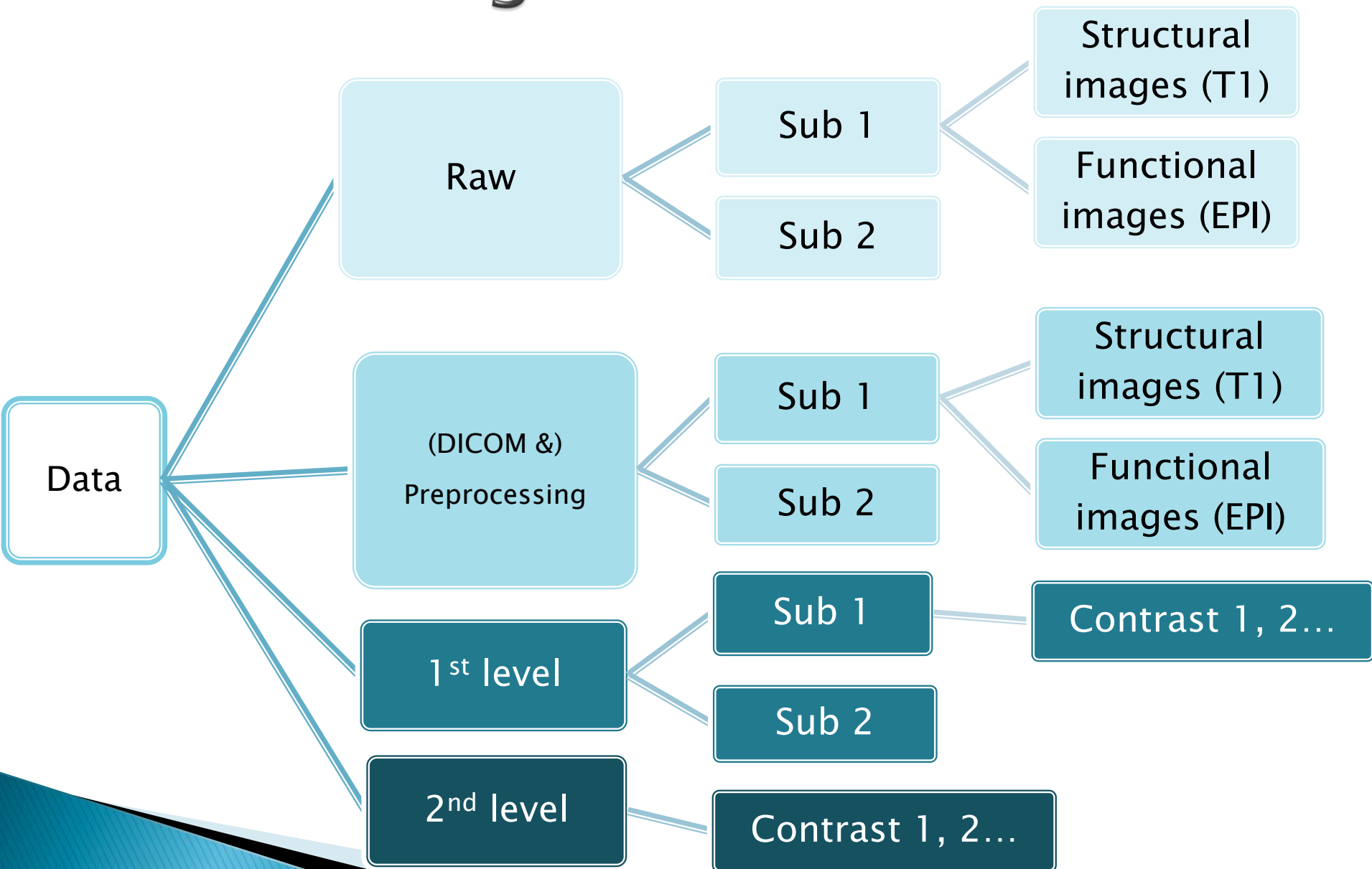


# Demo fMRI data analysis using SPM12

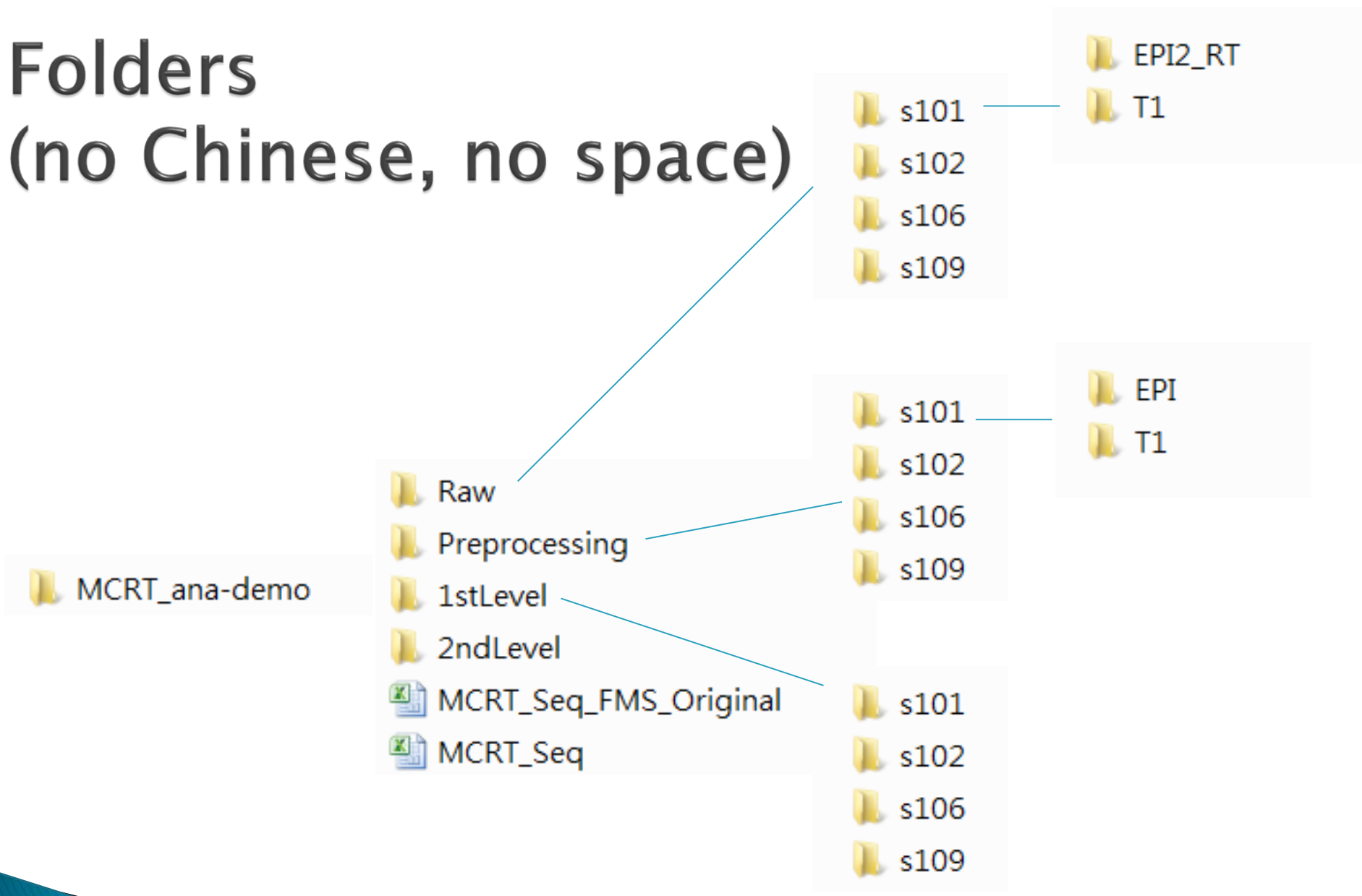
郭文瑞教授

陳尹華、蘇仲怡、李佩芳、盧毓文

# Data arrangement

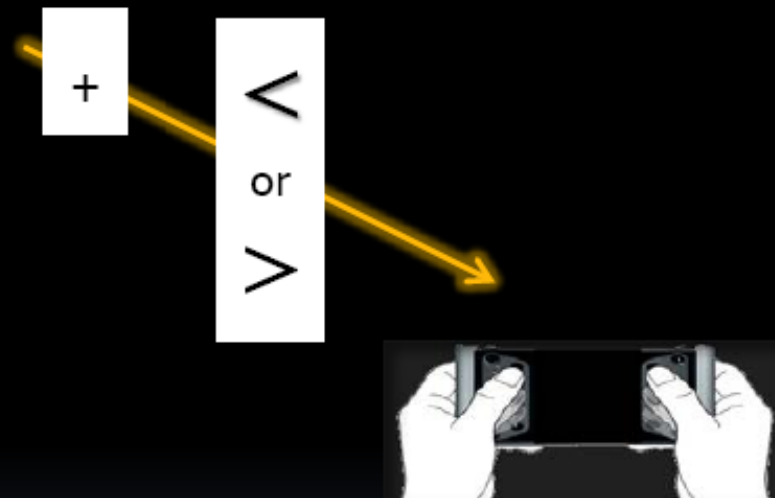


