

fMRI: 1st-level individual analysis, 2nd-level group analysis, and multiple regression

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Acknowledgement

- Der-Yow Chen, Ph.D.
- Yi-Ping Chao, Ph.D.

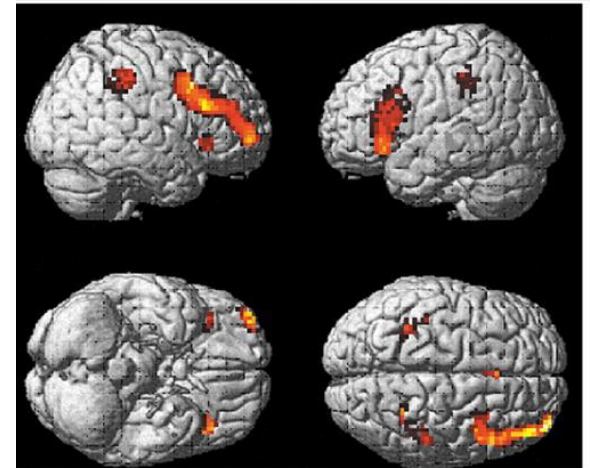
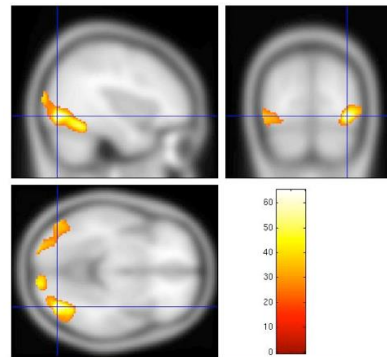
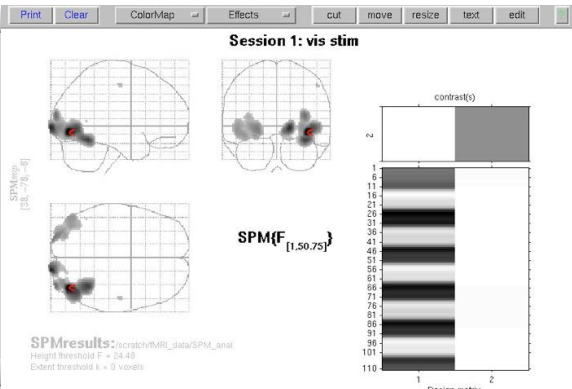
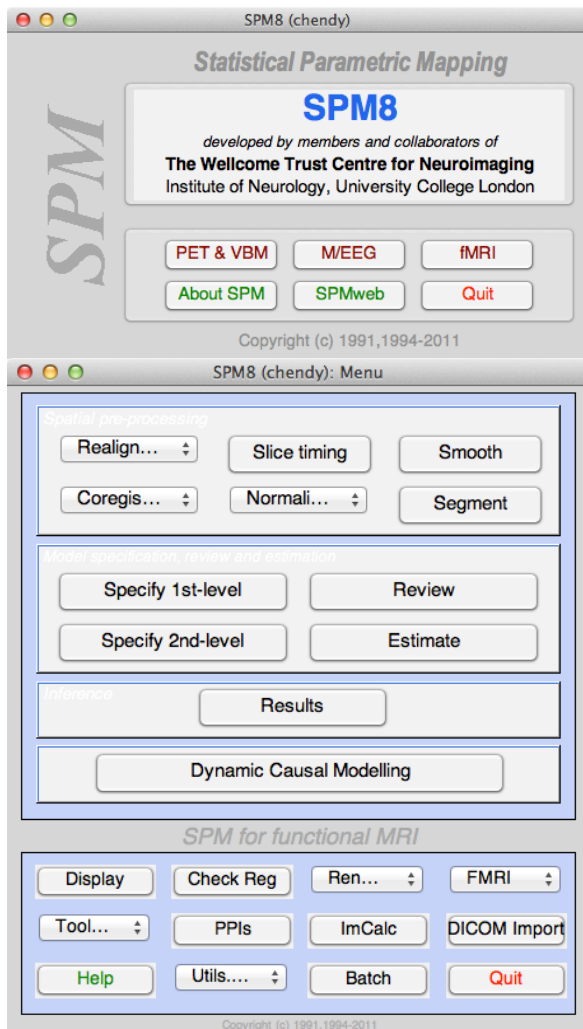
Outline

- Functional MRI data analysis
 - SPM pre-processing (Wesley Wu, Ph.D.)
 - 1st-level individual analysis
 - 2nd-level group analysis
 - multiple regression

fMRI analysis tools

- SPM (Statistical Parametric Mapping)
 - Wellcome Trust Centre for Neuroimaging, UCL, UK
 - <http://www.fil.ion.ucl.ac.uk/spm/software/>
- FSL (FMRIB Software Library)
 - Oxford, UK
 - <http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/>
- AFNI (Analysis of Functional NeuroImages)
 - NIH, USA
 - <http://afni.nimh.nih.gov/afni/download>
- REST (Resting-State fMRI Data Analysis Toolkit)
 - Lab of Cognitive Neuroscience and Learning, Beijing Normal University, China
 - <http://restfmri.net/forum/index.php>

SPM (Statistical Parametric Mapping)



statistics: volume summary (p-values corrected for entire volume)

set-level		cluster-level			voxel-level				x,y,z (mm)
<i>p</i>	<i>C</i>	<i>D</i> corrected	<i>K_E</i>	<i>D</i> uncorrected	<i>D</i> corrected	<i>F</i>	(<i>Z_u</i>)	<i>D</i> uncorrected	
0.000	4		2085		0.000	65.06	(6.34)	0.000	38 -78 -8
					0.000	57.02	(6.04)	0.000	16 -100 -2
					0.000	52.88	(5.88)	0.000	36 -54 -18
			1009		0.001	40.93	(5.33)	0.000	-24 -96 -4
					0.002	36.46	(5.03)	0.000	-50 -74 -4
					0.002	35.62	(5.04)	0.000	-42 -76 -10
			7		0.016	28.56	(4.59)	0.000	50 -14 52
			1		0.049	24.54	(4.30)	0.000	-48 -56 6

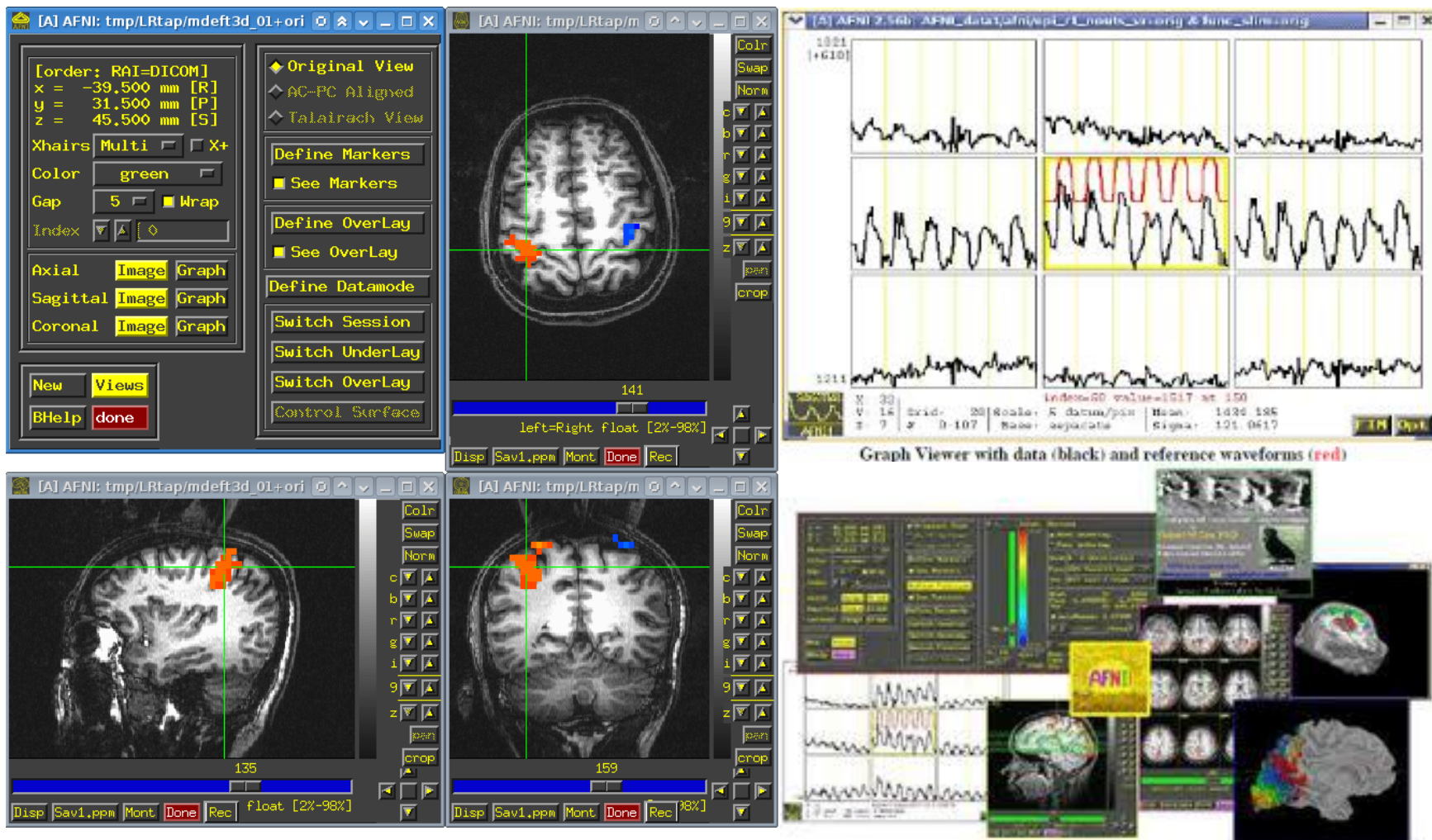
FSL (FMRIB Software Library)

The image displays the FSL (FMRIB Software Library) interface, specifically the FEAT (FMRIB Expert Analysis Tool) v5.4 window. The interface is divided into several panels:

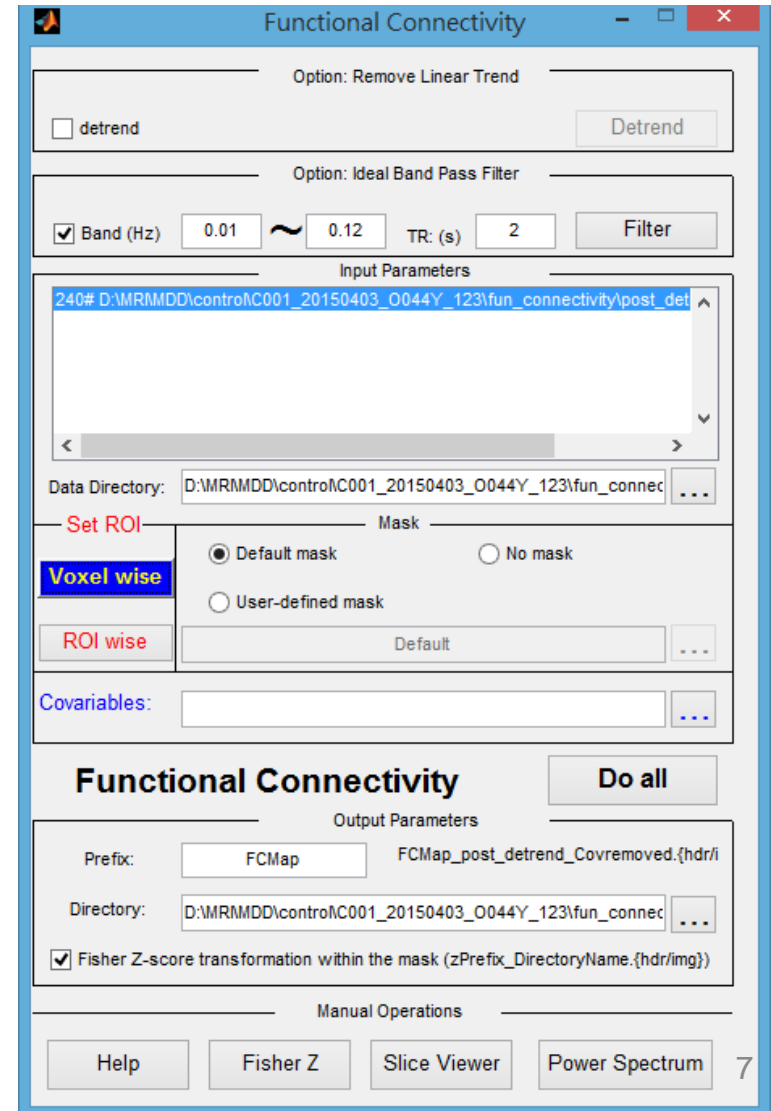
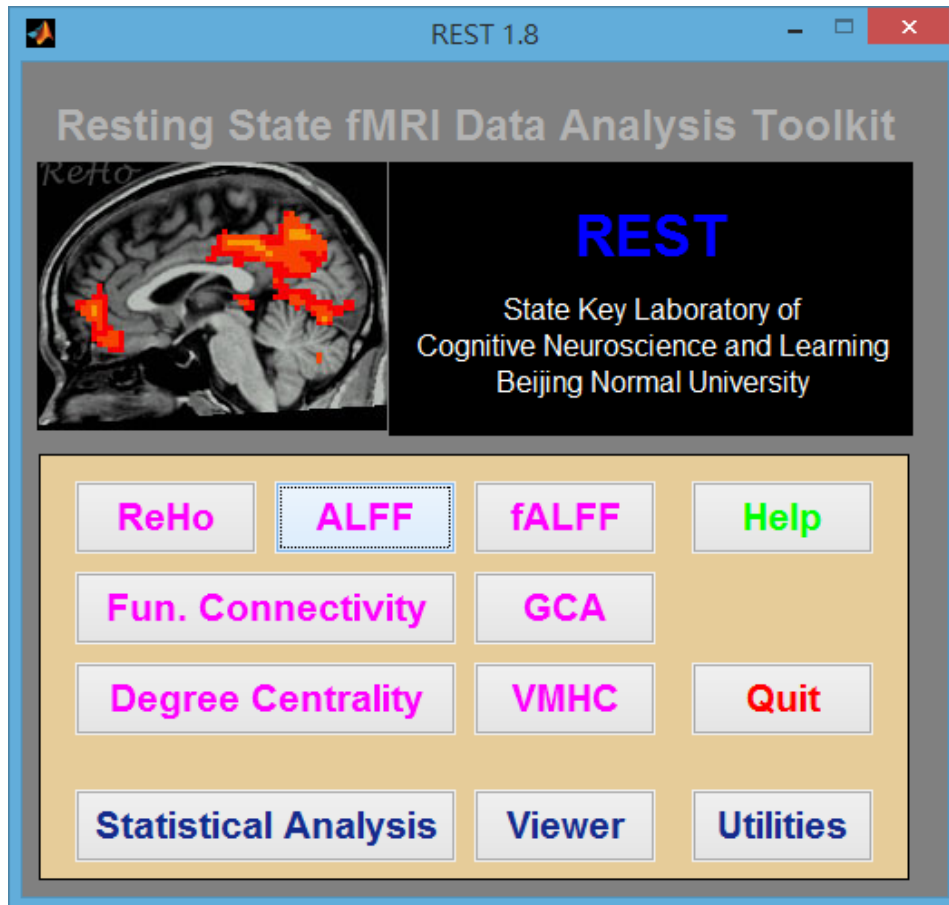
- FEAT - FMRIB Expert Analysis Tool - v5.4:** The main control window with tabs for "First-level analysis" and "Full analysis". It includes fields for "Number of analyses" (1), "Output directory", "Total volumes" (0), and "TR (s)" (3.0). A "Go" button is visible at the bottom left.
- FSL 3.2:** A smaller window showing the FSL logo and a list of tools:
 - BET Brain Extraction
 - SUSAN Noise Reduction
 - FAST Segmentation
 - FLIRT Linear Registration
 - FEAT FMRI Analysis
 - MELODIC ICA
 - FDT Diffusion
 - FSLView
 - Exit
 - Help
- Ortho view:** A window showing three orthogonal views (axial, sagittal, and coronal) of a brain slice. The top panel shows the axial view with a color scale from 0 to 23569. The bottom panel shows the sagittal view. The middle panel shows the coronal view. The views are overlaid on a grayscale brain slice.
- Timeseries:** A window showing a line graph titled "Timeseries - filtered_func_data". The y-axis is labeled "Value" and ranges from -400 to 500. The x-axis is labeled "Time" and ranges from 0 to 200. The graph shows a blue line with high-frequency oscillations and a green line with lower-frequency oscillations.

At the bottom of the FEAT window, there is a status bar showing "Loading.... /usr/local/feeds/data/fmri.feathresh_zstat2".

AFNI (Analysis of Functional NeuroImages)



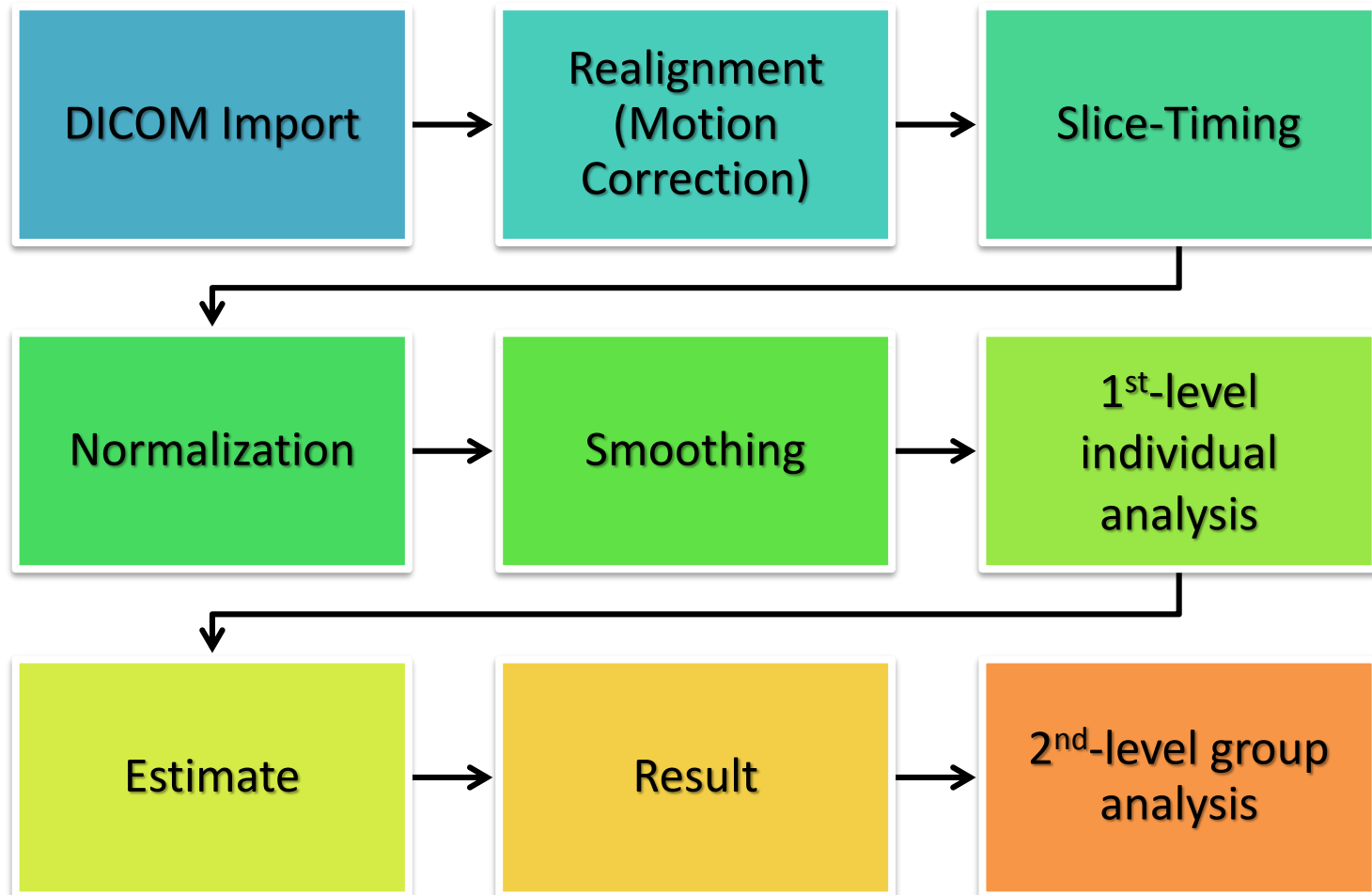
REST (Resting-State fMRI Data Analysis Toolkit)



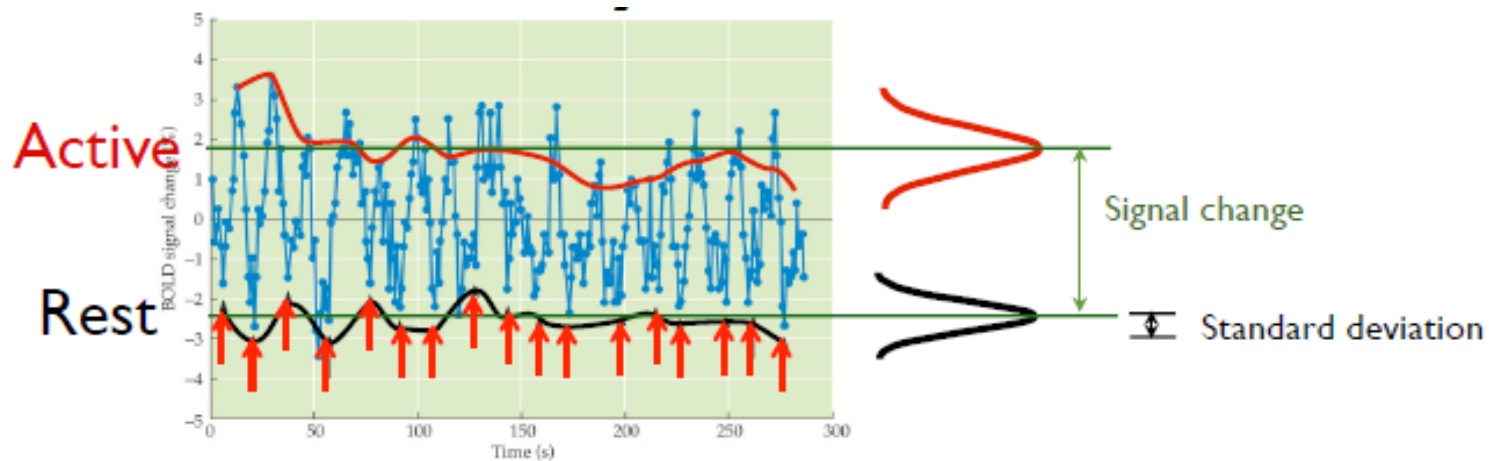
Analysis tools comparison

	SPM	FSL	AFNI	REST
Features	最多人使用，資料分析流程易標準化且便於操作，但細節不易作修改	資料分析流程亦適合初學者，為一免費之工具，並可由介面或是指令兩方面著手	資料分析流程適合略懂Unix指令人員，每一步驟均可做調整，有較大之自由度	適合resting-state fMRI初學者，為一免費之工具
Operating system	Any OS with Matlab	Mac, Linux, Windows	Mac, Linux, some Matlab-compatible scripts	Any OS with Matlab
User interface	MATLAB scripts and button-press	Unix functions and GUI	Unix functions and GUI	MATLAB scripts and button-press

Pre-processing and processing



Activity evaluation

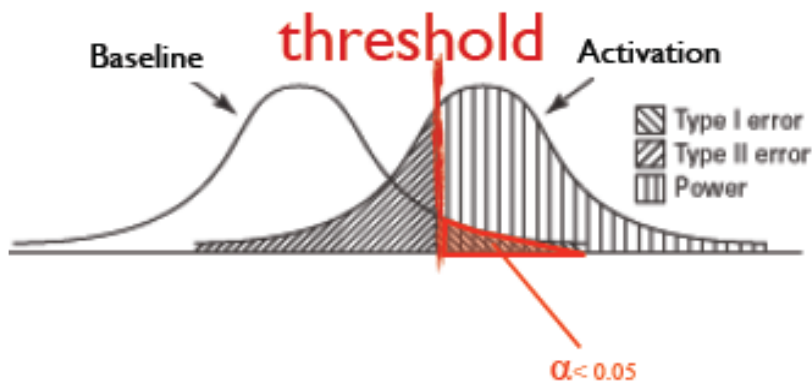


- Use concept of **normal distribution** to model **each condition** in BOLD signal.
- Find which voxels have time courses that match the predicted response.
- An unrelated brain region should have no response!

Statistical comparison

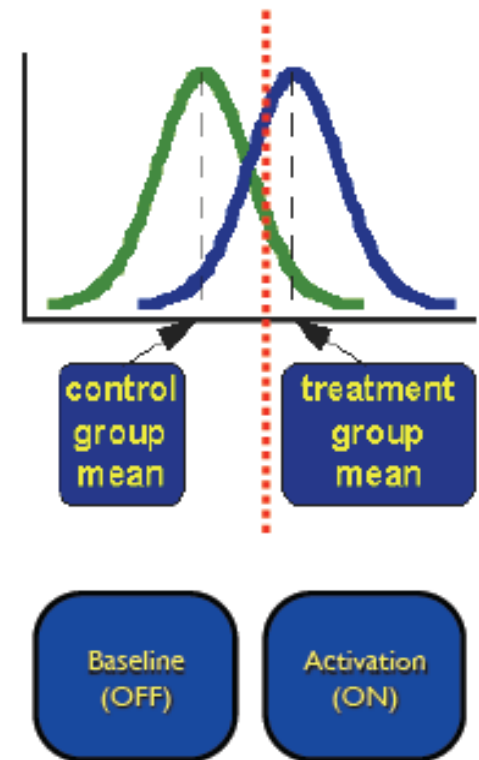
❖ Comparison between Conditions

- Conditions induced by IVs (treatments or tasks)
- DV: (fMRI data)



H_0 : Null Hypothesis: no difference

H_1 : Alternative Hypothesis: difference exists

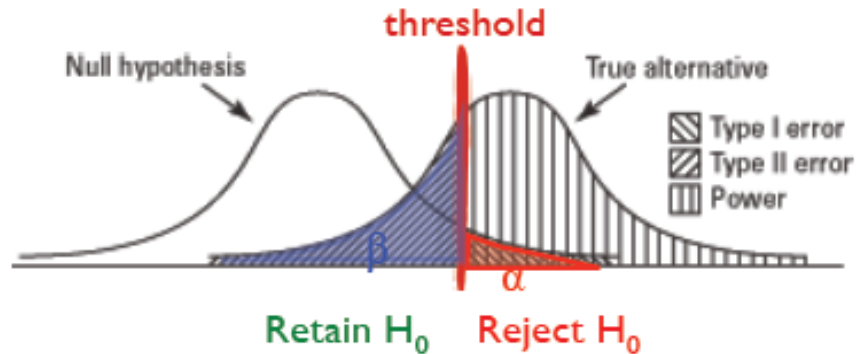


1. Grp1-Grp2

2. Task-Rest

Hypothesis testing in statistics

$H_0 : \text{ON} = \text{OFF}$
 $H_1 : \text{ON} \neq \text{OFF}$



		Nature/Truth	
		H_0 (inactive)	H_1 (active)
Statistical Decision	Reject H_0	Type I error α (false alarm)	Hit $1-\beta$ Power
	Retain H_0	Correct $1-\alpha$	Type II error β missed

significance level α
 < 0.05 (can be 0.01 or 0.001)

Statistics: t-test

- Identify differences in the “means”

- Single condition (compared to 0)

$$t = \frac{\bar{x} - \mu_0}{s/\sqrt{n}}$$

μ_0 : population mean
 s : sample standard deviation
 n : sample size
 Degree of freedom: (n-1)

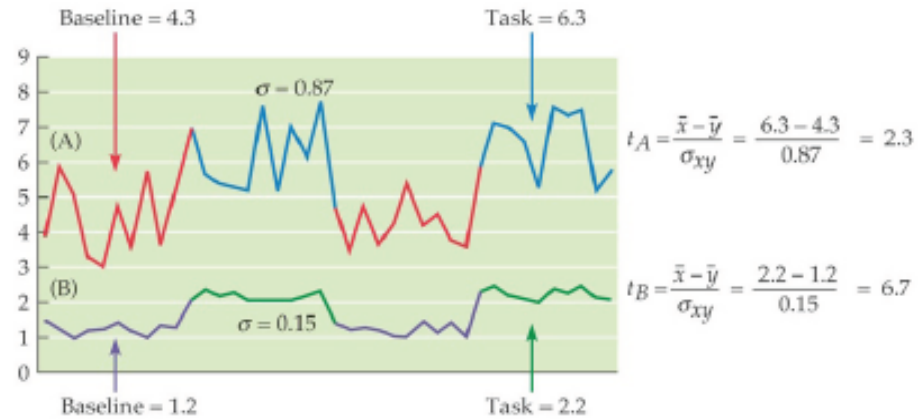
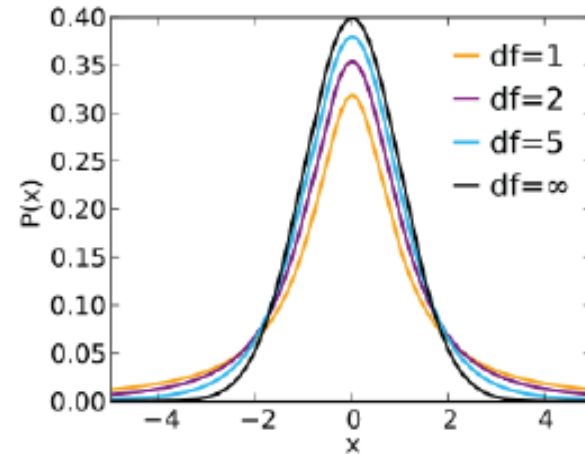
$t \uparrow \Rightarrow p \downarrow$
 \Rightarrow more likely has significant difference

- Two conditions (unequal sample size, unequal variance)

$$t = \frac{\bar{X}_1 - \bar{X}_2}{S_{X_1 X_2} \cdot \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

$$S_{X_1 X_2} = \sqrt{\frac{(n_1 - 1)S_{X_1}^2 + (n_2 - 1)S_{X_2}^2}{n_1 + n_2 - 2}}$$

\bar{X}_1 & \bar{X}_2 : population mean
 n_1 & n_2 : sample size
 $S_{X_1 X_2}$: standard deviation of 2 samples
 Degree of freedom: (n1 + n2 -2)



Statistics: correlation

- Quantify how well the data match HRF response.

- Strategy:

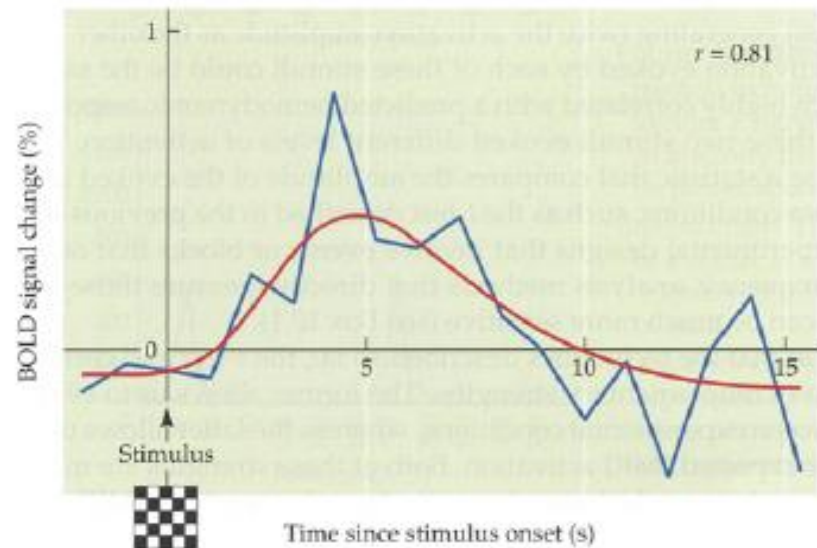
1. Paradigm + fMRI data
2. Covariance
3. Normalization (divide by std)

$$\rho_{X,Y} = \frac{\text{cov}(X, Y)}{\sigma_X \sigma_Y} = \frac{E((X - \mu_X)(Y - \mu_Y))}{\sigma_X \sigma_Y},$$

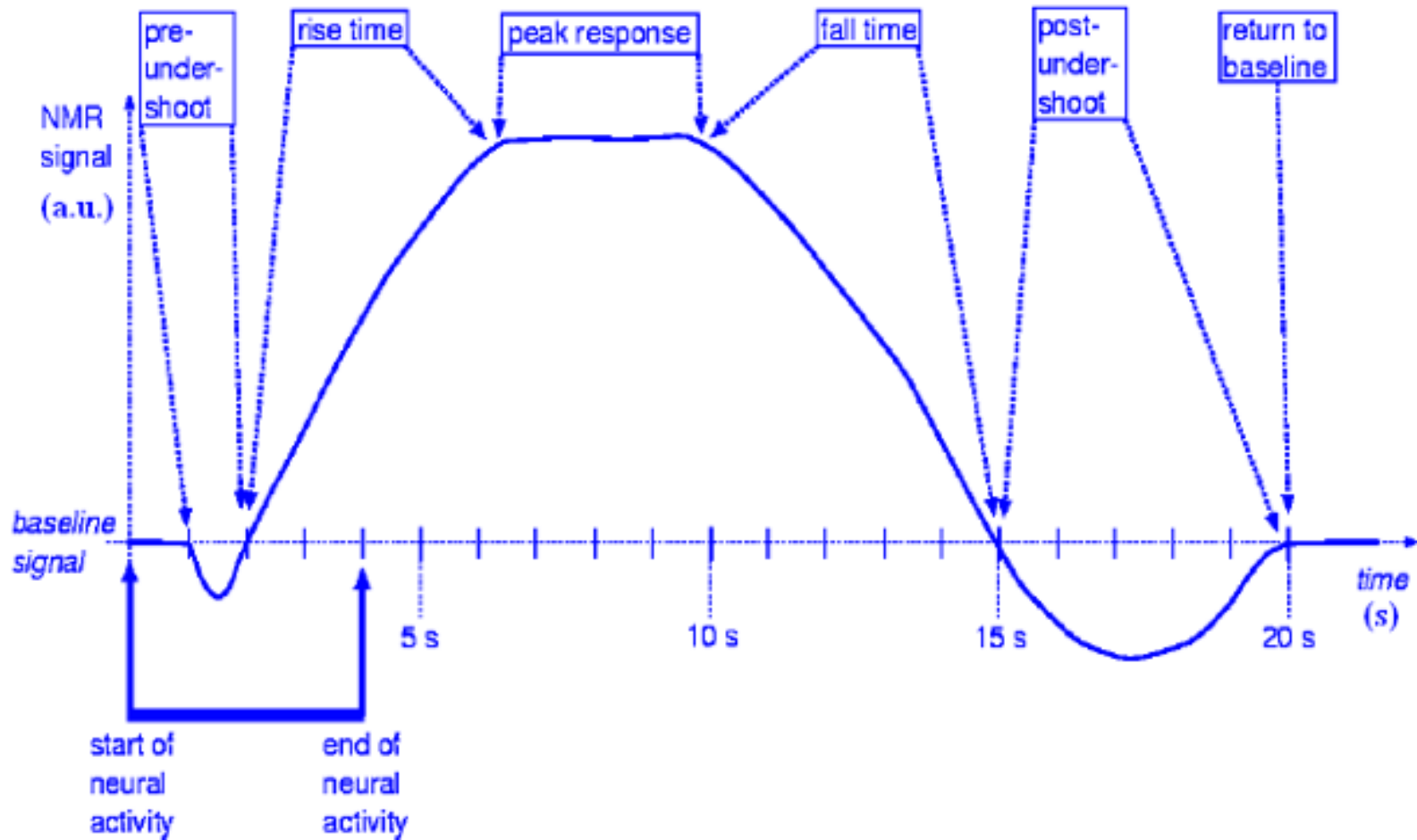
μ_X & μ_Y : population mean
 σ_X & σ_Y : standard deviation
Degree of freedom: $(n_X + n_Y - 2)$

