

2017 fMRI資料分析助理研習營

Spm8 is required!

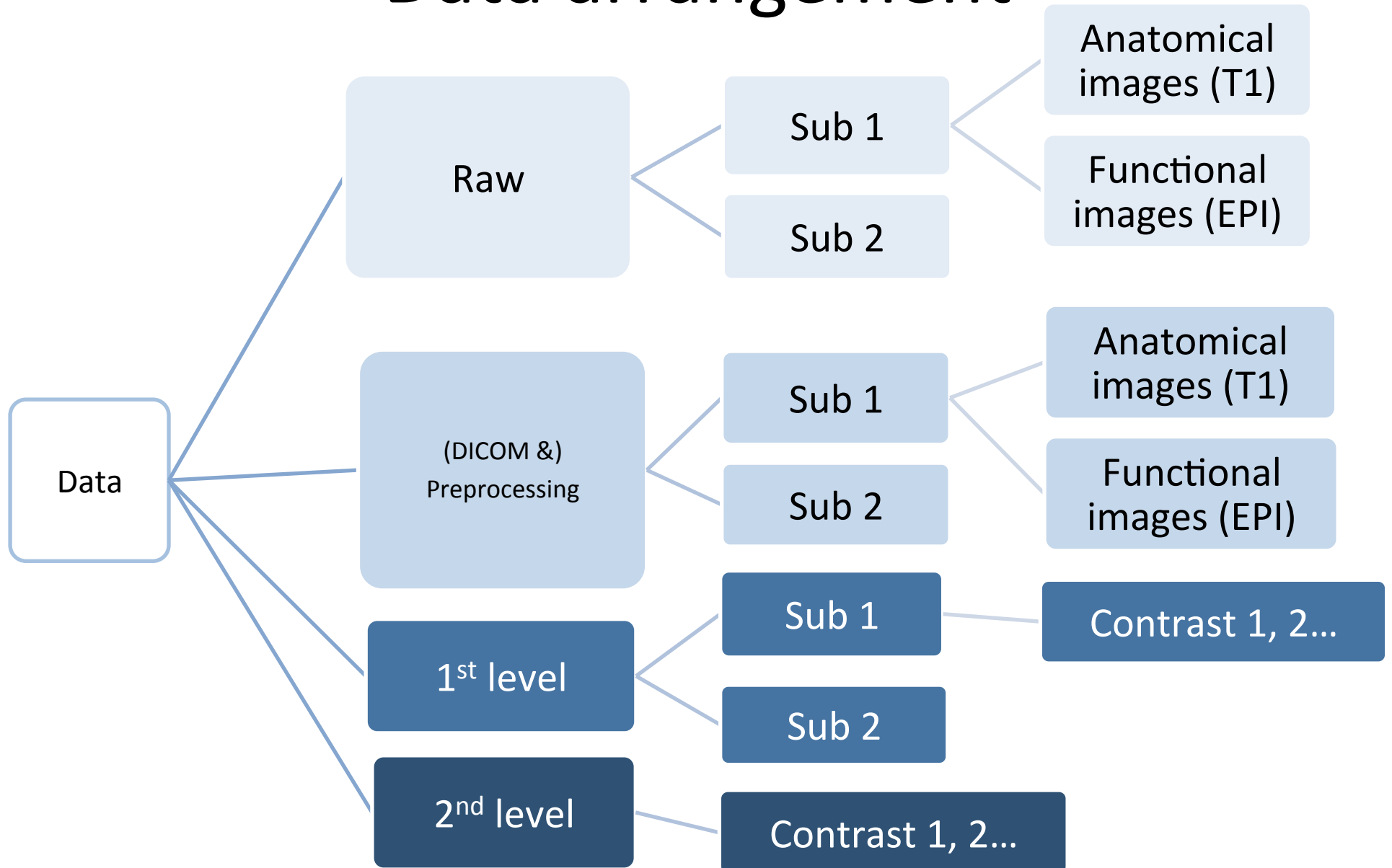
fMRI data analysis using SPM8

TMBIC

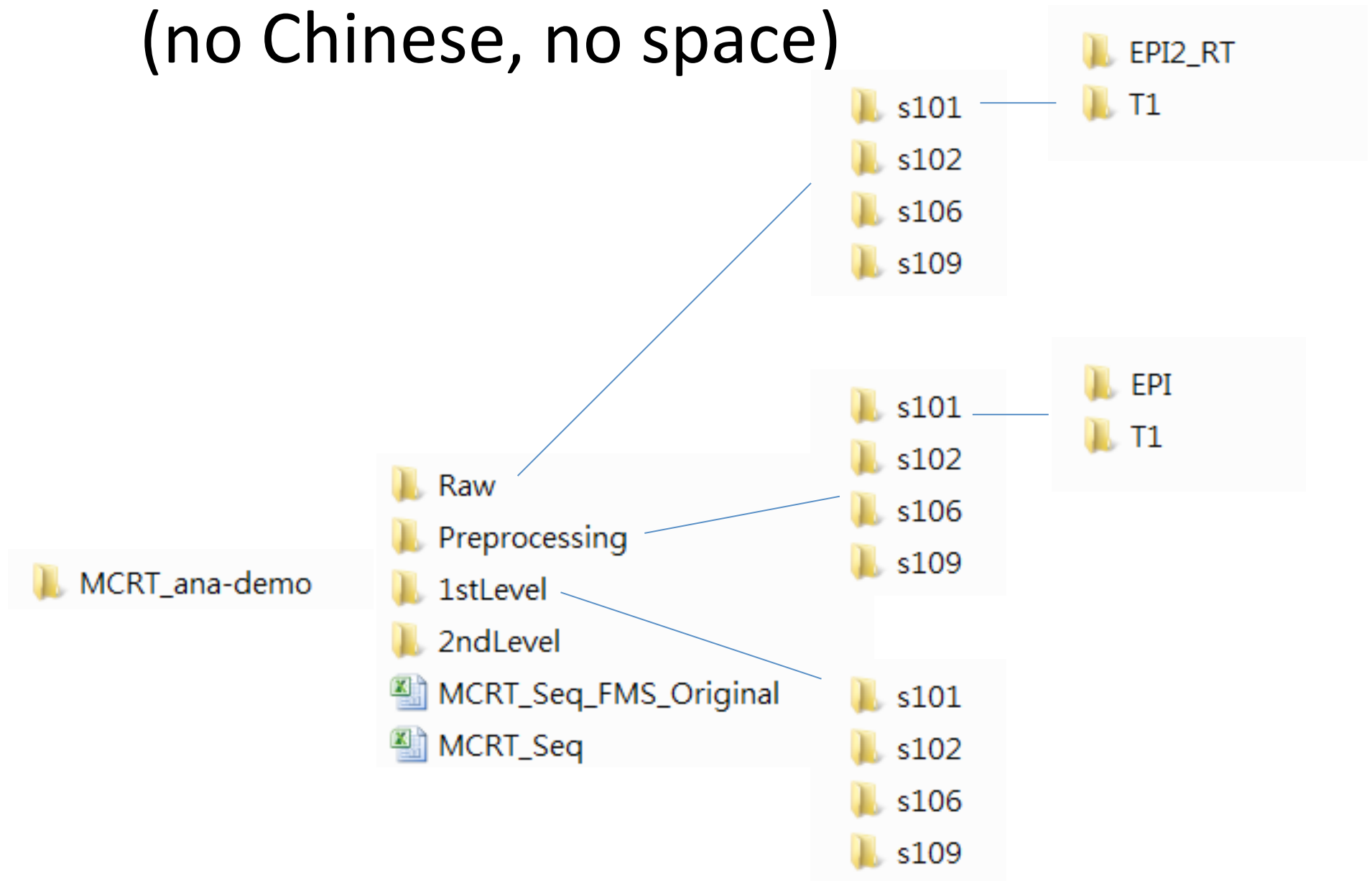
陳尹華、蔡文凱

李佩芳、盧毓文、鄭旭博

Data arrangement



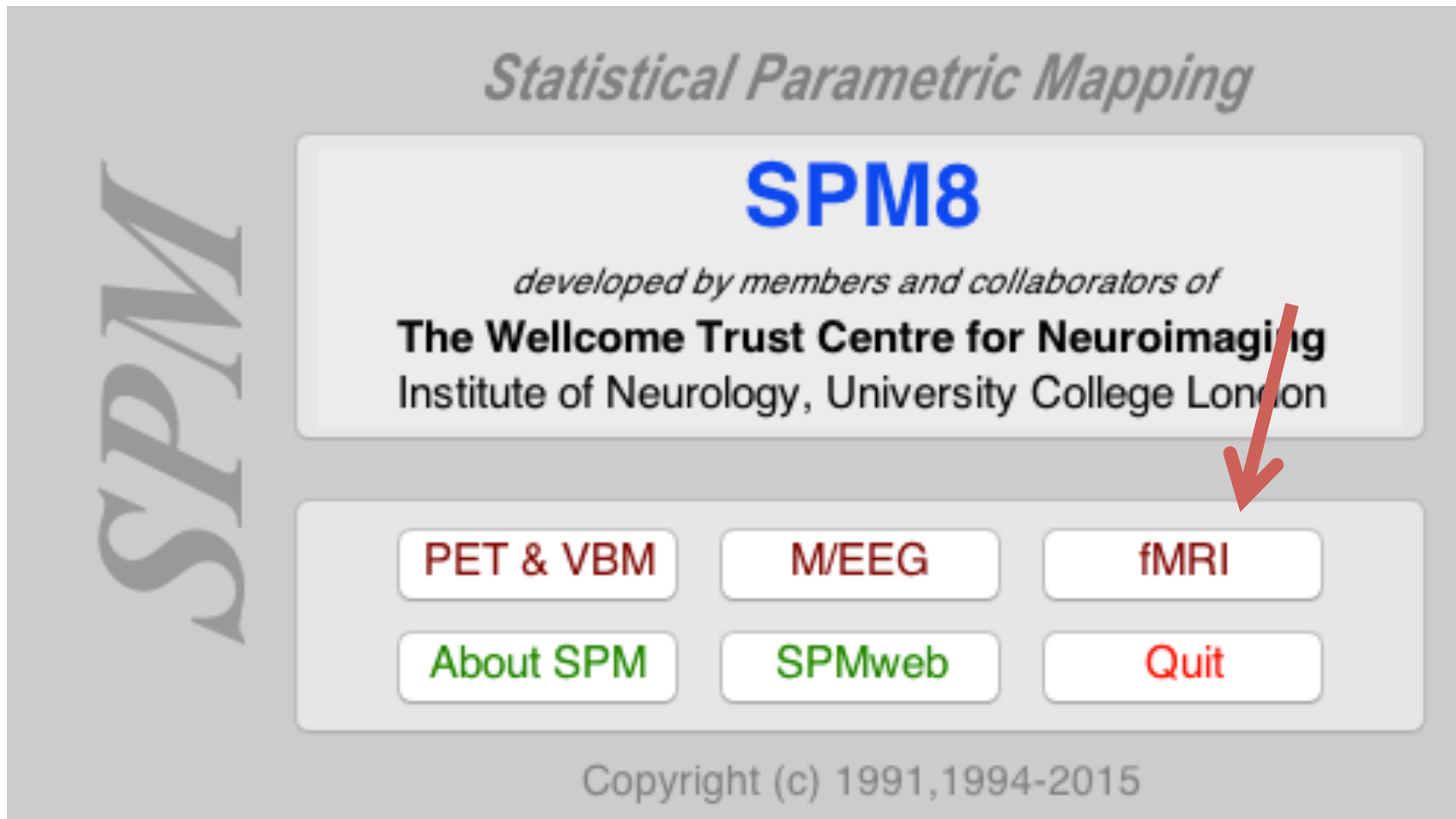
Suggested folder arrangement (no Chinese, no space)