# Folders (no Chinese, no space)




# 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 ....*



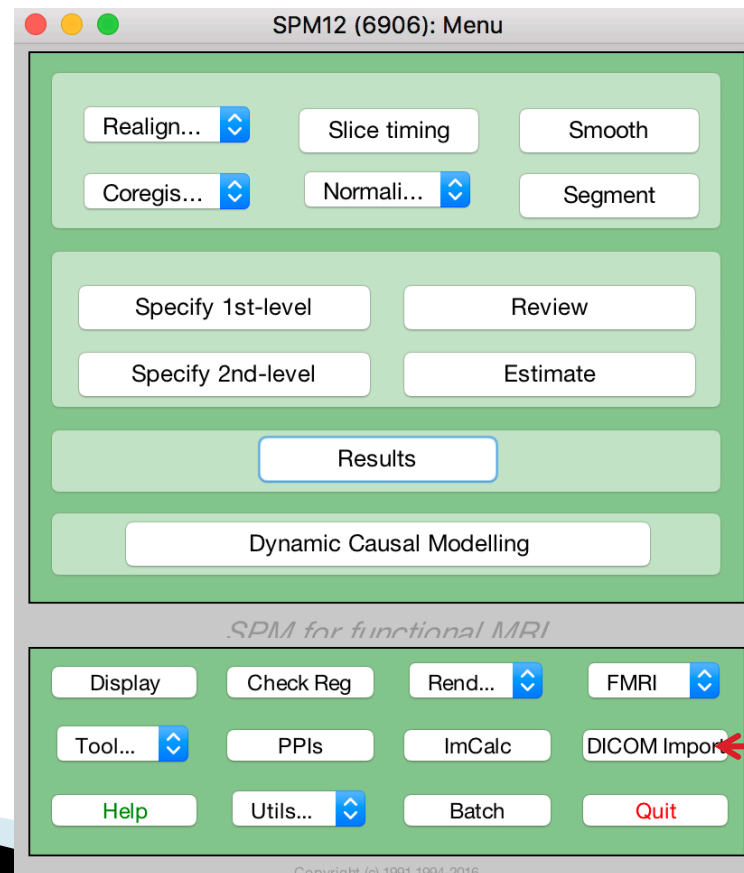
- *Event-related fMRI design*
- *There are 180 x 2 trials for response.*
- *RT and accuracy were recorded.*