- Correlation coefficients

- range: (-1, +1)
- irrelevant to amplitude

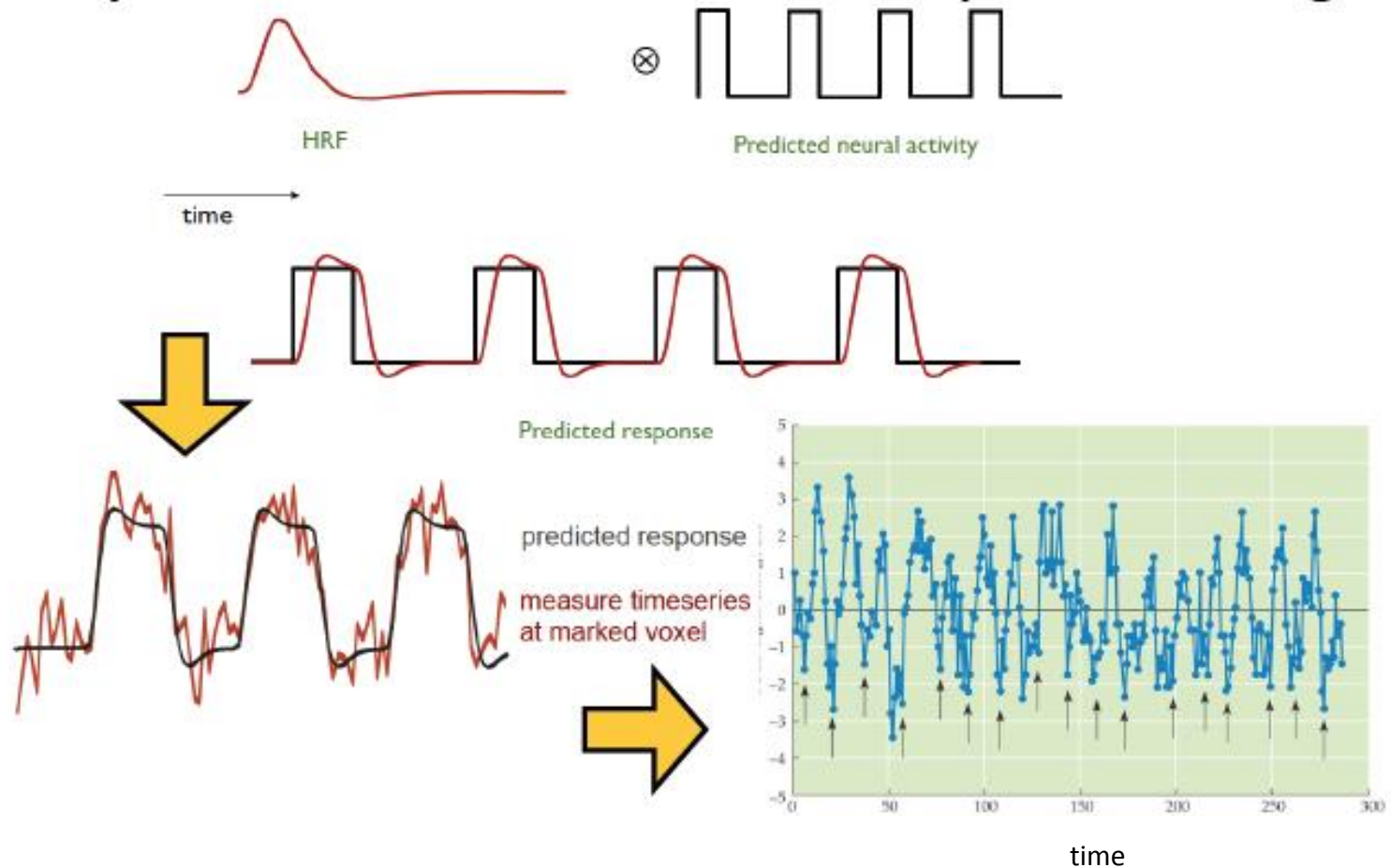


Hemodynamic response function (HRF)



BOLD fMRI signal and linear model

- Hemodynamic function *convolved* with experiment design



Basics of linear model: regression

- **Regression**: relationship between a response / outcome (dependent) variable and one or more explanatory (independent) variables (**regressors**)

- Simple regression: fit data with a straight line

$$y = \alpha + \beta x + \varepsilon$$

- α is the intercept (constant),
 β is the slope (like amplitude)

- Some statisticians just call it **linear model**

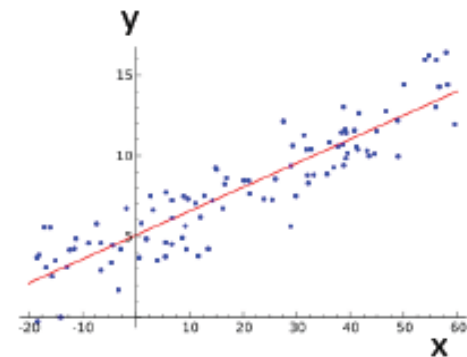
- **Mathematical crystallization**

- $y_i = \alpha + \beta x_i + \varepsilon_i$, or $y_i = \alpha + \beta_1 x_{1i} + \dots + \beta_k x_{ki} + \varepsilon_i$

- $y = X\beta + \varepsilon$, $X = [1, x_1, x_2, \dots, x_k]$

- Assumption

- linearity
- white noise (independence) and Gaussianity $\varepsilon \sim N(0, \sigma^2 I)$

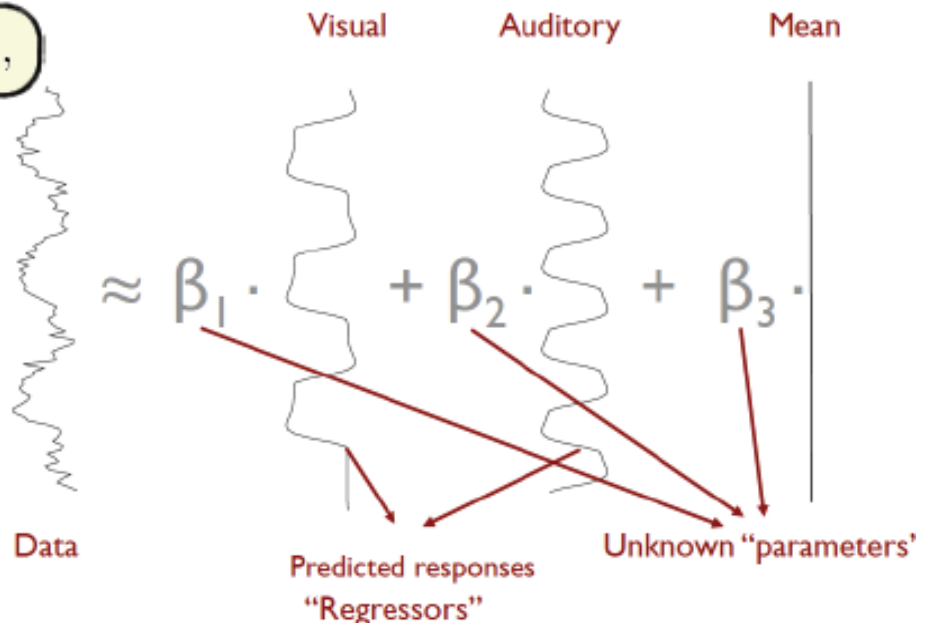
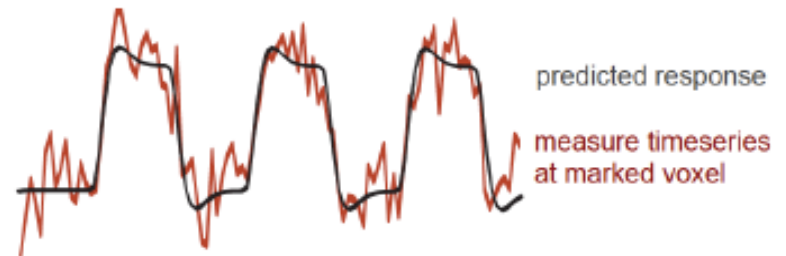


Statistics: regression

- Observed data (y_i)
 - regressors (x_i)
 - variable weighting (β_i)
 - residual noise (ϵ)

$$y_i = \beta_1 x_{i1} + \beta_2 x_{i2} + \dots + \beta_p x_{ip} + \epsilon_i,$$

- **Regressors for fMRI**
Curve fitting
- If β is non-zero, then voxel is “active”
 - β has *amplitude* info.



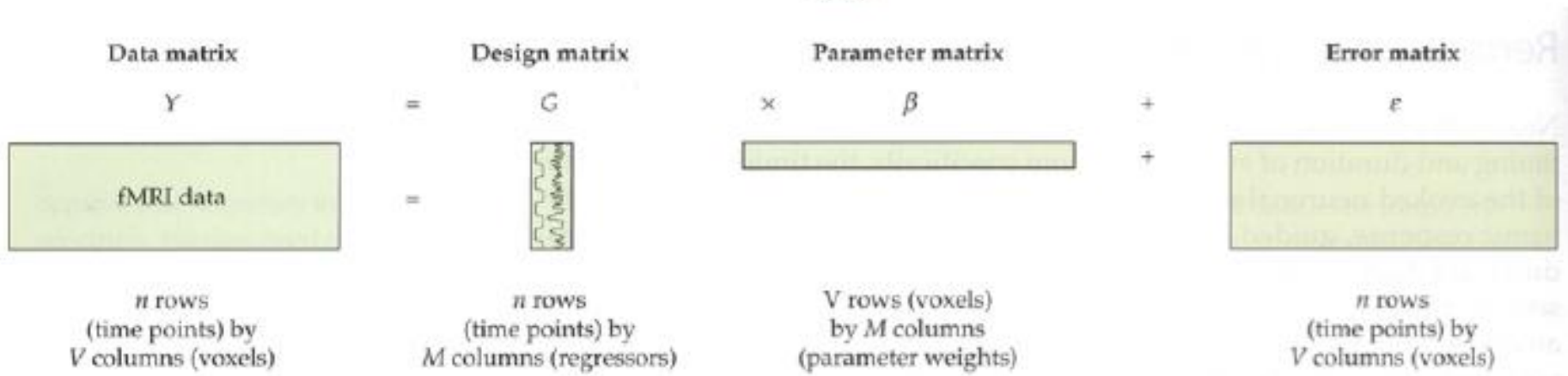
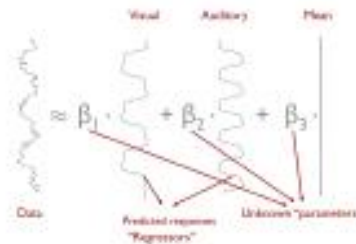
fMRI data

- Data partition: $\text{Data} = \text{Signal} + \text{Noise}$
 - Data = acquisition from scanner (voxel-wise time series)
 - What we have
 - Signal = BOLD response to stimulus; effects of interest + no interest
 - We don't really know the real signal!!!
 - Look for idealized components, or search for signal via repeated trials
 - Of interest: effect size (**response amplitude**) for each condition: *beta*
 - Of no interest: *baseline, slow drift, head motion effects, ...*
 - Noise = components in data that interfere with signal
 - Practically the part we have don't know and/or we don't care about; that is, noise is the part we can't explain in the model
 - Will have to make some assumptions about its distribution
- $\text{Data} = \text{baseline} + \text{slow drift} + \text{other effects of no interest} + \text{response}_1 + \dots + \text{response}_k + \text{noise}$

General linear model (GLM) model in fMRI

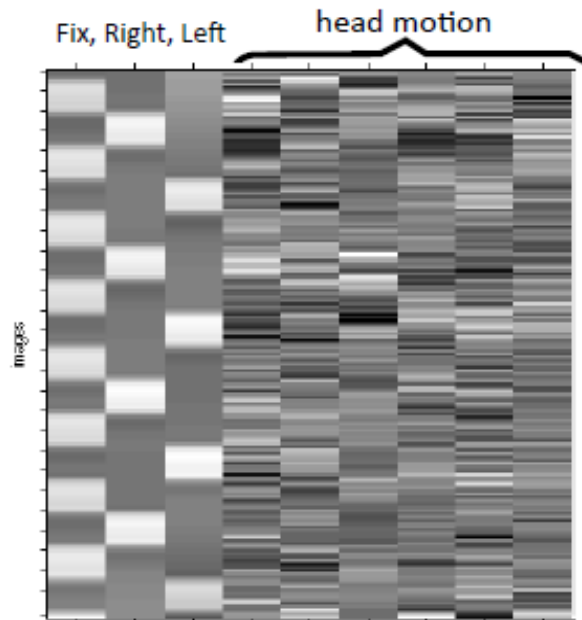
Data = baseline + slow drift + other effects of no interest + response₁ + ... + response_k + noise

$$y = X\beta + \varepsilon$$

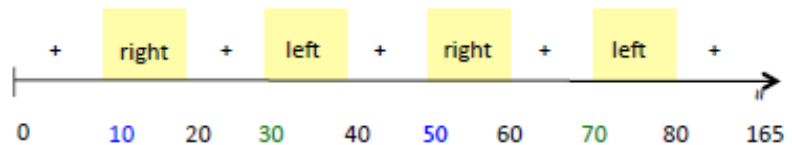


Design matrix

- Voxel-wise (massively univariate) linear model: $y = X\beta + \epsilon$
 - X : explanatory variables (regressors) – **same** across voxels
 - y : data (time series) at a voxel – **different** across voxels
 - β : regression coefficients (effects) – **different** across voxels
 - ϵ : anything we can't account for – **different** across voxels
- Visualizing design matrix $X = [x_1, x_2, \dots, x_k, \dots]$ in grayscale



- 3 regressors of interest (fix, right, left)
- 6 head motion regressors (3 rotations + 3 shifts)

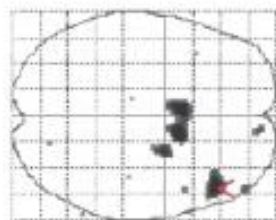
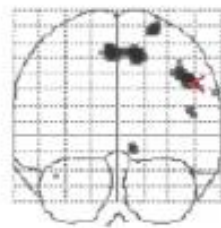
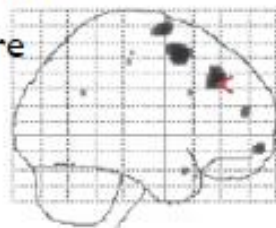


stimuli	Onset (for scan)
fixation	0 20 40 60 80 100 120 140 160
right	10 50 90 130
left	30 70 110 150

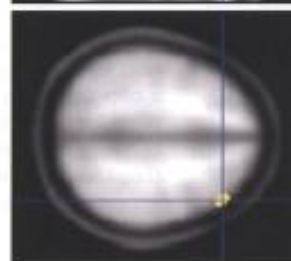
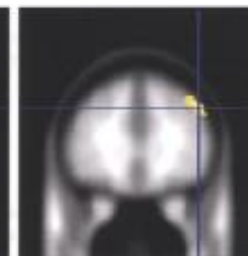
Displaying statistical results: statistical parametric mapping

Glass Brain View

All activations are visible in each orientation



(B)



Three orthogonal slices at specific location

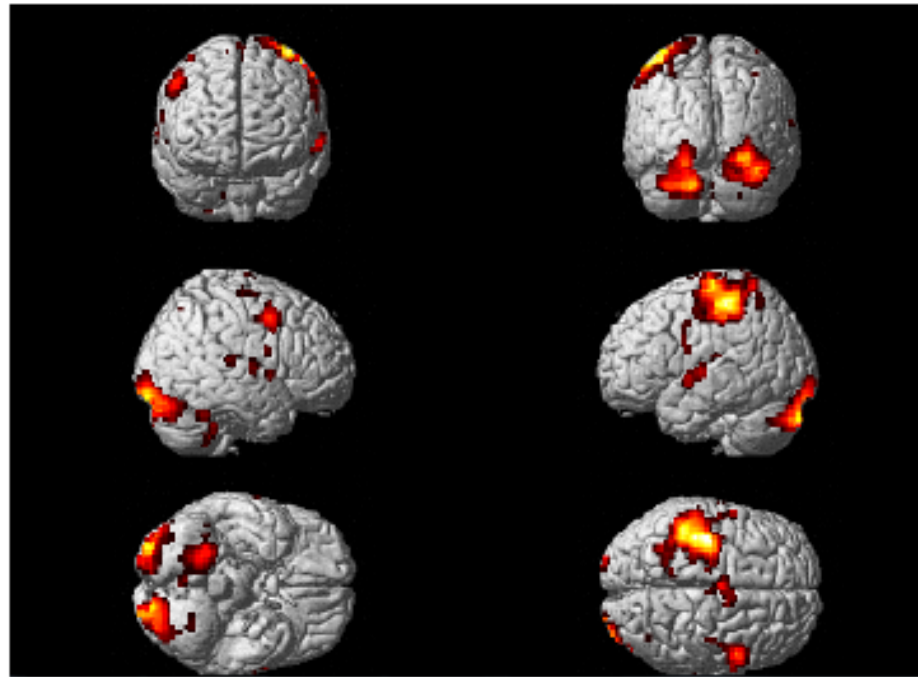
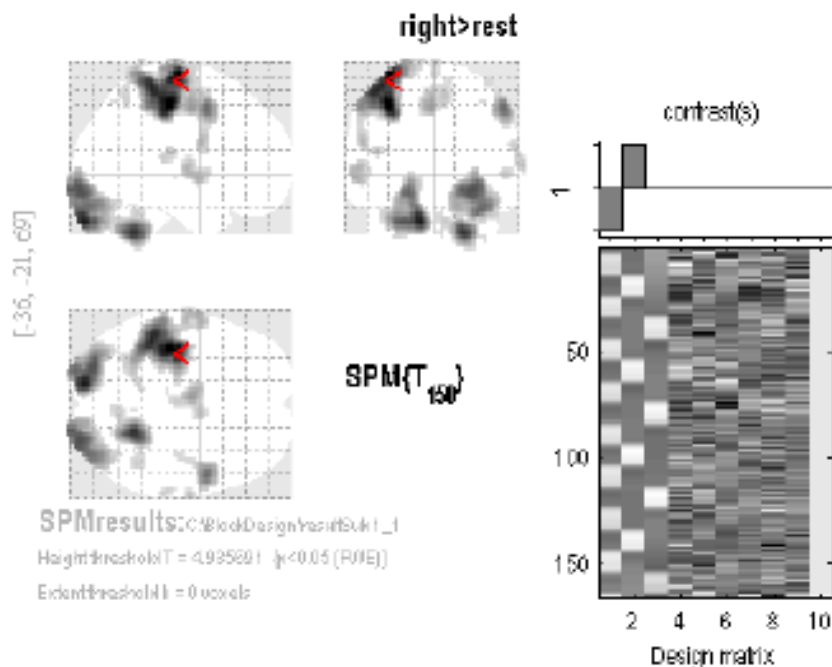
Rendered Brain View

(B)



Example result of single subject in SPM (1st level analysis)

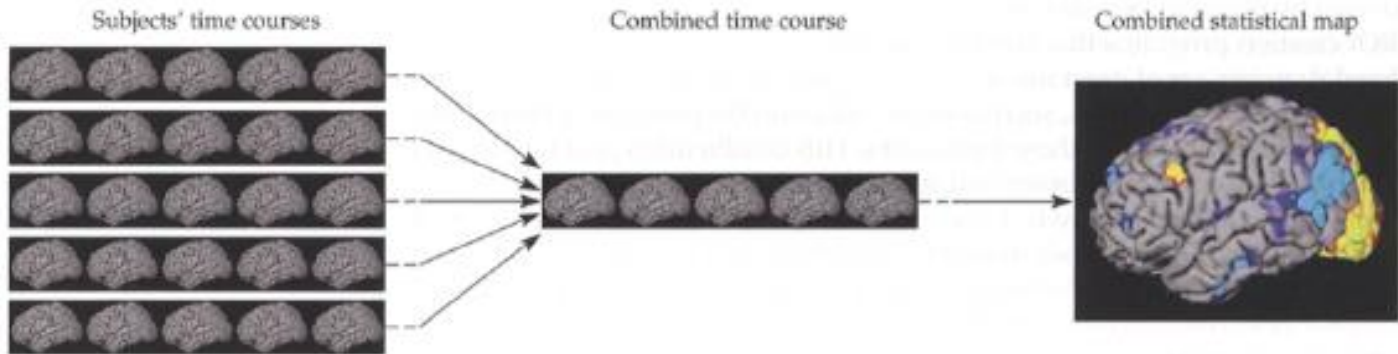
Right Finger Tapping > Left Finger Tapping



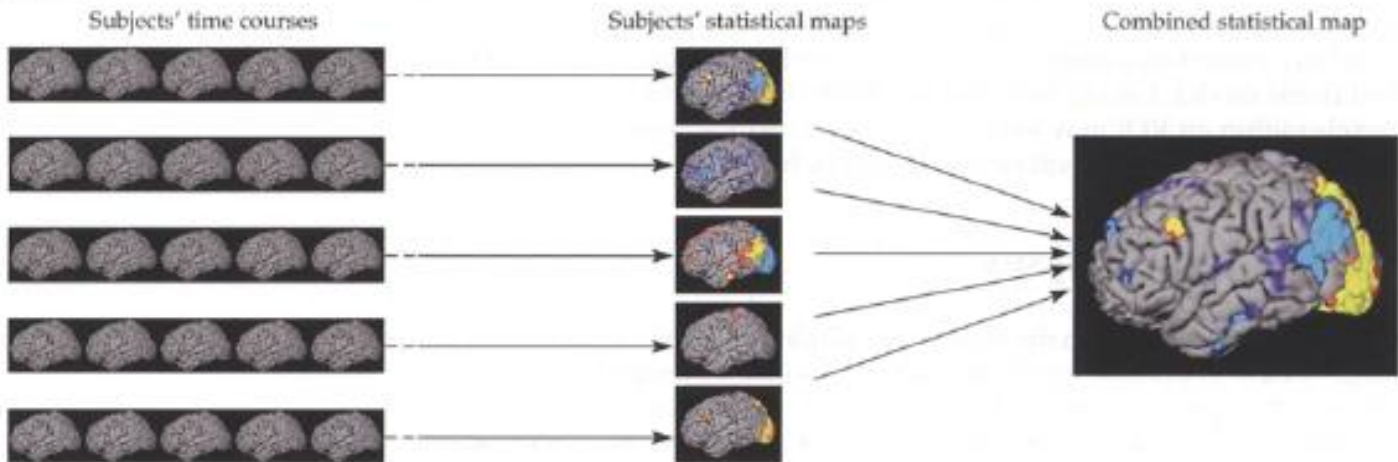
Significant difference can be found in the left hemisphere.

Group analysis: fixed effect vs. random effect

(A) Fixed effects



(B) Random effects



Examples of groups analysis

• One-Sample Case

- One group of subjects ($n \geq 10$)
 - One condition (house or face) effect
 - Linear combination of multiple effects (house - face)
- Null hypothesis H_0 : average effect = 0
 - Rejecting H_0 is of interest!
- Results
 - Average effect at group level
 - Significance: t-statistic

• Two-Sample Case

- Two groups of subjects ($n \geq 10$):
ex: males and females
 - One condition (house or face) effect
 - Linear combination of multiple effects (house - face)
 - Example: Gender difference in emotion effect?
- Null hypothesis H_0 : Group1 = Group2
 - Results
 - Group difference in average effect
 - Significance: t-statistic

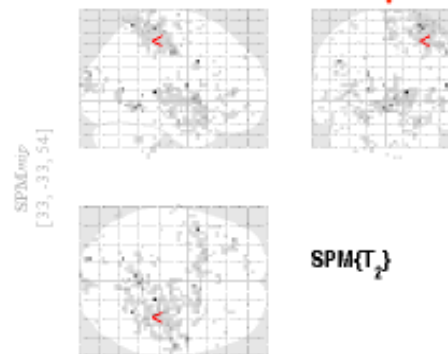
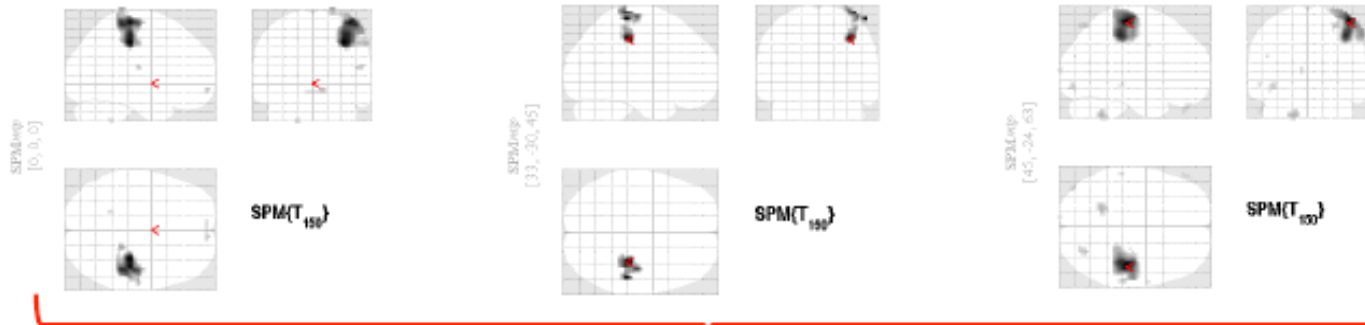
Example result of 3 subject in SPM (2nd level analysis)

Left Finger Tapping > Right Finger Tapping

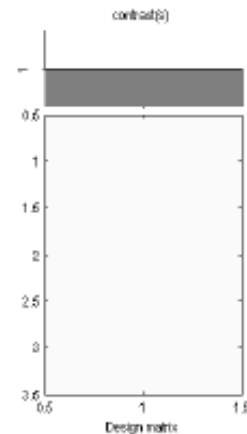
Subject 1

Subject 2

Subject 3



SPMresults: C:\BlockDesign2level
Height threshold T = 6.864568 (p < 0.01 (unc.))
Extent threshold k = 0 voxels



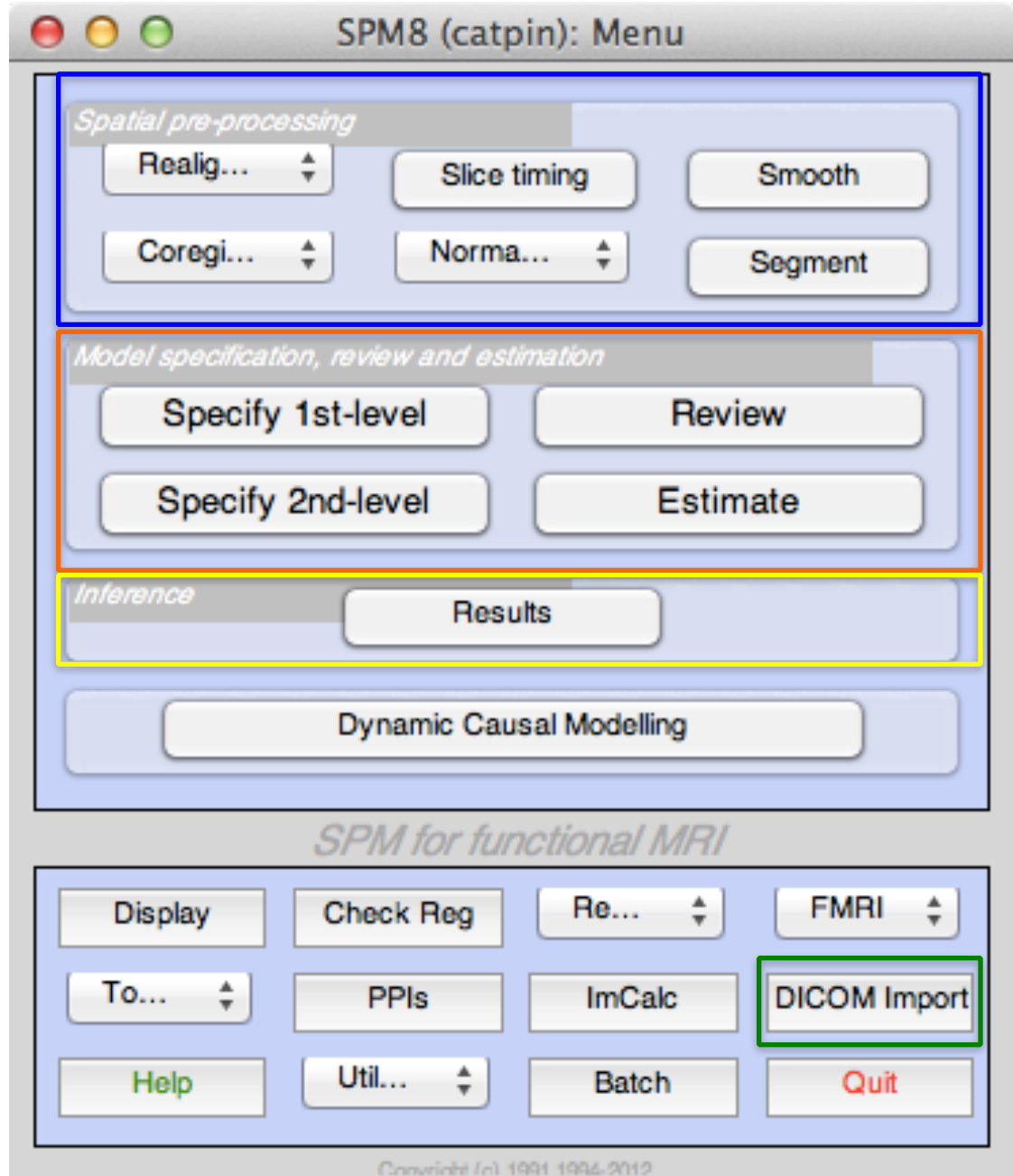
Demo

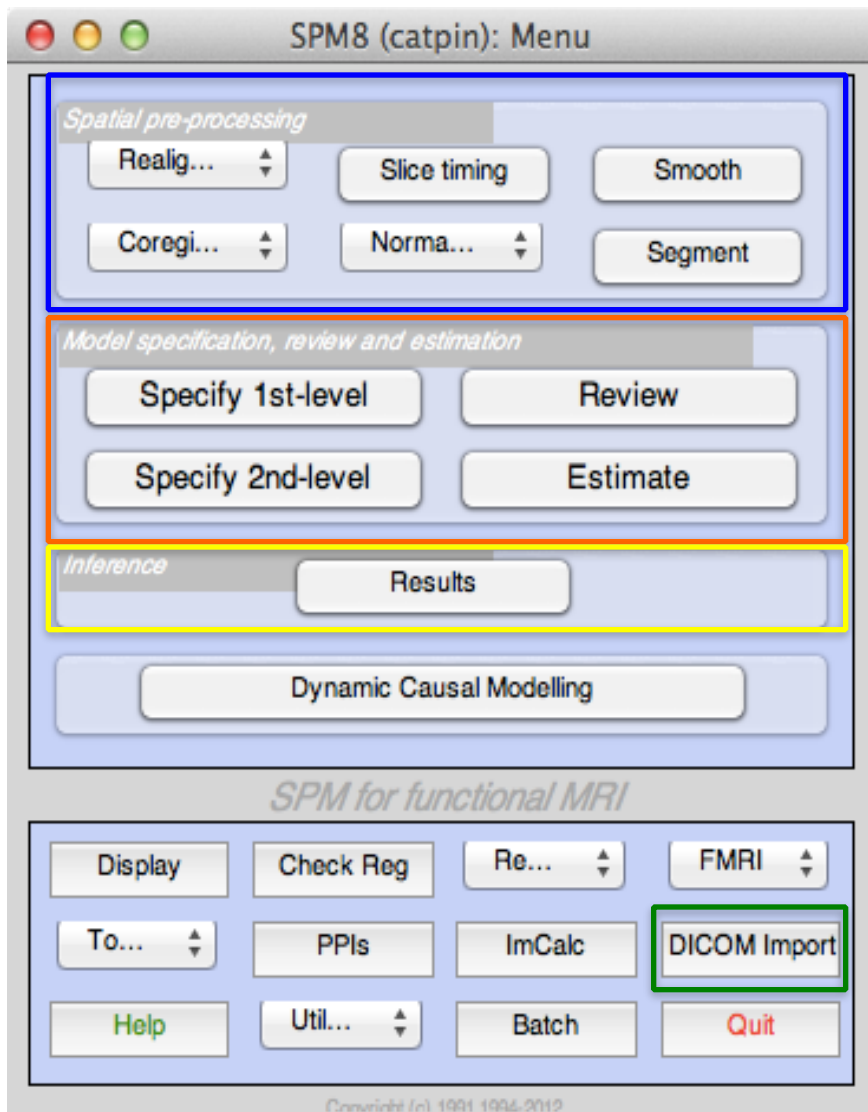
Preprocessing 前處理

Model specification,
review and estimation
時序分析/群組分析

Results 結果呈現

DICOM import 工具列





□ Preprocess

- *Realign*: Motion correction
- *Slice-Timing*: Slice timing correction
- *Smooth*: spatial smoothing
- *Coregister*: Modify A image into B image's orientation
- *Normalise*: Modify A image into brain template
- *Segment*: Separate the brain image into CSF, white matter, and gray matter parts.

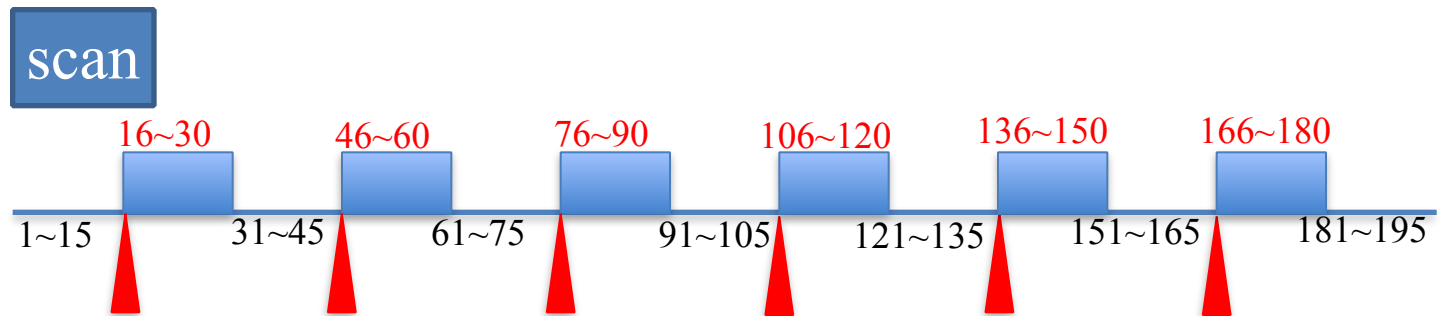
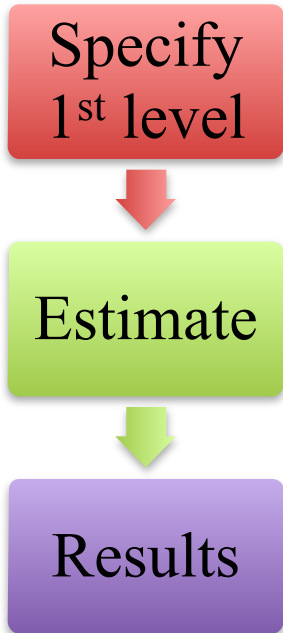
□ Analysis

- *Specify 1st -level*: 1st -level analysis paradigm design
- *Specify 2nd -level*: Group-level analysis pattern design
- *Review*
- *Estimate*: Analysis pattern calculating

- **Results**: Show results

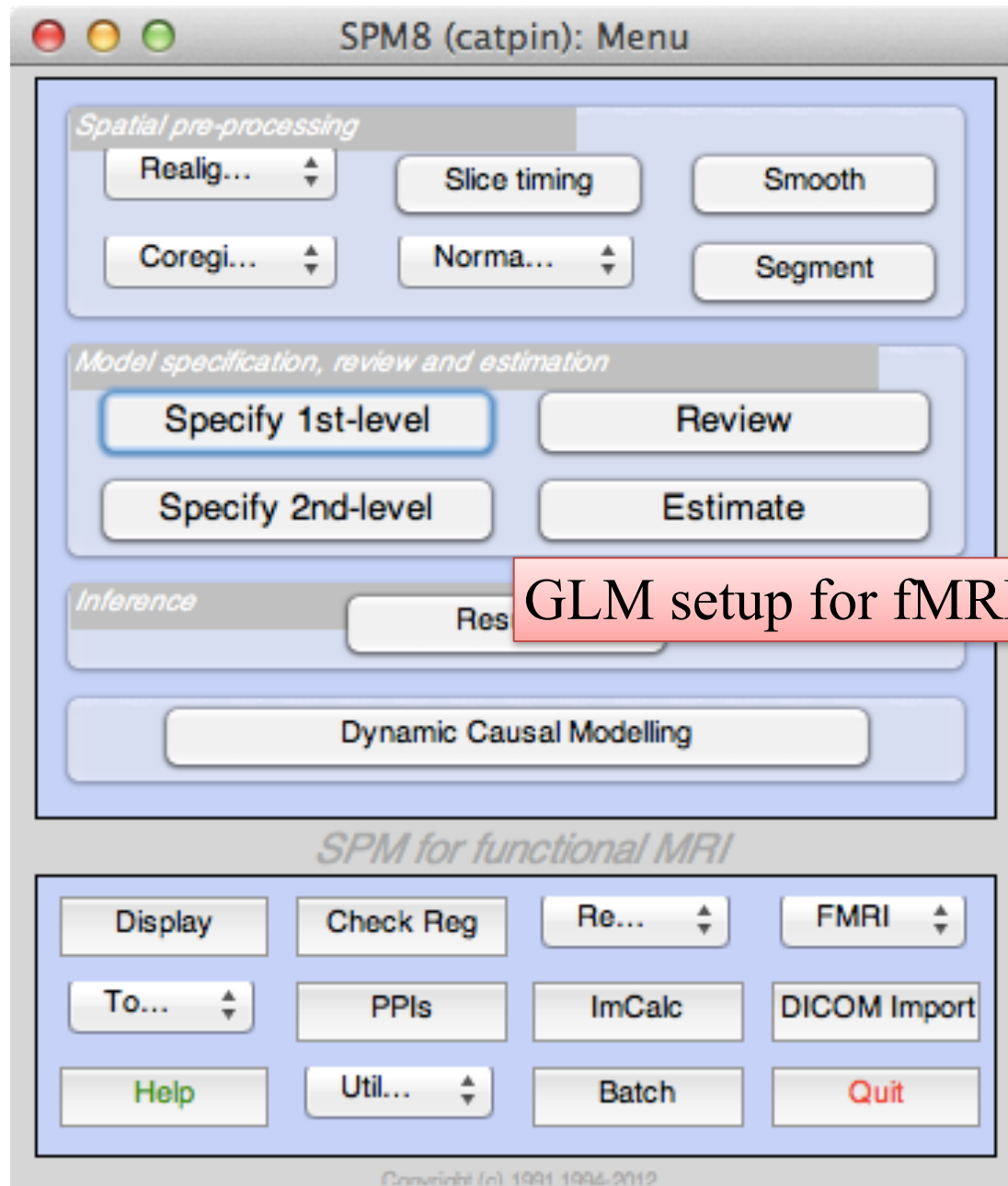
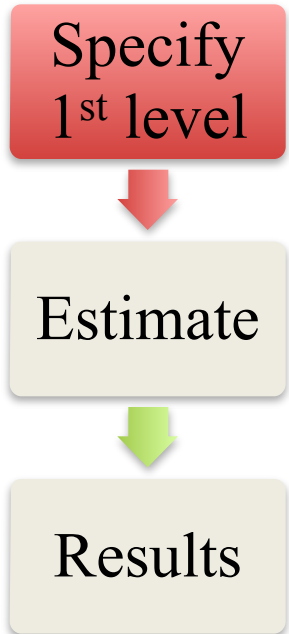
Single Subject Analysis