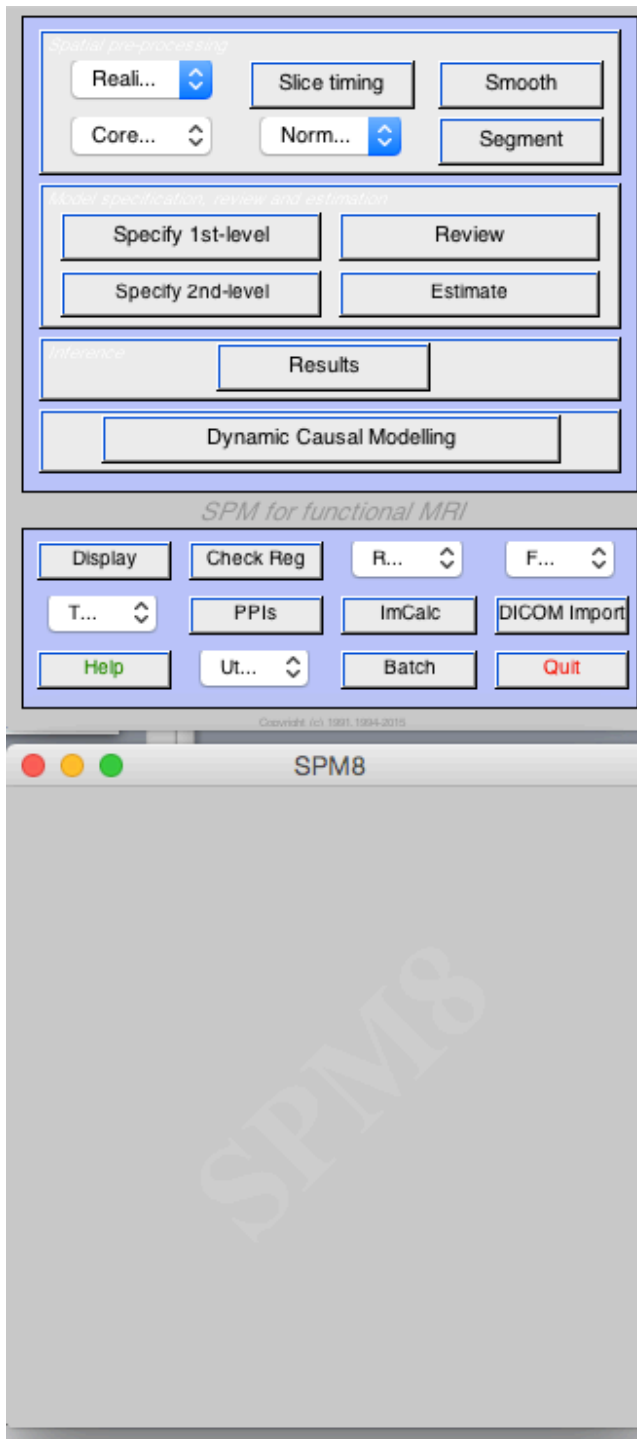


Start SPM package

- >> spm

-





SPM8

Welcome to SPM8

Please refer to this version as "SPM8" in papers and communications.

SPM is developed under the auspices of Functional Imaging Laboratory (FIL), The Wellcome Trust Centre for Neuroimaging, in the Institute of Neurology at University College London (UCL), UK.

Although SPM8 will read image files from previous versions of SPM, there are differences in the algorithms, templates and models used. Therefore, we recommend you use a single SPM version for any given project.

The SPM8 Release Notes can be found online:
<http://www.fil.ion.ucl.ac.uk/spm/software/spm8/>

Further information may be found at the SPMweb site:
<http://www.fil.ion.ucl.ac.uk/spm/>
 where details of the SPM email discussion list can be found:
<http://www.fil.ion.ucl.ac.uk/spm/support/>

A PDF manual is also available in the 'man' folder of SPM and online:
<http://www.fil.ion.ucl.ac.uk/spm/doc/manual.pdf>

SPM is free but copyright software, distributed under the terms of the GNU General Public Licence as published by the Free Software Foundation (either version 2, as given in file spm_LICENCE.man, or at your option, any later version). Further details on "copyleft" can be found at <http://www.gnu.org/copyleft/>.

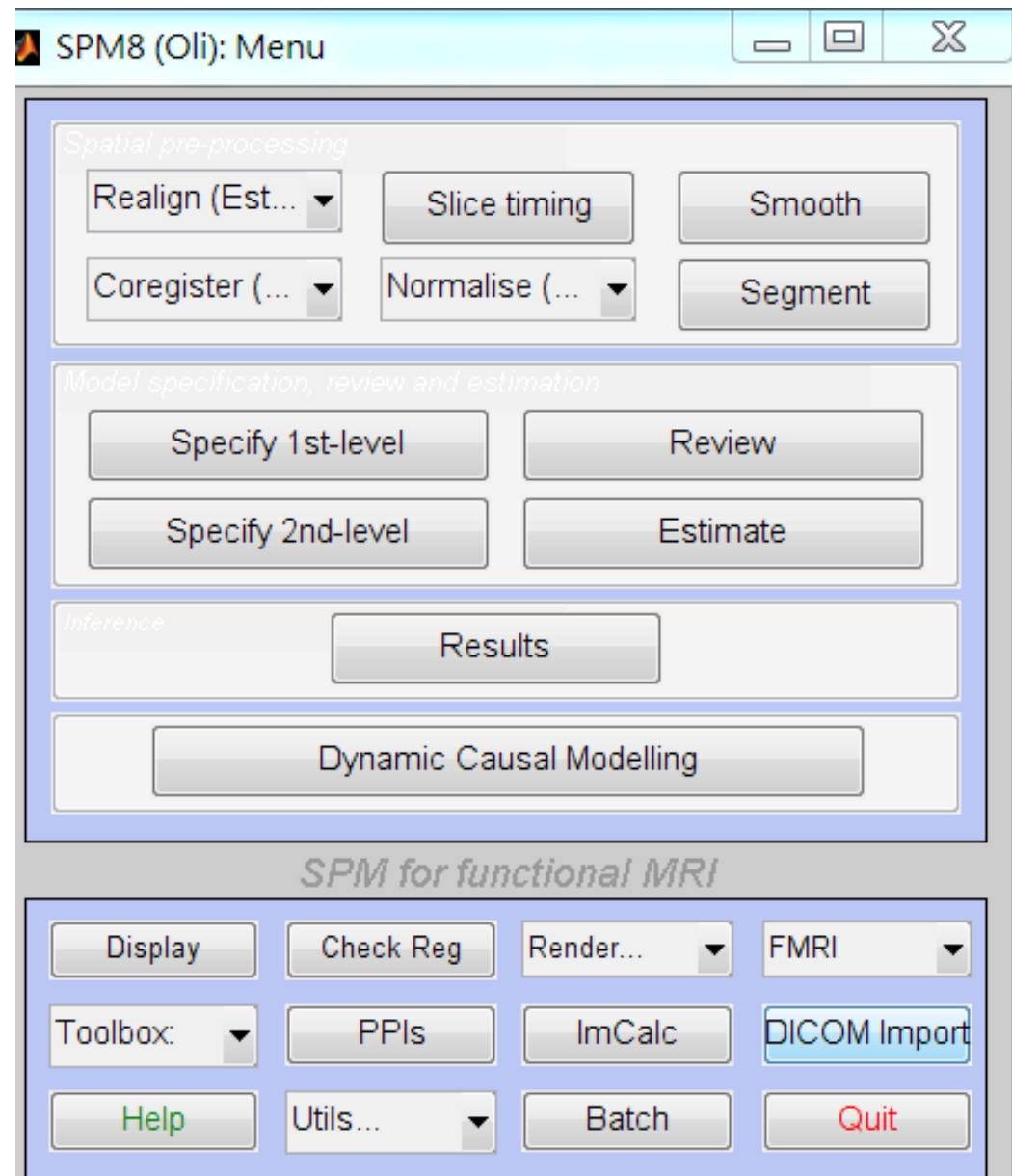
Copyright (C) 1991, 1994-2015 Wellcome Trust Centre for Neuroimaging

