.001)
SPM($F_{3,322}$)
contrast(s)
50
100
150
200
250
300
350
5
10
15
Design matrix
Statistics

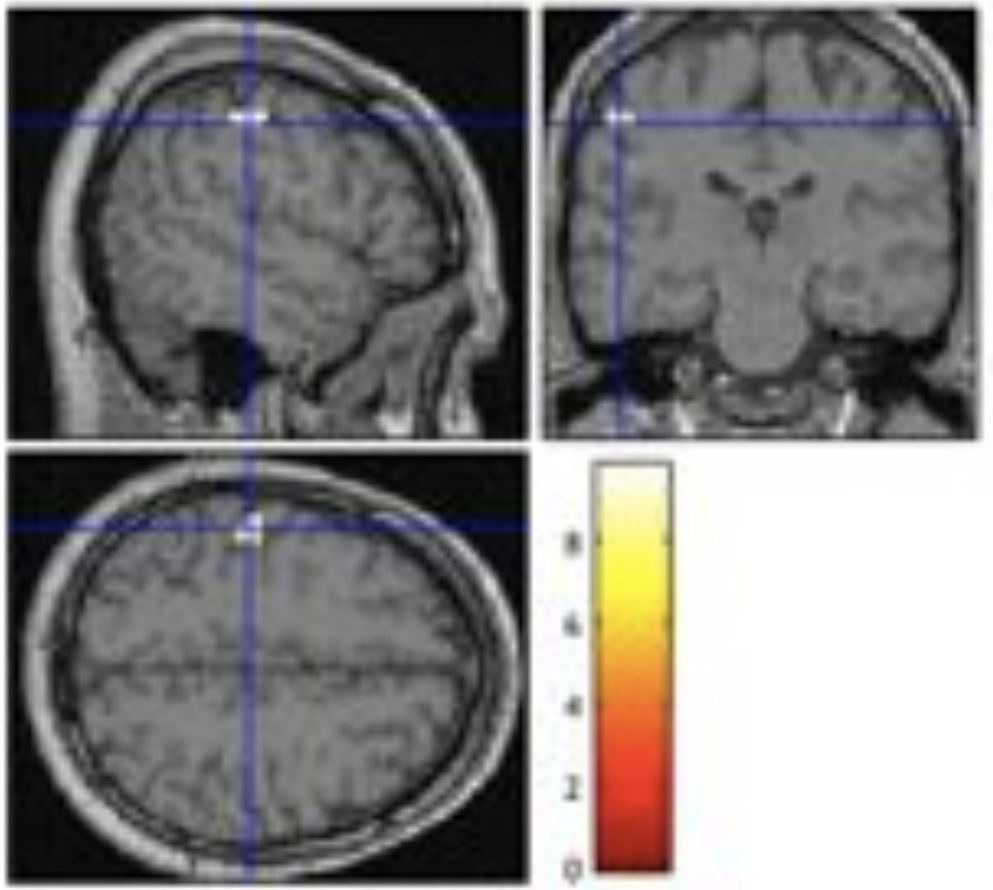
F-Test on movement parameters





Parametric Modulation

Lag Effect



END