# Summary of preprocessing procedure

- ▶ **Slice timing**: temporal adjustment of images sampling
  - ▶ **Realignment**: adjustment for participant's head movement between slices
  - ▶ **Co-registration**: link functional images to structural image
  - ▶ **Normalize**: all into a common anatomical space (template)
  - ▶ **Smoothing**: better signal to noise ratio
- 

# DICOM Import

- ▶ Input of T1 & EPIs, respectively
- ▶ Output of T1 & EPIs, respectively



# Slice Timing

Help on: Slice Timing	
Data	
. Session	488 files
Number of Slices	33
TR	2
TA	1.9393939393939394
Slice order	1x33 double
Reference Slice	33
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 1<sup>st</sup> and the last slice within one scan.
- ▶ **Slice order**: interleaved (ex: Simens Skyra)  
Odd #: 1 3 5 7 **9** 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

# Realign → Est & Res

Help on: Realign: Estimate & Reslice

## Data

. Session 488 files

## Estimation Options

. Quality 0.9

. Separation 4

. Smoothing (FWHM) 5

. Num Passes Register to mean

. Interpolation 2nd Degree B-Spline

. Wrapping No wrap

. Weighting 0 files

## Reslice Options

. Resliced images All Images + Mean Image

. Interpolation 4th Degree B-Spline

. Wrapping No wrap

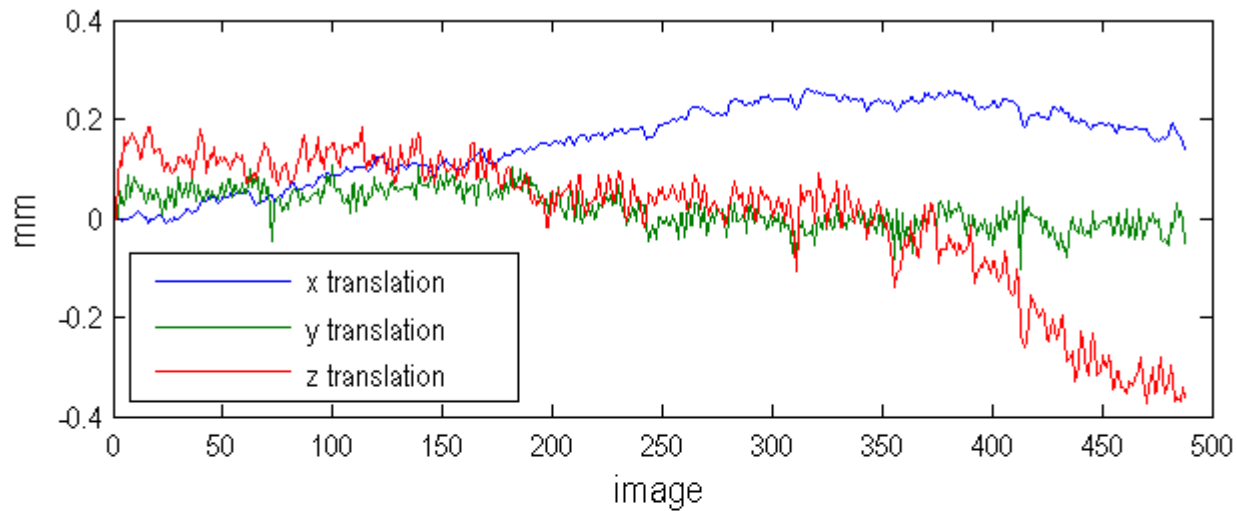
. Masking Mask images

. Filename Prefix r

- ▶ Input: ^af
- ▶ Output:
  1. mean EPIs (mean\_...),
  2. realigned EPIs (raf\*),
  3. .txt (rp\_ar...)