Summary of preprocessing procedure

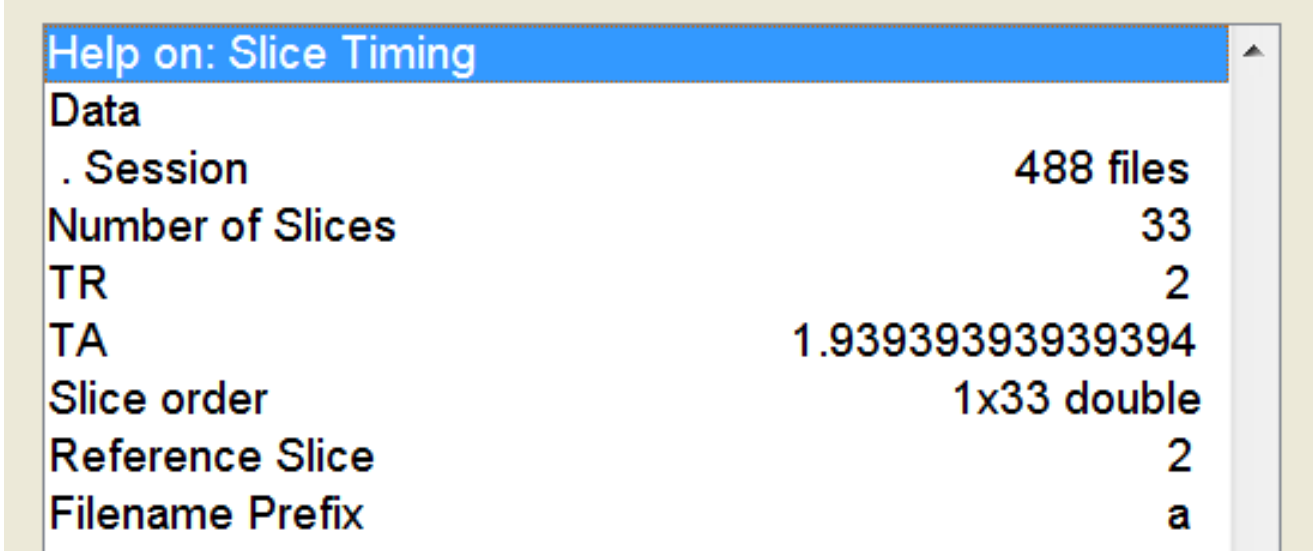
- **Slice timing:** temporally adjust image sampling
- **Realignment:** suppress subject's head motion
- **Segmentation:** parcellate subject's anatomic image into different tissue types
- **Co-registration:** spatially align between functional and anatomic images
- **Normalize:** morph functional images into a "standard" brain
- **Smoothing:** get better signal to noise ratio

DICOM Import

- Input of T1 & EPIs
- Output of T1 & EPIs



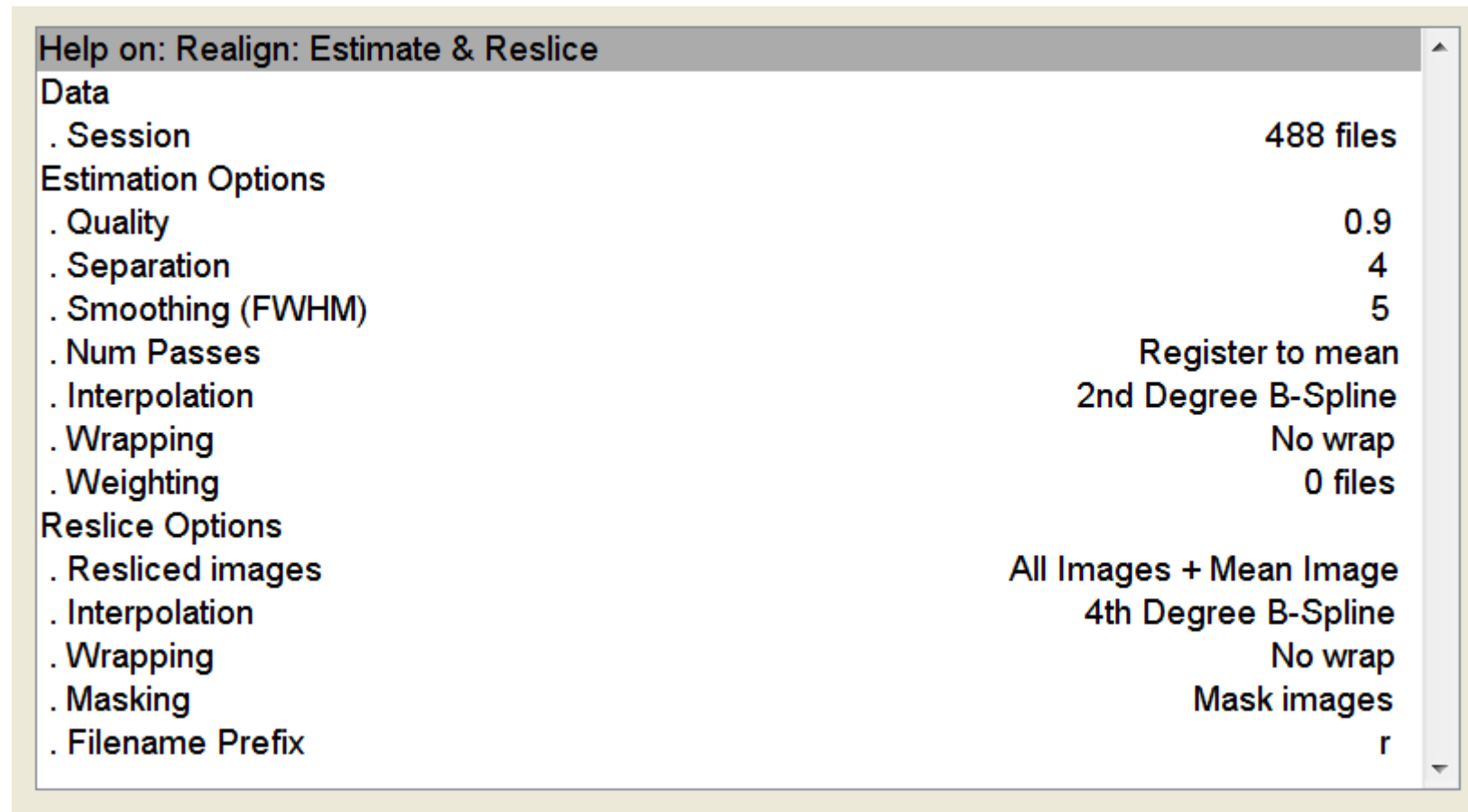
Slice Timing



Help on: Slice Timing	
Data	
. Session	488 files
Number of Slices	33
TR	2
TA	1.93939393939394
Slice order	1x33 double
Reference Slice	2
Filename Prefix	a

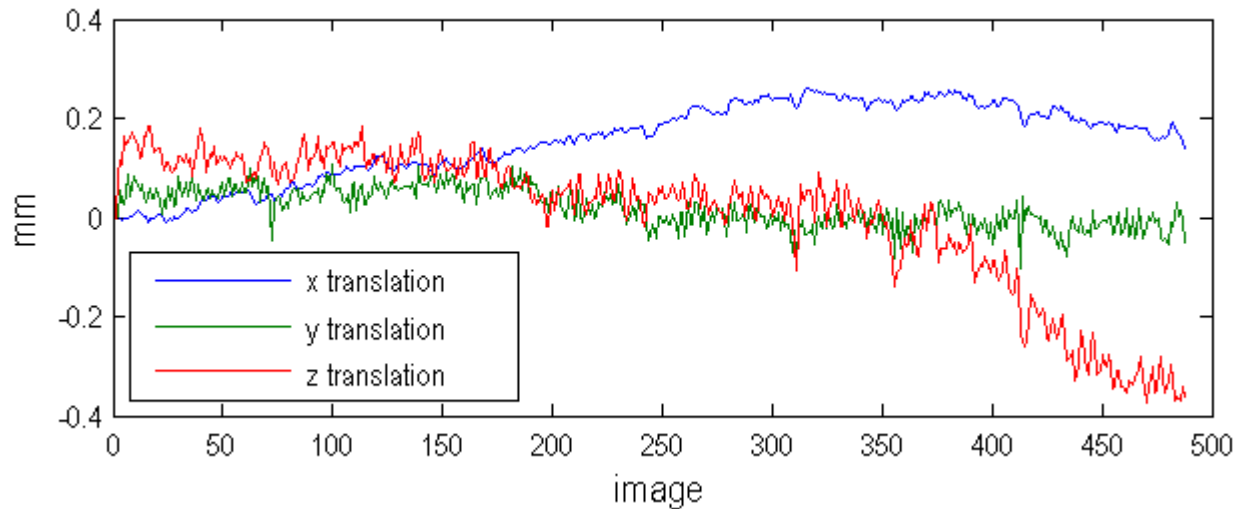
- Input: EPIs after DICOM
- **TR** = time of each scan; **TA** = $TR - (TR / \# \text{ of slices})$
TA is the time b/w the 1st and the last slice within one scan.
- **Slice order**: interleaved (ex: Siemens Skyra)
Odd #: 1 3 5 7 ... 2 4 6 8 [1:2:# 2:2:(#-1)]
Even #: 2 4 6 8 ... 1 3 5 7 [2:2:# 1:2:(#-1)]
- **Reference slice**: middle one (2 or 1 depending on slice #)

Realign → Est & Res



- Input: ^af
- Output:
 1. mean EPIs (mean_...),
 2. realigned EPIs (raf*),
 3. .txt (rp_ar...)

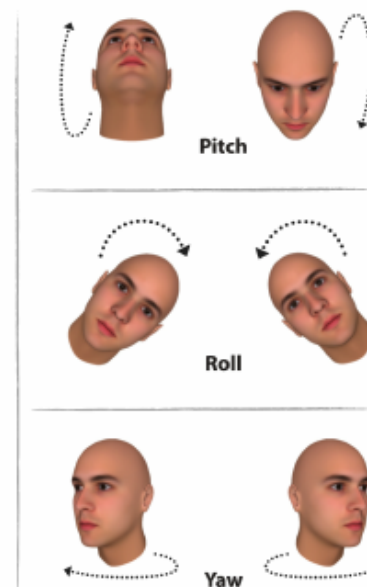
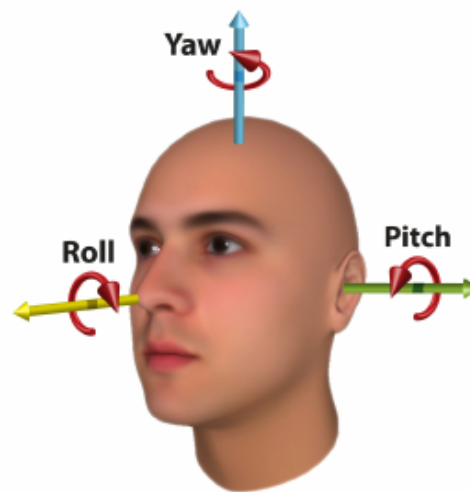
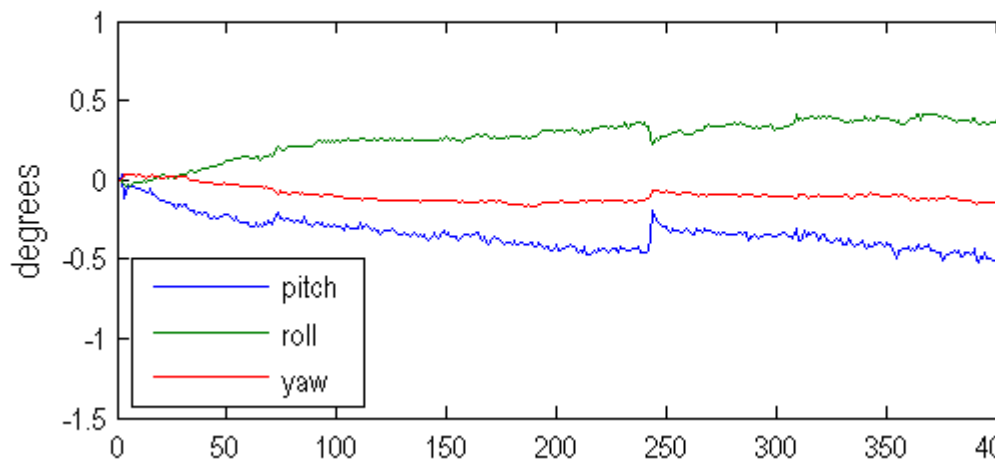
translation