- 此部份與實驗設計以及所欲進行的統計運算有極大的關係，請參閱此次講習的其他課程內容。
- 再複習一下這堂課所展示的範例實驗設計

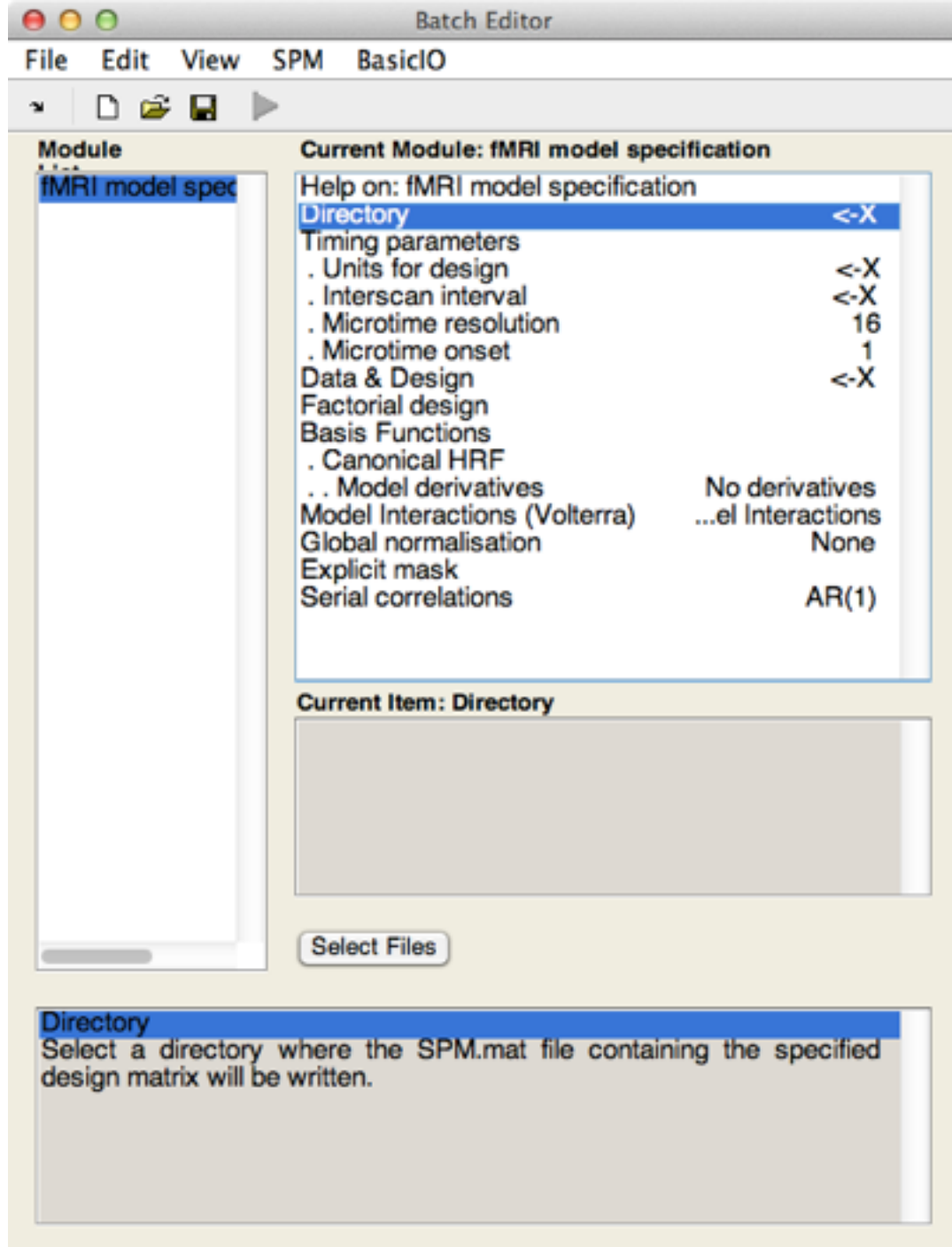


兩種Condition:

- 無雙手抓握(OFF), duration: 15 scans,
Onsets(每一段狀況開始的scan): 0 30 60 90 120 150 180
- 有雙手抓握(ON), duration: 15 scans
Onsets(每一段狀況開始的scan): 15 45 75 105 135 165



GLM setup for fMRI analysis



- ***Directory***

- 存放GLM設計的資料夾
- 所以要先建立一個資料夾

- ***Units for design***

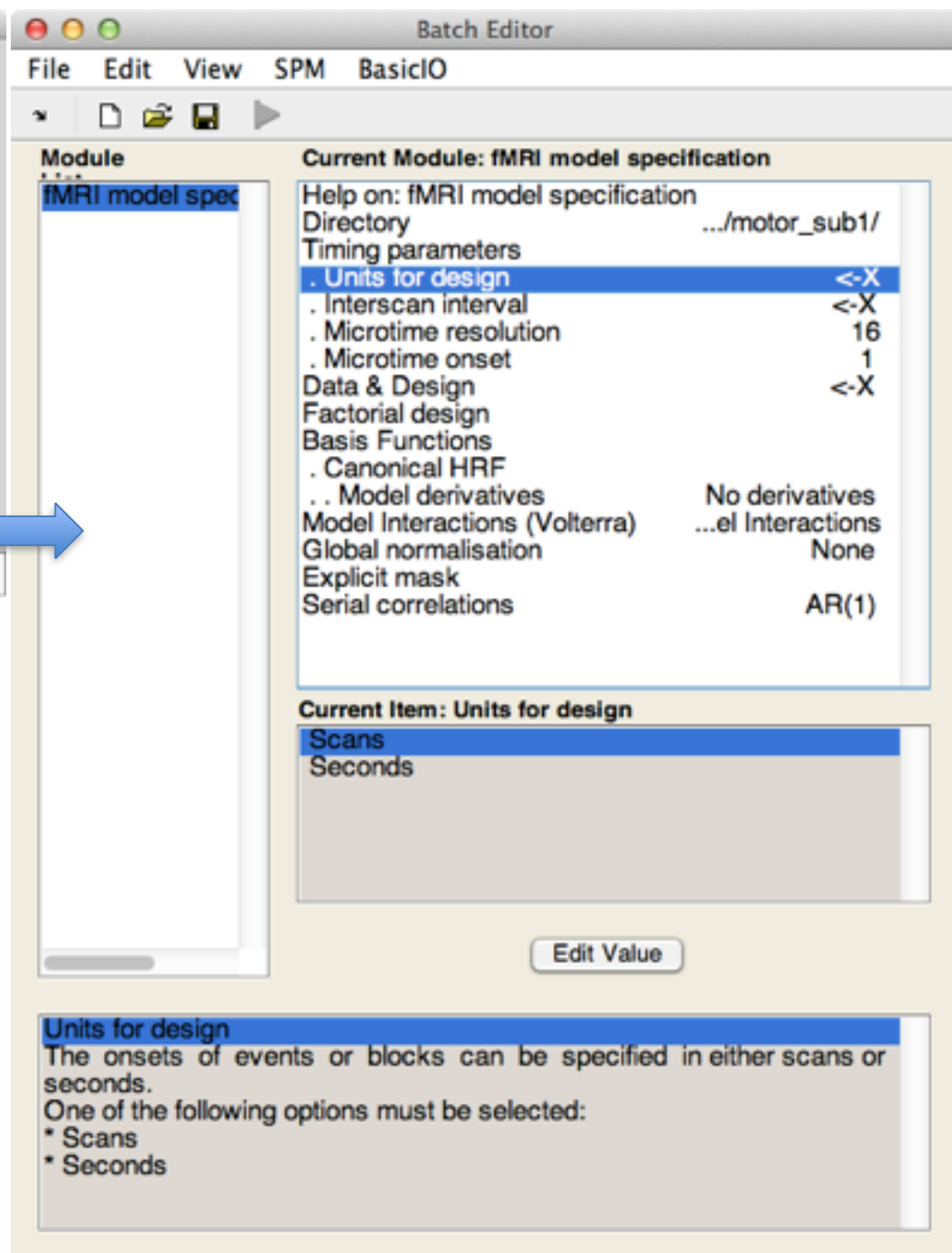
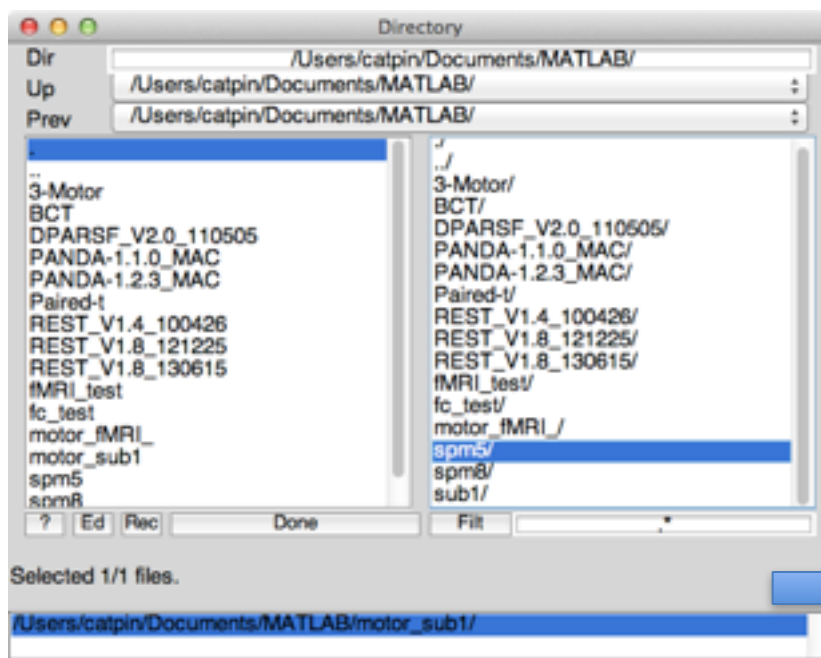
- 設計使用的單位
- Scan/Second

- ***Interscan Interval***

- Scan之間的時間
- TR

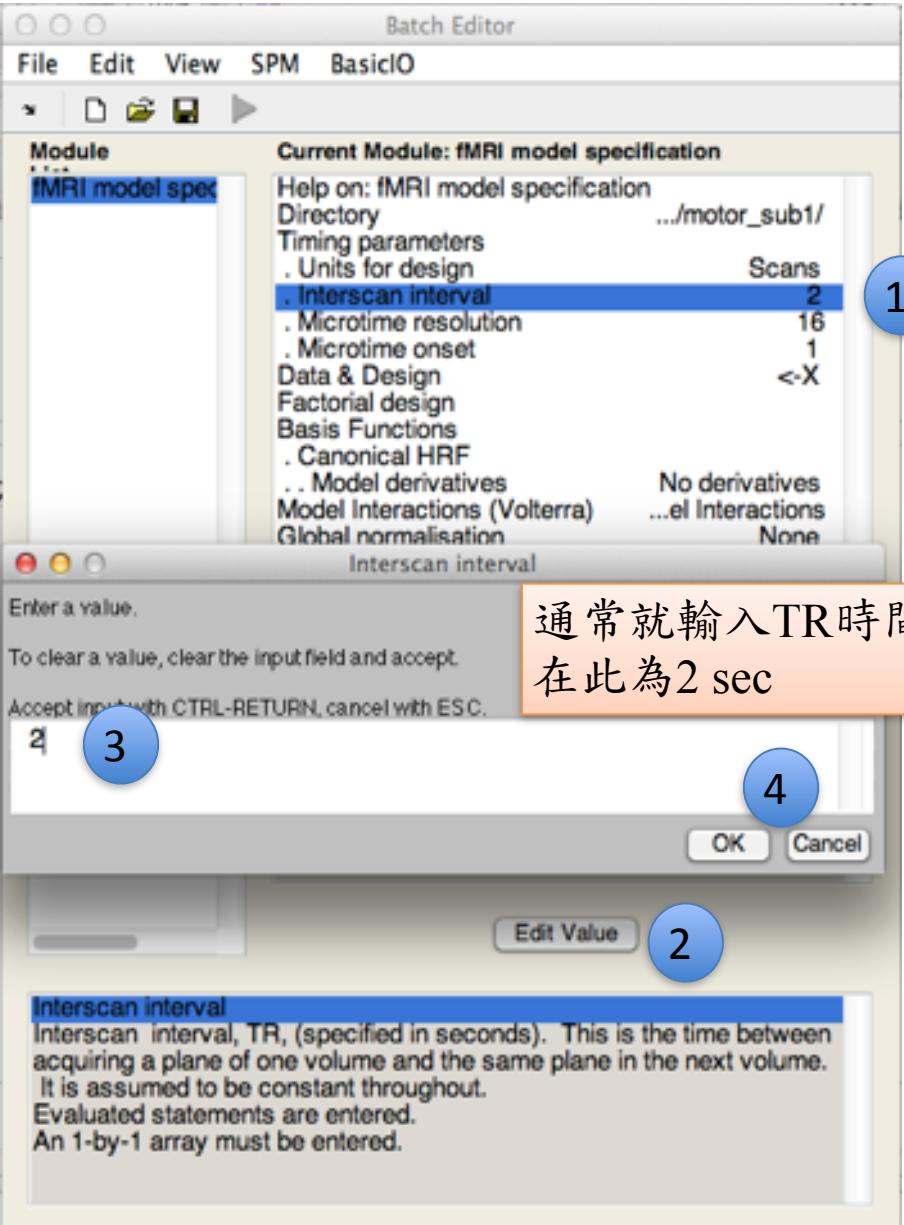
- ***Data & Design***

- 資料與設計

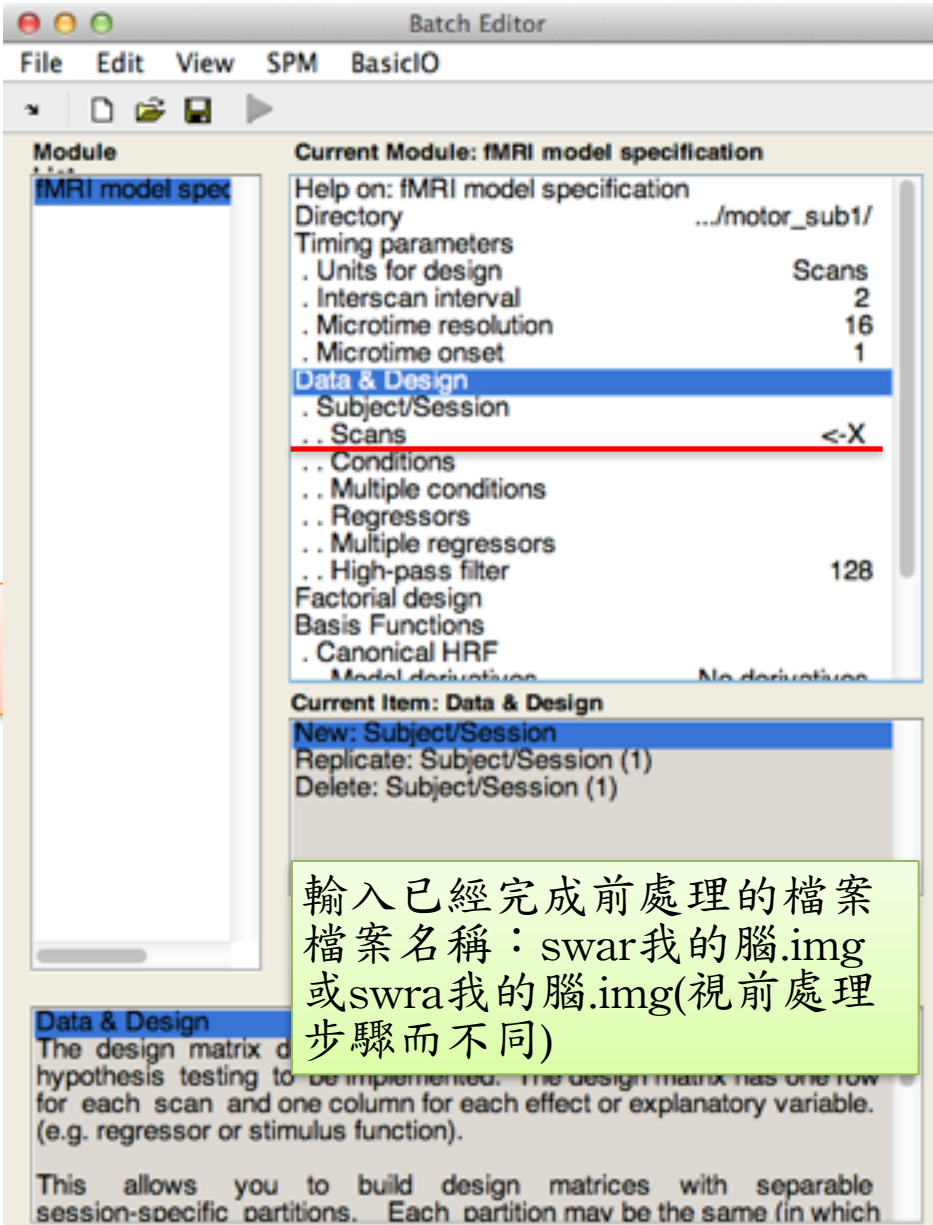


先建立一個資料夾來存放GLM設計，並由右邊視窗點選該資料夾路徑後，按下Done。

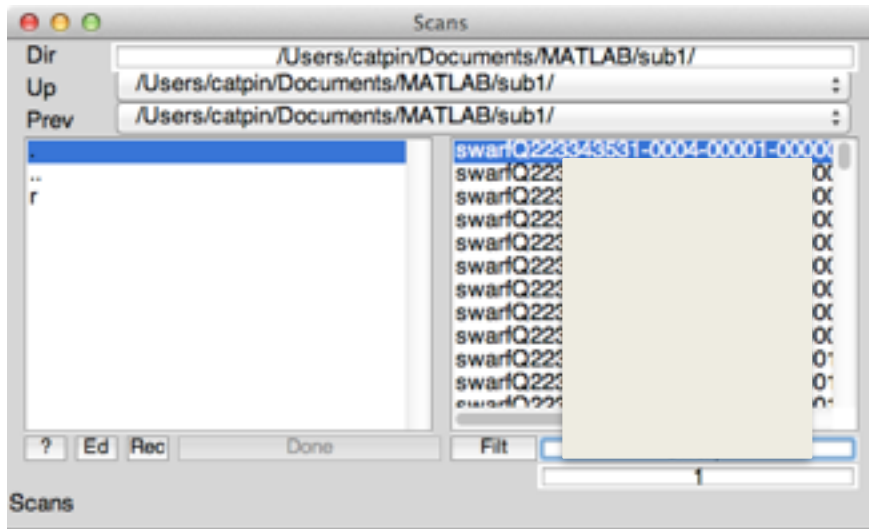
視實驗設計方式，在此可以選擇Scans(block design)或Seconds(event-related)，本實驗則選擇Scans



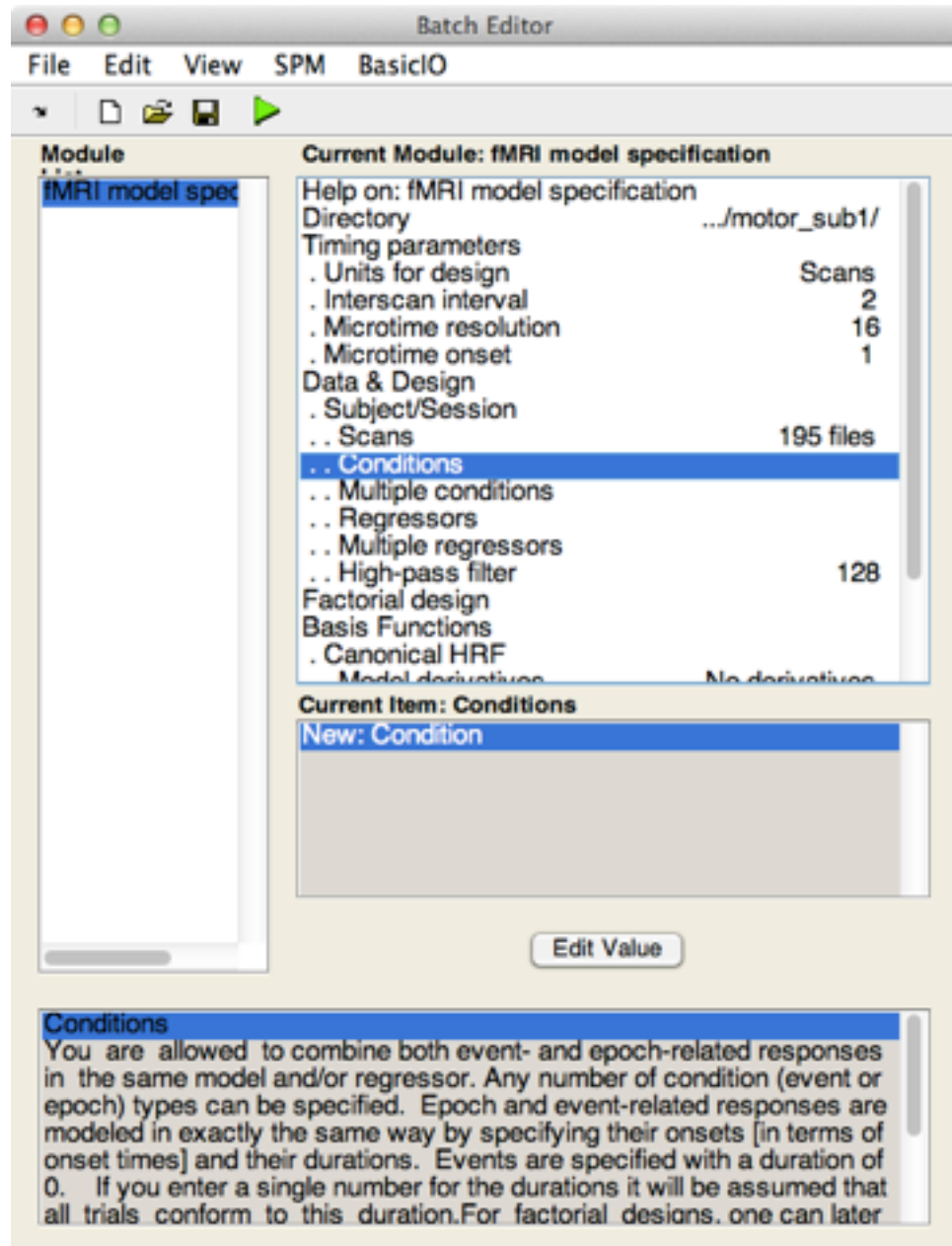
通常就輸入TR時間
在此為2 sec



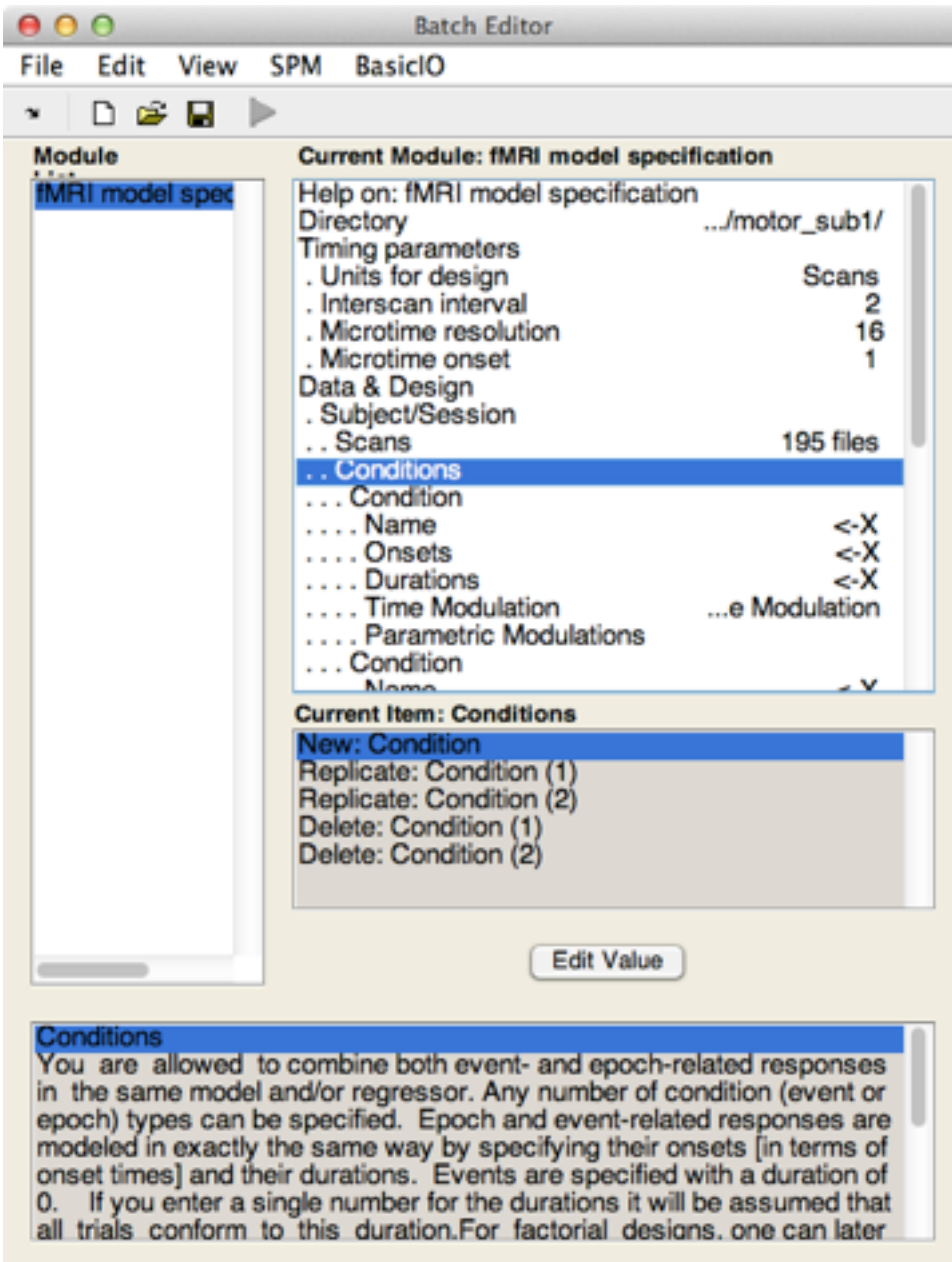
輸入已經完成前處理的檔案
檔案名稱：swar我的腦.img
或swra我的腦.img(視前處理
步驟而不同)



選取已經完成前處理的檔案
選取後即可按下Done



接下來是Conditions的部份
在這個實驗當中可視為兩種狀況
一種是無雙手抓握(OFF)
一種是進行雙手抓握(ON)
因此必須在New:Condition點兩次



Conditions 設計

Condition 命名簡單且容易辨識即可

- Name
 - OFF
- Onsets
 - 1:30:195
 - 或 0 30 60 90 120 130 150 180

• Durations

- 15

Condition

- Name
 - ON
- Onsets
 - 15:30:195
 - 或 15 45 75 105 135 165
- Durations
 - 15

Batch Editor

File Edit View SPM BasicIO

Module: fMRI model specification

- . Subject/Session
- .. Scans 195 files
- .. Conditions
- ... Condition
- Name OFF
- Onsets 7x1 double
- Durations 15
- Time Modulation ...e Modulation
- Parametric Modulations
- ... Condition
- Name ON
- Onsets 6x1 double
- Durations 15
- Time Modulation ...e Modulation
- Parametric Modulations
- .. Multiple conditions
- .. Regressors
- .. Multiple regressors
- High pass filter 128

Current Item: Durations

15

Conditions設定完成

Edit Value

Durations

Specify the event durations. Epoch and event-related responses are modeled in exactly the same way but by specifying their different durations. Events are specified with a duration of 0. If you enter a single number for the durations it will be assumed that all trials conform to this duration. If you have multiple different durations, then the number must match the number of onset times. Evaluated statements are entered.

Batch Editor

File Edit View SPM BasicIO

Module: fMRI model specification

- . Subject/Session
- .. Scans 195 files
- .. Conditions
- ... Condition
- Name OFF
- Onsets 7x1 double
- Durations 15
- Time Modulation ...e Modulation
- Parametric Modulations
- ... Condition
- Name ON
- Onsets 6x1 double
- Durations 15
- Time Modulation ...e Modulation
- Parametric Modulations
- .. Multiple conditions
- .. Regressors
- .. Multiple regressors
- High pass filter 128

Current Item: Multiple regressors

Select Files

Multiple regressors

如果有其他的變量會影響GLM分析可以在這邊輸入

Ex: realignment parameters

所以在此將載入在前處理realignment所產出的rp-我的腦.txt

點選完成之後即可按下 ▶ 開始執行

Multiple regressors

如果有其他的變量會影響GLM分析可以在這邊輸入

Ex: realignment parameters

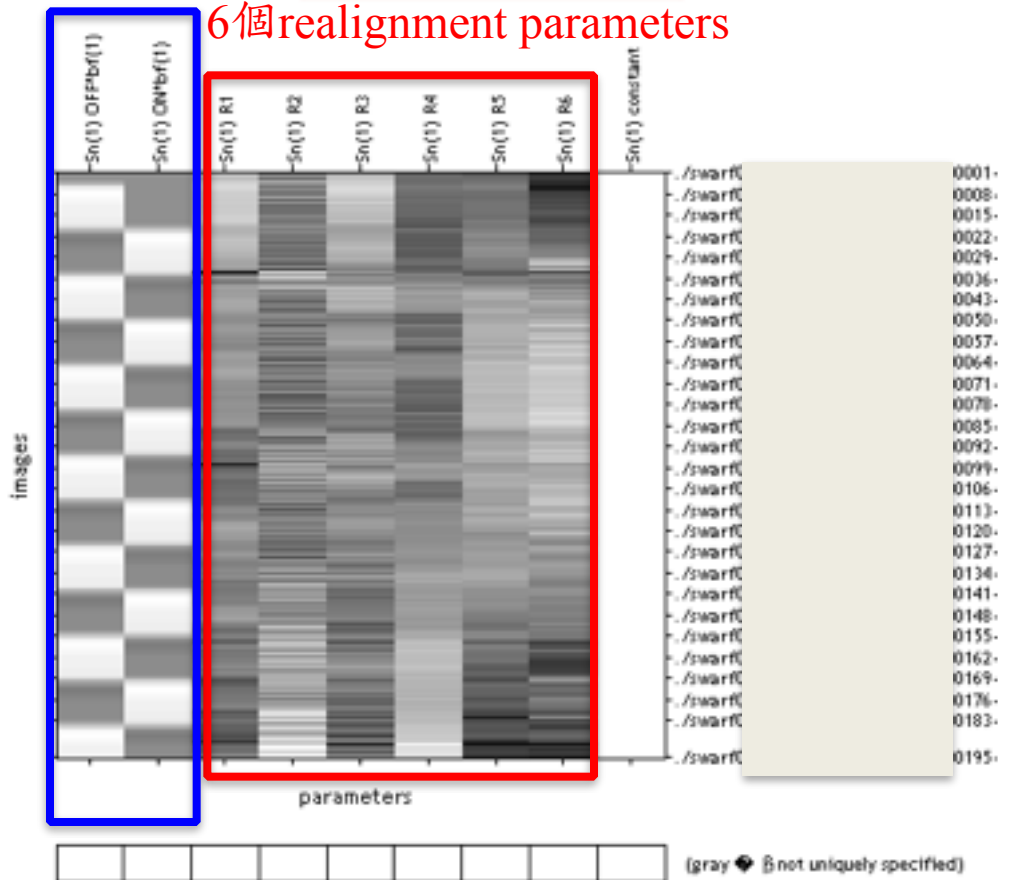
所以在此將載入在前處理realignment所產出的rp-我的腦.txt

點選完成之後即可按下 ▶ 開始執行

Statistical analysis: Design

6個realignment parameters

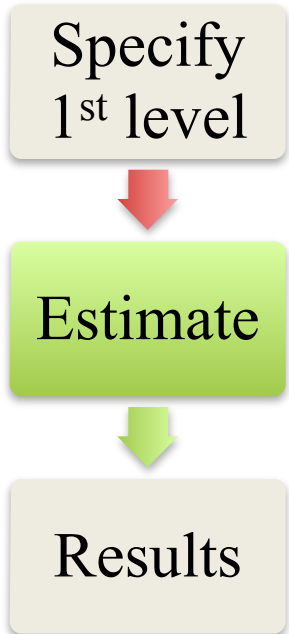
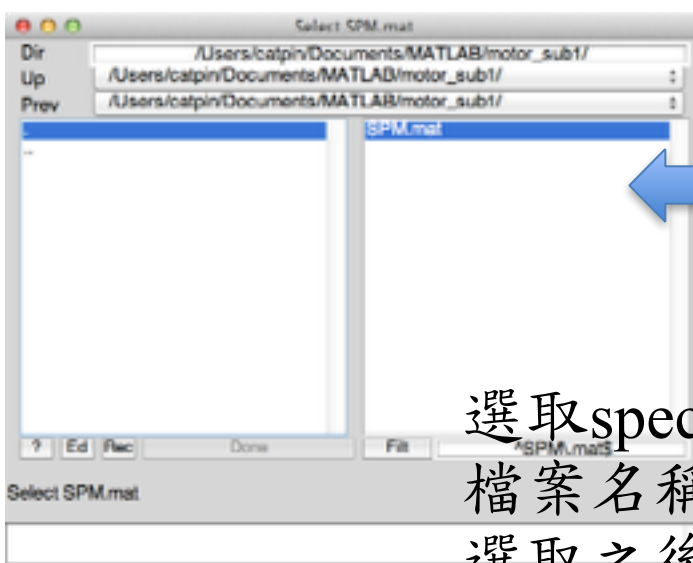
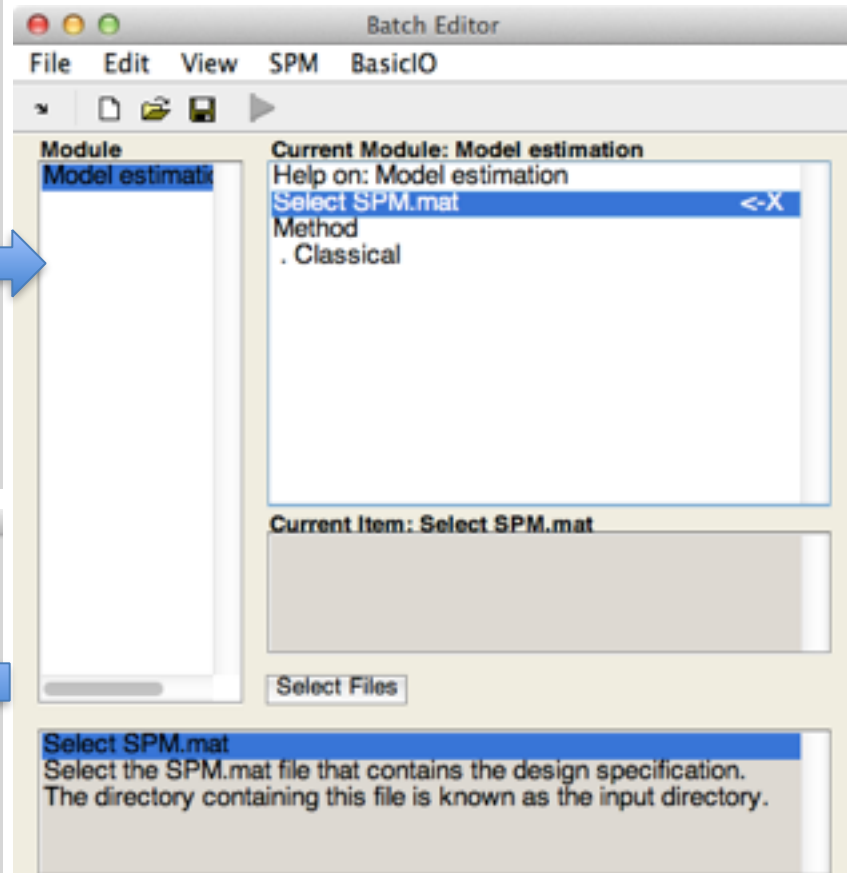
實驗設計
 Block design



Design description...