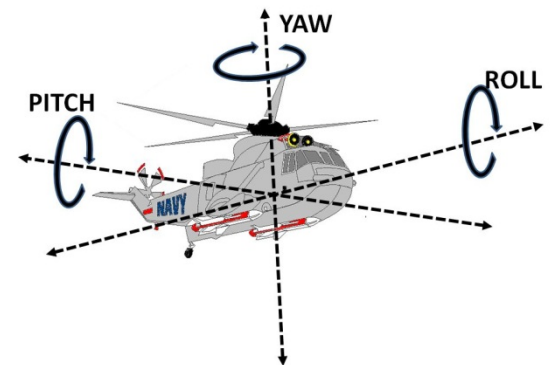
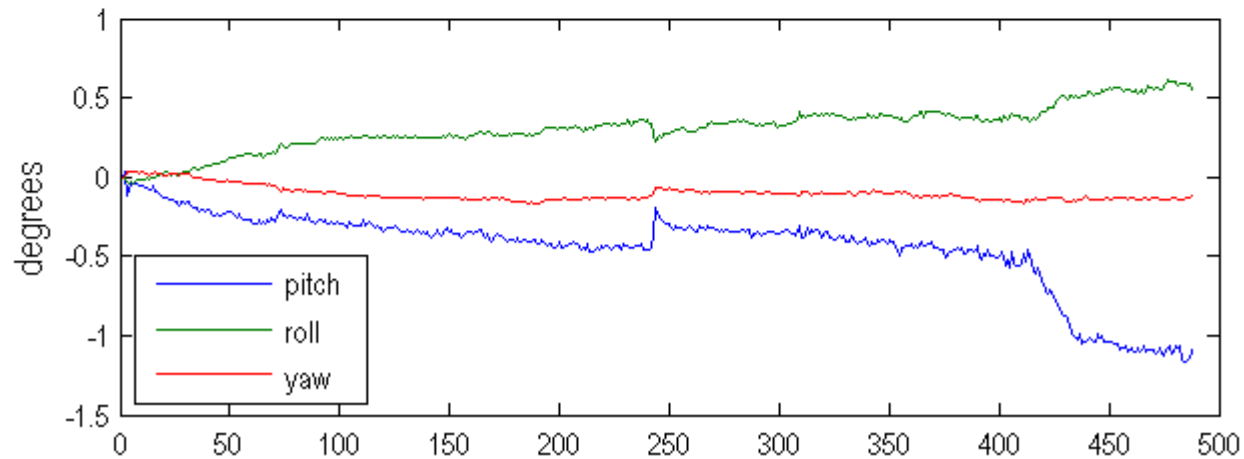


## translation



- ▶  $< 1$  voxel (3mm;  $2^\circ$ )
- ▶ Spike  $< 0.5$  voxel (1.5 mm;  $1^\circ$ );

## rotation



# Coregister (Est)

## Help on: Coregister: Estimate

Reference Image	...ing/s101/T1_3/sA126941105-0004-00001-000192-01.nii,1
Source Image	...1/EPI_3/meanafA126941105-0003-00001-000001-01.nii,1
Other Images	488 files
Estimation Options	
. Objective Function	Normalised Mutual Information
. Separation	[4 2]
. Tolerances	1x12 double
. Histogram Smoothing	[7 7]

- ▶ Reference Image (template image): 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

## Help on: Normalise: Estimate & Write

### Data

. Subject

. . Image to Align ...sA126941105-0004-00001-000192-01.nii,1

. . Images to Write 488 files

### Estimation Options

. Bias regularisation very light regularisation (0.0001)

. Bias FWHM 60mm cutoff

. Tissue probability map /Applications/spm12/tpm/TPM.nii

. Affine Regularisation ICBM space template - East Asian brains

- ▶ Image to Align (to be warped to match the template): T1
- ▶ Images to Write: coregistered EPIs
- ▶ Affine Regularisation: East Asian brains
- ▶ Output: wraf\*

# Spatial → Smooth

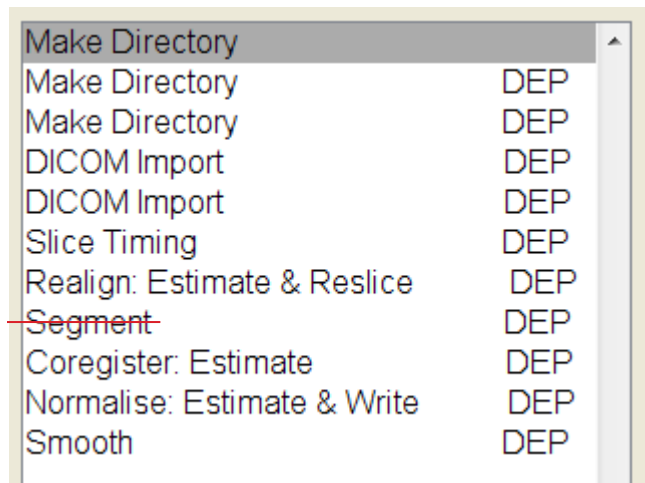
Help on: Smooth	
Images to Smooth	488 files
FWHM	[8 8 8]
Data Type	SAME
Implicit masking	No
Filename Prefix	s

- ▶ Input: normalized EPIS, wraf\*
- ▶ Output: swraf\*

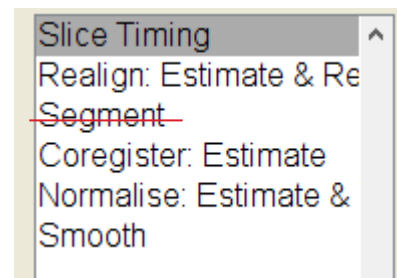
# Check the results

- ▶ .ps → PDF (automatically saved)