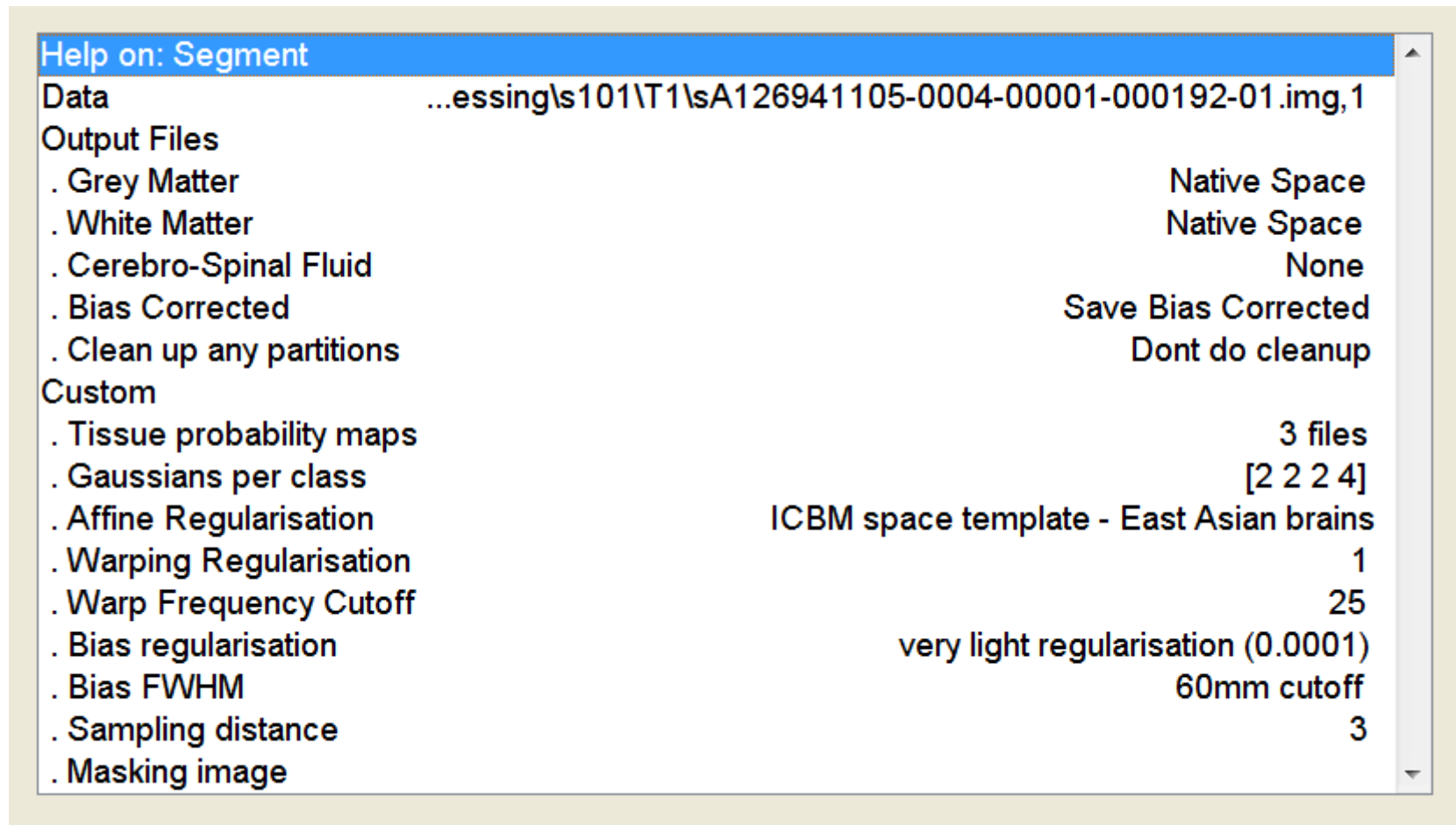
- < 1 voxel (3mm; 2°)
- Spike < 0.5 voxel (1.5 mm; 1°);

RAS system

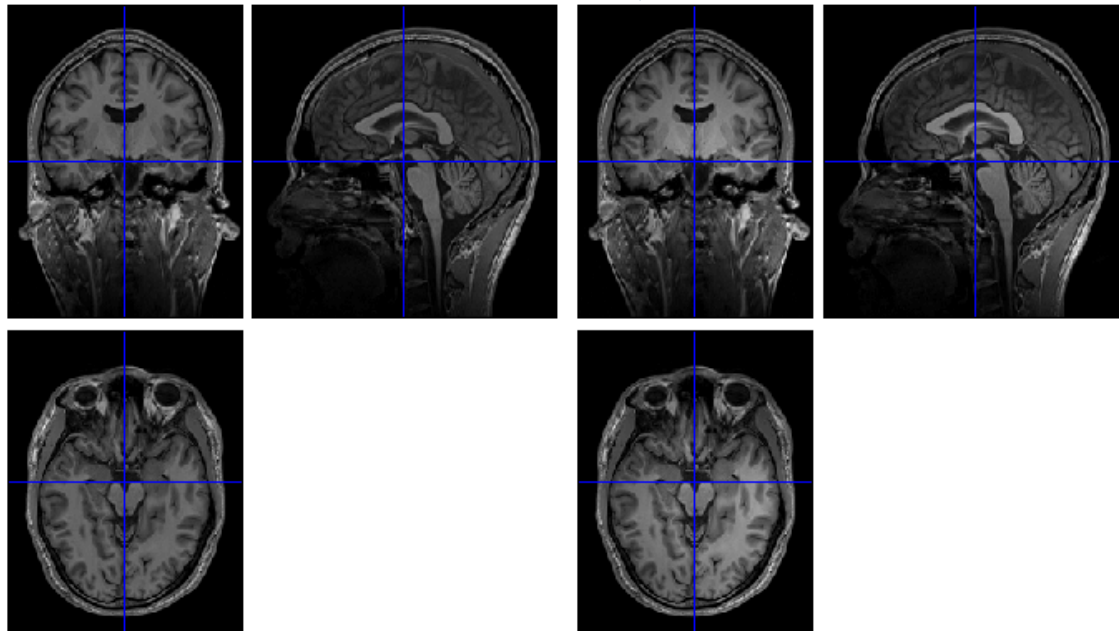
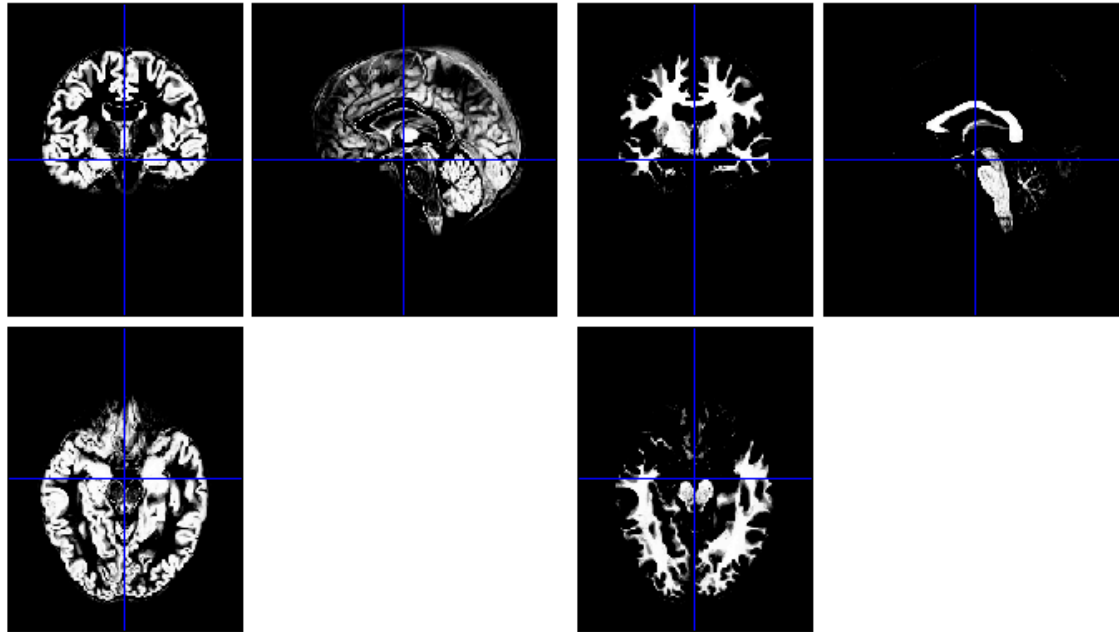
rotation