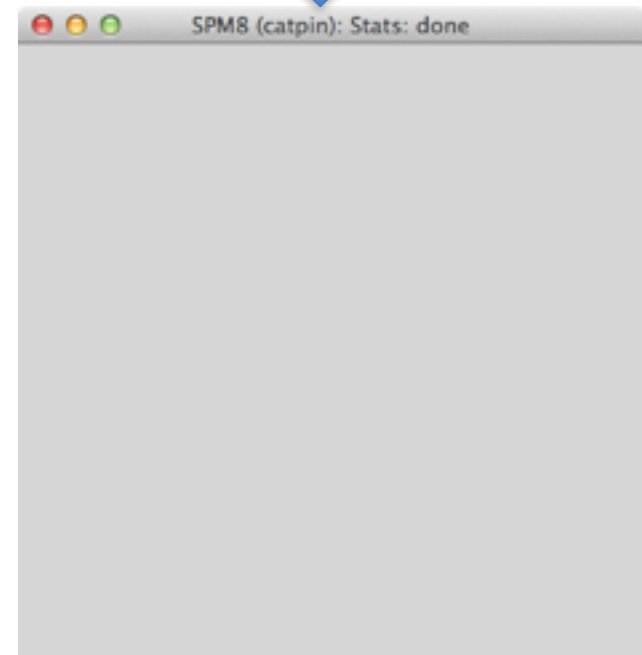
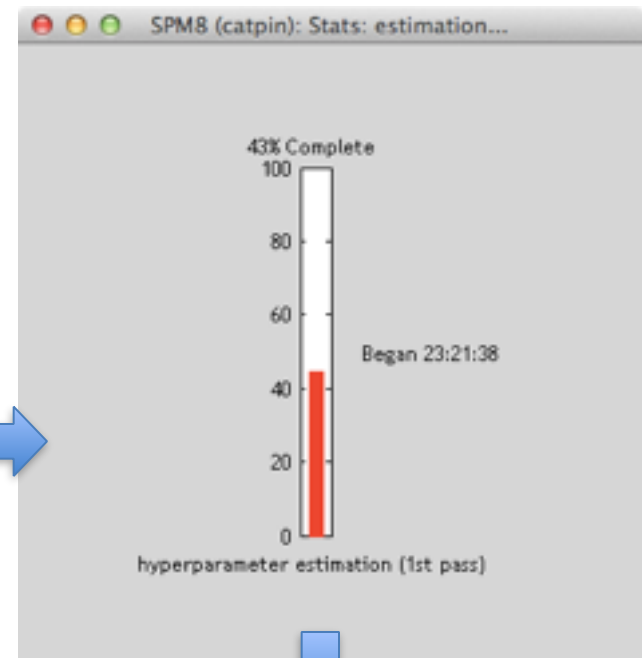
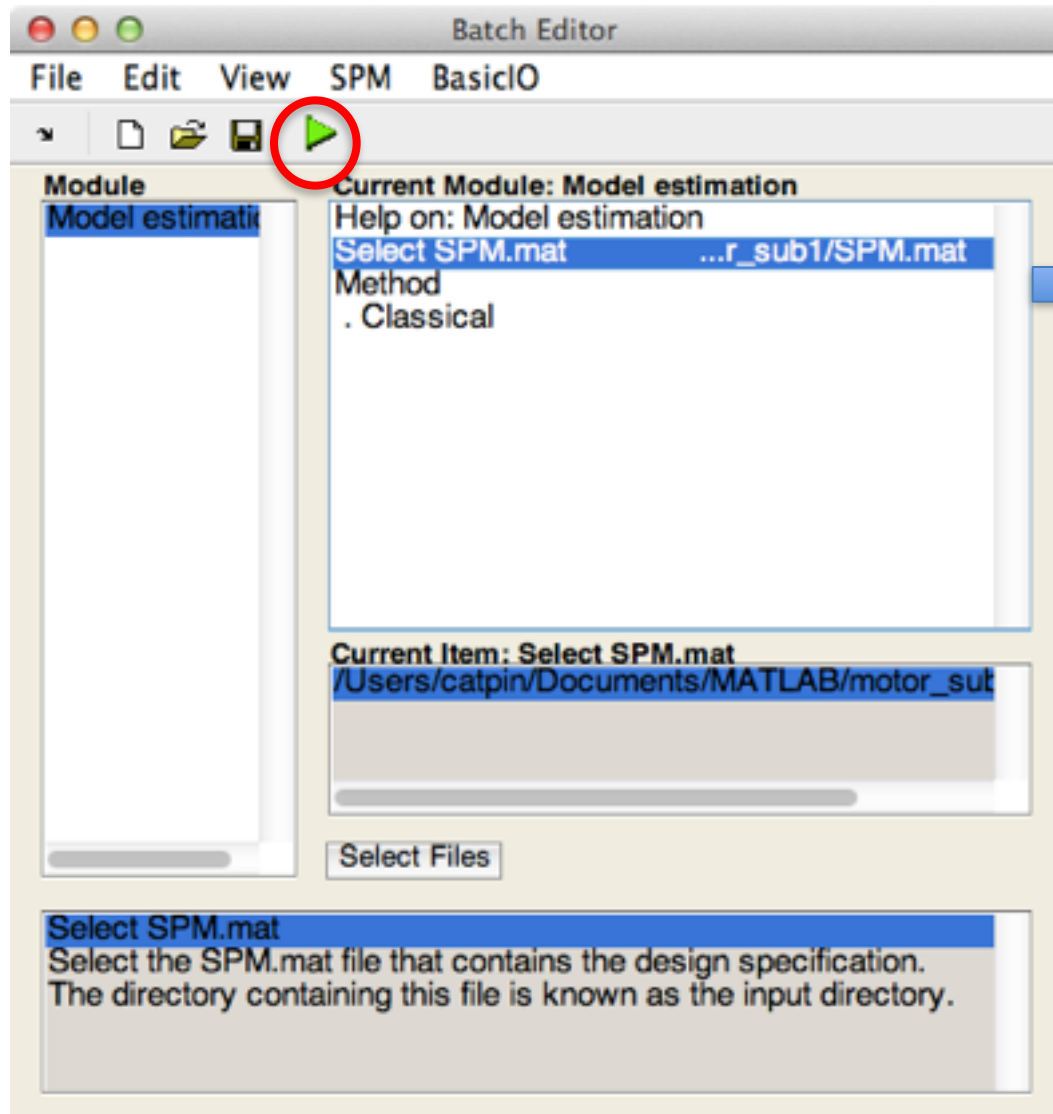
- Basis functions hrf
- Number of sessions 1
- Trials per session 2
- Interscan interval 2.00 [s]
- High pass Filter : Cutoff: 128 [s]
- Global calculation mean voxel value
- Grand mean scaling session specific
- Global normalisation None

在此必須再一次確認所輸入的Condition資訊是否正確，尤其是onsets, duration

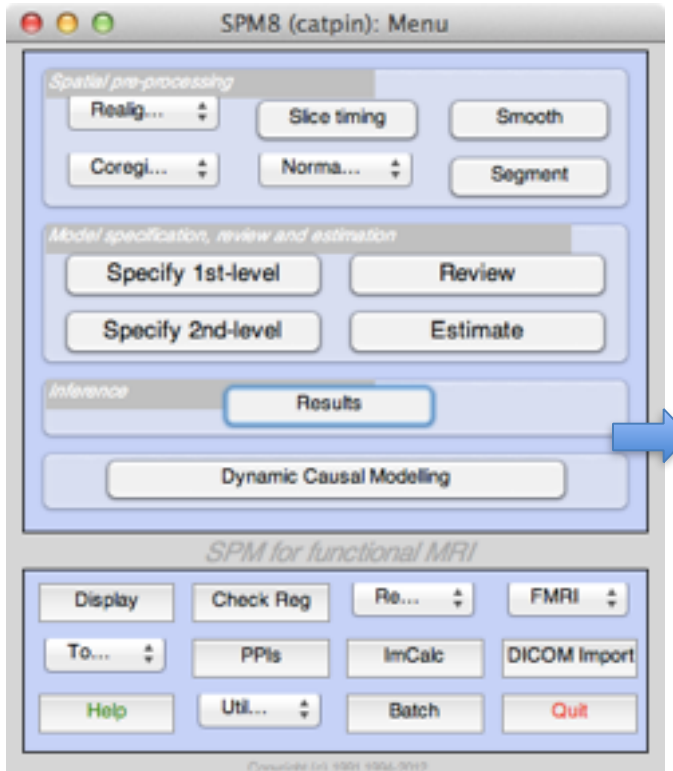
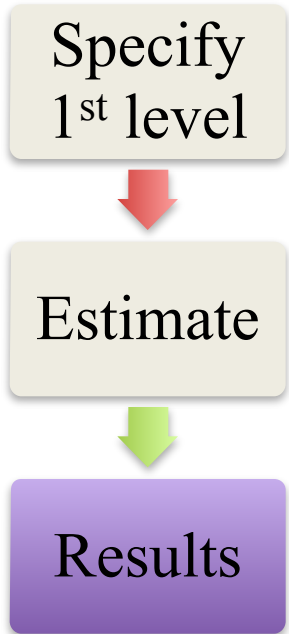


選取specify 1st level所完成的GLM設計
檔案名稱為:SPM.mat
選取之後按下Done

選取SPM.mat後即可開始執行

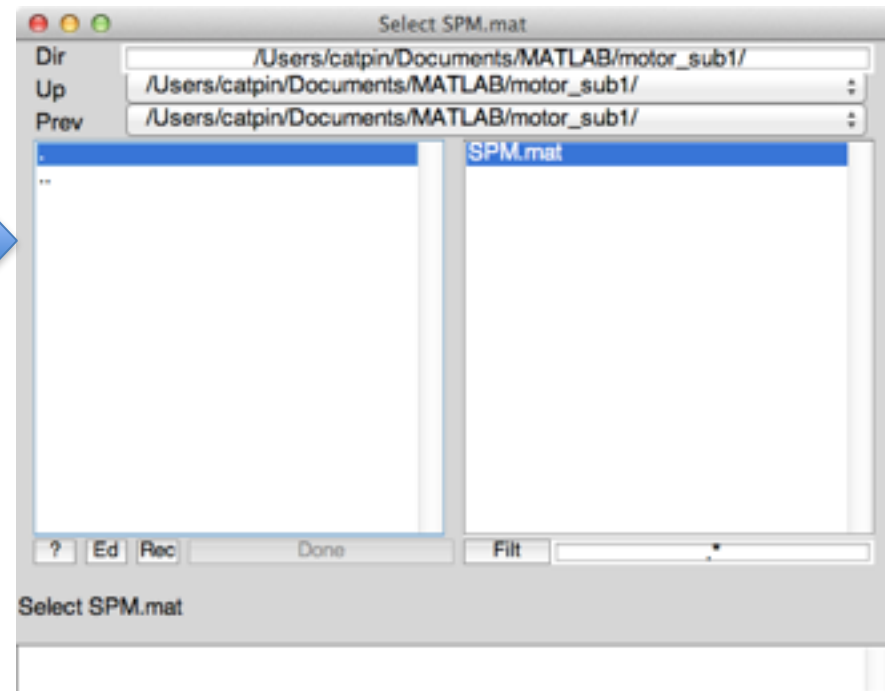


結果呈現



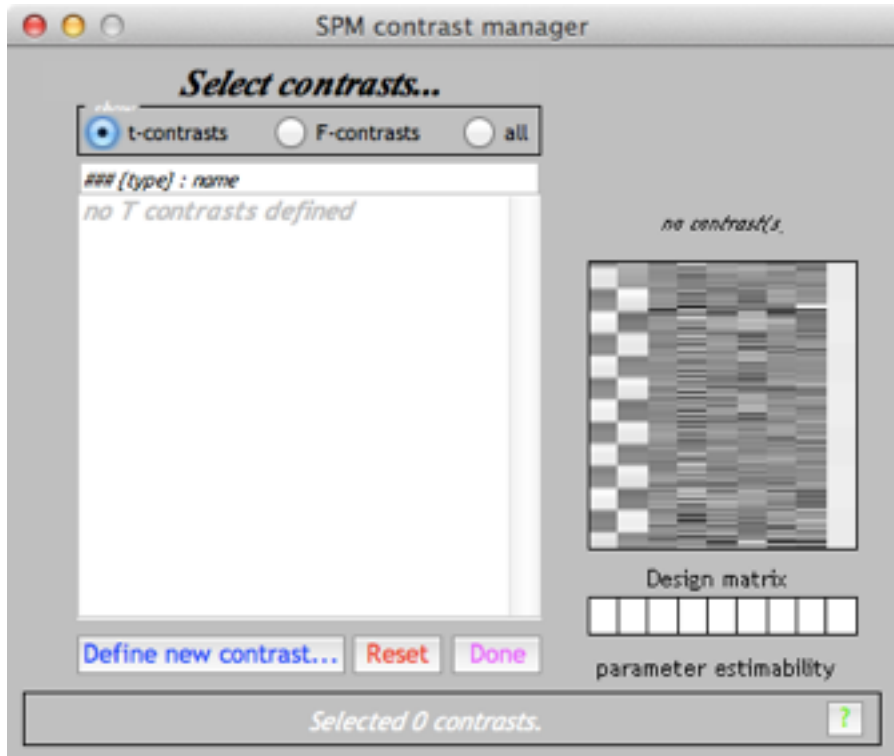
點選Results

跳出點選SPM.mat視窗



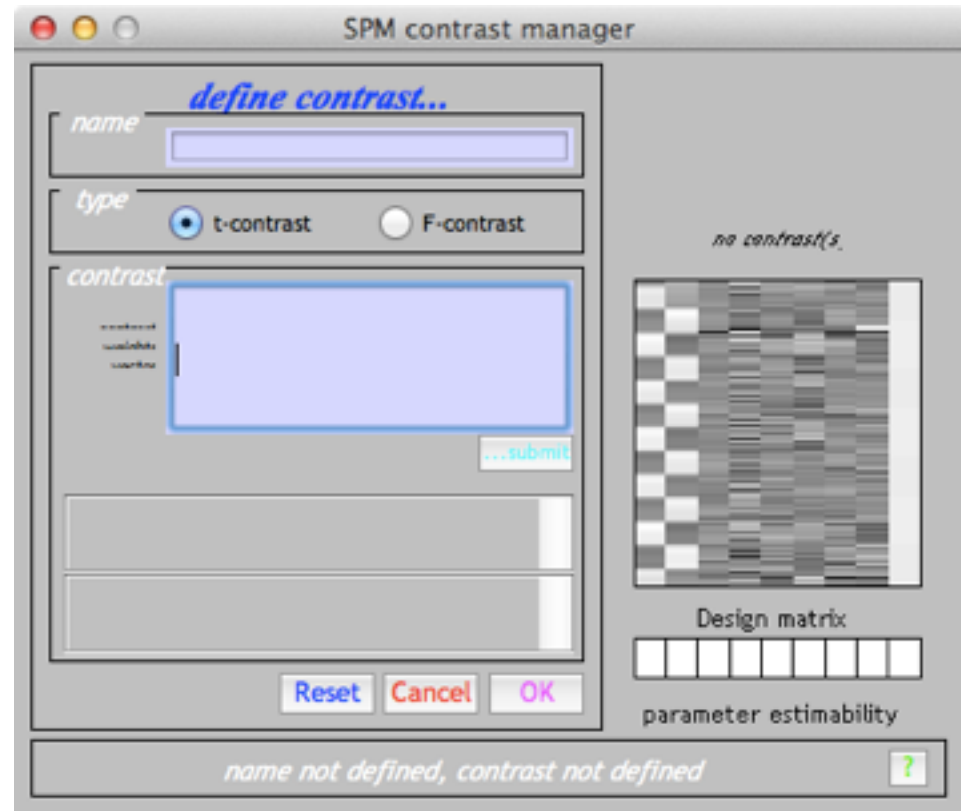
選取存放GLM設計資料夾內的SPM.mat

開始進行結果呈現的設計



Select contrasts

1. 點選t-contrasts
2. Define new contrast



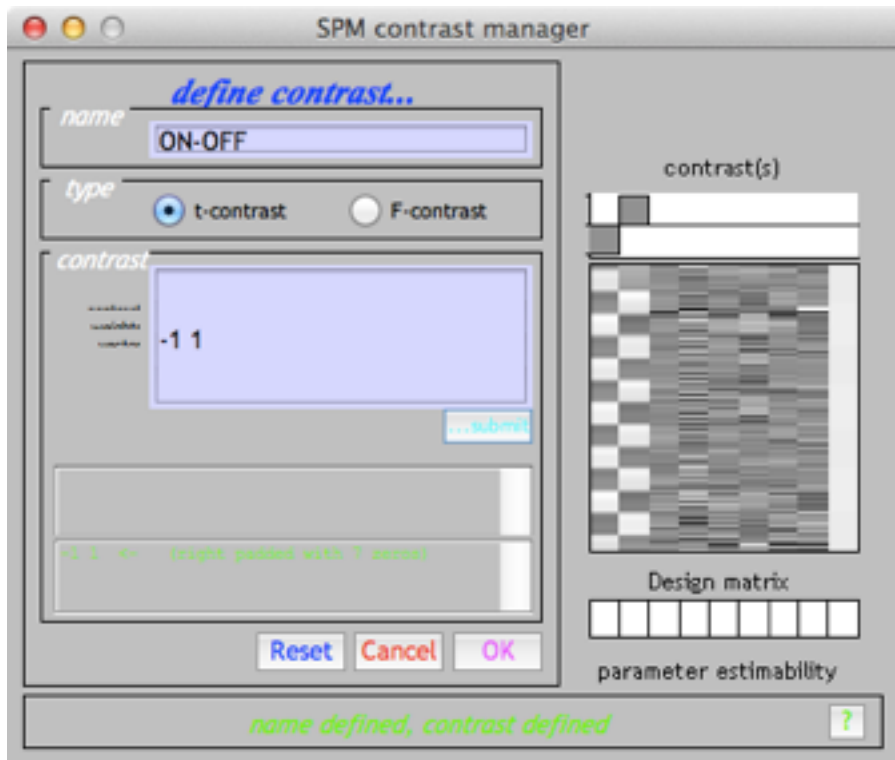
Name (可以自行定義contrast名稱)

Contrast(必須根據Design Matrix以及所欲觀察的統計對比)

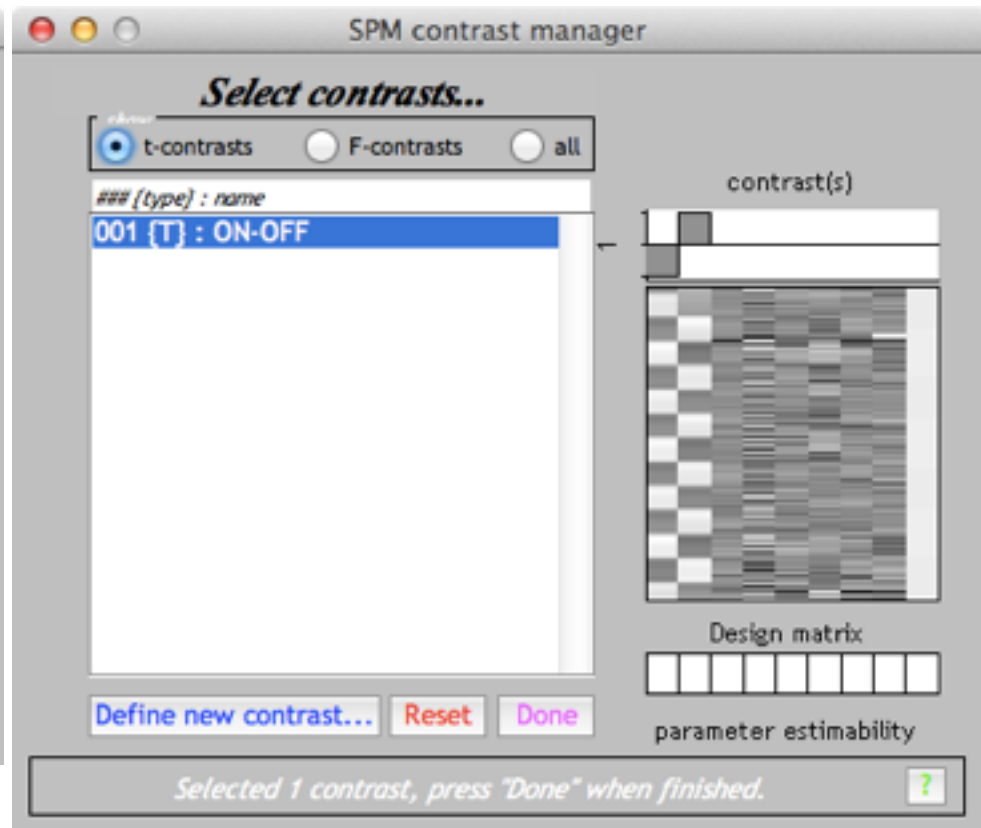
Ex: 欲了解有雙手抓握(ON)與無雙手抓握之差異(OFF)，在此則必須設定為

-1 1

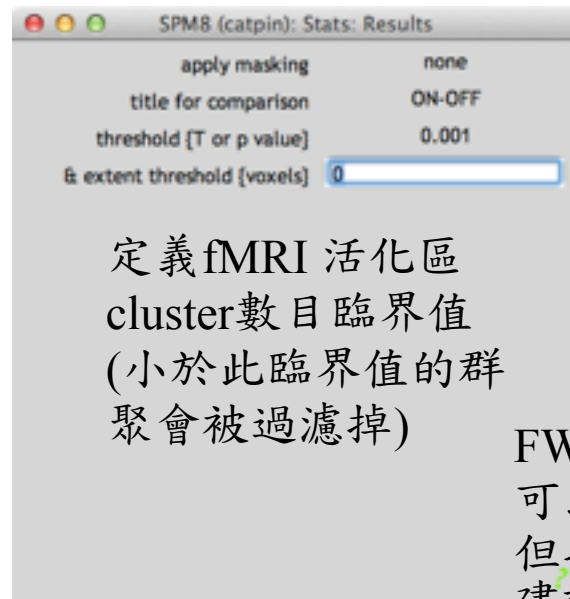
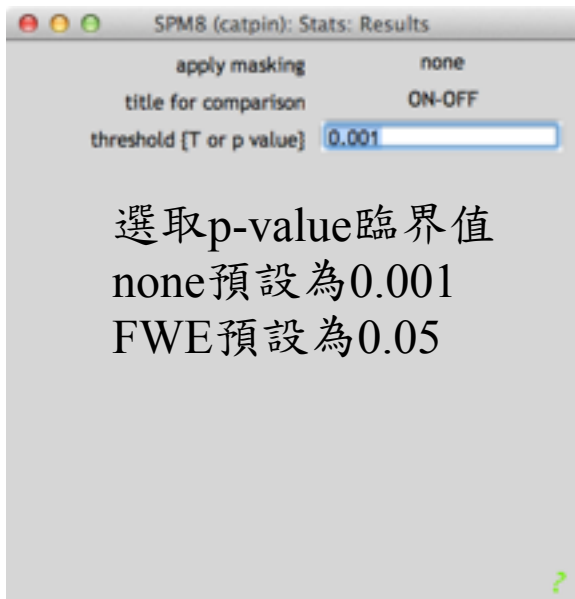
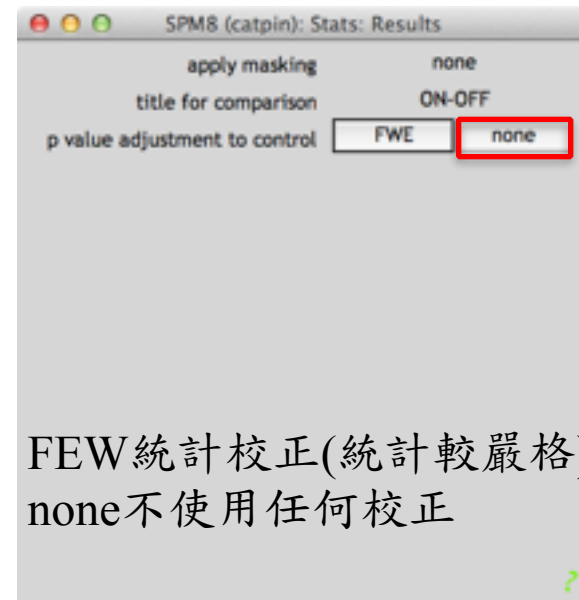
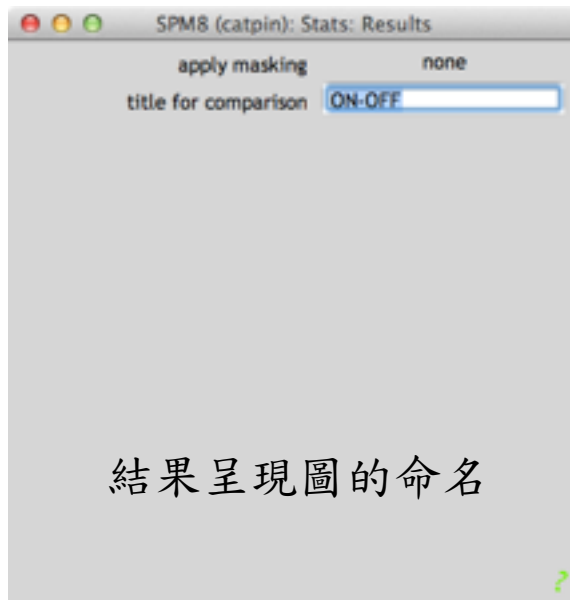
(第一項為design matrix之設計：OFF，第二項為ON，所以為(-1)*OFF+(1)*ON)



輸入contrast：-1 1之後，即可按下submit，然後按下OK



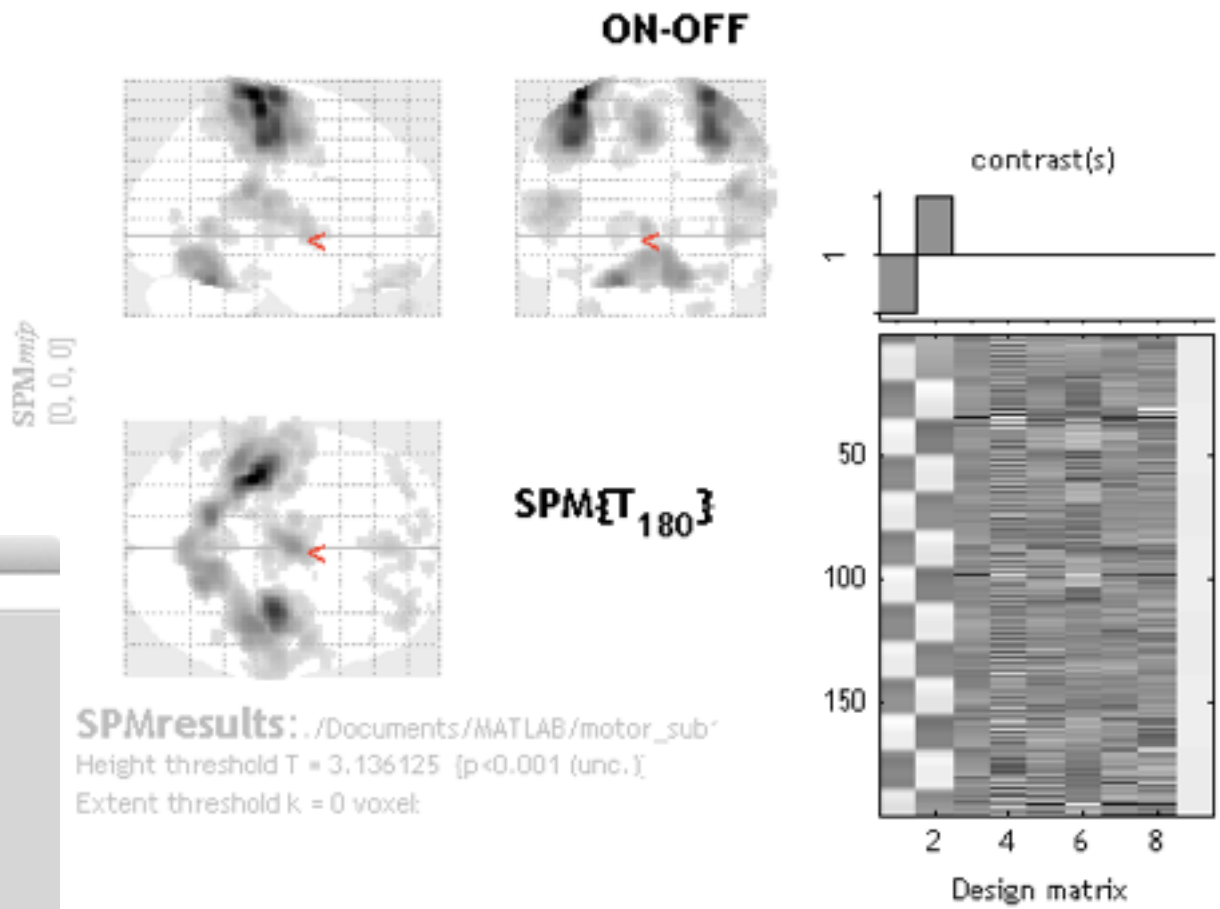
完成建立contrast後，按下Done



FWE: Familywise error rate
可以減少false positive，可信度提高
但也可能太過嚴謹，而沒有結果
建議先用無校正了解實驗設計
再採用FWE校正觀察結果

結果顯示

SPM8 (catpin): Graphics
 File Edit View Insert Tools Desktop Window SPM Figure Help



SPM8 (catpin): SPM{T}: Results
 Design Contrasts

結果顯示操控視窗

n-values
 whole brain
 current cluster
 small volume

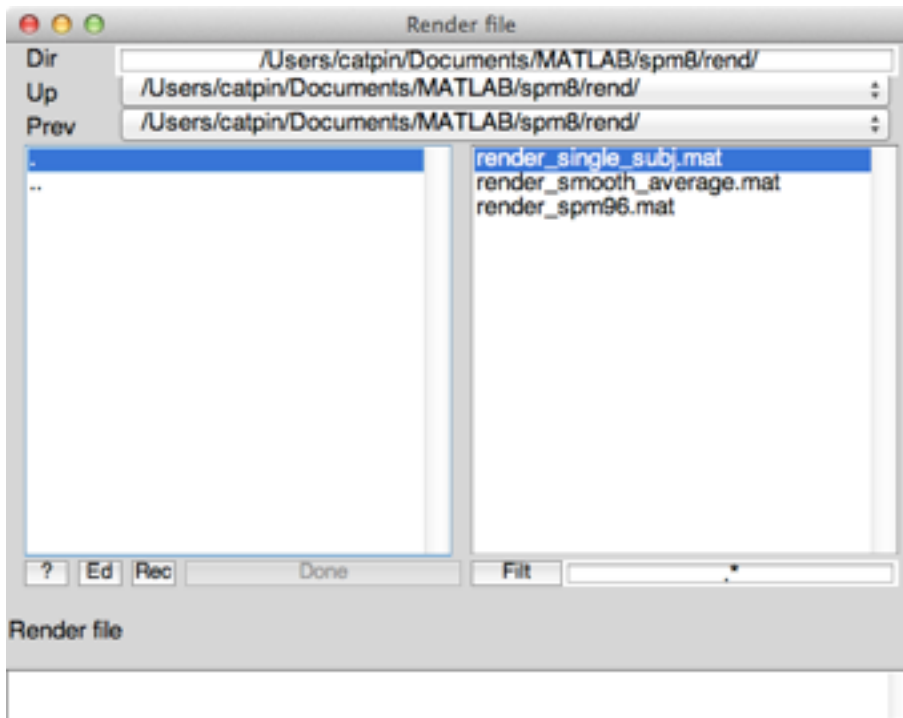
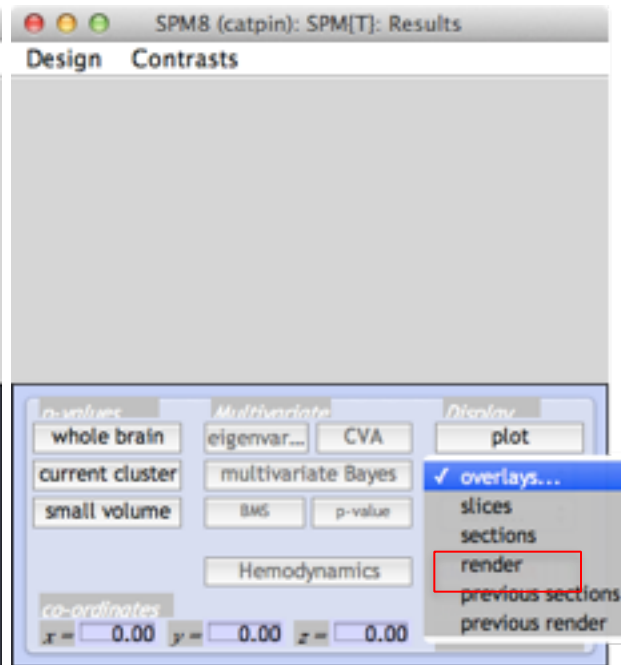
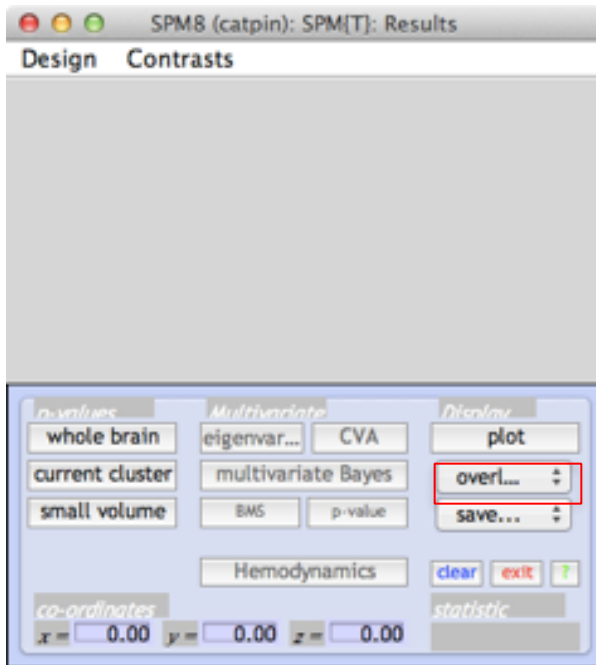
Multivariate
 eigenvar...
 multivariate Bayes
 BMS
 p-value
 Hemodynamics

Display
 plot
 overl...
 save...
 clear
 exit
 ?

co-ordinates
 x = 0.00 y = 0.00 z = 0.00

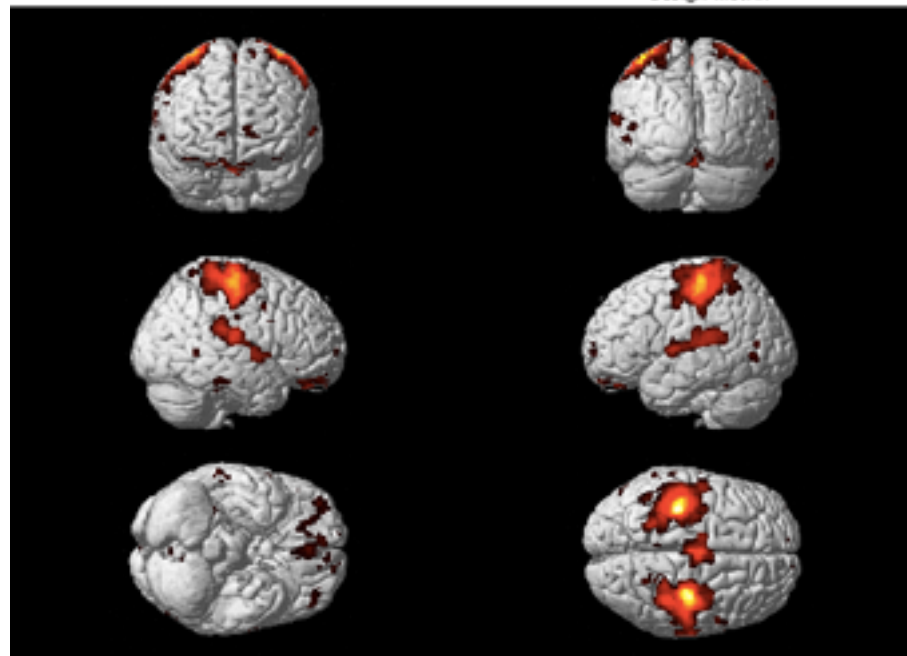
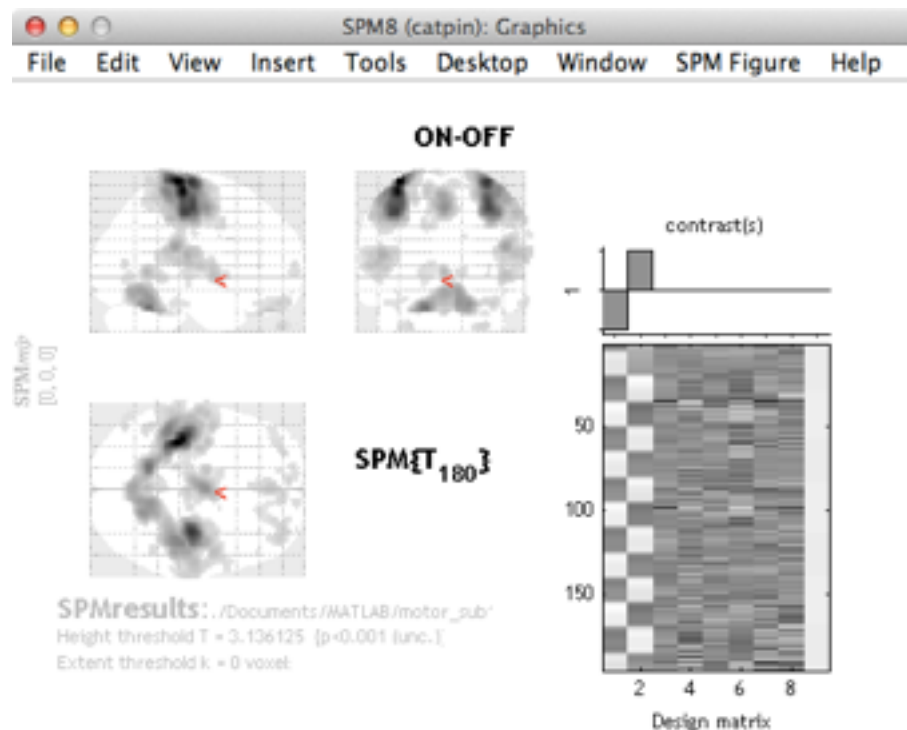
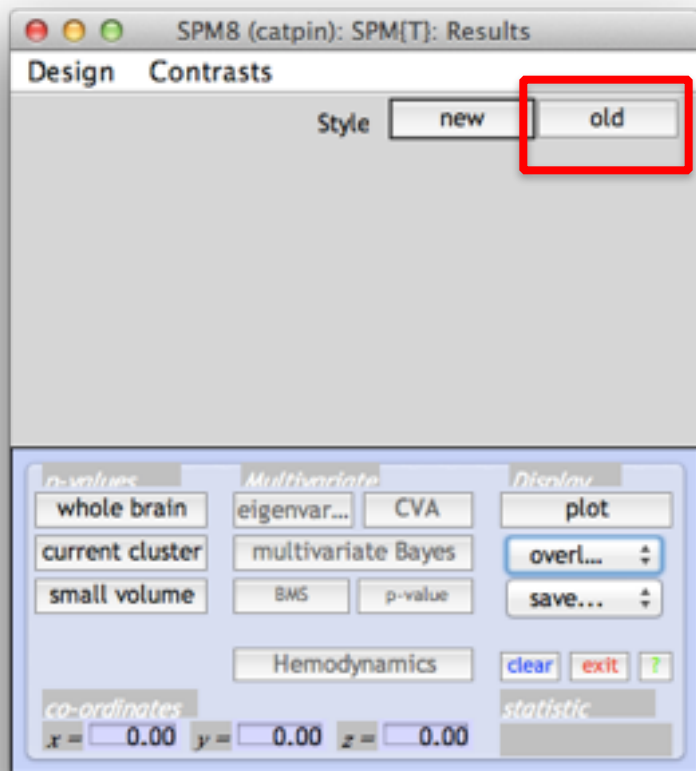
statistic