# Link all the preprocessing steps



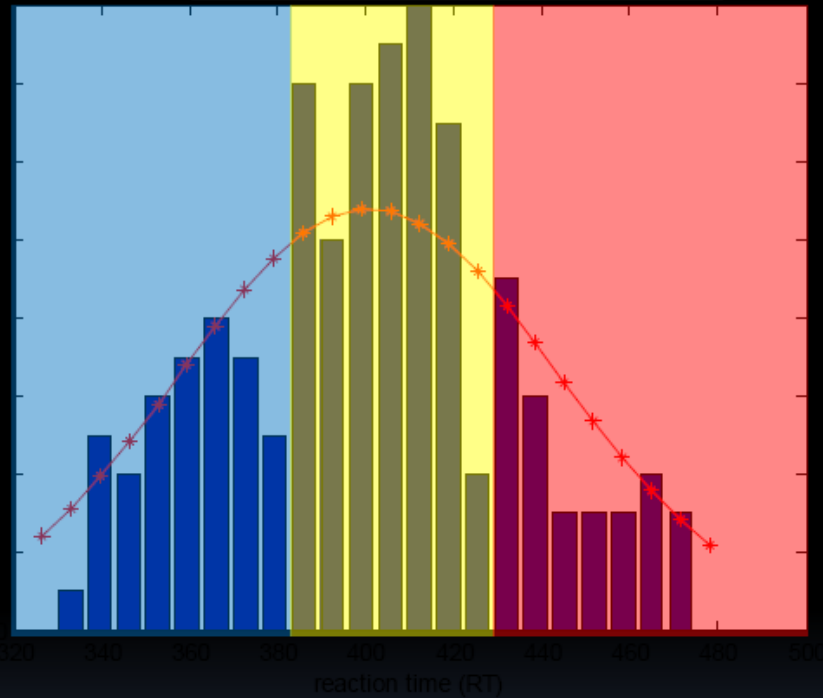
Step	Dependency
Make Directory	
Make Directory	DEP
Make Directory	DEP
DICOM Import	DEP
DICOM Import	DEP
Slice Timing	DEP
Realign: Estimate & Reslice	DEP
<del>Segment</del>	DEP
Coregister: Estimate	DEP
Normalise: Estimate & Write	DEP
Smooth	DEP



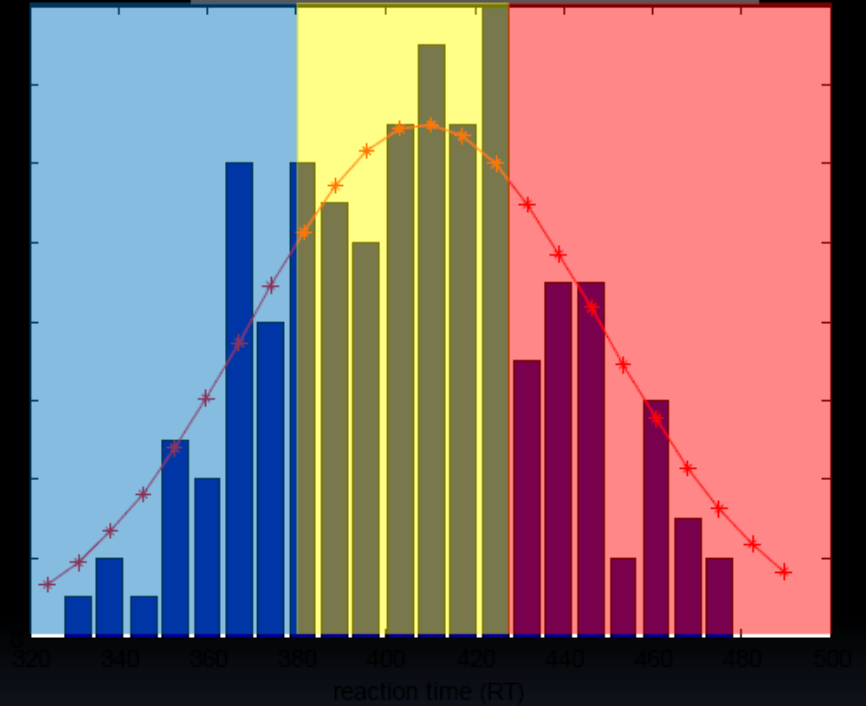
Step	Dependency
Slice Timing	
Realign: Estimate & Re	
<del>Segment</del>	
Coregister: Estimate	
Normalise: Estimate &	
Smooth	