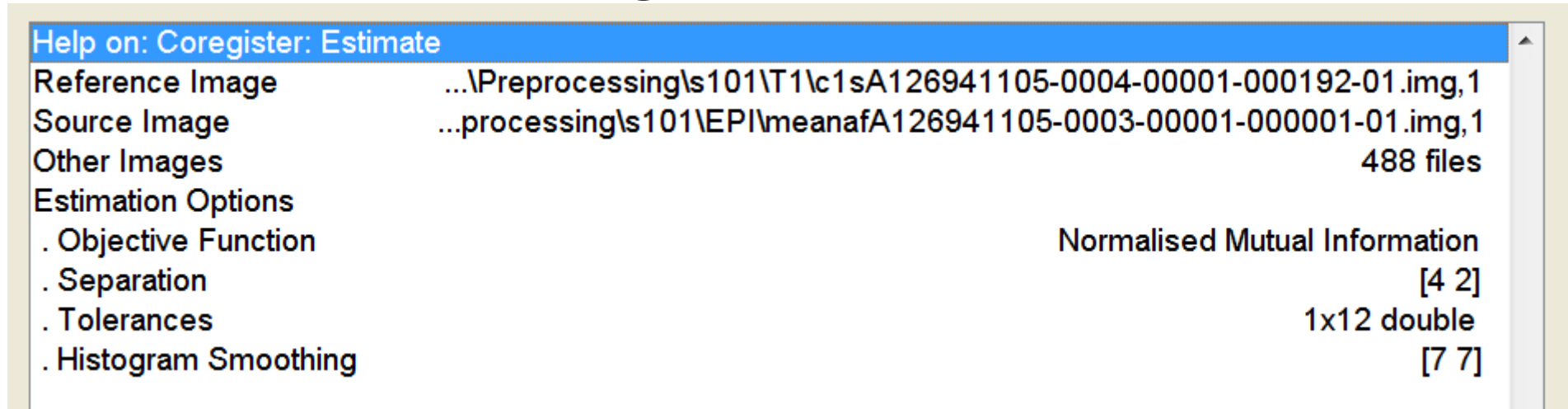
Segment



- Input: T1image after DICOM
- ICBM space template → East Asian brains
- Output: C1, C2, ms

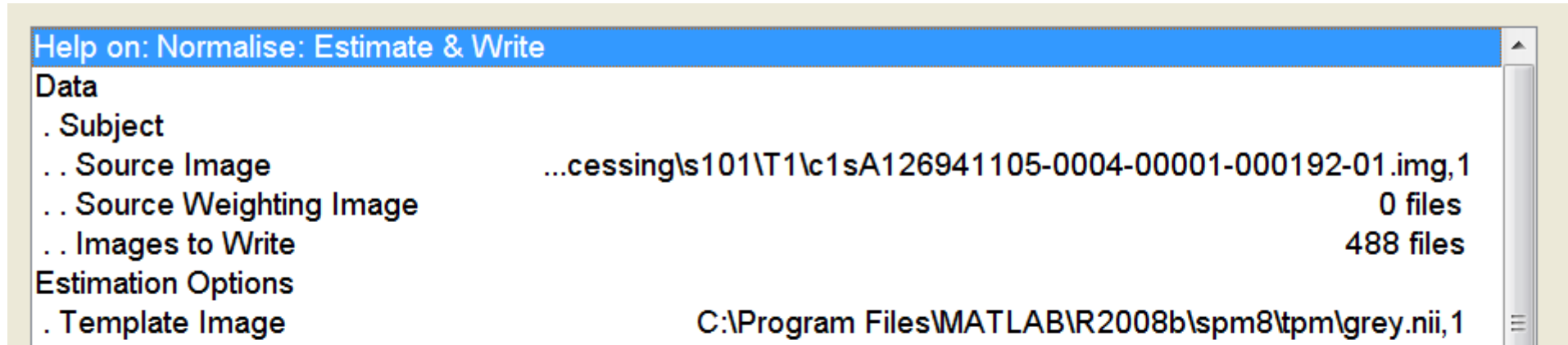


Coregister (Est)



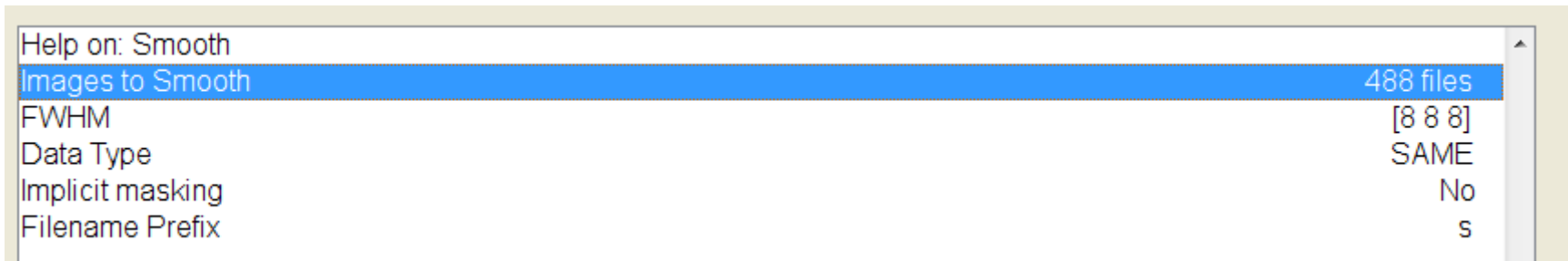
- Reference Image (template image): C1 of T1
- Source image (the image to best match reference image): mean of Realigned EPIs
- Other images (images to be remain in alignment with the source image): Realigned EPIs (raf*)

Normalize → Est & Wri



- Source image (to be warped to match the template): C1
- Images to write: coregistered EPIs
- Template image: spm8\tpm\grey.nii.1
- Output: wraf*

Spatial → Smooth



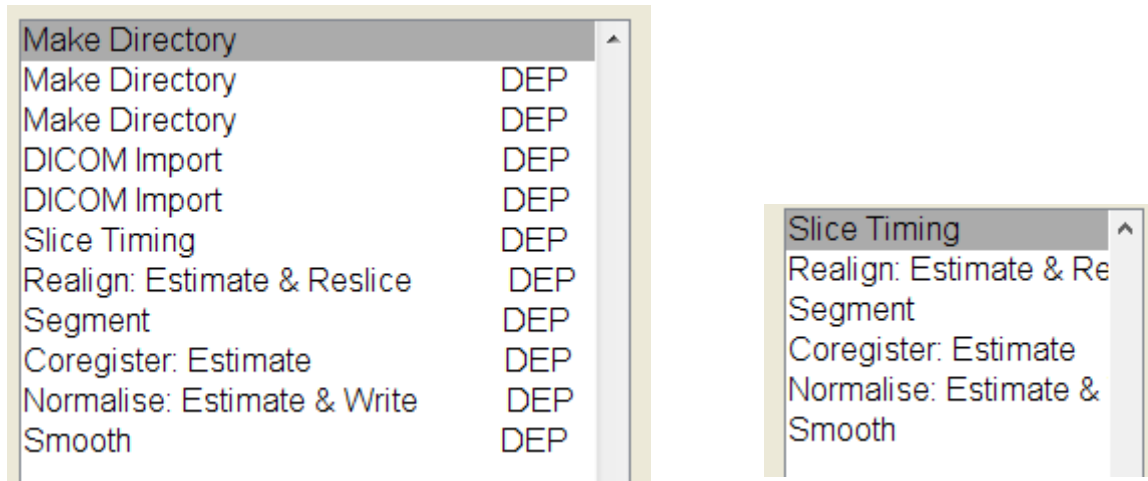
Help on: Smooth	
Images to Smooth	488 files
FWHM	[8 8 8]
Data Type	SAME
Implicit masking	No
Filename Prefix	s

- Input: normalized EPIs, wraf*
- Output: swraf*

Check the results

- .ps → PDF (automatically saved)

Link all the preprocessing steps

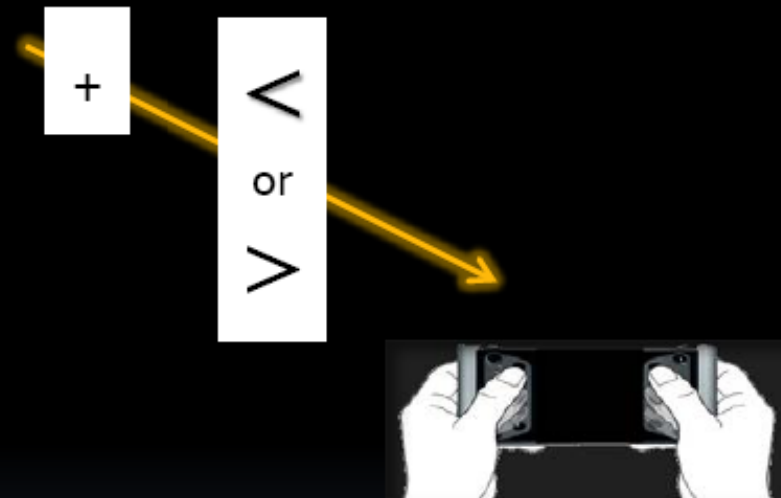


- DEP (dependency)
the previously processed images
- Create individual batch for each subject

Do you know what kind of experiment
for this data set?

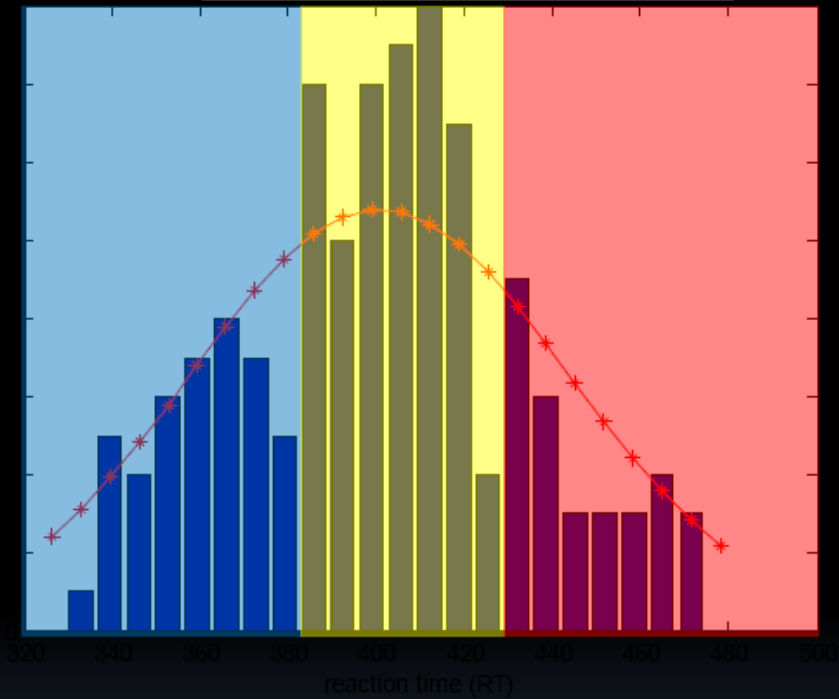
Demo experiment

- ✓ *Neural effects related to simple RT variations ...*
- ✓ *At behavioral level, we recorded reaction time for post hoc separation of the trials. For each trial, it begins with*