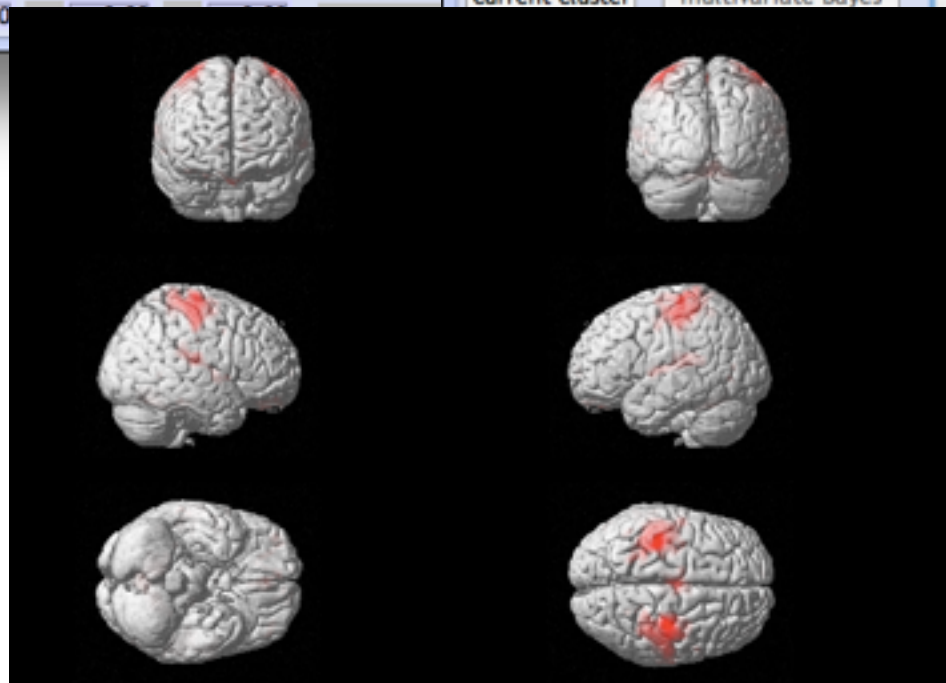
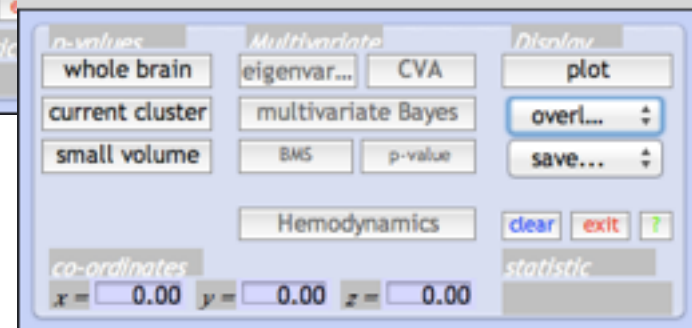
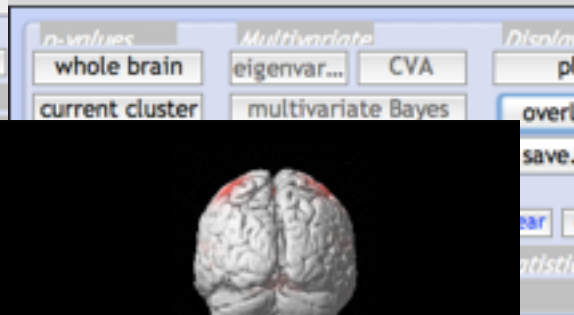
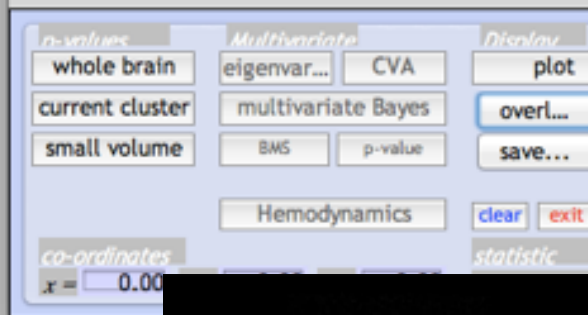
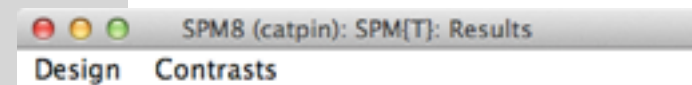
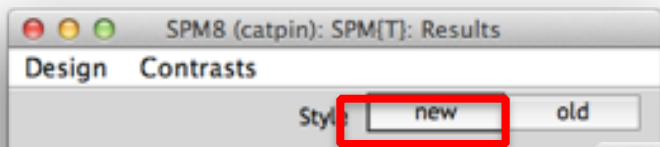
立體顯示 模式

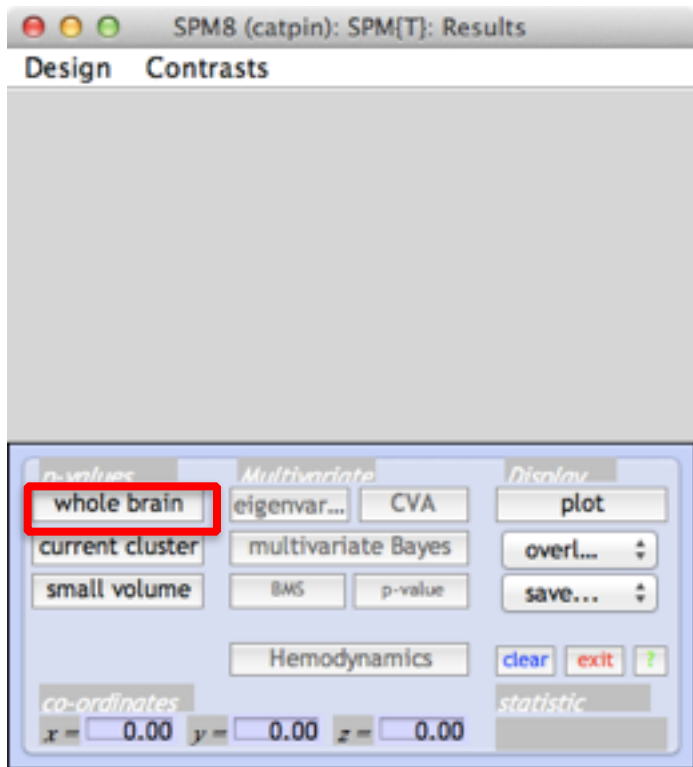


找到spm8所在位置下
spm8/rend/render_single_subj.mat

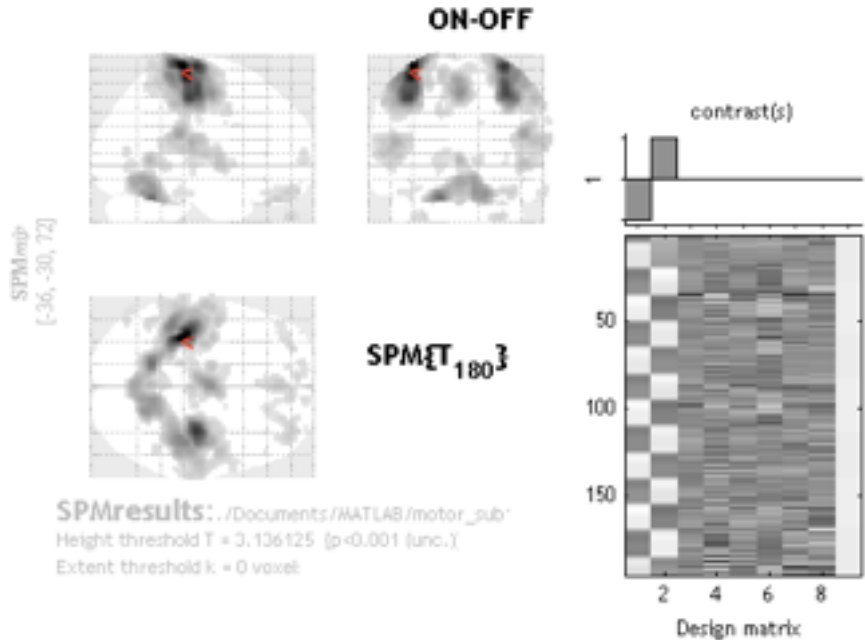
選取後按下Done







顯示全腦所有群聚區域
(在此即顯示大腦中對於雙手
抓握實驗有活化之區域)



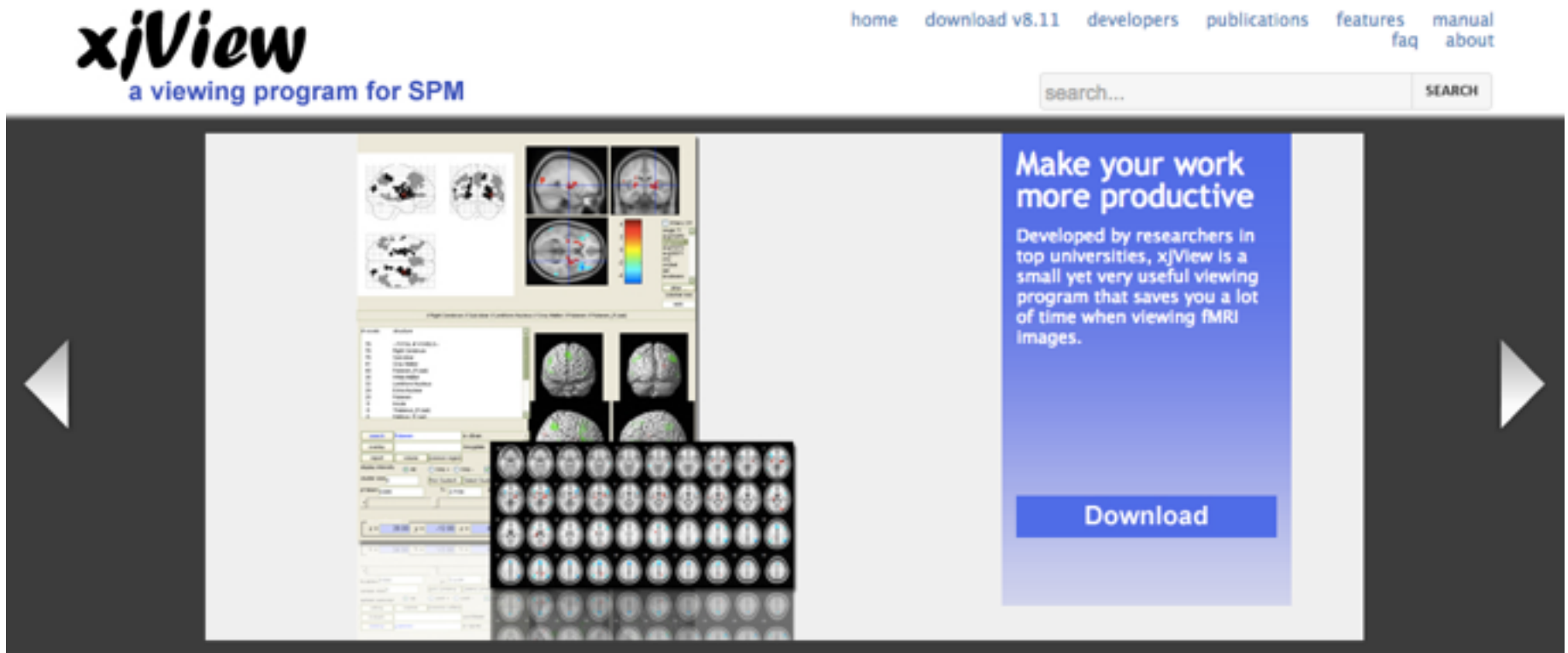
Statistics: *p-values adjusted for search volume*

set-level		cluster-level				peak-level					mm mm mm		
<i>P</i>	<i>κ</i>	<i>P</i> _{FWE,cor}	<i>P</i> _{FDR,cor}	<i>k</i>	<i>P</i> _{FWE,cor}	<i>P</i> _{FDR,cor}	<i>T</i>	<i>Z</i> ₀	<i>P</i> _{FWE,cor}				
0.000	31	0.000	0.000	3183	0.000	0.000	0.000	25.65	Inf	0.000	-34	-33	32
											-32	-32	66
											-32	-24	50
											34	-32	32
											26	-20	54
											62	-32	66
											-54	-58	-28
											20	-40	-24
											34	-54	-20
											0	-10	52
											-12	-10	66
											4	-24	54
											50	-38	22
											32	-32	32

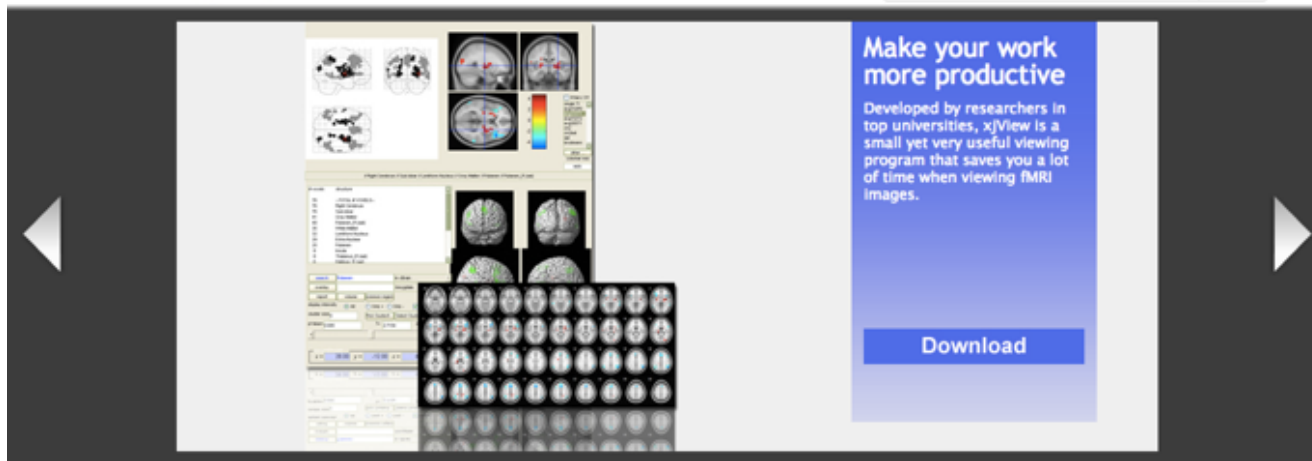
點選座標點，上方小紅箭頭游標
即會指向此群聚中心座標。
(注意：此座標為MNI座標)
可利用其他軟體來查詢解剖位置

結果呈現 - xjview

- A viewing program for SPM
- <http://www.alivelearn.net/xjview8/>



提供一個瀏覽結果以及圖形呈現的介面



Download v8.11

xjView has been downloaded >15,000 times.

To run xjView you need:

1. MatLab 6.5 or above
2. SPM2, SPM5 or SPM8. You need to add SPM to your MatLab path. How? In matlab, enter spm folder, then run `addpath(genpath(pwd))`

Simply fill out your information and click "Submit" button. An email will be sent to you with the download link so please enter a valid email address.

Your name *

Your institute *

Your institute email *

Email has to be valid.

You are a * Professor

Student

Postdoc

Medical Doctor

Other

Hi, yiping,

Please download xjView at

<http://www.alivelearn.net/xjview8/blog/download/>

Questions? Comments? <http://groups.google.com/group/xjview-discuss-group>

Sincerely,

[Cui, Xu](#) at Stanford University 崔旭

[Li, Jian](#) at Peking University 李健

[Song, Xiaowei](#) 宋晓伟

Download

Download the following two files (required to run xjView)

To download, right-click your mouse on the links below to bring up the context menu, and then click "Save Link As" or "Save Target As".

1. [xjview.m](#) (270K)
2. [TDdatabase.mat](#) (12M)

將這兩個檔案複製到spm8的資料夾內即可

... and two example images (optional). They are T-test images. In SPM the T-test images are usually named like "spmT_0001.img" etc

1. [example1.img](#) (275K)
2. [example1.hdr](#) (1K)
3. [example2.img](#) (275K)
4. [example2.hdr](#) (1K)

Keyin “xjview” in command window

開啟檔案



Click menu
File | Open
Images

Welcome to xjView 8
Download at
<http://www.sivaleem.net/xjview>

search in xBrain

overlay Amygdala

report volume Small volu... common r... slice view

display intensity All Only + Only - Render

cluster sig 5 Pick Clust... Select Clu... Clear Sele...

pValue 0.001 FDR p inters 0 df:



MATLAB 7.10.0 (R2010a)

File Edit Debug Parallel Desktop Window Help

/Users/catpin/Documents/MATLAB

Shortcuts How to Add What's New

Command Window

```
f> >> xjview
```

spm fr
xjview
%-- 12/
spm fr
xjview
%-- 12/
spm fr
xjview
%-- 12/
spm fr

Start Ready

xjView

File Edit View Insert Tools Desktop Window Help

Click menu
File | Open
Images

XMairs O
wv11011
wvq15212
wvq305T1
ch2
ef2bal
sal
brodmann
other ...
colorbar max
auto

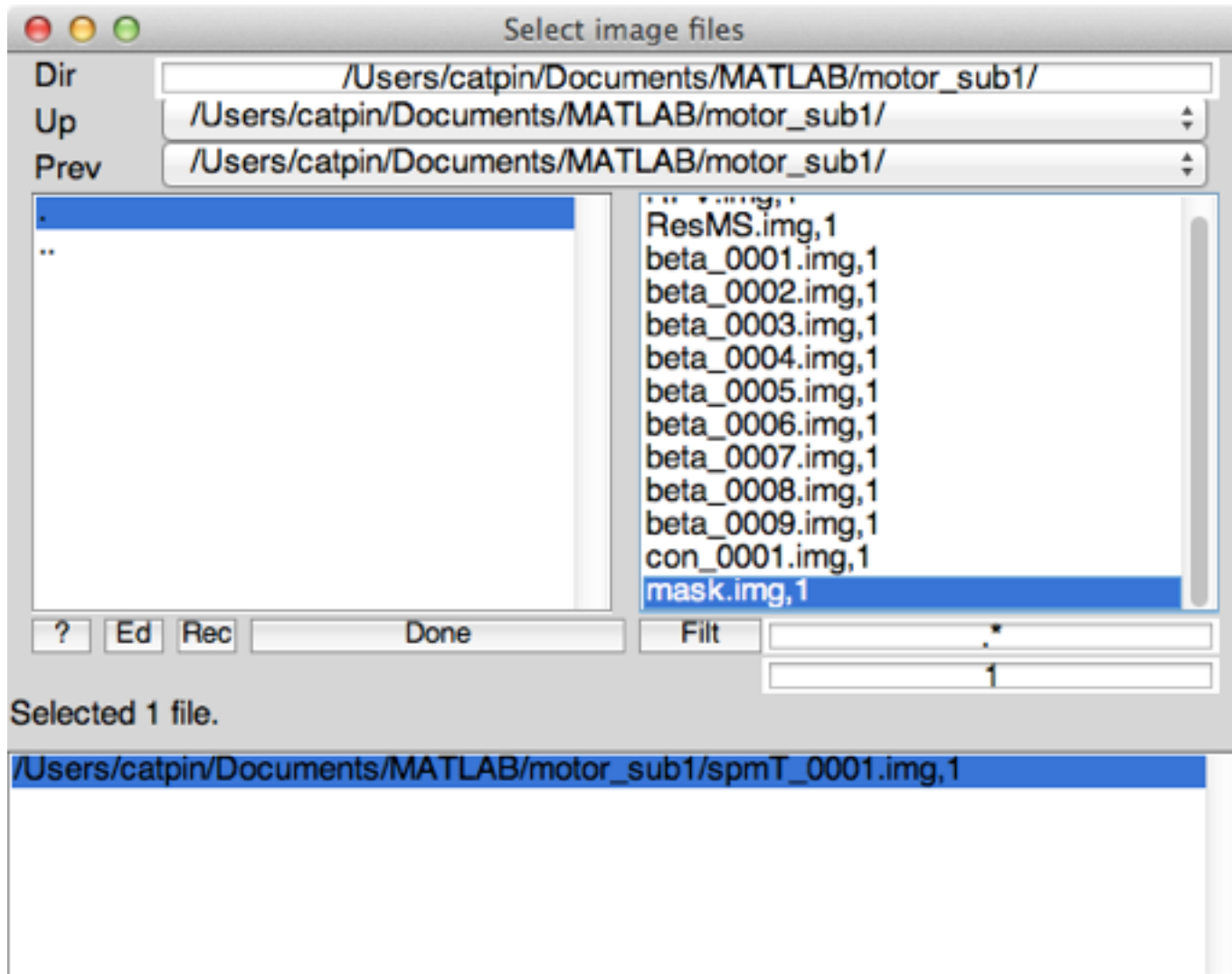
Search

display intensity All Only + Only - Render

cluster sig 5 Pick Clust... Select Clu... Clear Sele...

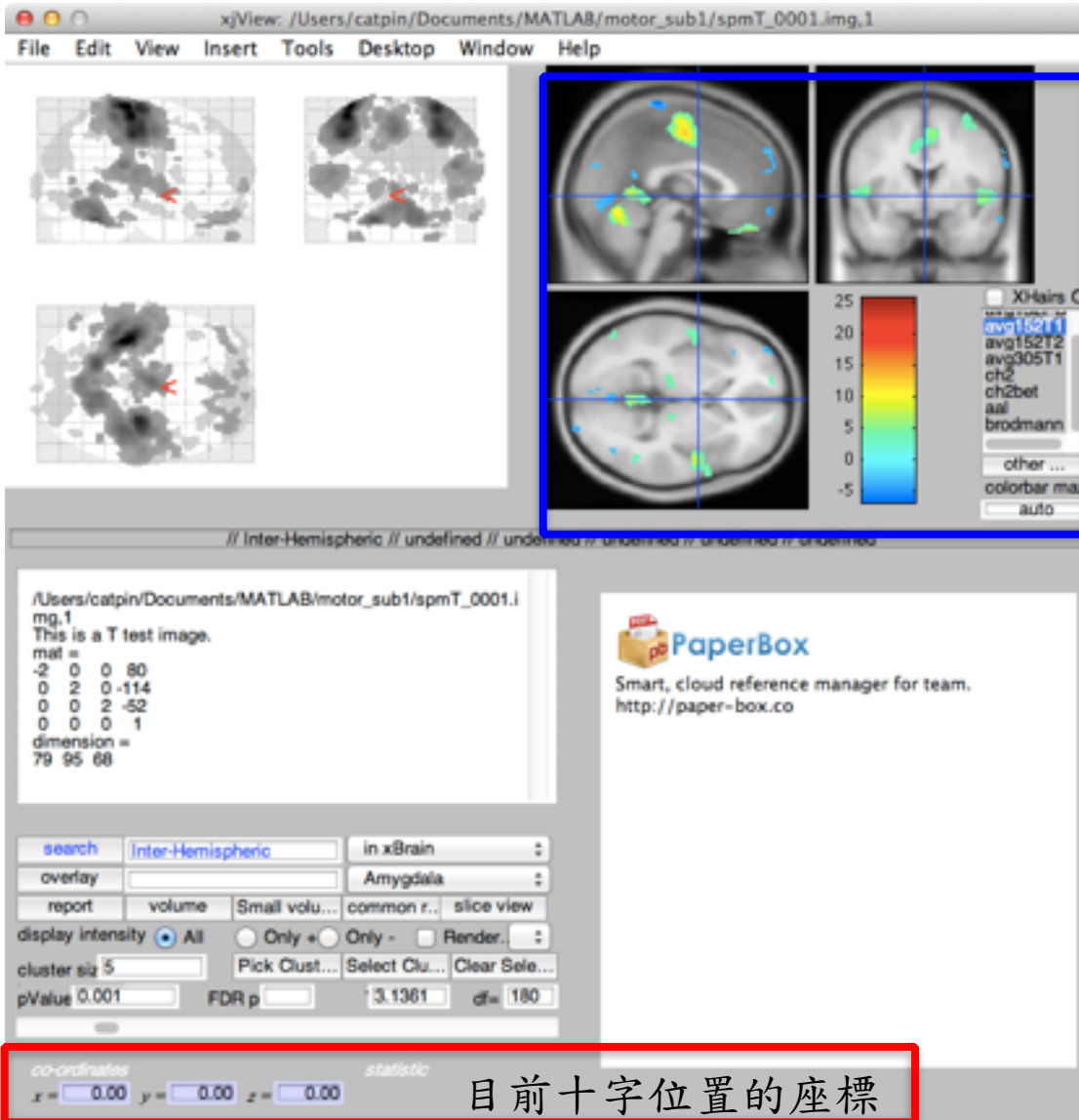
pValue 0.001 FDR p inters 0 df:

PaperBox
Smart, cloud reference manager for team.
<http://paper-box.co>

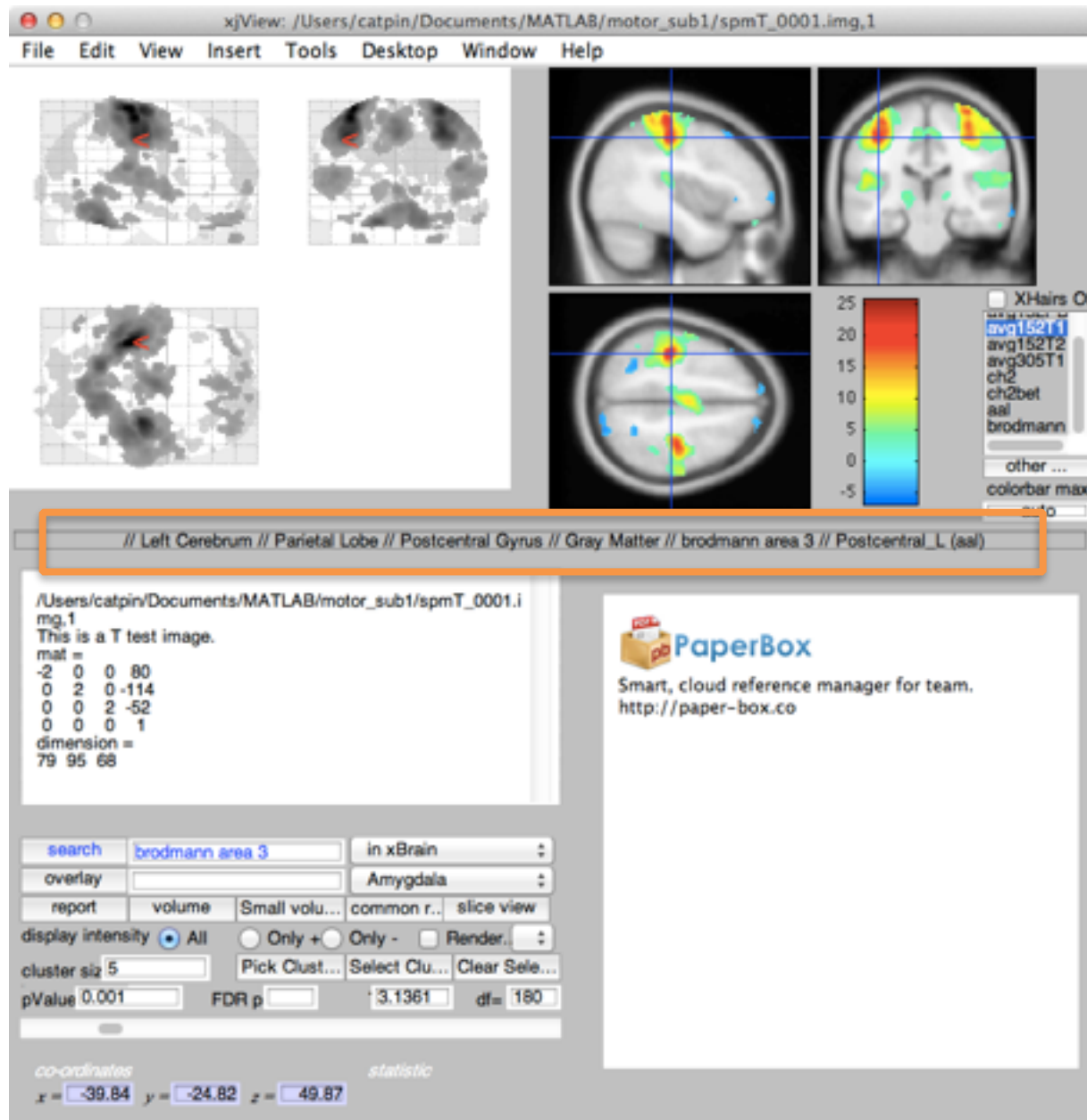


點選資料夾至擺放結果的資料夾處，並點選spmT_0001.img檔案
然後按下Done

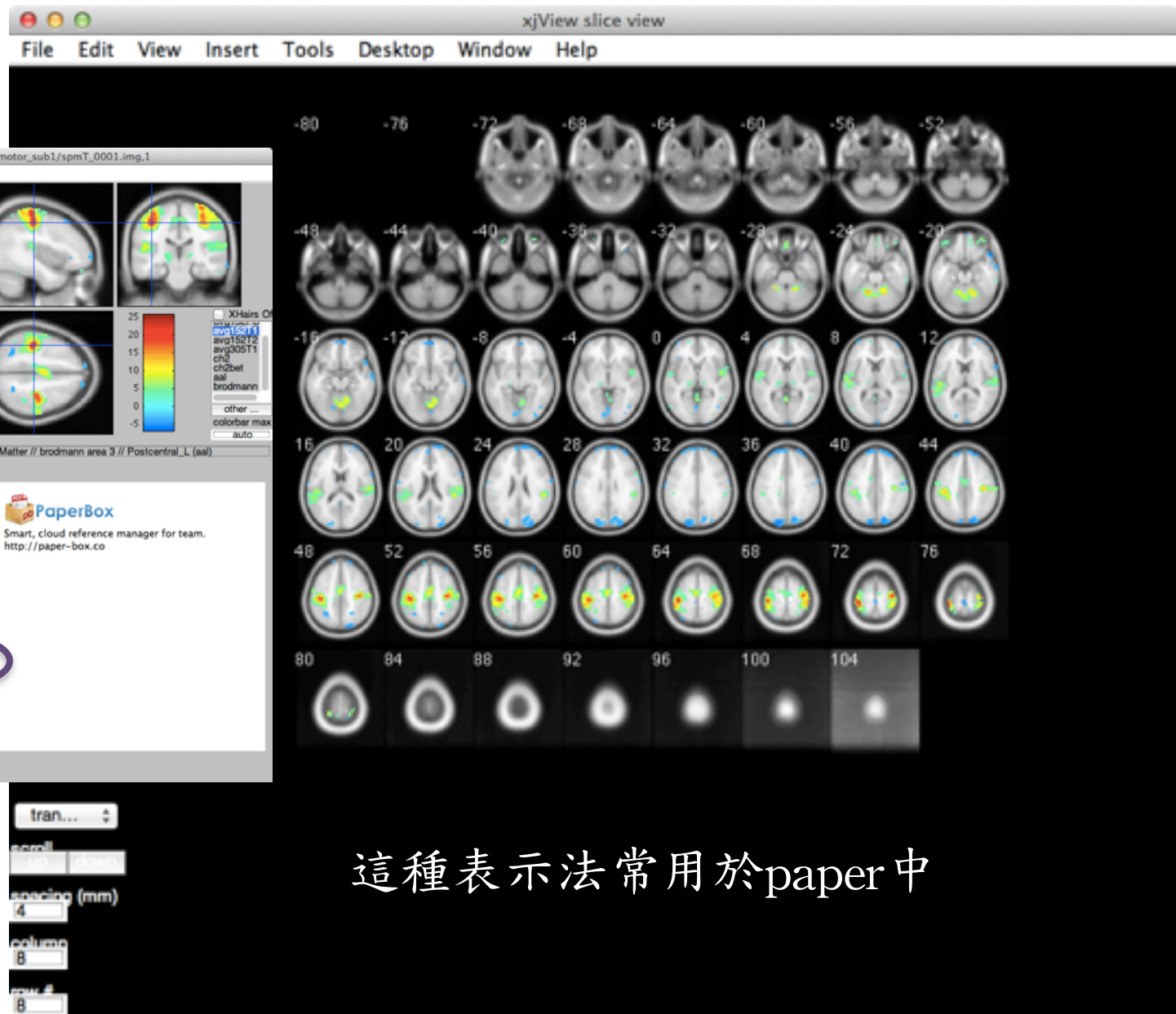
Xjview主介面



- T-value Map
- T-value color coding：可以修改彩色對應方式
- Overlap：可以選擇底圖
- Xhairs: 勾選時會將十字取消

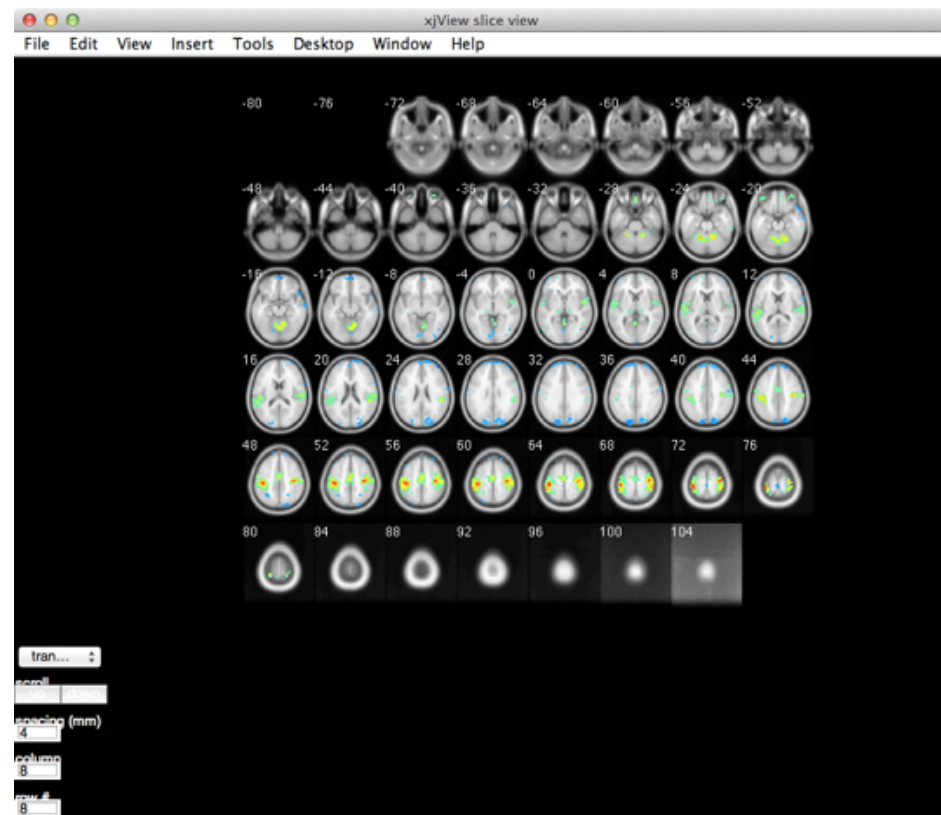


將十字移動時，會直接對應出Talairach座標，並將座標所對應Talairach大腦圖譜的五層資訊及AAL(automated anatomical labeling)圖譜資訊顯示出來