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

*Left-hand response*



*Right-hand response*

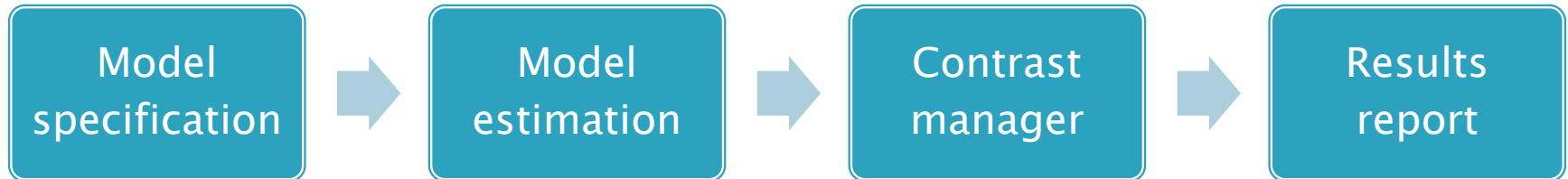


*Response levels separated by mean RT →*

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

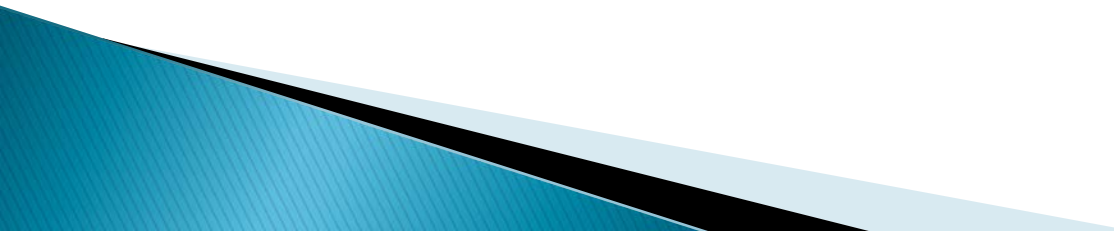
*R-fast, R-medium, R-slow*

# 1<sup>st</sup> level analysis (individual level)





# 1<sup>st</sup> 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

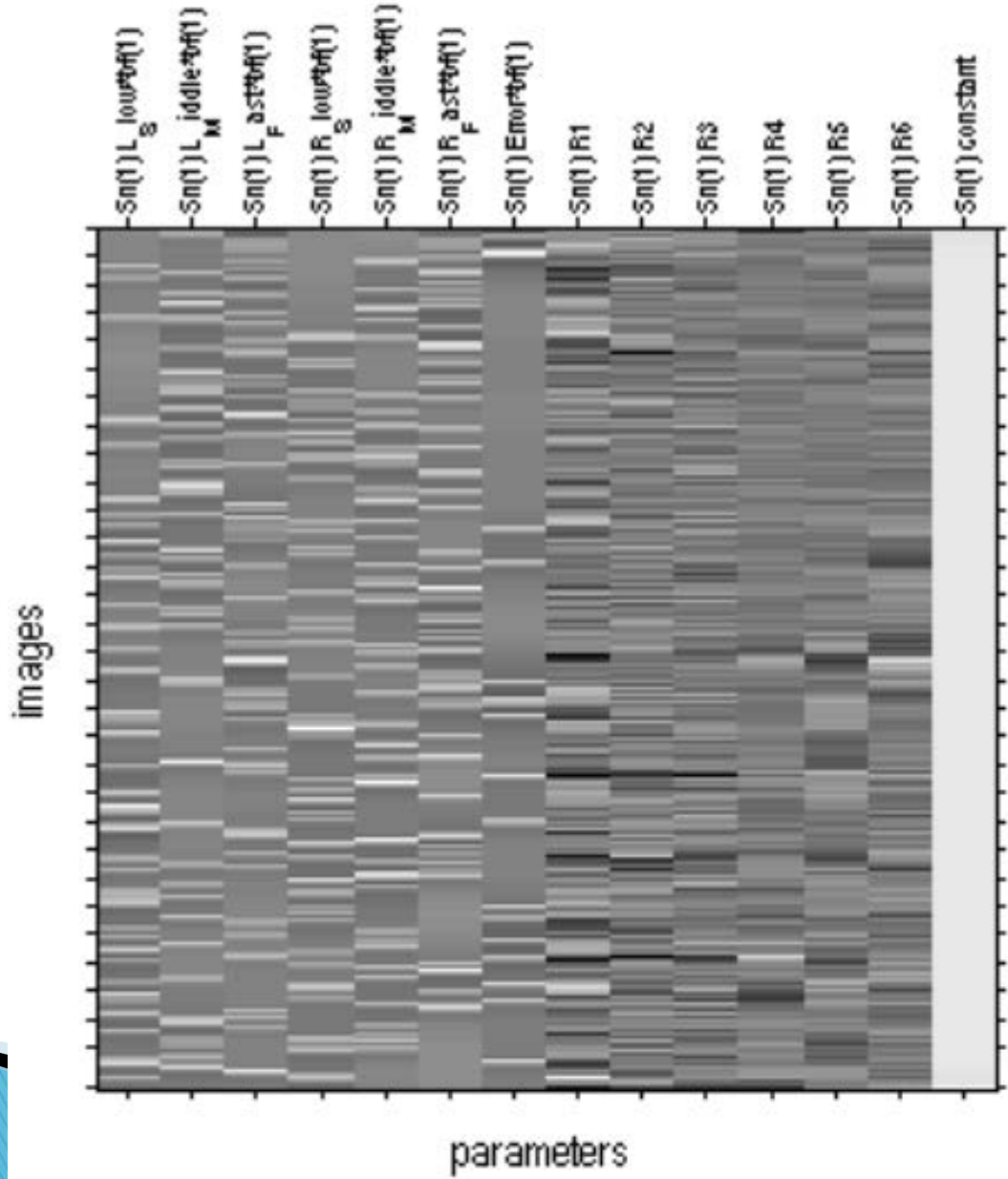
- . Units for design Scans
- . Interscan interval 2
- . Microtime resolution 16
- . Microtime onset 1

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...