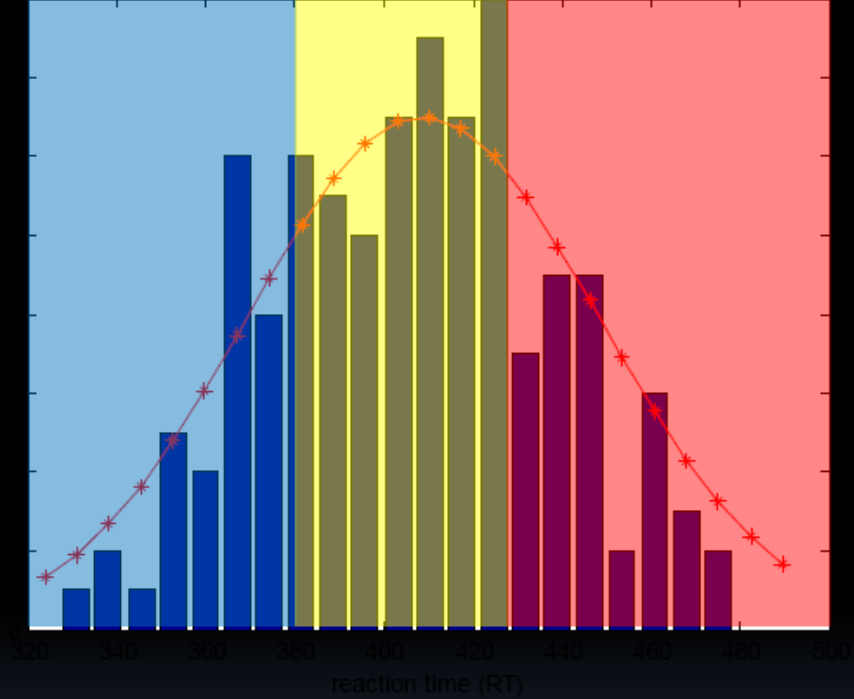


- *Event-related fMRI design*
- *There are 180 x 2 trials for response.*
- *RT and accuracy were recorded.*

Left-hand response



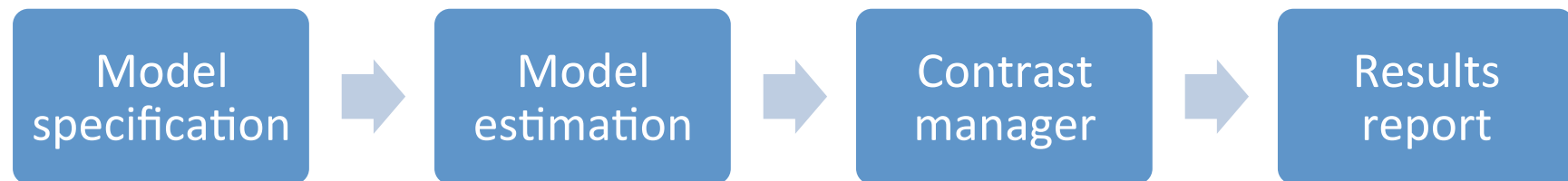
Right-hand response



Response levels separated by mean RT →

*L-fast, L-medium, L-slow
R-fast, R-medium, R-slow*

1st level analysis (individual level)



1st level analysis: Model specification

1. Unit of design: scans (488 scans)
2. Time interval = TR = 2s
3. Input: preprocessed EPIs ([swraf*](#))
4. **Conditions: 2 (handedness) x 3 (RT) +1 (error)**
5. **Regressor: head motion ([.txt](#))**
6. Basis function: canonical hrf

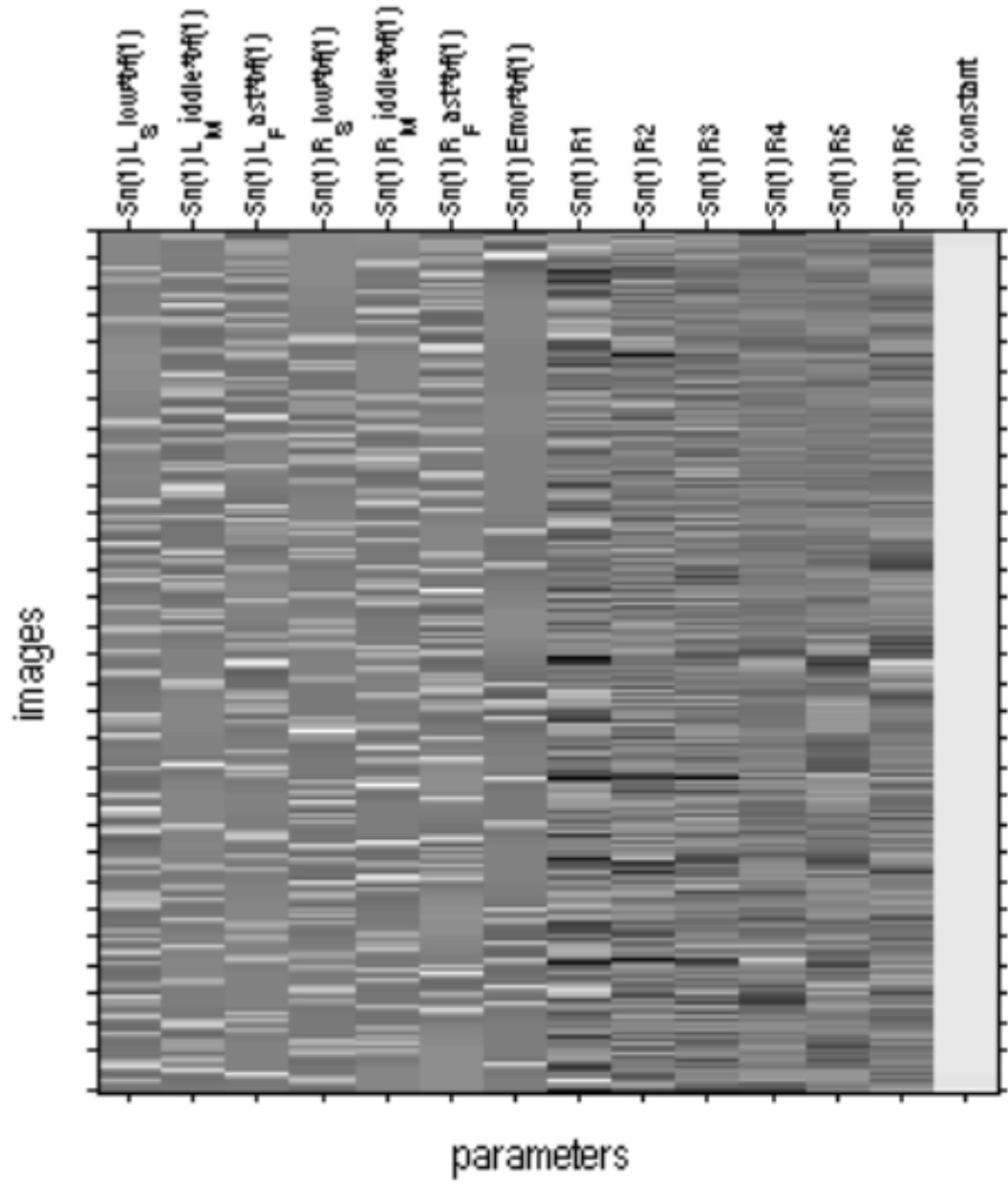
Module List

fMRI model specification ^
Model estimation
Contrast Manager
Results Report

Current Module: fMRI model specification

Help on: fMRI model specification ^
Directory ..._ana-demo\1stLevel\101\
Timing parameters
. Units for design Scans
. Interscan interval 2
. Microtime resolution 16
. Microtime onset 1
Data & Design
. Subject/Session
.. Scans 488 files
.. Conditions
... Condition
.... Name L Slow v
.... Onsets 59x1 double ^
.... Durations 0
.... Time Modulation No Time Modulation
.... Parametric Modulations
... Condition
.... Name L_Middle
.... Onsets 51x1 double
.... Durations 0
.... Time Modulation No Time Modulation
.... Parametric Modulations