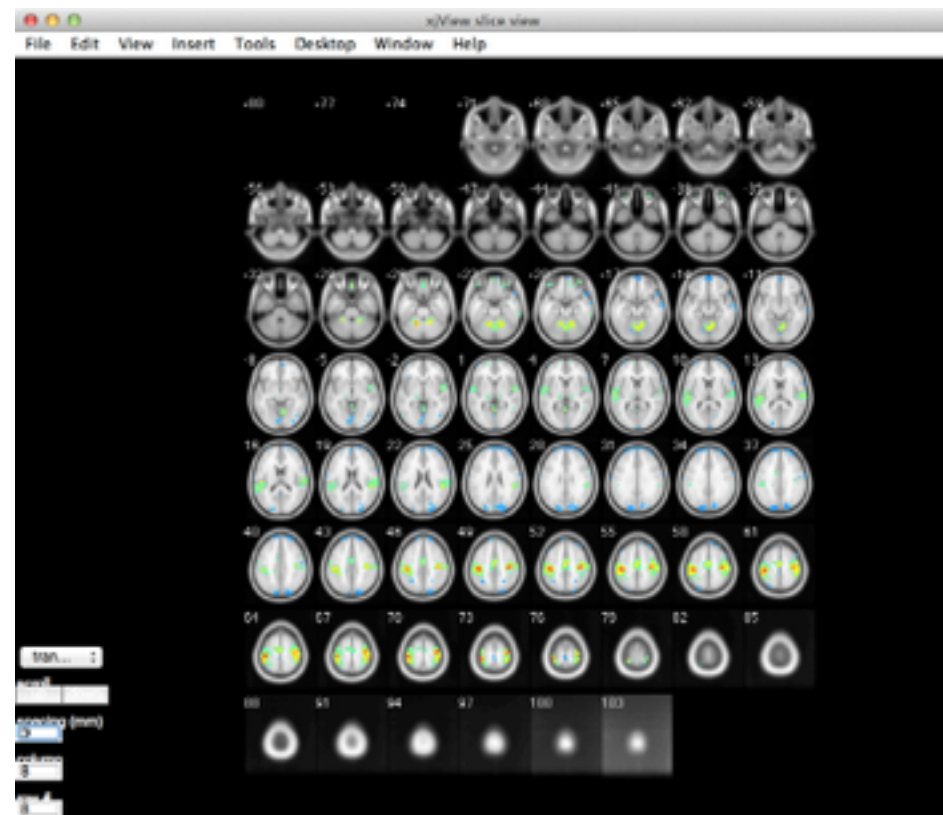
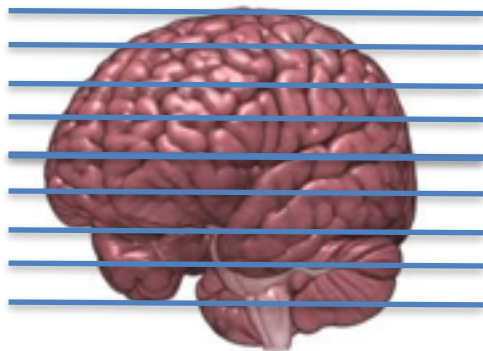


Slice View

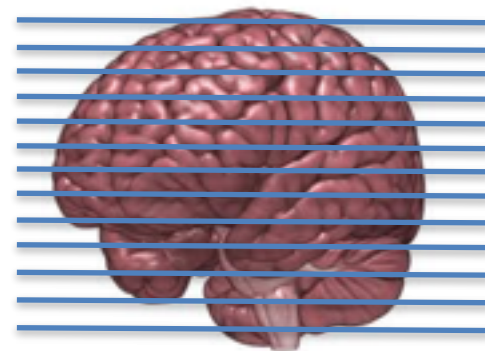
這種表示法常用於paper中

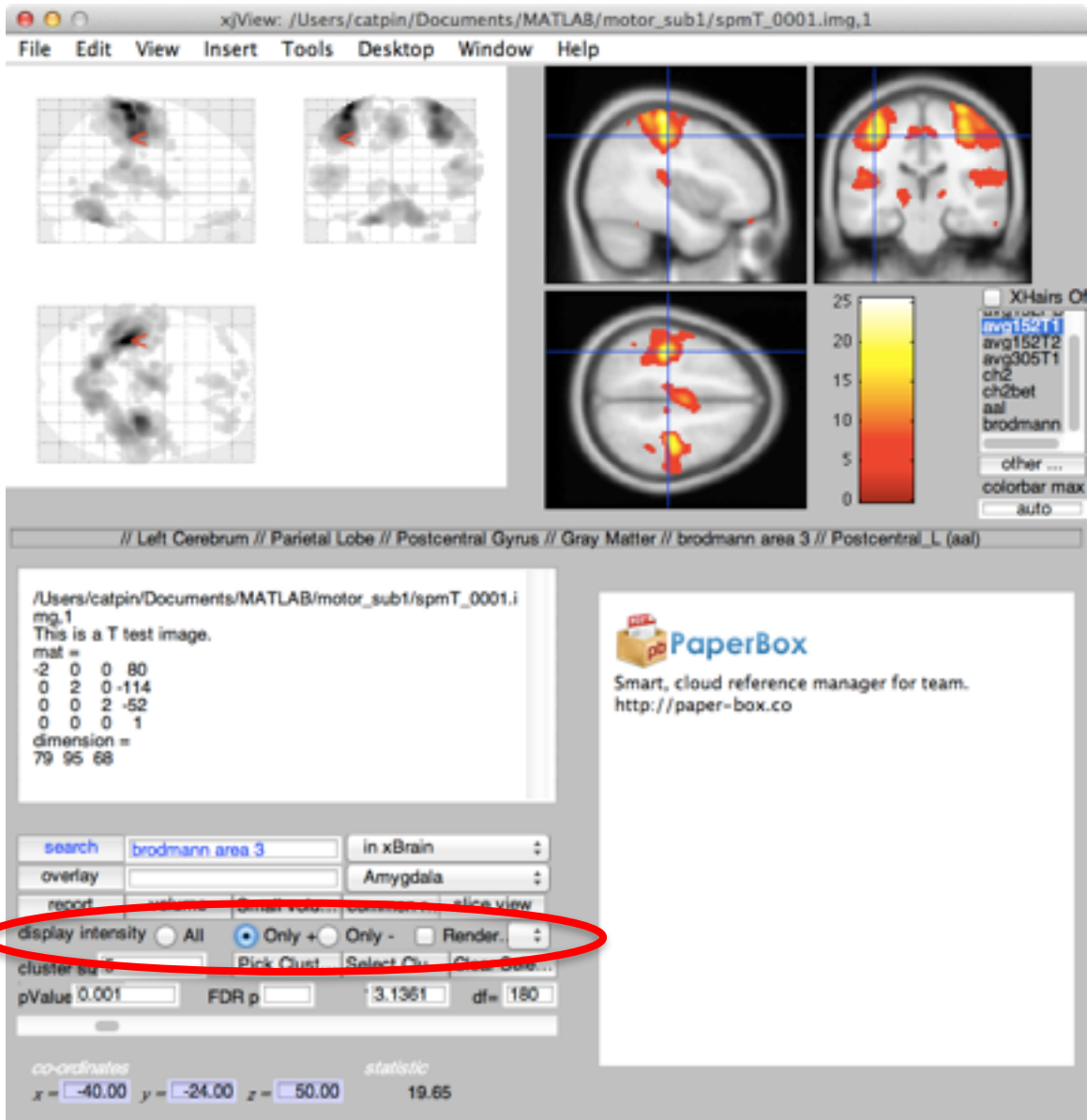


spacing: 4mm

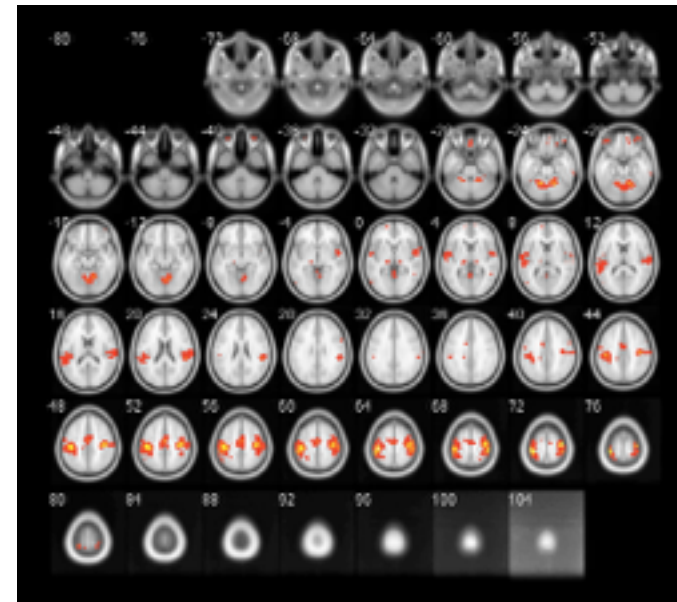


spacing: 3mm



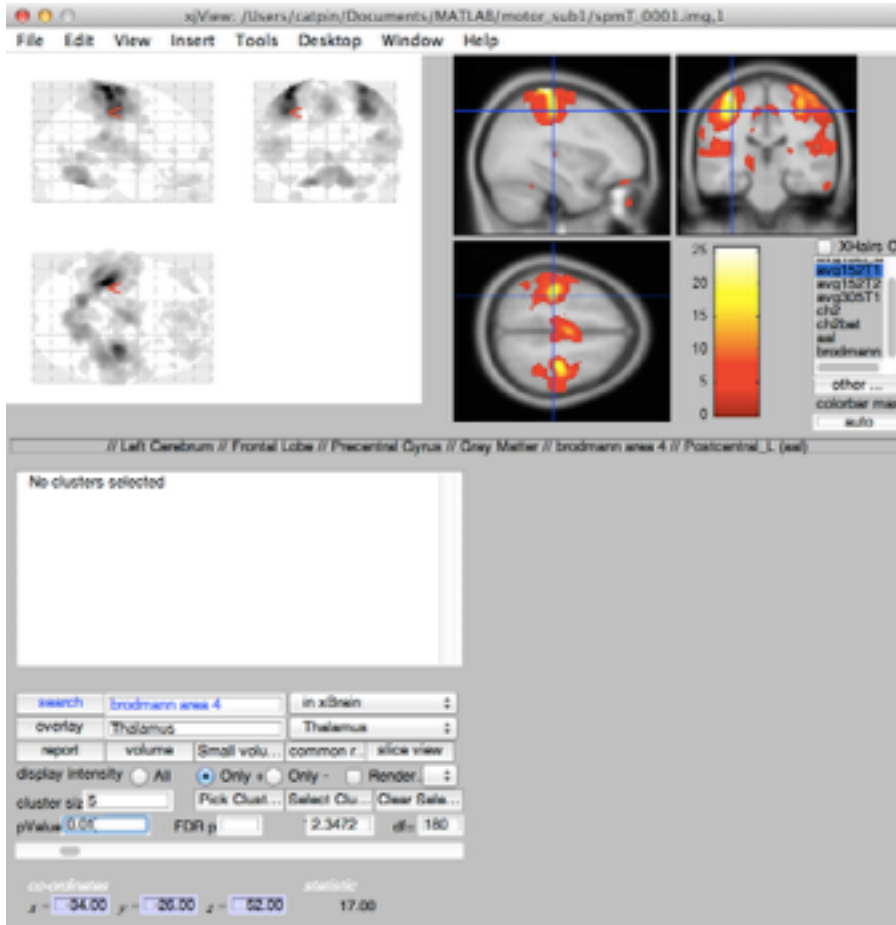


Only +
 可以調整欲觀察的T map

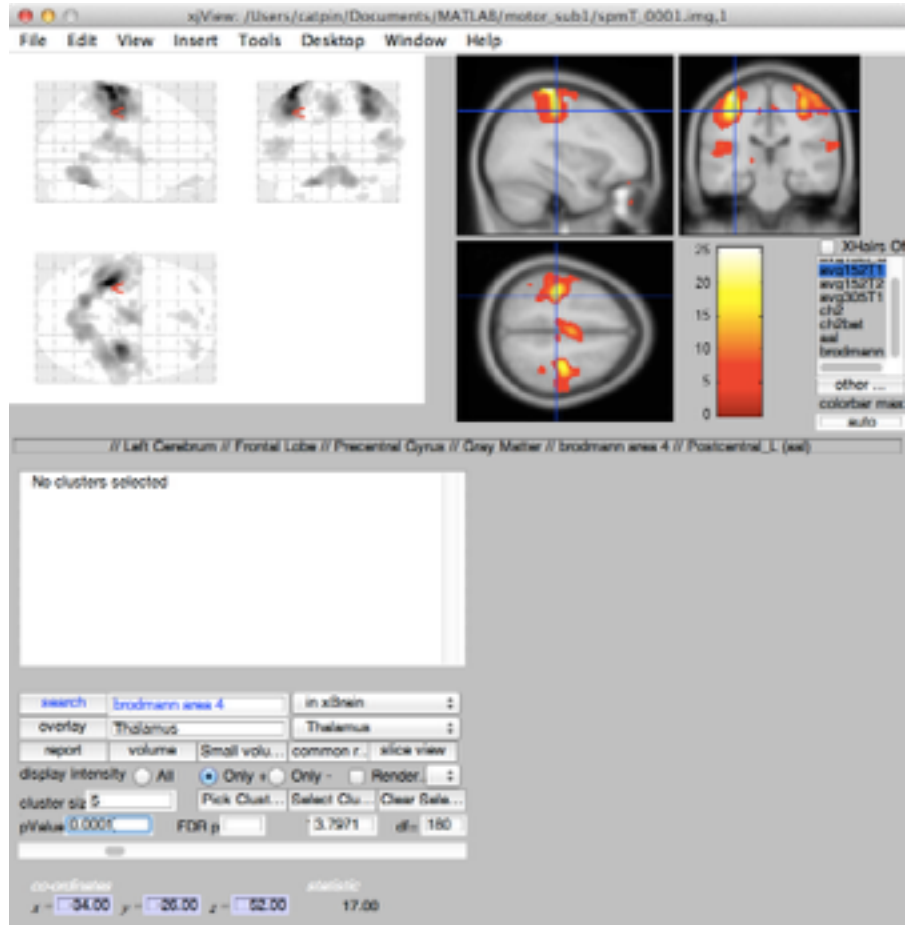


Display Intensity: All(全部顯示), Only +(與實驗設計正相關的活化區), Only -(與實驗設計負相關的活化區)

改變不同的p-value threshold



pValue=0.01



pValue=0.0001

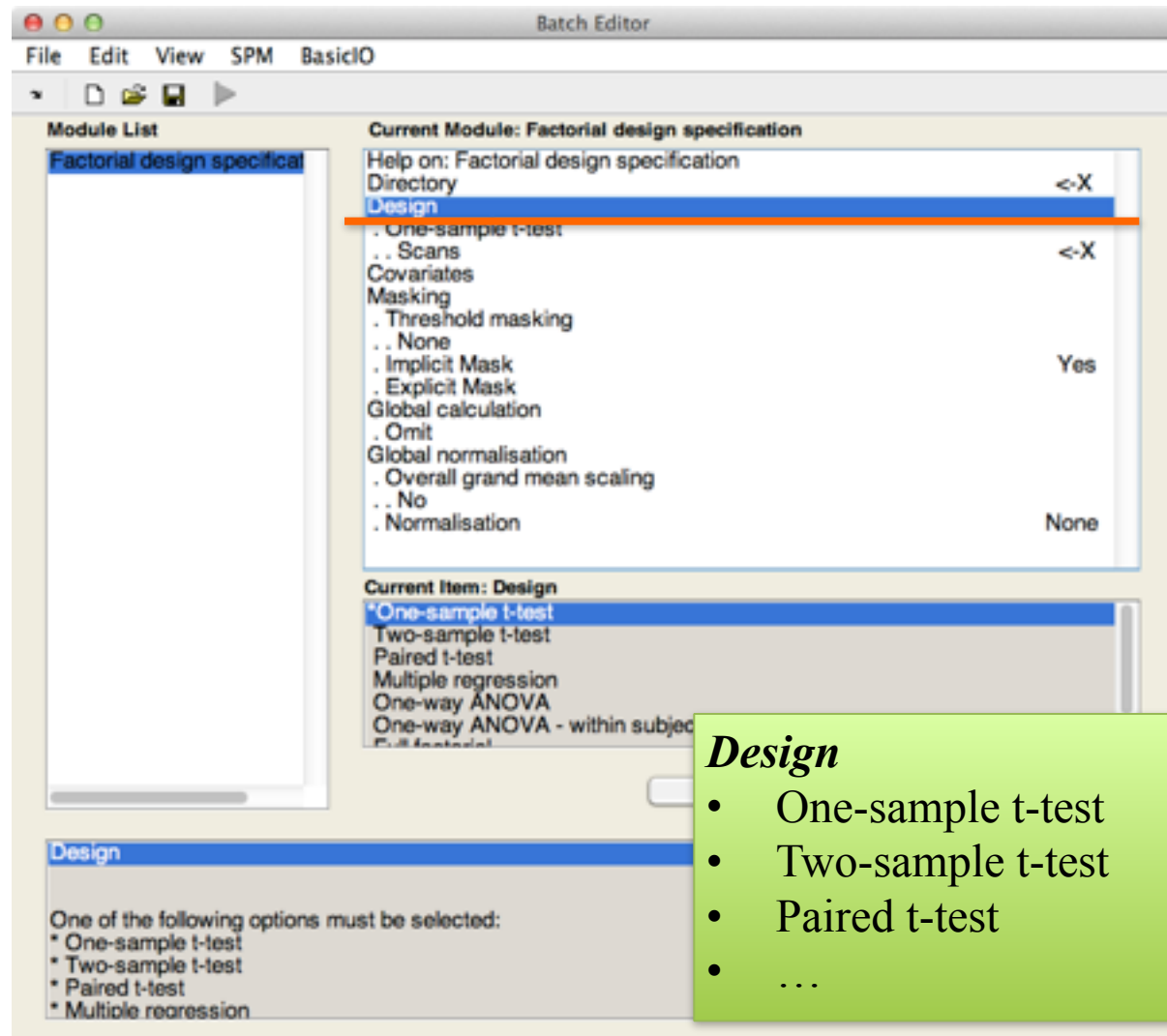
當然也可以改變FDR統計的p值threshold
FDR: False Discovery Rate, 介於FWE與none之間的校正

Group Analysis



- 完成1st level 的個體分析後，已經分析出各single subject對於實驗刺激相關的活化區域
- 接著就可以開始進行群組分析
- 群組分析分為三部分
 - 設計統計分析模型
 - 建立模型與處理
 - 最後結果呈現

Specify 2nd-level

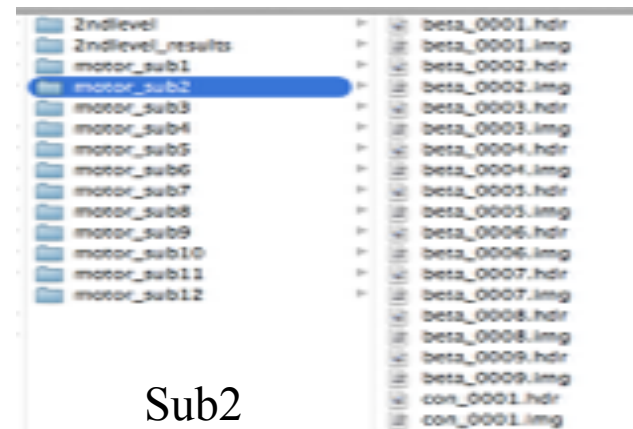


Design

- One sample t-test
 - 針對同一組群體進行各voxel間之活化程度統計運算
 - Ex: 了解一組資料對於雙手抓握實驗中，倒底有哪些共同的腦功能區，相較於其他沒有反應的區域，其統計上表現出顯著差異
- Two sample t-test
 - 針對兩組不同的群體進行各voxel間之活化程度統計運算
 - Ex: 了解無經過訓練與經過訓練之受試者兩群體間，倒底有經過訓練的群體在哪些腦功能區是與沒經過訓練之群體上之活化程度在統計表現上有差異
- Paired t-test
 - 針對同一組群體於訓練前後進行各voxel間之活化程度統計運算
 - Ex: 了解經過訓練前與訓練後之同一群受試者，倒底經過訓練後在哪些腦功能區是與訓練前上之活化程度在統計表現上有差異

事前準備

- 先建立一個資料夾
 - 用以存放2nd level 之設計模型
- 另外建立一個資料夾用以存放1st level所分析出之結果
 - 由於每一組資料分析之結果都是spmT_0001.img/hdr
 - 所以必須重新命名，否則沒有辦法放在同一個資料夾內



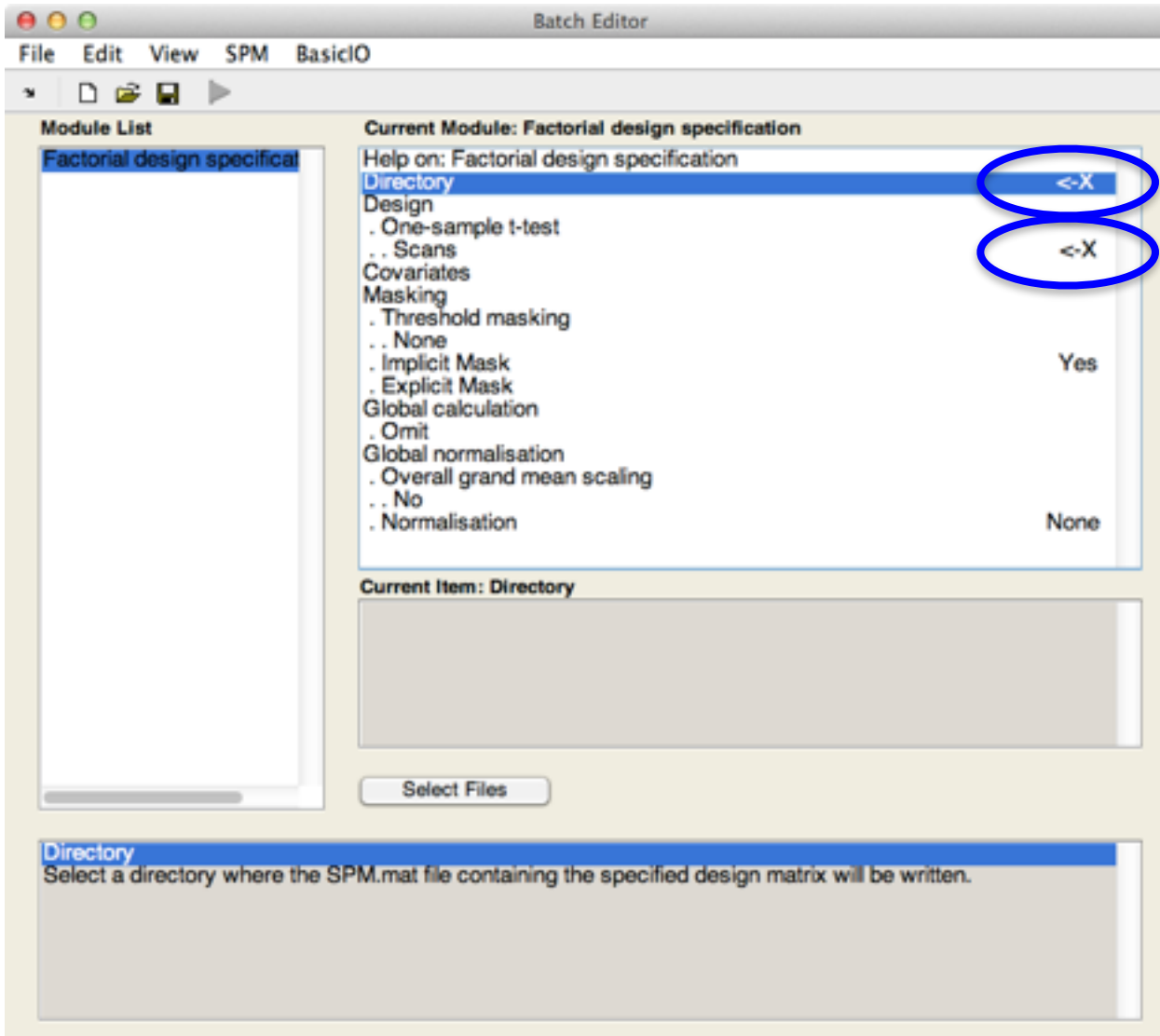
Sub2



Sub10

新建一個2ndlevel資料夾，將所有的結果都先複製到裡面，並重新命名，以方便2nd-level分析時的資料匯入

One sample t-test (default)

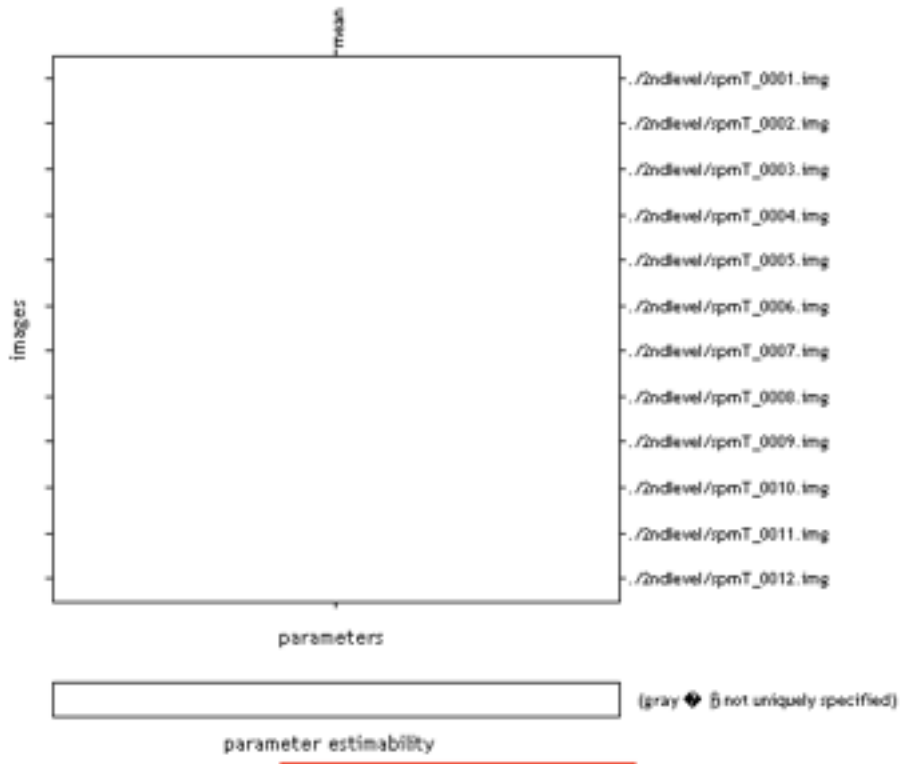
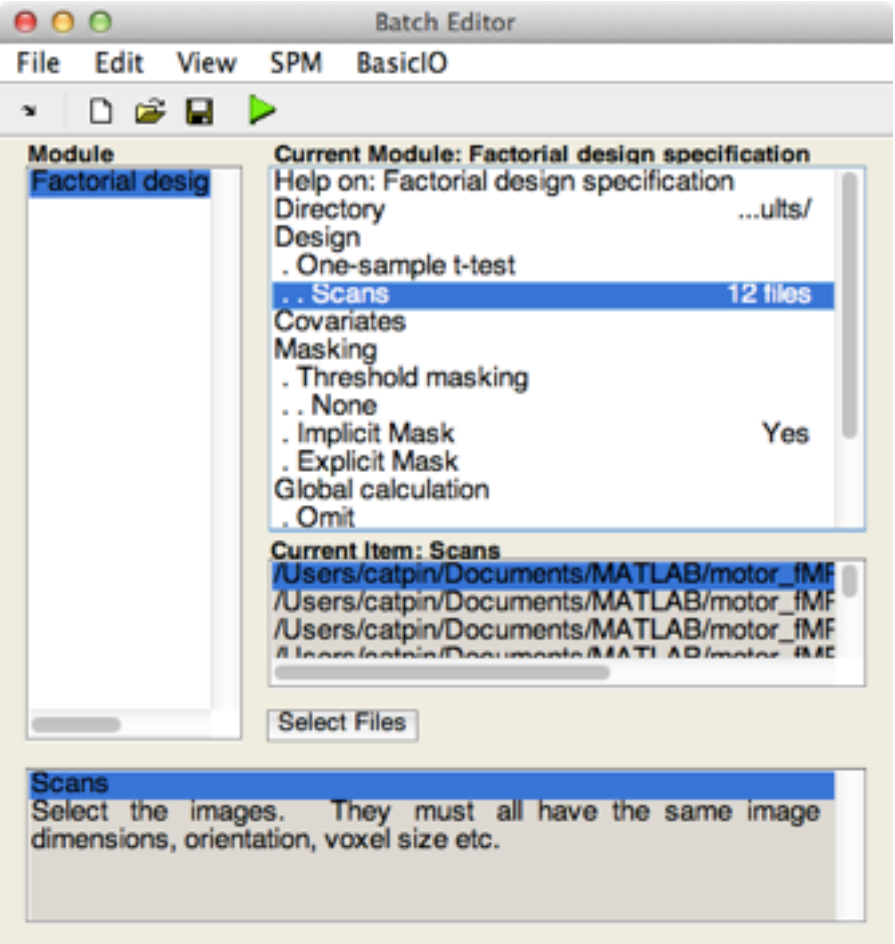


- 只有兩個<-X (輸入)

- **Directory**
選擇資料夾用以存放2nd level之設計模組
Ex: 2ndlevel_results

- **Scans**
選擇同一群組資料於1st level分析處理所完成之結果影像
Ex: 從剛剛建立的2ndlevel內選取
con_0001.img
con_0002.img
...
con_0012.img

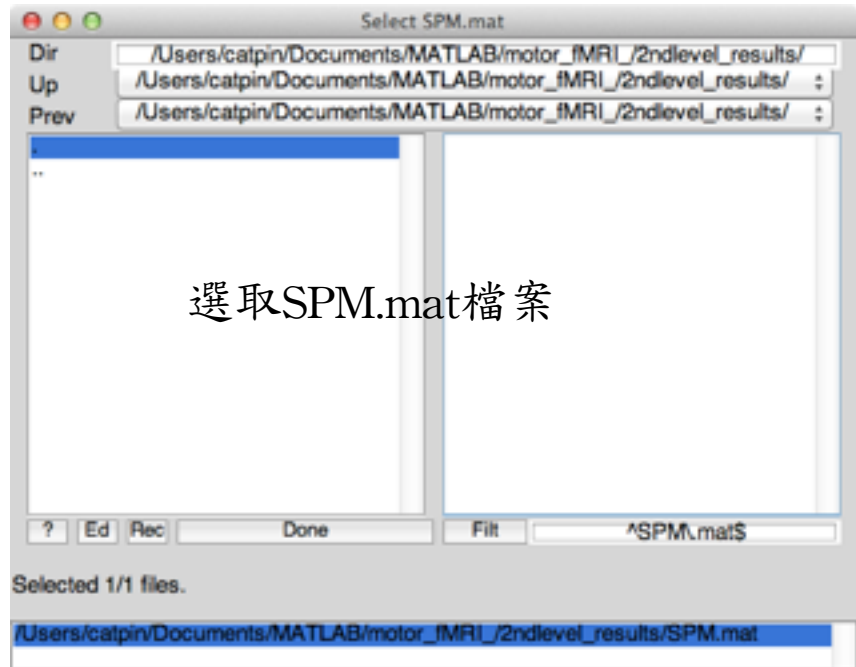
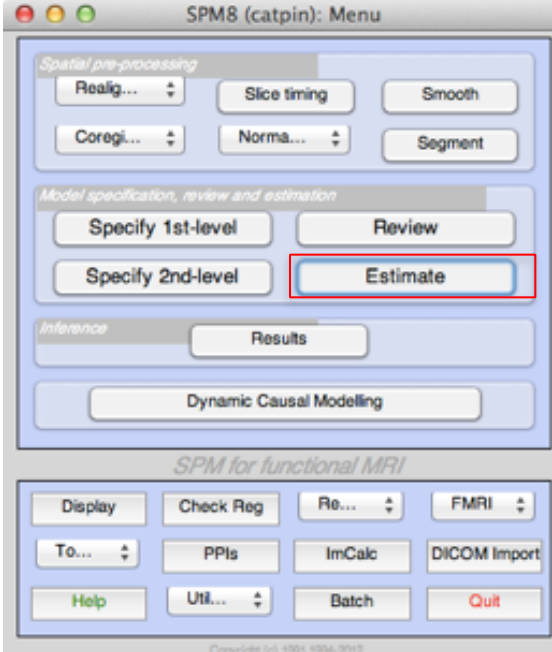
Statistical analysis: Design
One-sample t-test



Design description...

Design : One sample t-test
Global calculation : omit
Grand mean scaling : <no grand Mean scaling>
Global normalisation : <no global normalisation>
Parameters : 1 condition, +0 covariate, +0 block, +0 nuisance
 1 total, having 1 degrees of freedom
 leaving 11 degrees of freedom from 12 Images

選擇好要輸出基本統計模型設計的資料夾
 也選擇好所有1st level之結果後
 就可以按下執行開始建立統計模型設計



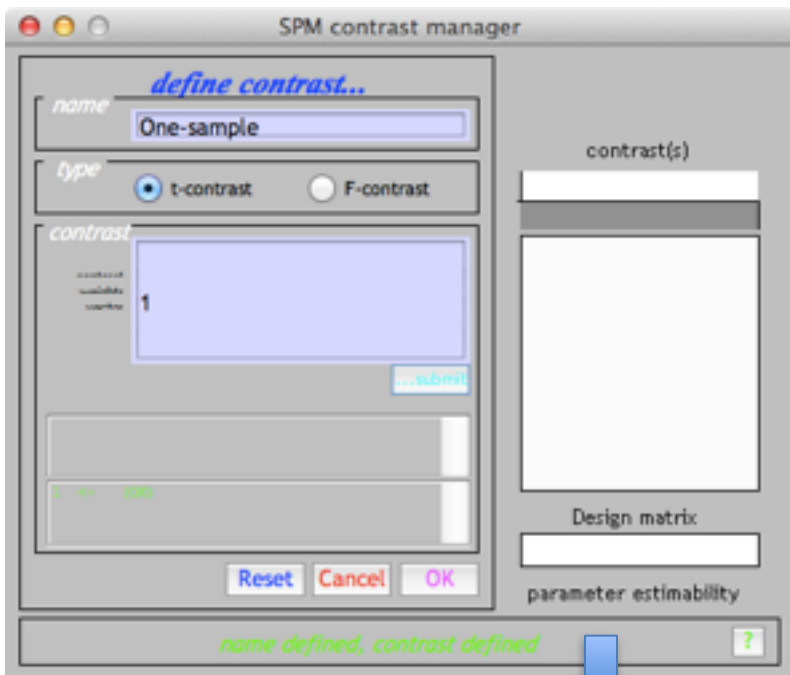
選取SPM.mat檔案



選取已經完成的統計模型設計



建立contrast
一樣選擇t-contrast



給予命名，而contrast中
 在one-sample test中只能輸入1
 (two-sample, paired t-test比較有變化)
 輸入完畢後按下submit與OK



完成後選擇剛剛建立的contrast
 : One-sample，然後按下Done



依次選取

none

命名

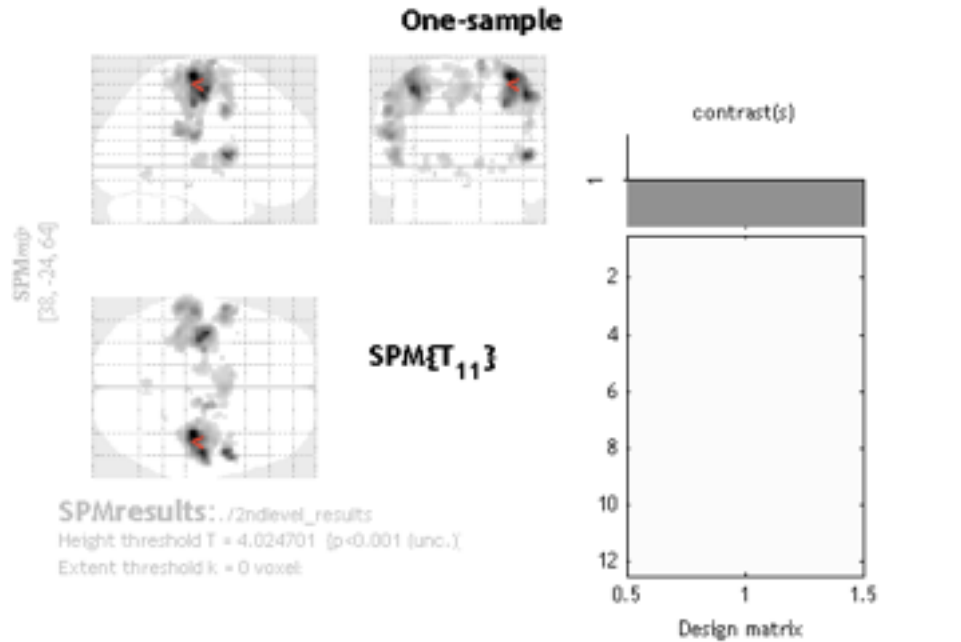
FWE/none

0.001

(跟1st level部分相同)

群組分析結果

- 結果呈現操控與1st level single subject analysis相同
- 在存放統計模型設計SPM.mat的資料夾內也會有一個spmT_0001.img結果圖，可以利用xjview或其他軟體開啟繪圖。
- 結果呈現後可以改變不同之contrast、不同之統計校正(FWE)、改變不同p-value threshold，以獲取不同之結果呈現
- 接著就是結果解釋



Statistics: *p-values adjusted for search volume*

set-level		cluster-level				peak-level				mm mm mm			
<i>P</i>	<i>C</i>	<i>P_{HECov}</i>	<i>P_{HECov}</i>	<i>k_E</i>	<i>P_{SPCov}</i>	<i>P_{HECov}</i>	<i>P_{HECov}</i>	<i>T</i>	<i>(σ^2_{ϕ})</i>	<i>P_{SPCov}</i>			
0.988	23	0.000	0.000	1885	0.000	0.000	0.032	13.34	5.58	0.000	38	-21	44
						0.011	0.032	12.21	5.22	0.000	50	-10	52
						0.044	0.045	10.22	5.09	0.000	24	-24	66
		0.000	0.000	2628	0.000	0.012	0.032	12.11	5.32	0.000	-38	-18	56
						0.382	0.151	8.57	4.65	0.000	-54	-22	22
						0.532	0.132	8.14	4.54	0.000	-32	-14	62
		0.001	0.000	168	0.000	0.039	0.037	10.88	5.18	0.000	50	2	4
						1.000	0.675	5.09	2.57	0.000	20	4	4
						1.000	0.675	4.95	2.52	0.000	64	4	14
		0.057	0.084	85	0.002	0.494	0.129	8.27	4.57	0.000	-56	0	40
		0.000	0.000	203	0.000	0.749	0.148	7.43	4.34	0.000	-50	0	8
		0.000	0.000	461	0.000	0.976	0.322	6.32	4.03	0.000	4	0	56
						0.999	0.629	5.75	2.01	0.000	-2	4	64
						1.000	0.549	5.24	2.67	0.000	0	-2	60
		0.911	0.158	23	0.049	0.593	0.381	6.01	3.92	0.000	12	-20	50
		0.788	0.112	29	0.044	1.000	0.552	5.29	3.64	0.000	12	-22	0
		0.189	0.019	41	0.004	1.000	0.552	5.28	3.65	0.000	-10	-22	4
						1.000	0.675	4.97	2.52	0.000	-12	-16	-2
		1.000	0.471	8	0.244	1.000	0.435	4.97	2.53	0.000	-10	-16	50
		0.991	0.254	15	0.134	1.000	0.454	4.85	2.47	0.000	-2	-60	-6
		1.000	0.514	5	0.380	1.000	0.489	4.74	2.44	0.000	4	-28	-16
		1.000	0.714	2	0.591	1.000	0.703	4.78	2.41	0.000	-20	-2	-8

Table shows 3 local maxima more than 8.0mm apart

Height threshold: $T = 4.02$, $p = 0.001$ (1.000) Degrees of freedom = [1.0, 11.0]
 Extent threshold: $k = 0$ voxels, $p = 1.000$ (1.000) FWHM = 10.0 10.3 9.4 mm mm mm; 5.0 5.1 4.7 [voxels]
 Expected voxels per cluster, $\langle k \rangle = 6.984$ Volume: 1820576 = 227572 voxels = 1746.3 resels
 Expected number of clusters, $\langle c \rangle = 35.23$ Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 121.30 voxels)
 FWEp: 10.532, FDRp: 10.281, FWEc: 168, FDRc: 61 Page 7

如果操作上遇到問題

- 看看操作說明，再試著以範例資料分析一次，檢驗步驟是否正確
- 先分析品質佳之資料並確立其流程，再應用至群組中之其他資料
- 寫信詢問此系列課程的講師們
- SPM與xjview均有其討論區及電子郵件群組，可留言詢問，以解決您的疑問



By members & University College London Wellcome Trust Centre for Neuroimaging

[Introduction](#) | [Software](#) | [Documentation](#) | [Courses](#) | [Email list](#) | [Data](#) | [Extensions](#)

Discussion List

Introduction

The SPM discussion list is an electronic mailing list for discussion and help with the methodology, implementation and use of Statistical Parametric Mapping and the SPM package. The list is not moderated, but is monitored and owned by members of the [Wellcome Trust Centre for Neuroimaging](#).