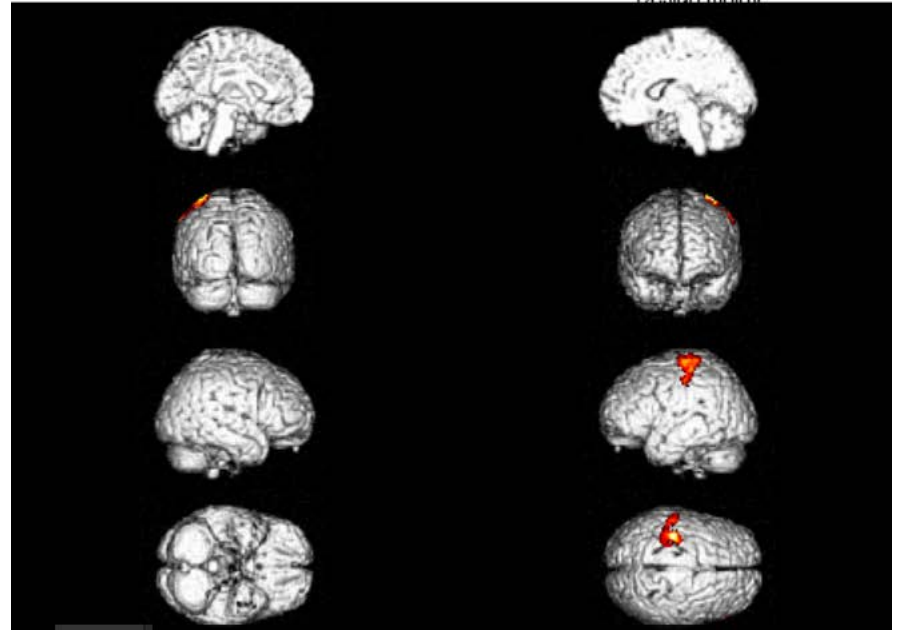
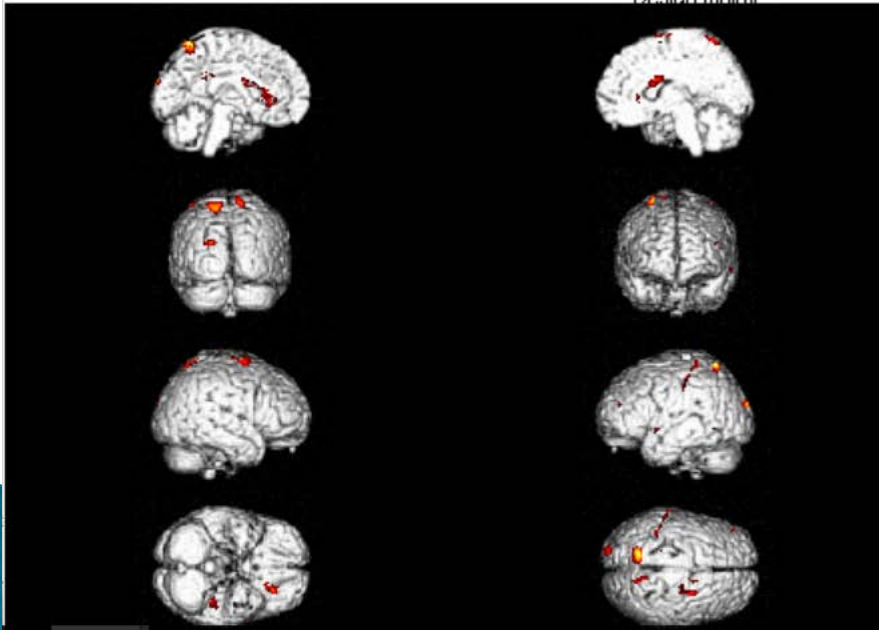
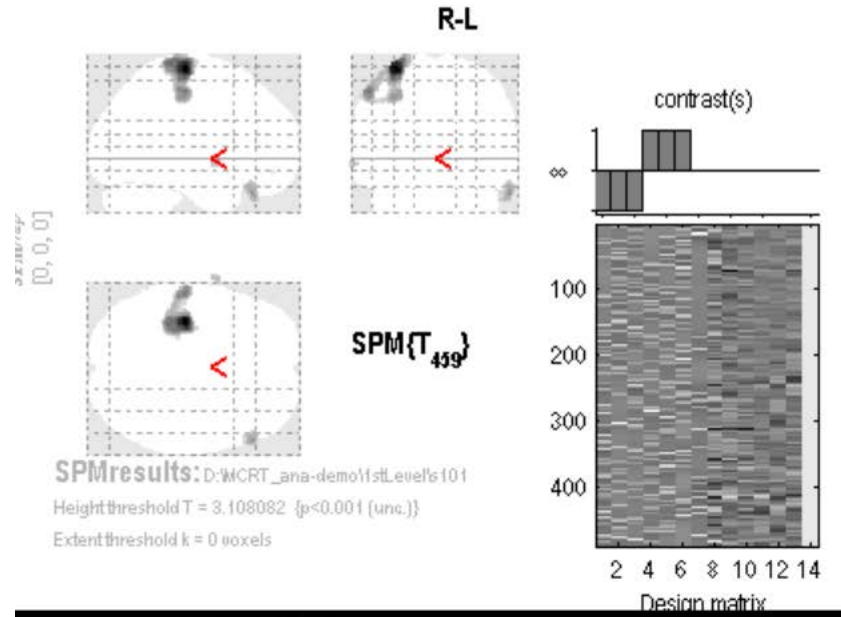
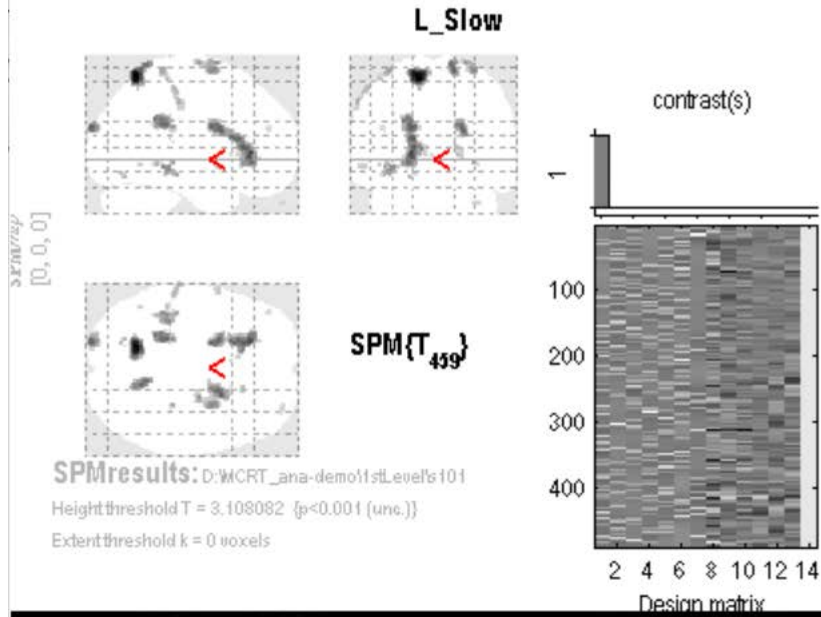
- ▶ Contrast:

L\_Slow, L\_Middle, L\_fast,  
R\_Slow, R\_Middle, R\_Fast, L-R, R-L,...

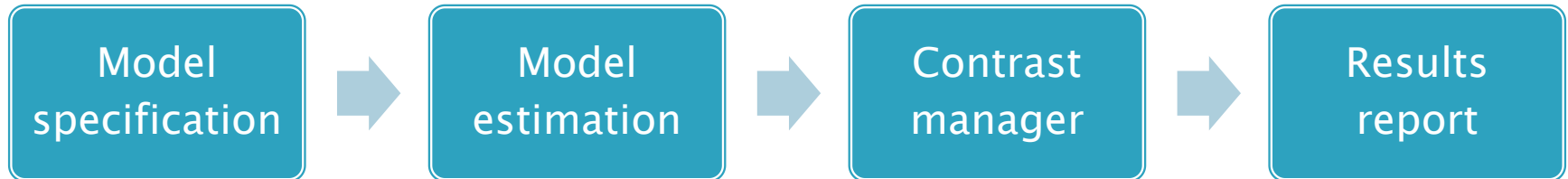
Output: Con(conditions [6]), SPMT(conditions[6])...

- ▶ Report: Threshold  $p < .001$

- ▶ Plot: render → SPM12 \rend



# 2<sup>nd</sup> level analysis (group level)



# 2<sup>nd</sup> level analysis

- ▶ Design: One-sample t-test

Module List	Current Module: Factorial design specification
Make Directory	Help on: Factorial design specification
Factorial design specification DE	Directory DEP Make Directory: Make Directory '2ndLevelTtest'
Model estimation DE	Design
Contrast Manager DE	. One-sample t-test
	. . Scans 4 files
	Covariates
	Multiple covariates
	Masking
	. Threshold masking
	. . None
	. Implicit Mask Yes
	. Explicit Mask
	Global calculation

# Whole Brain Report

Statistics: *p-values adjusted for search volume*

set-level		cluster-level				peak-level					mm mm mm		
$p$	$c$	$P_{\text{FWE-corr}}$	$q_{\text{FDR-corr}}$	$k_E$	$P_{\text{uncorr}}$	$P_{\text{FWE-corr}}$	$q_{\text{FDR-corr}}$	$T$	$(Z_{\equiv})$	$P_{\text{uncorr}}$			
0.999	4	0.000	0.000	1442	0.000	0.000	0.002	10.36	5.84	0.000	-16	-54	-20
						0.092	0.023	6.94	4.78	0.000	-12	-86	-10
						0.208	0.032	6.36	4.55	0.000	-10	-62	-18
		0.000	0.000	5172	0.000	<b>0.018</b>	<b>0.012</b>	<b>8.10</b>	<b>5.20</b>	<b>0.000</b>	<b>38</b>	<b>-16</b>	<b>44</b>
						0.021	0.012	7.97	5.15	0.000	30	-18	44
						0.049	0.019	7.38	4.95	0.000	32	-24	54
		0.372	0.095	286	0.007	<b>0.208</b>	<b>0.032</b>	<b>6.36</b>	<b>4.55</b>	<b>0.000</b>	<b>-14</b>	<b>-94</b>	<b>8</b>
		0.996	0.837	101	0.086	1.000	0.504	3.94	3.30	0.000	16	-20	8

*table shows 3 local maxima more than 8.0mm apart*

Height threshold:  $T = 2.55$ ,  $p = 0.010$  (1.000)  
 Extent threshold:  $k = 50$  voxels,  $p = 0.215$  (1.000)  
 Expected voxels per cluster,  $\langle k \rangle = 34.889$   
 Expected number of clusters,  $\langle c \rangle = 13.63$   
 FWEp: 7.366, FDRp: 6.031, FWEc: 1442, FDRc: 1442

Degrees of freedom = [1.0, 18.0]  
 FWHM = 10.6 10.8 10.7 mm mm mm; 5.3 5.4 5.3 {voxels}  
 Volume: 1416888 = 177111 voxels = 1069.8 resels  
 Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 152.19 voxels)



# Useful tools

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

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