Statistical analysis: Design



Estimate → Contrasts → Report

- Model estimation

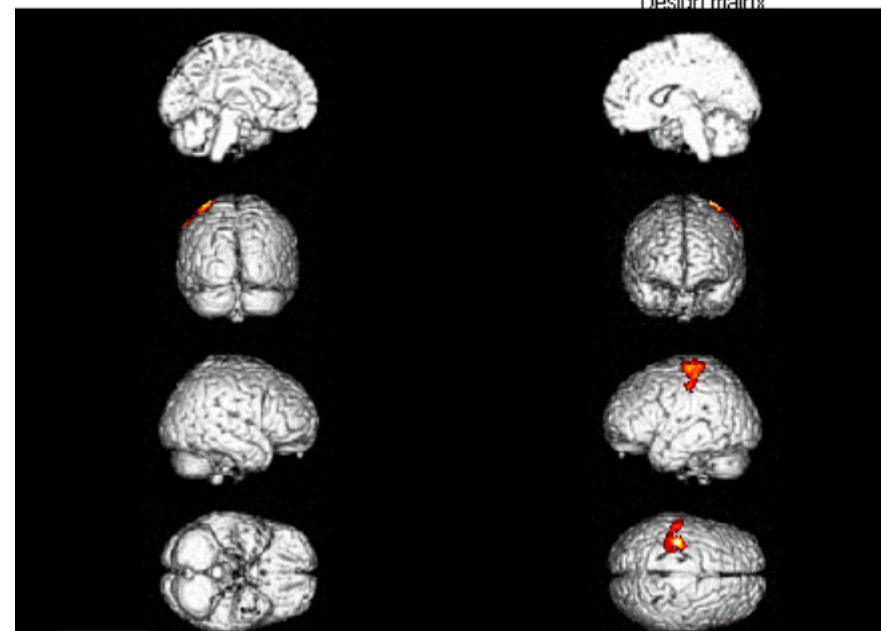
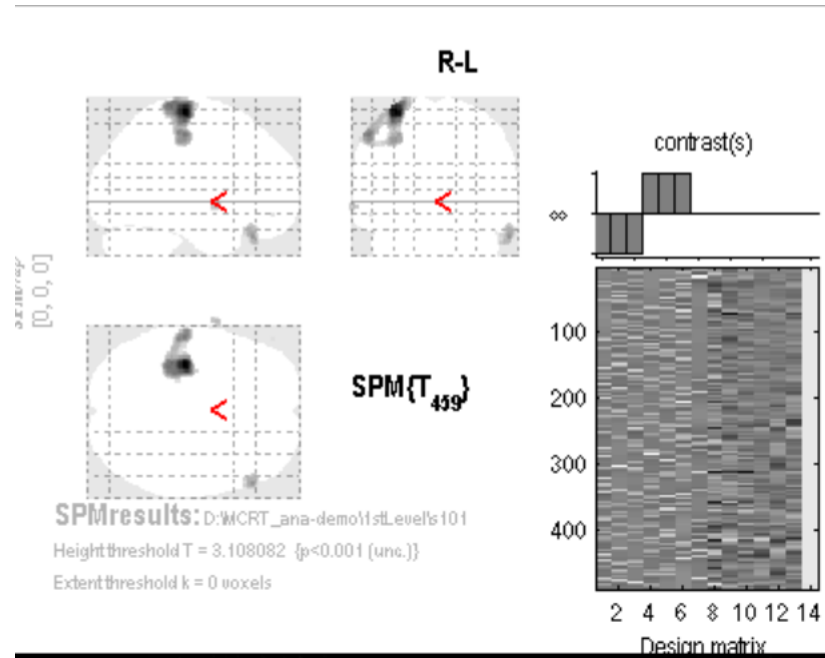
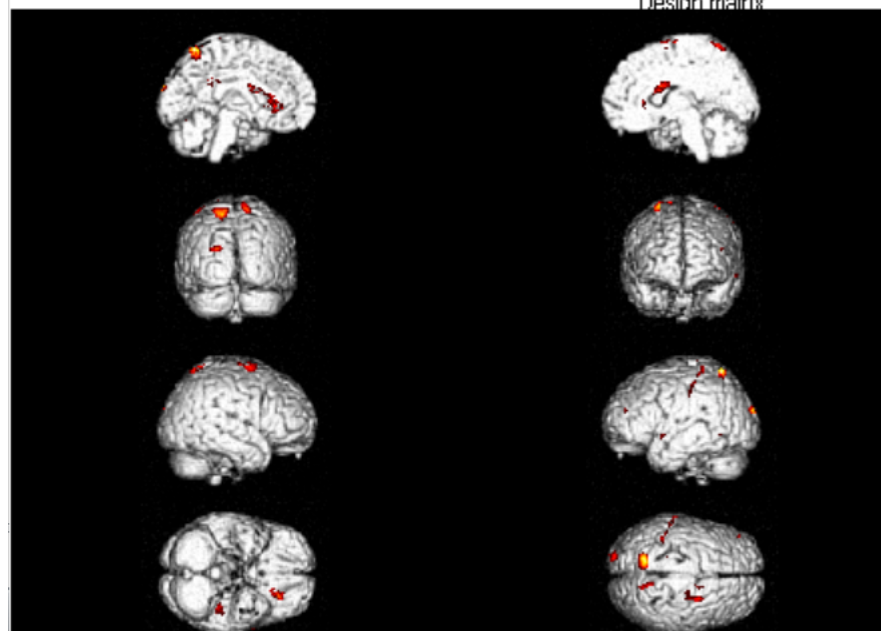
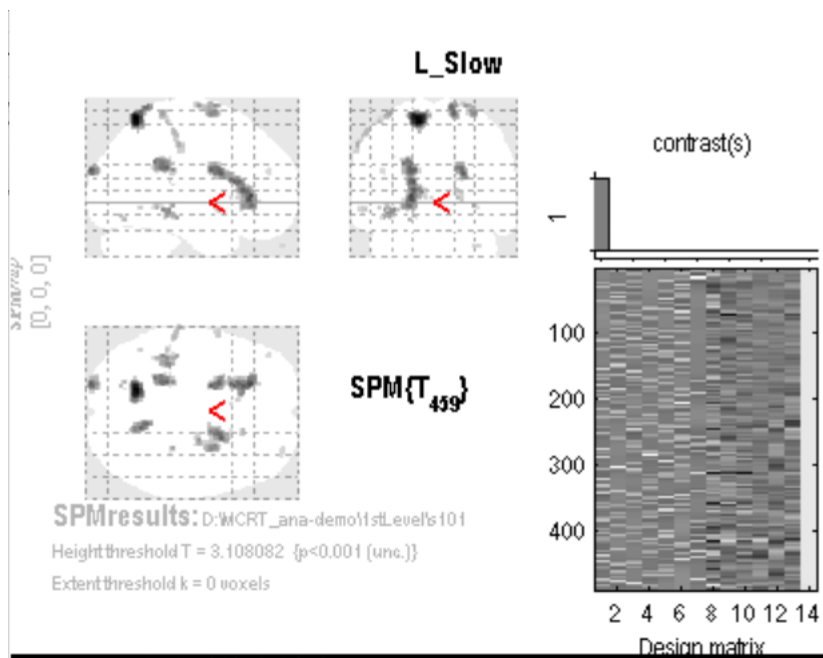
Output: beta (conditions [6+1] + motion [6] + constant [1] =14), Res...

- Contrast:

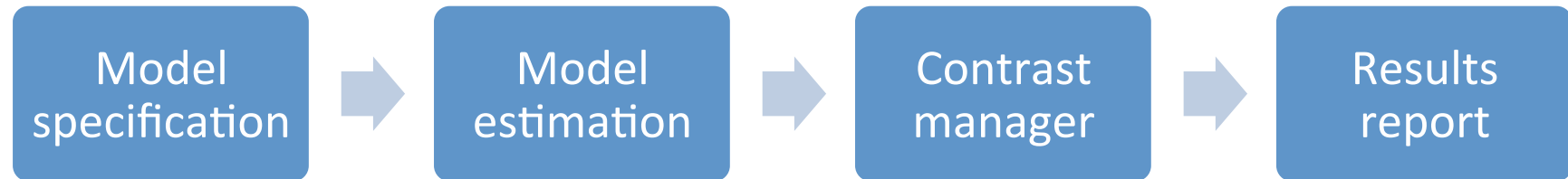
L_Slow, L_Middle, L_fast,
R_Slow, R_Middle, R_Fast, L-R, R-L,...

Output: Con(conditions [6]), SPMT(conditions[6])...

- Report: Threshold $p < .001$
- Plot: render → SPM8 \rend



2nd level analysis (group level)



2nd level analysis: Model specification

- Design: full factorial design: 2 way (2 x 3)

The screenshot displays a software interface with two main panels. The left panel, titled 'Module List', contains two entries: 'Factorial design specificati' and 'Model estimation'. The right panel, titled 'Current Module: Factorial design specification', shows a tree view of design options. The 'Full factorial' option is selected and highlighted in blue. Below it, a list of parameters is shown with their corresponding values:

Parameter	Value
Name	Handedness
Levels	2
Independence	No
Variance	Equal
Grand mean scaling	No
ANCOVA	No

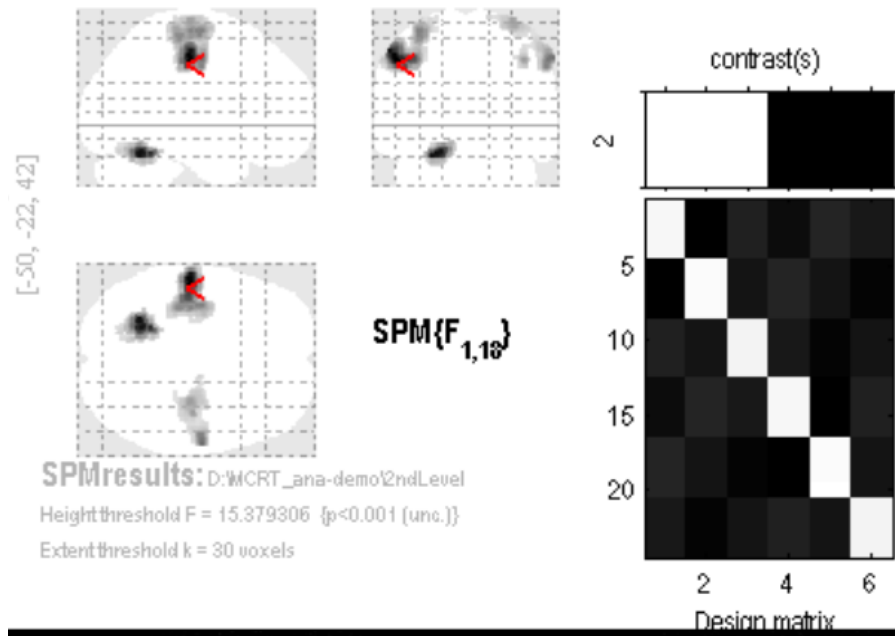
Below this table, there are two sections for specifying cells. The first section is for a 2x2 design:

Cell	Levels	Scans
[1 1]	2	4 files

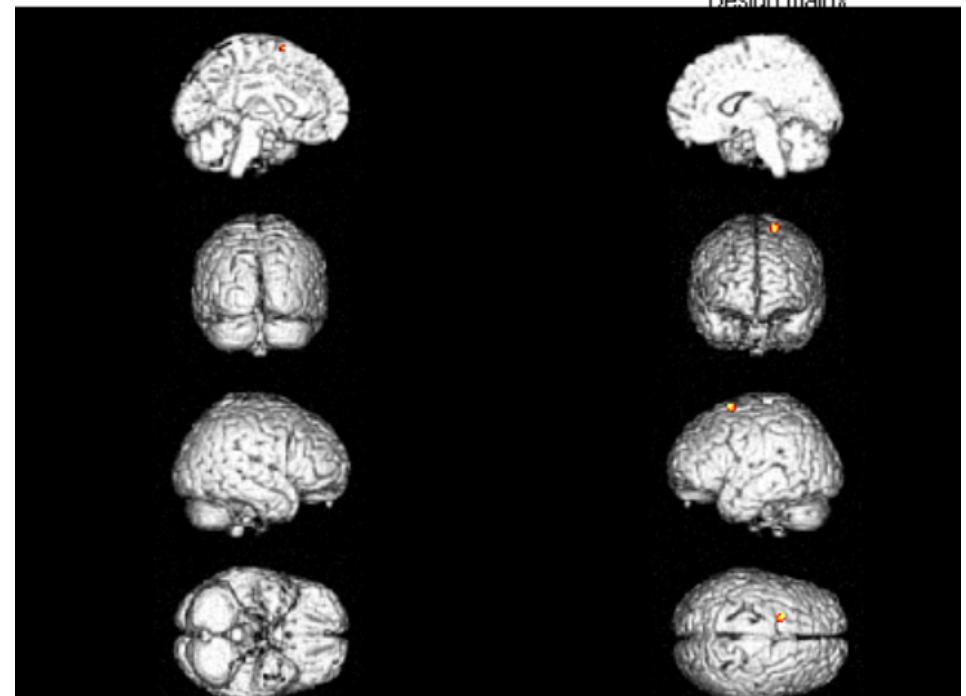
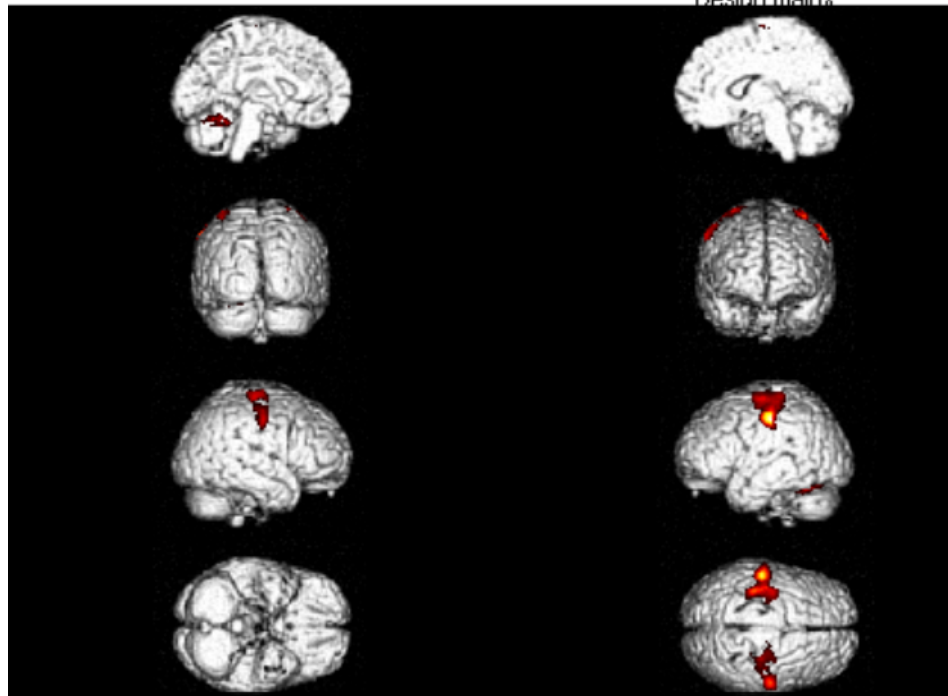
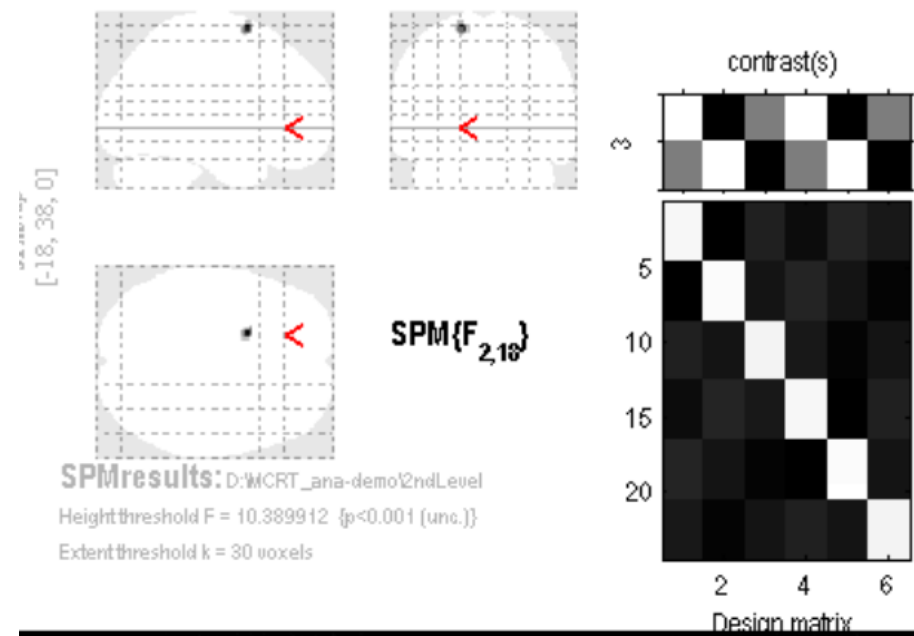
The second section is for a 2x3 design:

Cell	Levels	Scans
[1 2]	3	4 files

Main effect of Handedness



Main effect of RT



Whole Brain Report

Statistics: *p-values adjusted for search volume*

set-level	cluster-level				peak-level					mm	mm	mm
	$\rho_{FWE_{corr}}$	$q_{FDR_{corr}}$	k_E	ρ_{uncorr}	$\rho_{FWE_{corr}}$	$q_{FDR_{corr}}$	F	(Z _≡)	ρ_{uncorr}			
5			1369		0.026	0.018	71.24	5.18	0.000	-50	-22	42
					0.053	0.018	64.39	5.04	0.000	-58	-20	50
					0.637	0.141	38.09	4.32	0.000	-36	-12	64
			471		0.044	0.018	66.19	5.08	0.000	-26	-58	-24
					0.112	0.025	57.74	4.89	0.000	-20	-50	-22
					0.999	0.592	24.82	3.73	0.000	-16	-66	-18
			287		0.433	0.105	42.86	4.48	0.000	62	-12	46
					0.613	0.141	38.61	4.33	0.000	56	-12	40
					1.000	0.905	19.21	3.38	0.000	52	-18	56
			285		0.898	0.238	31.95	4.07	0.000	32	-20	70
					1.000	0.805	21.39	3.53	0.000	32	-12	66
					1.000	0.905	18.95	3.37	0.000	14	-14	74
			71		0.924	0.252	31.10	4.04	0.000	40	-18	44
					1.000	0.941	16.89	3.21	0.001	40	-16	54

table shows 3 local maxima more than 8.0mm apart

Height threshold: F = 15.38, p = 0.001 (1.000)

Extent threshold: k = 30 voxels, p =

Expected voxels per cluster, <k> = 7.195

Expected number of clusters, <c> =

FWE_p: 64.988, FDR_p: 57.740

Degrees of freedom = [1.0, 18.0]

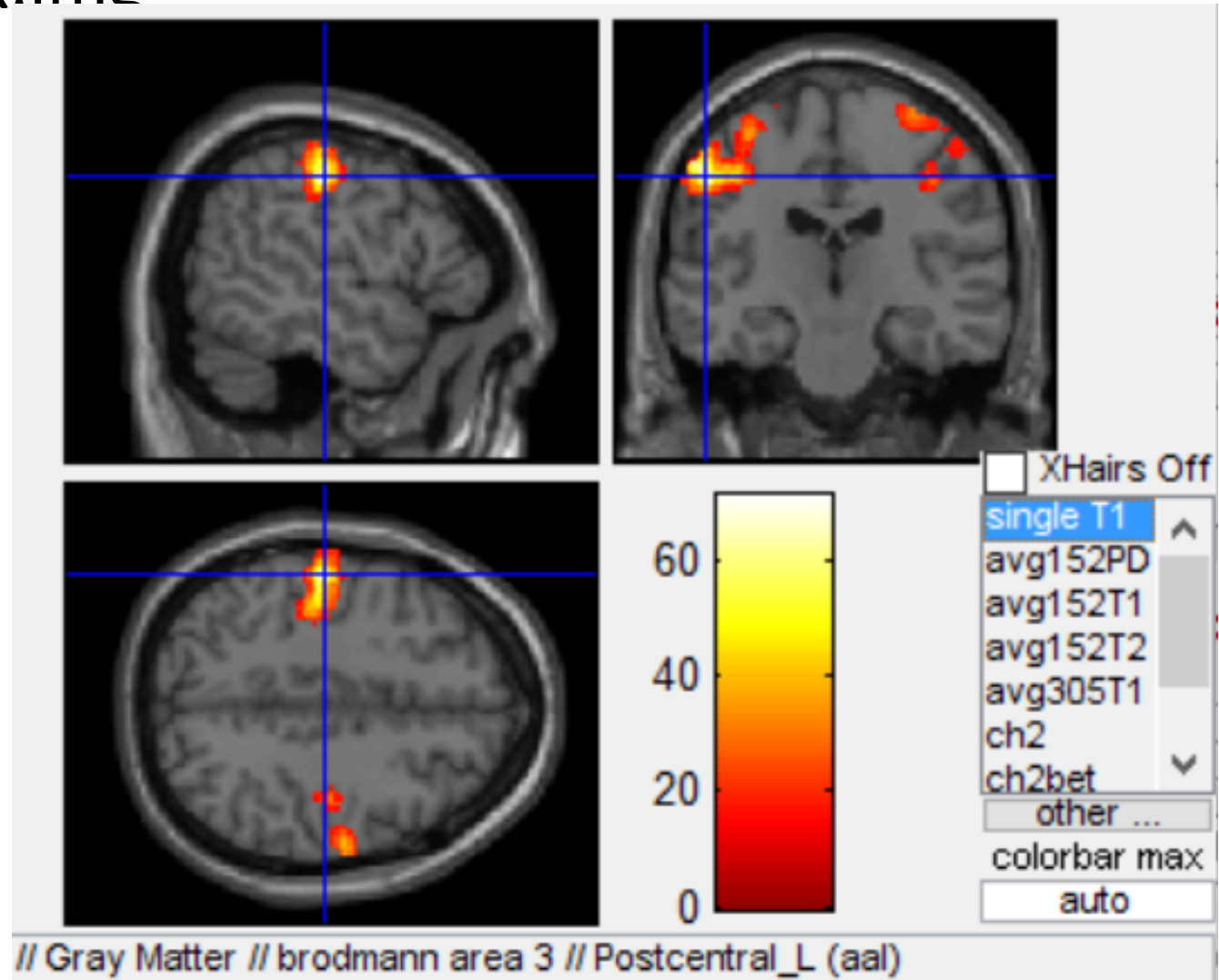
FWHM = 9.8 10.1 9.7 mm mm mm; 4.9 5.0 4.8 {voxels}

Volume: 1820680 = 227585 voxels = 1768.3 resels

Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 119.52 voxels)

Xj-view

- SPMFxxx.img



Useful tools

軟體名稱	連結
SPM	http://www.fil.ion.ucl.ac.uk/spm/software/download/
MRicro	http://www.mccauslandcenter.sc.edu/mricro/mricro/mricro.html#Installation
MRicron	http://www.mccauslandcenter.sc.edu/mricro/mricron/install.html
xjView	http://www.alivelearn.net/xjview8/download/
MarsBaR	http://marsbar.sourceforge.net/download.html
ImageJ	http://rsb.info.nih.gov/ij/download.html
cuifindstructure	http://www.alivelearn.net/?p=1456

<http://tmbic.nccu.edu.tw>