Much of the approach and use of SPM is described in the [documentation](#). Subscribers are urged to consult these sources, and any local expertise, before using the discussion list as a helpline. A response from one of the SPM authors cannot be guaranteed, due to resource limitations. Experienced list members are therefore encouraged to address issues within their experience, posting their responses & discussion to the list for general enlightenment.

Searching archives

- [Archives](#) of SPM messages.
- [Search](#) SPM archives.

Subscription

The list is run at the UK's automated [JISCmail](#) service.

To **subscribe** or **unsubscribe** to the SPM list:

Enter your details at <http://www.jiscmail.ac.uk/cgi-bin/webadmin?SUBED1=spm&A=1>

To **send a message** to all the people currently subscribed to the SPM list:

Just send a mail to spm@jiscmail.ac.uk after subscription.

If you have difficulties, then have a look to the [frequently asked questions](#) about JISCmail or email the list owner at fil.spm@ucl.ac.uk, for assistance.

<http://www.fil.ion.ucl.ac.uk/spm/support/>

Google 搜尋主題

網上論壇 新增主題 全部標為已讀 篩選器

我的群組 首頁 已加星號

我的收藏

最近瀏覽過的群組

最近搜尋的內容

隱私權政策 - 服務條款

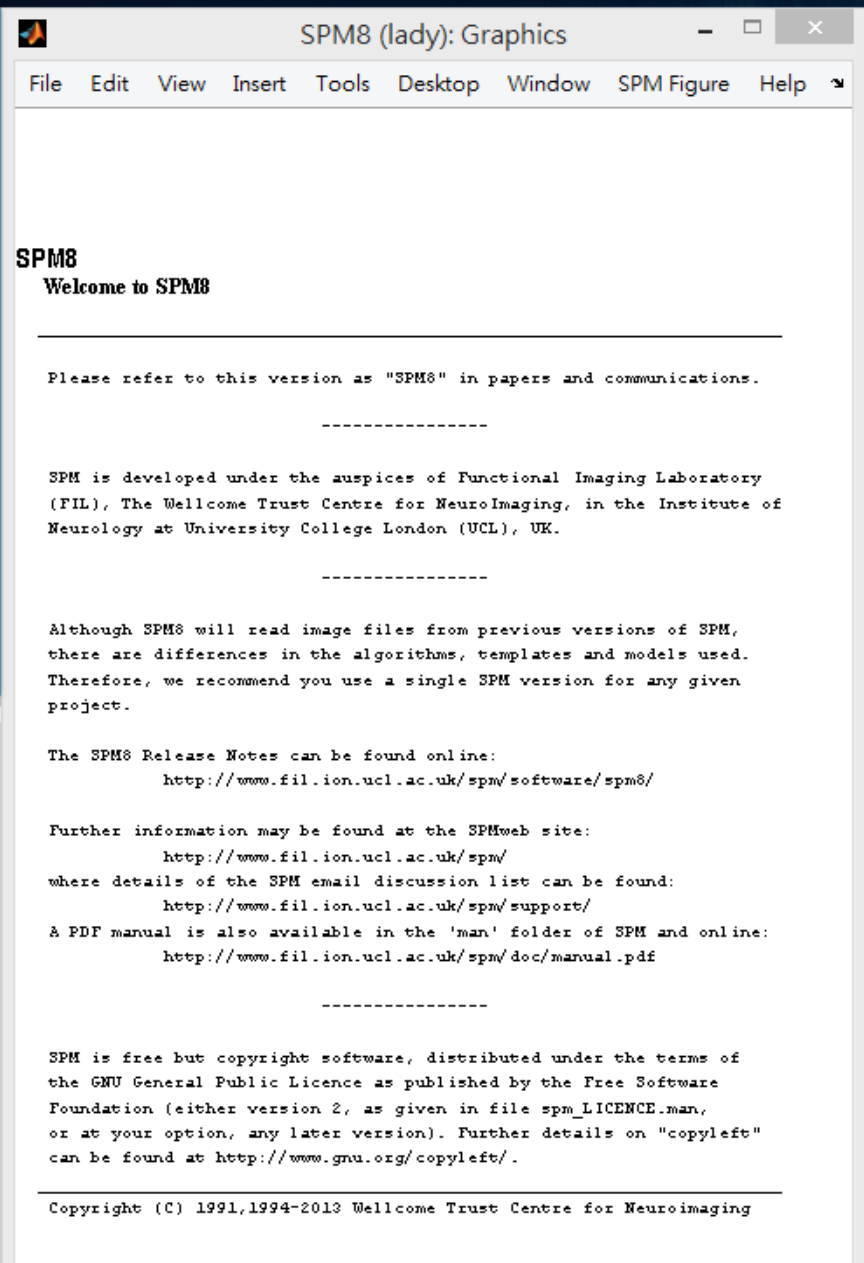
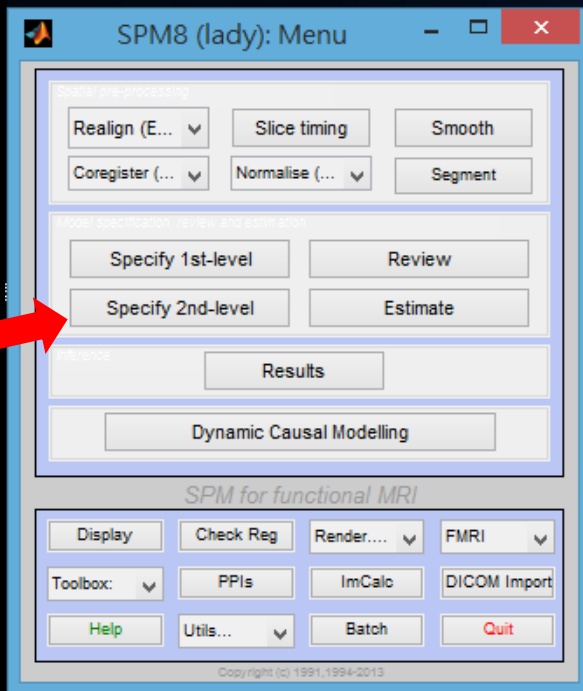
xjView discuss group 公開分享

第 60 個主題, 共 87 個 (85 個未讀取) ☆ 加入群組即可張貼留言 8+1

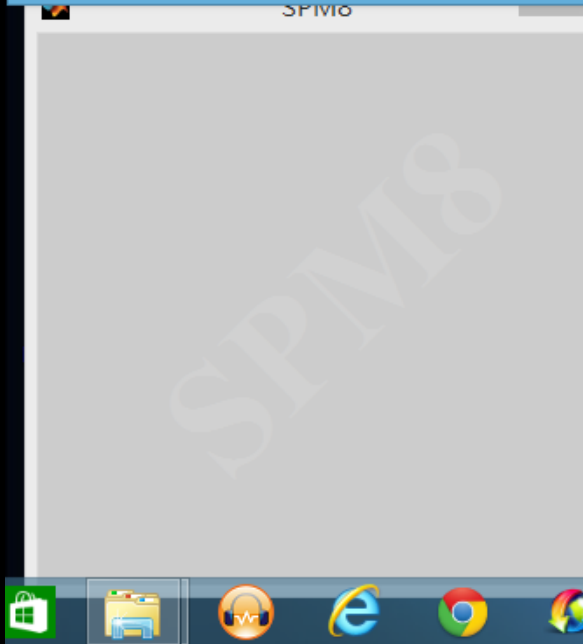
-  p value of FDR was more liberal than uncorrected ones. (3)
作者: Chunliang Feng - 3 則留言 - 瀏覽次數: 2
-  fdr function error in Matlab 2013a (1)
作者: TH - 1 則留言 - 瀏覽次數: 4
-  message error mask based on anatomy (2)
作者: tarik - 2 則留言 - 瀏覽次數: 4
-  Error message: Undefined function or variable 'xjview' (2)
作者: Tianyi Li - 2 則留言 - 瀏覽次數: 6
-  Error message when starting xjview
作者: djw...@gmail.com - 6 則留言 - 瀏覽次數: 26
-  Small volume correction with Display intensity = All (1)
作者: bettyann - 1 則留言 - 瀏覽次數: 9
-  How to change the colors of color bar in xjView? (5)
作者: Letty - 5 則留言 - 瀏覽次數: 92
-  help needed- basics of SPM & xjView (2)
作者: Daria - 2 則留言 - 瀏覽次數: 30
-  Help with error: "Reference to non-existent field 'TF'" (1)
作者: lisa.br...@googlemail.com - 1 則留言 - 瀏覽次數: 5
-  problem with coordinates/crosshairs (2)
作者: Chaleece - 2 則留言 - 瀏覽次數: 19
-  contrast interpretation (6)
作者: karyn - 6 則留言 - 瀏覽次數: 43

- <https://groups.google.com/forum/#!forum/xjview-discuss-group>

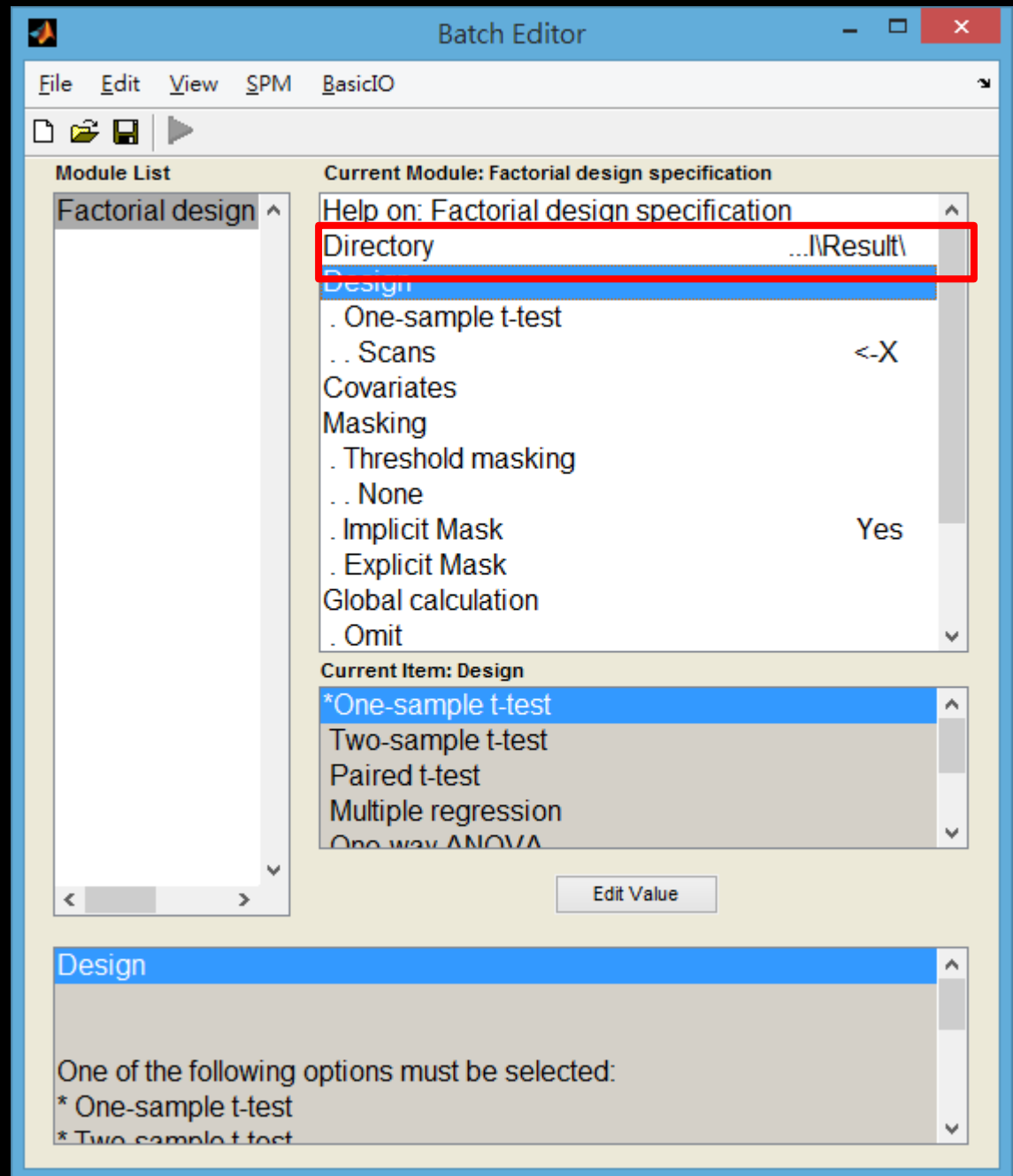
Two sample t -test



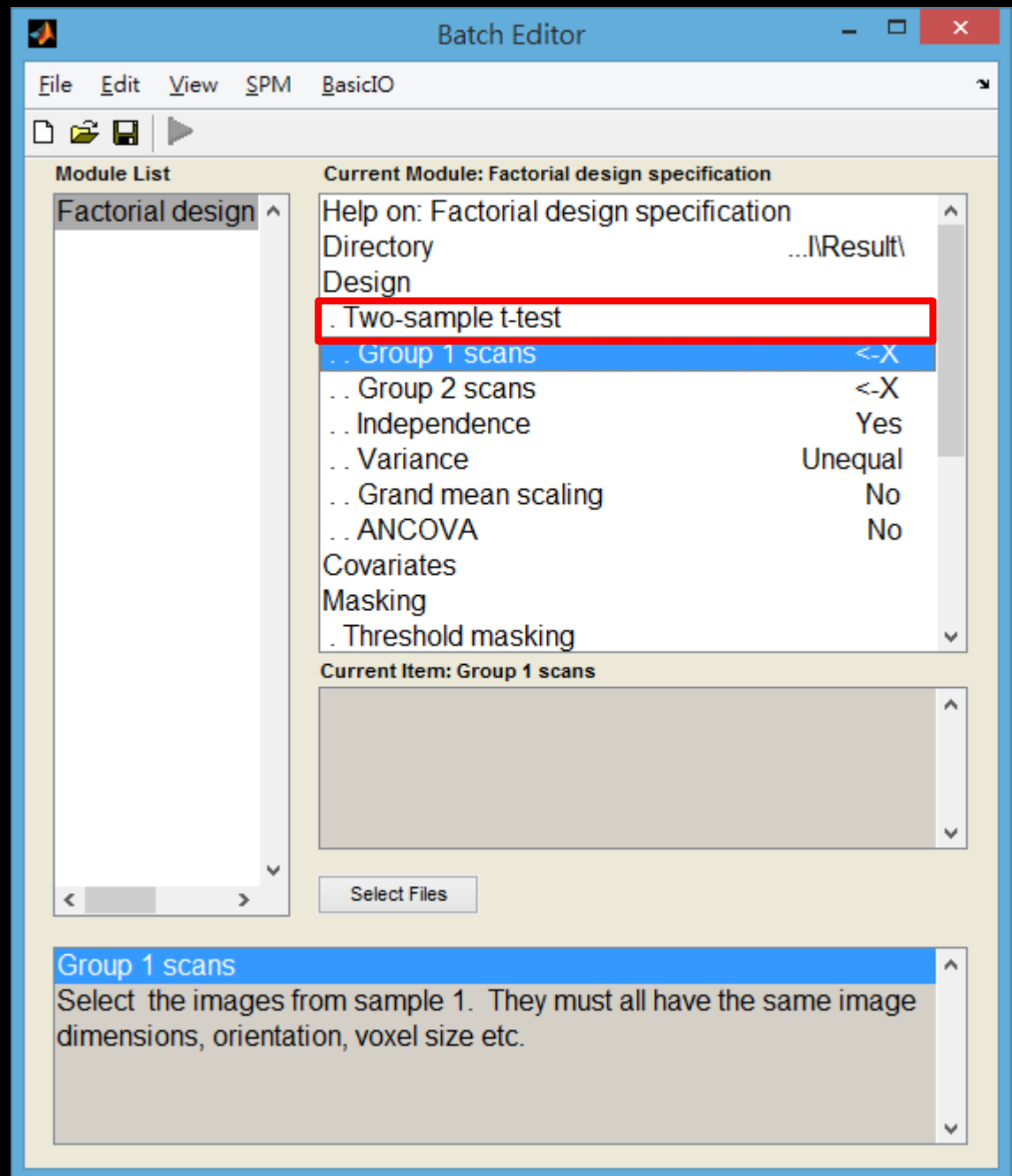
選Specify
2nd-level

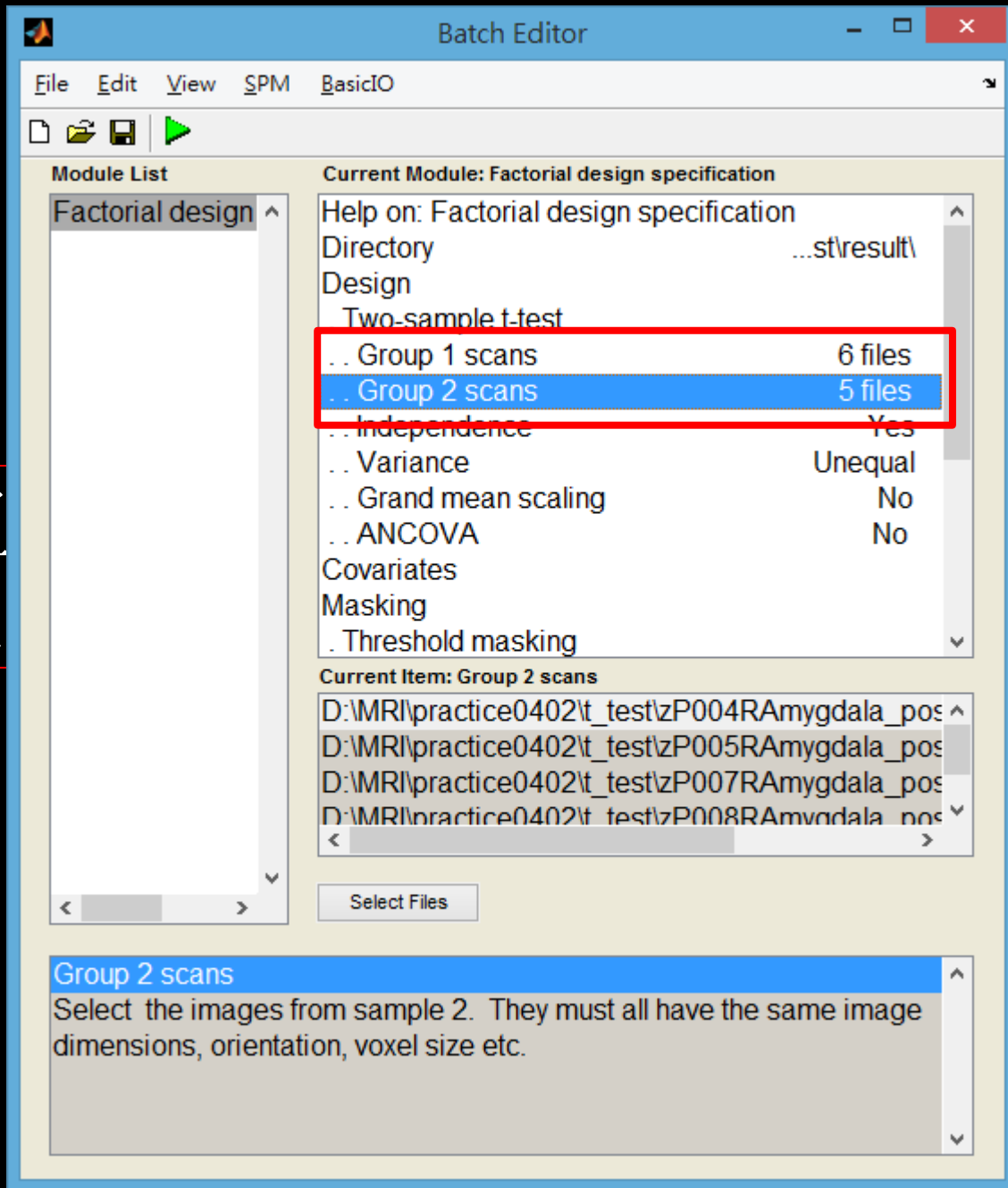


Directory 選擇檔案輸出位置



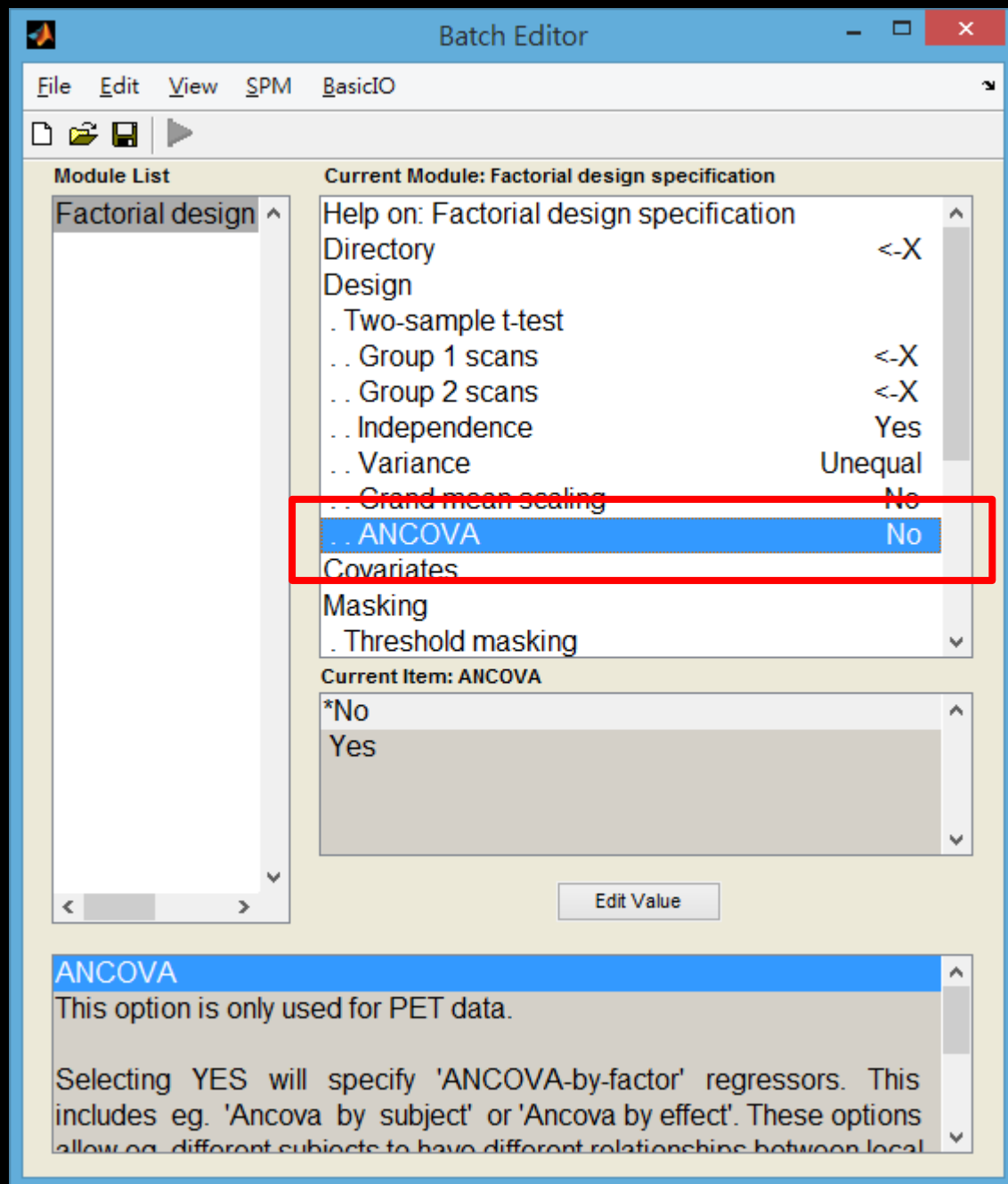
點選Design 選擇 Two-sample t-test





Group 1 選 Control組
Group 2 選 Patient組

ANCOVA的部分
選No



點選Covariates
並選New:Covariate
目的在於排除共變數對
影像所造成的影響

Batch Editor

File Edit View SPM BasicIO

Module List

Factorial design

Current Module: Factorial design specification

- . Two-sample t-test
- .. Group 1 scans <-X
- .. Group 2 scans <-X
- .. Independence Yes
- .. Variance Unequal
- .. Grand mean scaling No
- .. ANCOVA Yes
- Covariates**
- . Covariate
- .. Vector <-X
- .. Name <-X
- .. Interactions None
- .. Centering ...all mean

Current Item: Covariates

- New: Covariate**
- Replicate: Covariate (1)
- Delete: Covariate (1)

Edit Value

Covariates

This option allows for the specification of covariates and nuisance variables. Unlike SPM94/5/6, where the design was partitioned into effects of interest and nuisance effects for the computation of adjusted data and the F-statistic (which was used to thresh out voxels where there appeared to be no effects of interest), SPM does not partition the

輸入共變數的名稱

The screenshot shows the 'Batch Editor' window with the 'Current Module: Factorial design specification' selected. The 'Module List' on the left shows 'Factorial design' expanded. The main panel displays a list of options for the current module, with 'Name' highlighted in blue and enclosed in a red box. Below this list, the 'Current Item: Name' section is visible, containing a text input field and an 'Edit Value' button. At the bottom, a detailed description for the 'Name' item is shown.

Option	Value
.. ANCOVA	Yes
Covariates	
.. Covariate	
.. Vector	<-X
.. Name	<-X
.. Interactions	None
.. Centering	...all mean
Masking	
.. Threshold masking	
.. None	
.. Implicit Mask	Yes
.. Explicit Mask	
Global calculation	

Current Item: Name

Name
Name of covariate
A String is entered.
The string must have at least 1 characters.

選No centering
才不會做多餘的
計算

The screenshot shows the 'Batch Editor' window with the 'Factorial design specification' module selected. The 'Module List' on the left shows 'Factorial design' expanded. The main panel displays the following settings:

Setting	Value
.. ANCOVA	Yes
Covariates	
. Covariate	
.. Vector	<-X
.. Name	<-X
.. Interactions	None
.. Centering	...entering
Masking	
. Threshold masking	
.. None	
. Implicit Mask	Yes
. Explicit Mask	
Global calculation	

The 'Current Item: Centering' section shows the following options:

- Factor 2 mean
- Factor 3 mean
- *No centering
- User specified value
- As implied by ANCOVA

An 'Edit Value' button is located below the 'Current Item' list.

The 'Centering' section at the bottom provides the following explanation:

Centering
The appropriate centering option is usually the one that corresponds to the interaction chosen, and ensures that main effects of the interacting factor aren't affected by the covariate. You are advised to choose this option, unless you have other modelling considerations.

Batch Editor

File Edit View SPM BasicIO

Module List

Current Module: Factorial design specification

- .. Intercept
- Covariates
- .. Covariate
- .. Vector
- .. Name
- .. Interactions
- .. Centering
- .. Covariate
- .. Vector
- .. Name
- .. Interactions
- .. Centering
- Masking

Current Item: Centering

Centering

The appropriate centering option for the interaction chosen, and ensure that the factor aren't affected by the covariate option, unless you have other modules



Vector

Enter a value.

To clear a value, clear the input field and accept.

Accept input with CTRL-RETURN, cancel with ESC.

OK Cancel



輸入要排除
共變數的數
值



Vector

Enter a value.

To clear a value, clear the input field and accept.

Accept input with CTRL-RETURN, cancel with ESC.

261
261
262
262
910
910
226
226
255
255
274
274
237
237
227
227
297
297
333

OK Cancel

RUN

The screenshot shows the 'Batch Editor' window with a menu bar containing 'File', 'Edit', 'View', 'SPM', and 'BasicIO'. A red box highlights the 'View' menu and the 'Run' button (a green play icon) in the toolbar. The main area is titled 'Current Module: Factorial design specification' and contains a list of parameters:

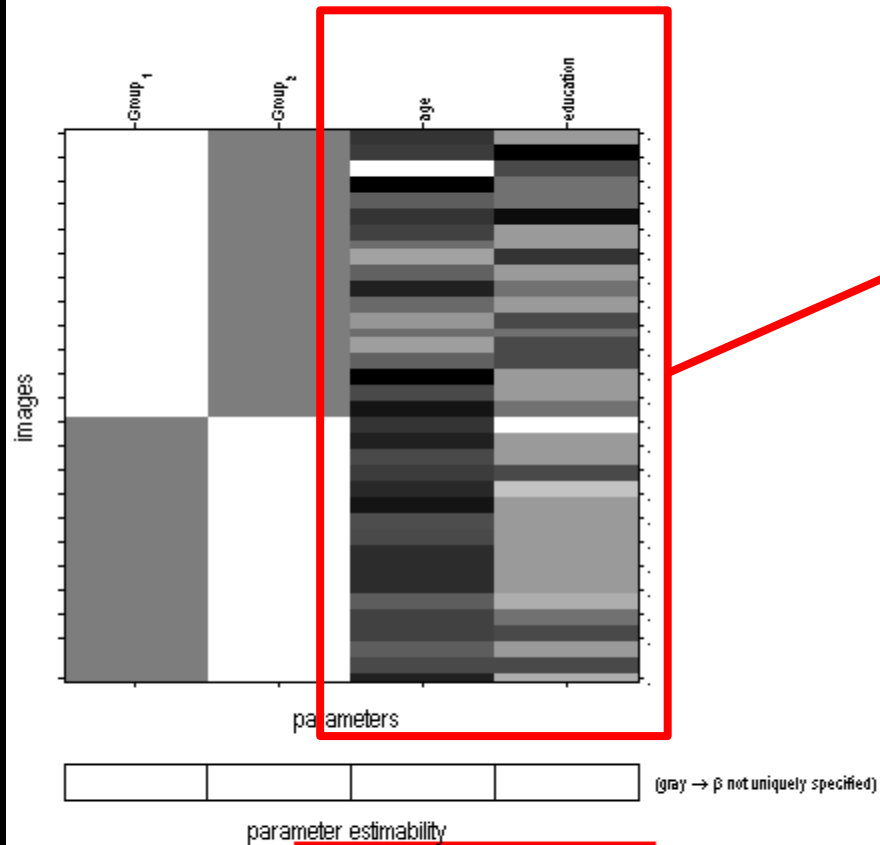
- .. Intercept ...Intercept
- Covariates
- . Covariate
- .. Vector ...1 double
- .. Name age
- .. Interactions None
- .. Centering ...entering
- . Covariate
- .. Vector ...1 double
- .. Name education
- .. Interactions None
- .. Centering ...entering

The 'Centering' option is highlighted in blue. Below this list is a section for 'Current Item: Centering' with a scrollable list of options: 'Overall mean', 'Factor 1 mean', 'Factor 2 mean', 'Factor 3 mean', and '*No centering'. An 'Edit Value' button is located below the list.

At the bottom of the window, a text box titled 'Centering' provides the following explanation:

Centering
The appropriate centering option is usually the one that corresponds to the interaction chosen, and ensures that main effects of the interacting factor aren't affected by the covariate. You are advised to choose this option, unless you have other modelling considerations.

Statistical analysis: Design

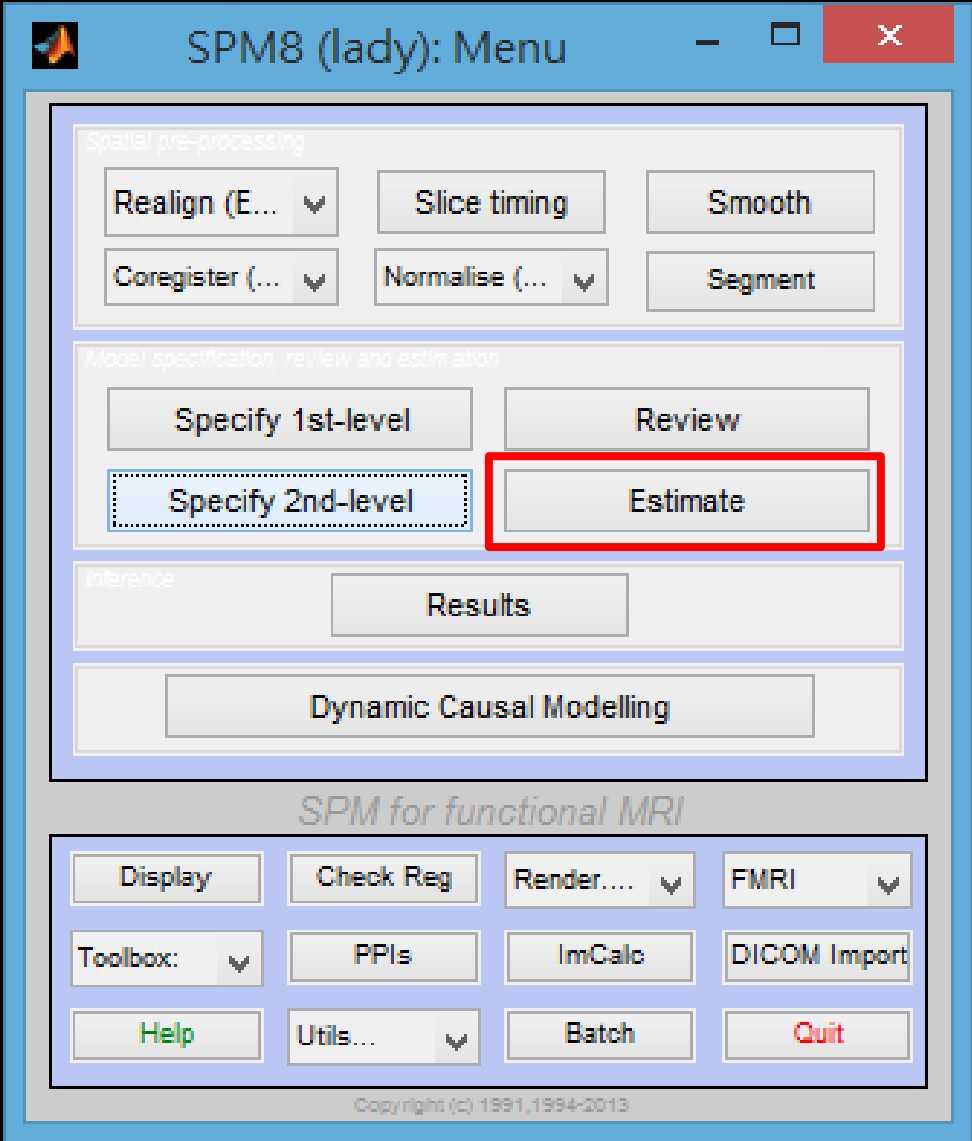


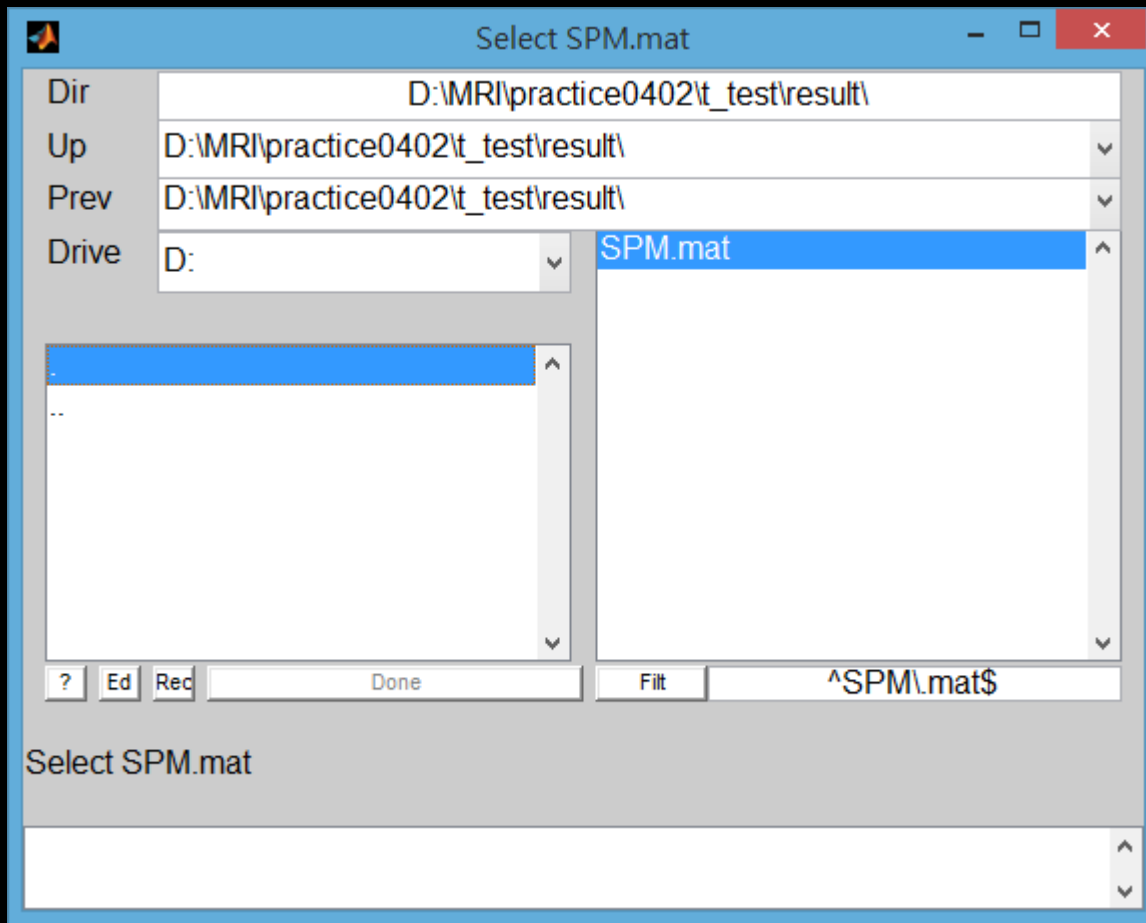
要排除的共變數

Design description...

Design : Two-sample t-test
Global calculation : omit
Grand mean scaling : <no grand Mean scaling>
Global normalisation : <no global normalisation>
Parameters : 2 condition, +2 covariate, +0 block, +0 nuisance
4 total, having 4 degrees of freedom
leaving 65 degrees of freedom from 69 images

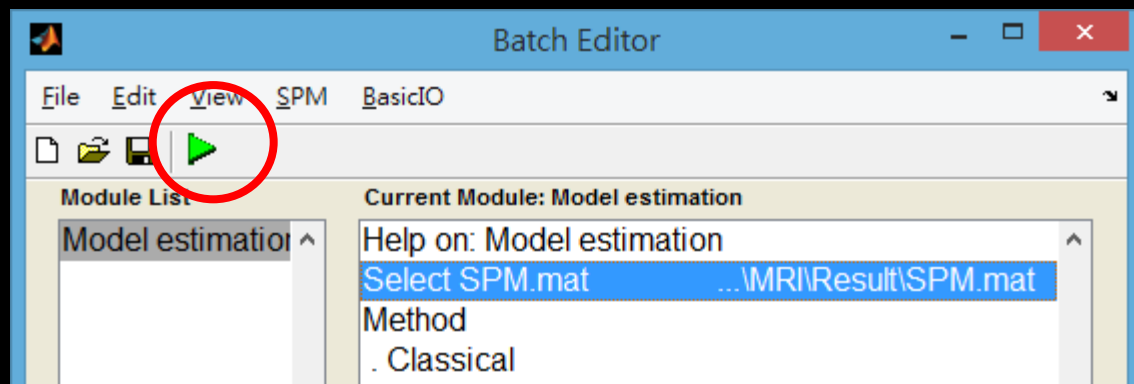
選Estimate



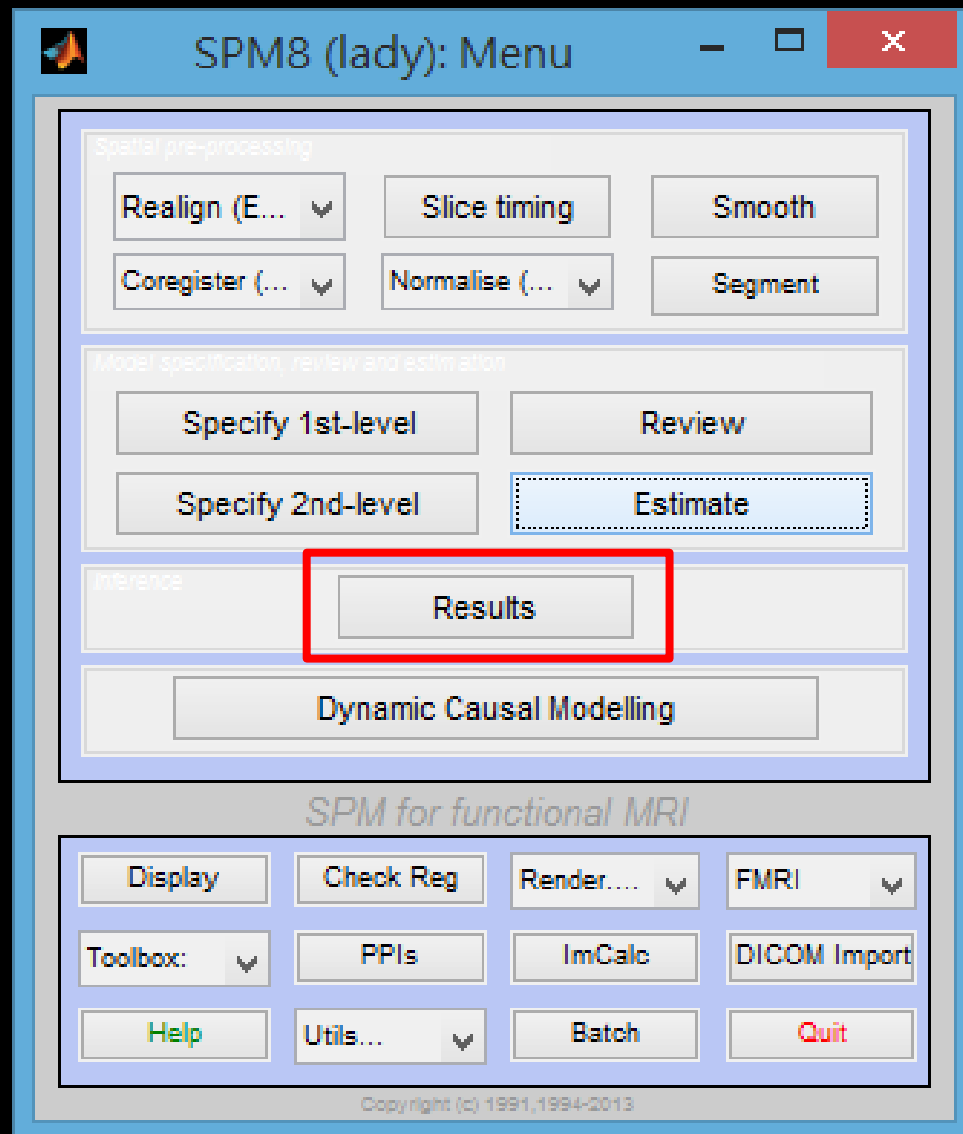


到原本設定
輸出檔案的
資料夾.選擇
SPM.mat

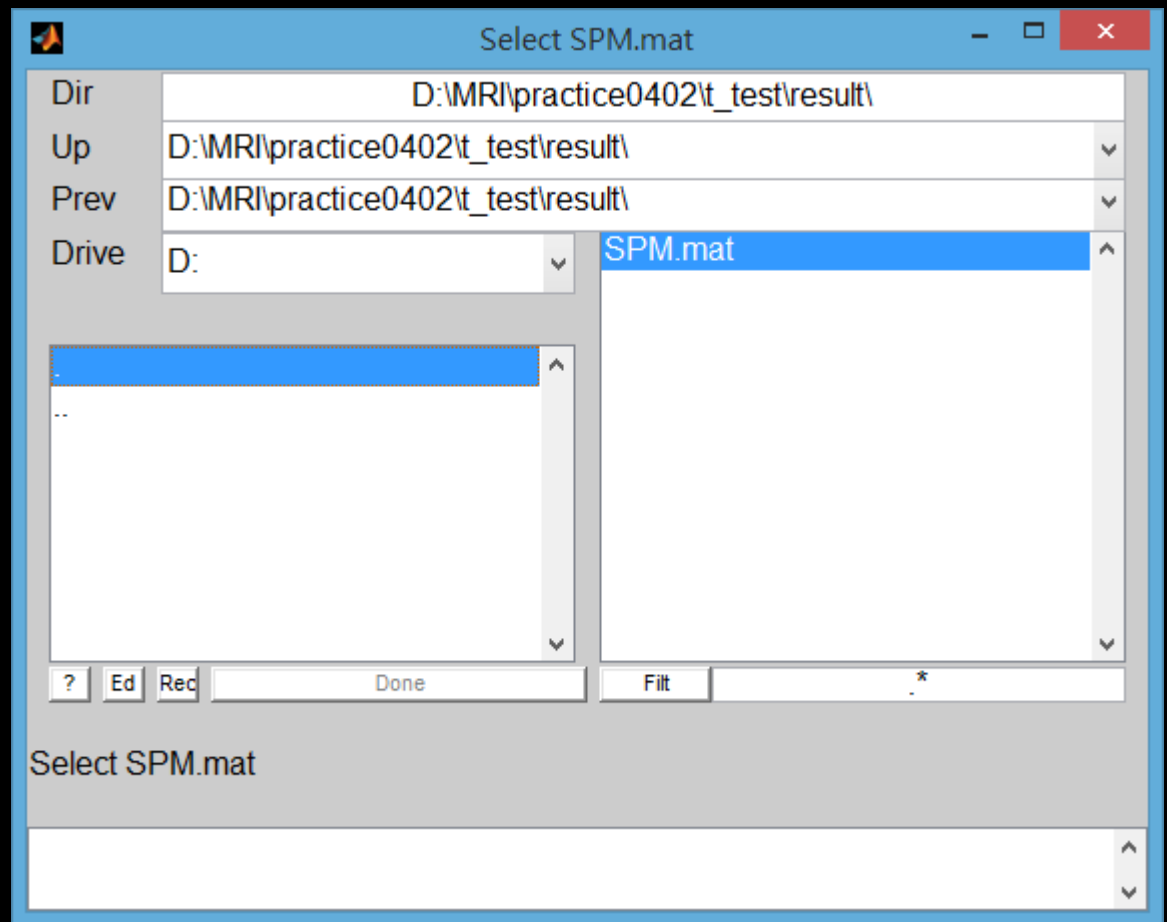
開始跑Data

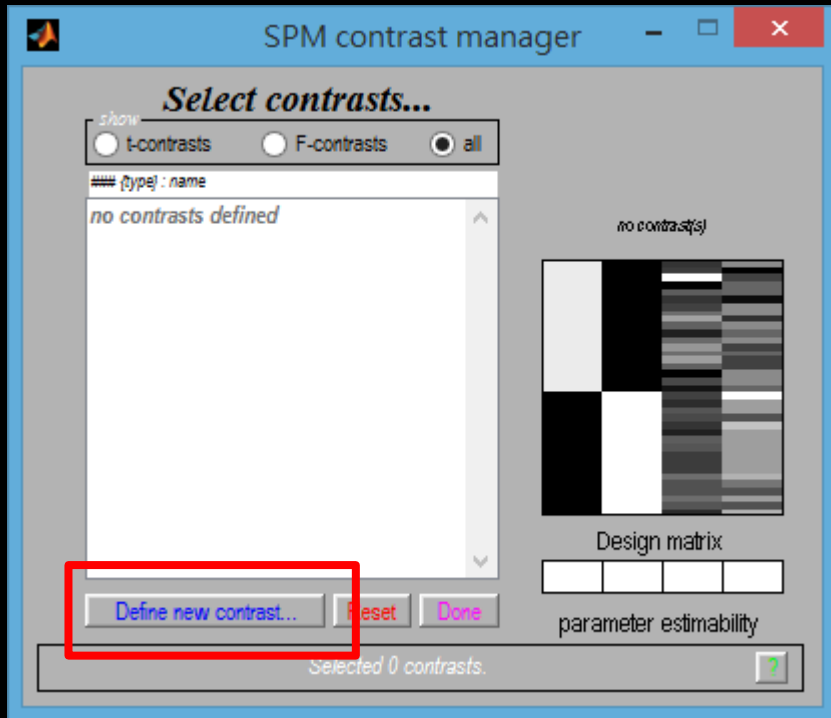


點選Result



選擇Estimate
後的檔案

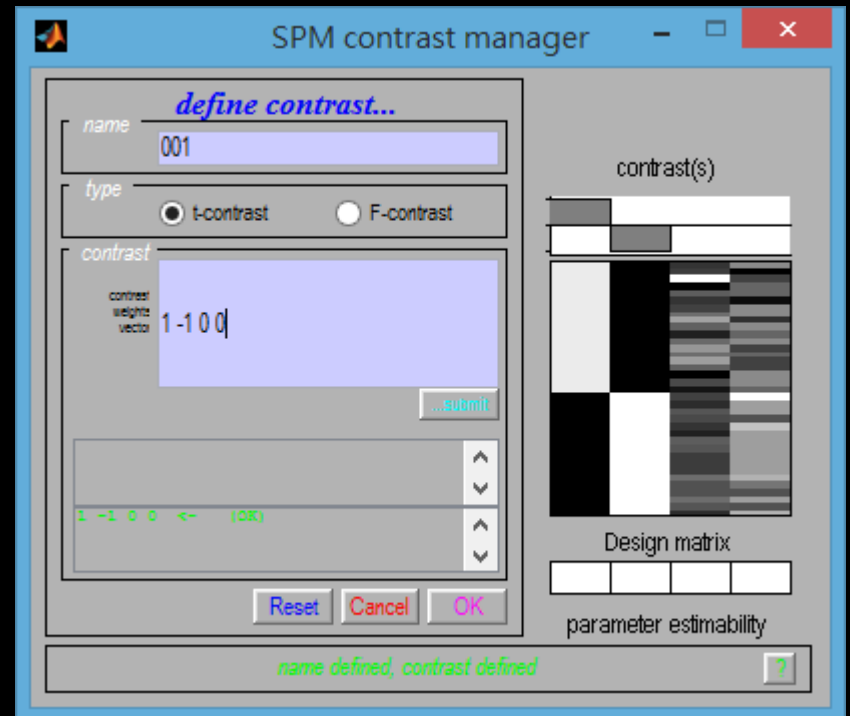




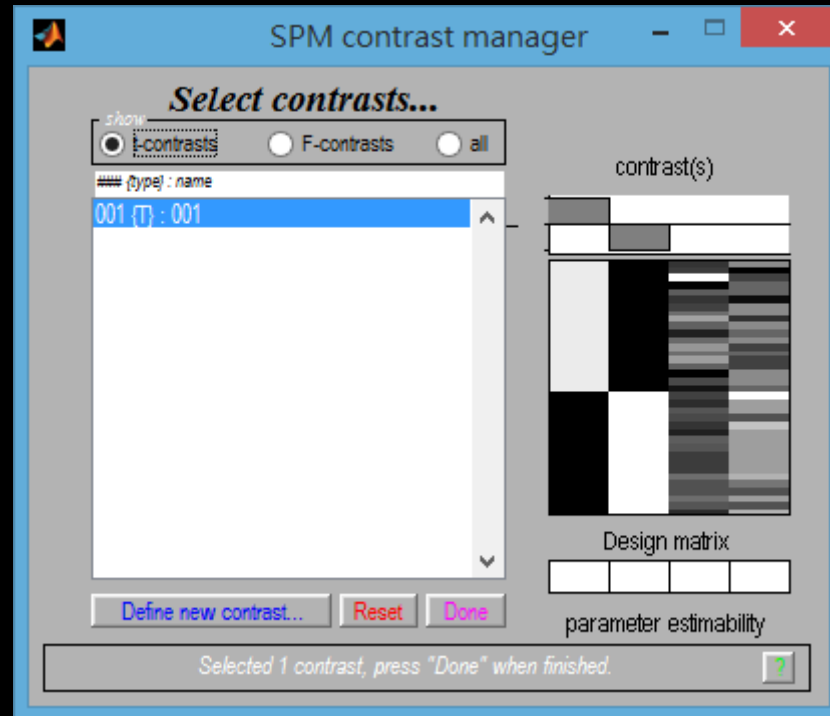
按Define new contrast

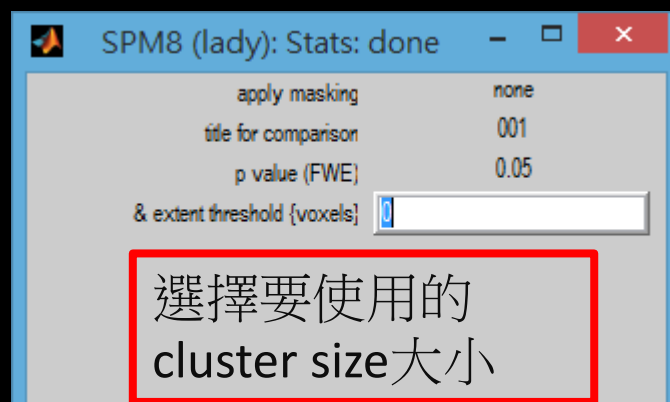
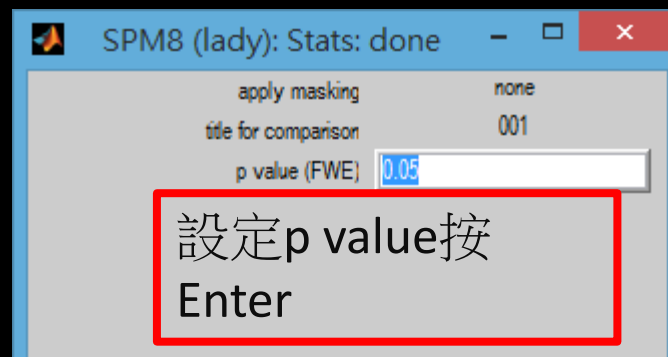
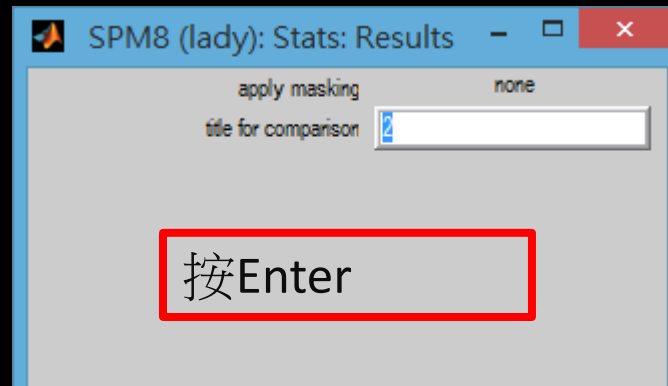
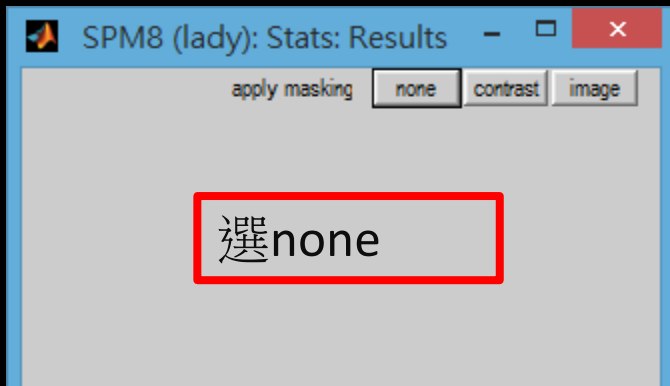
影像的權重給[1 -1] or [-1 1]
 [1 -1] Group 1 > Group 2
 [-1 1] Group 1 < Group 2
 Covariate 因為要排除所以給0

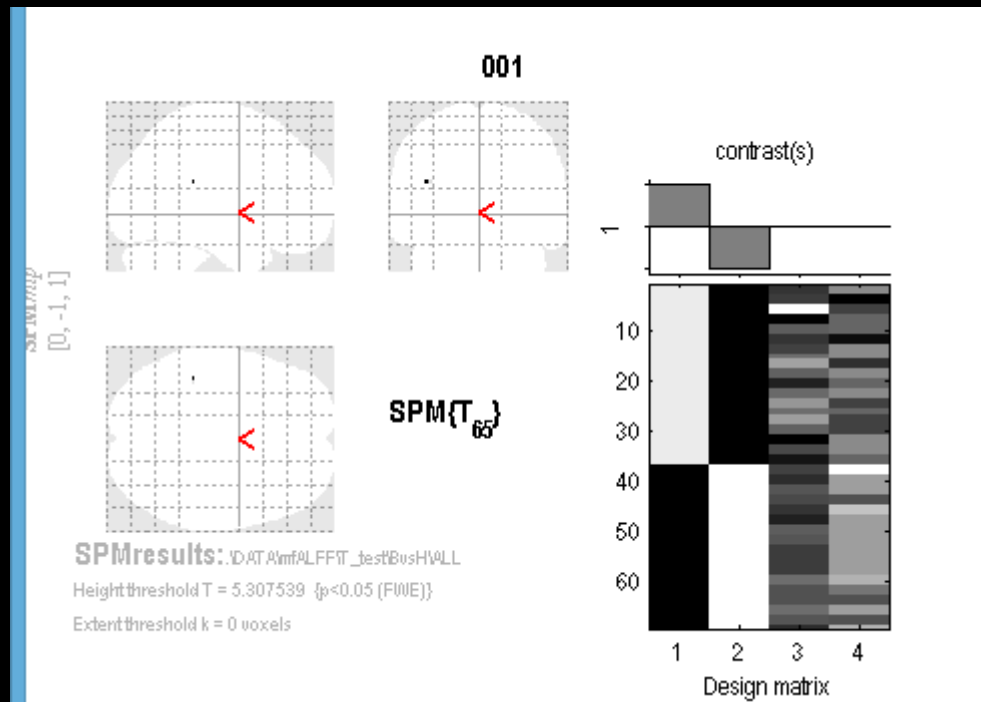
最後權重設為
 [1 -1 0 0] or [-1 1 0 0]



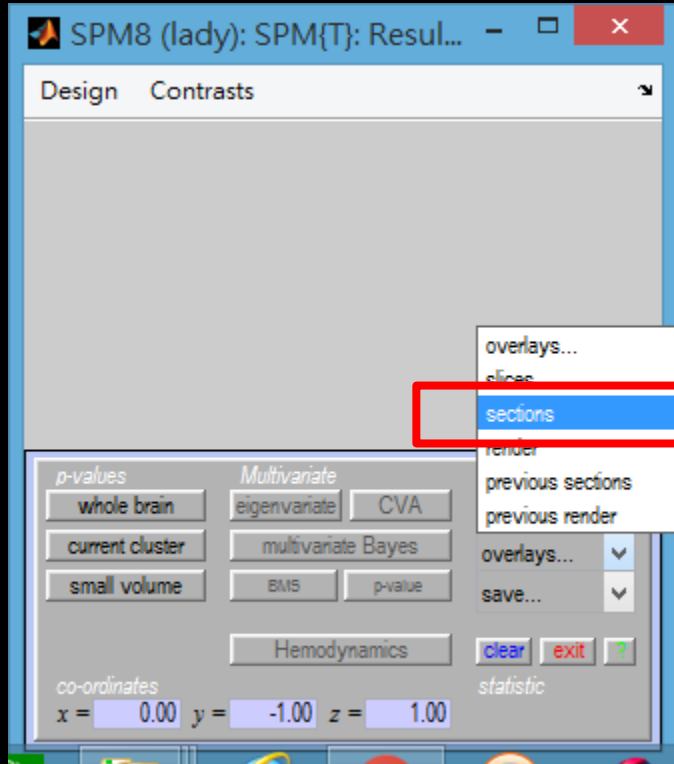
選擇要使用的權重



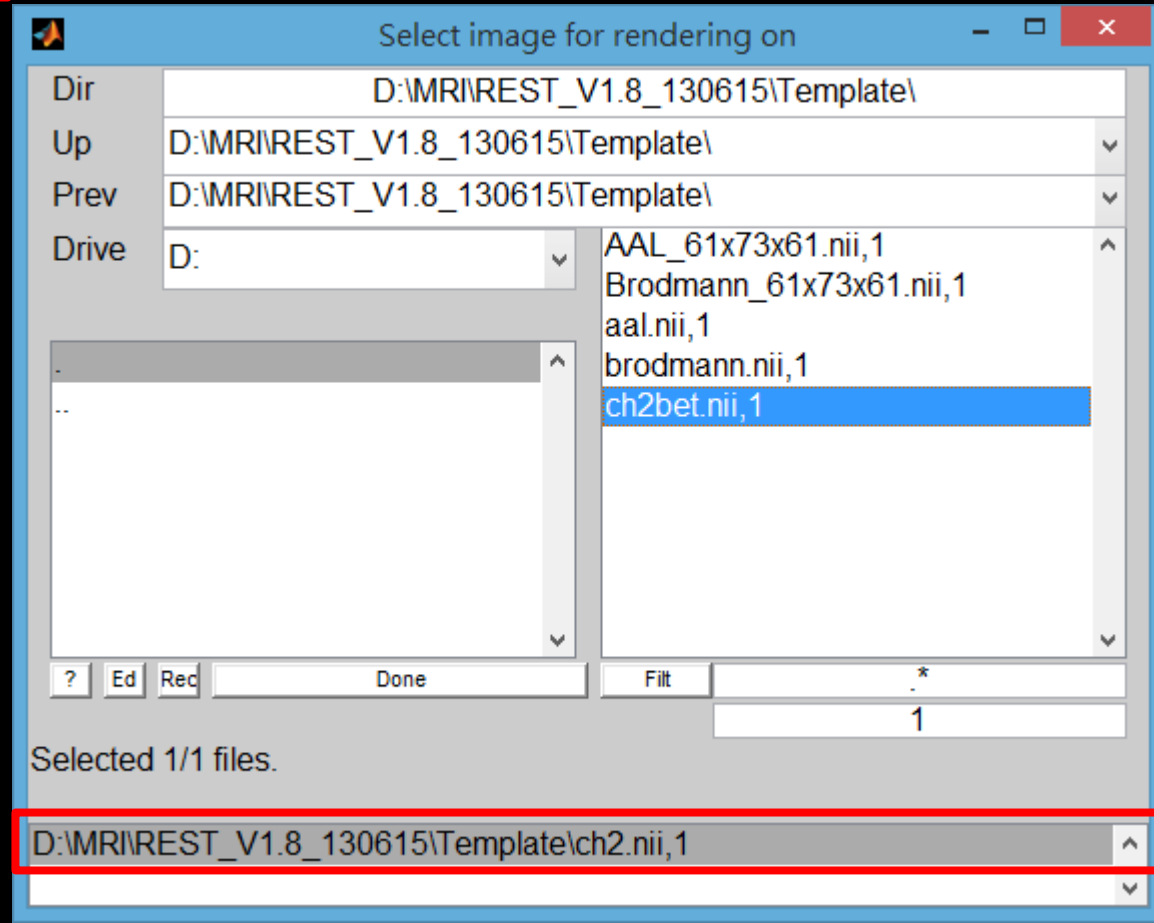




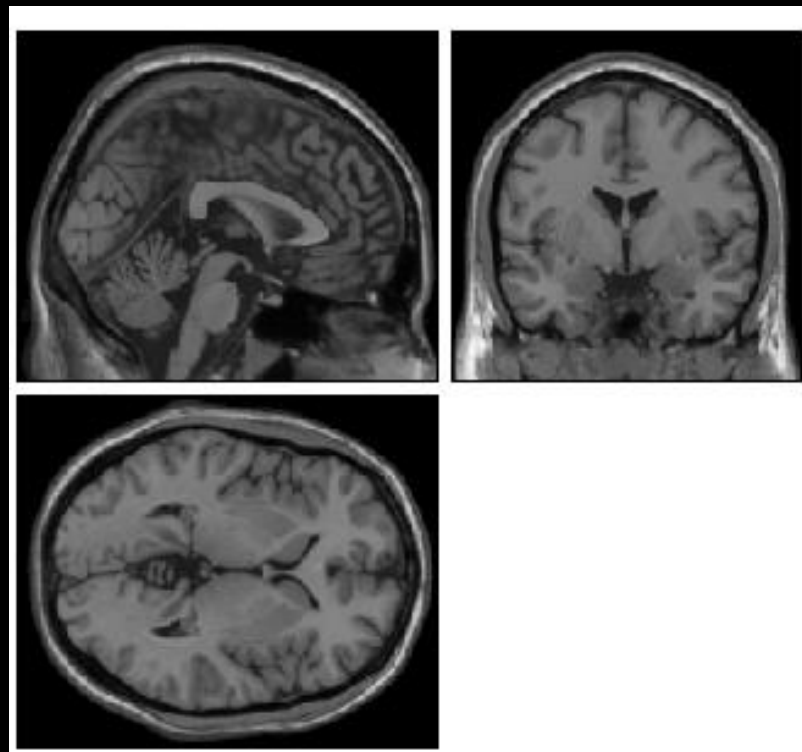
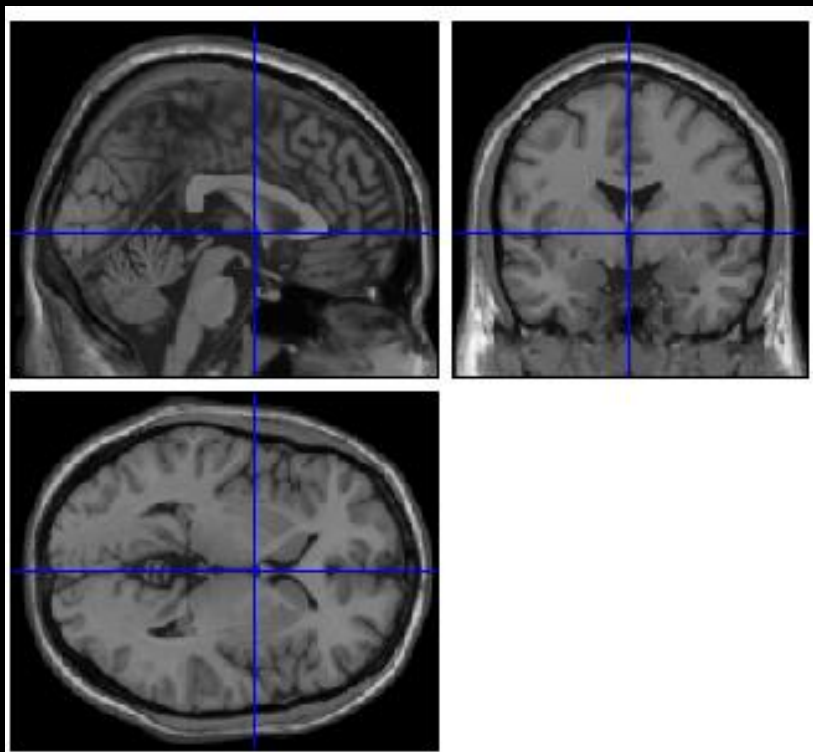
以SPM呈現結果，之後再開
 xjview，對照腦區



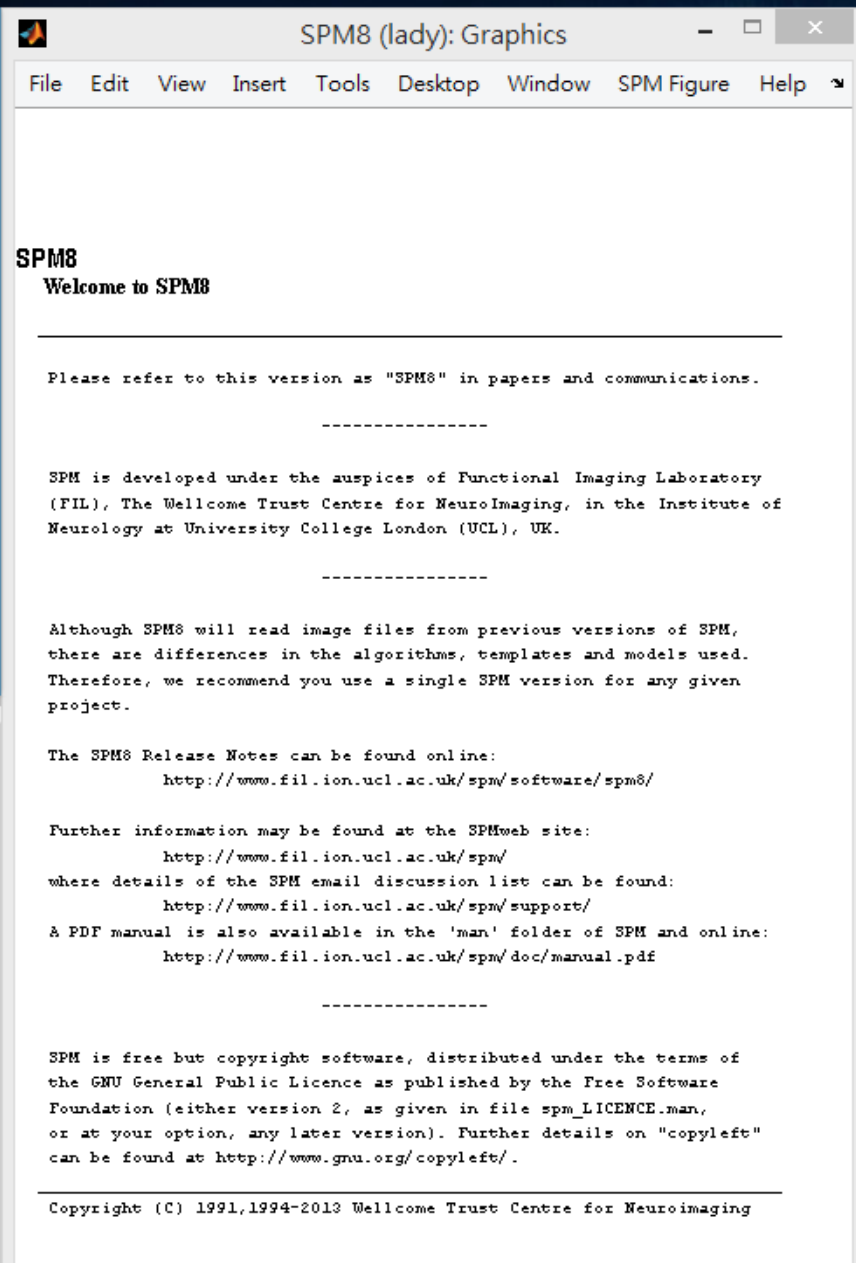
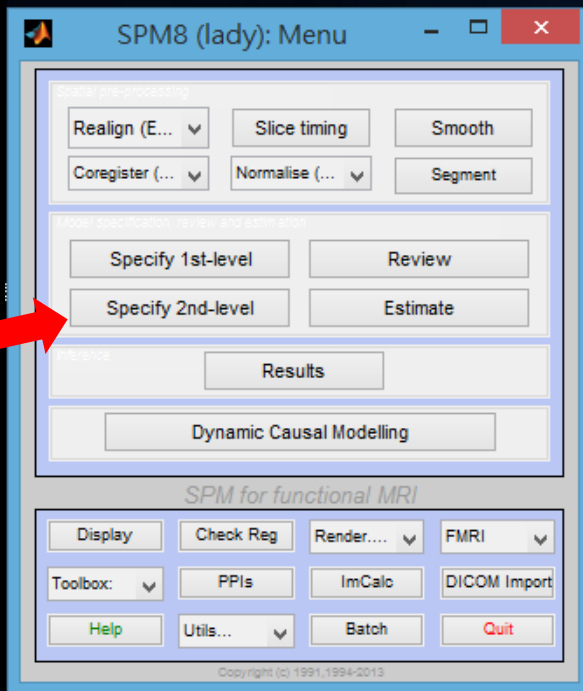
Overlays→sections→
REST→Template→ch2.nii



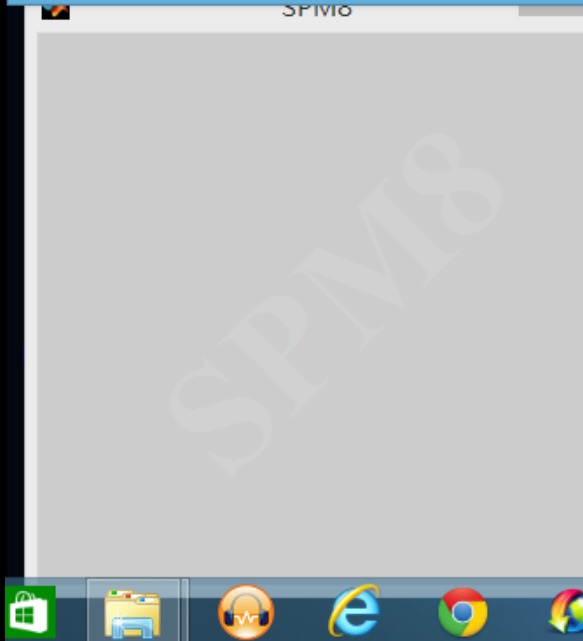
右鍵→crosshair→Off
把十字拿掉



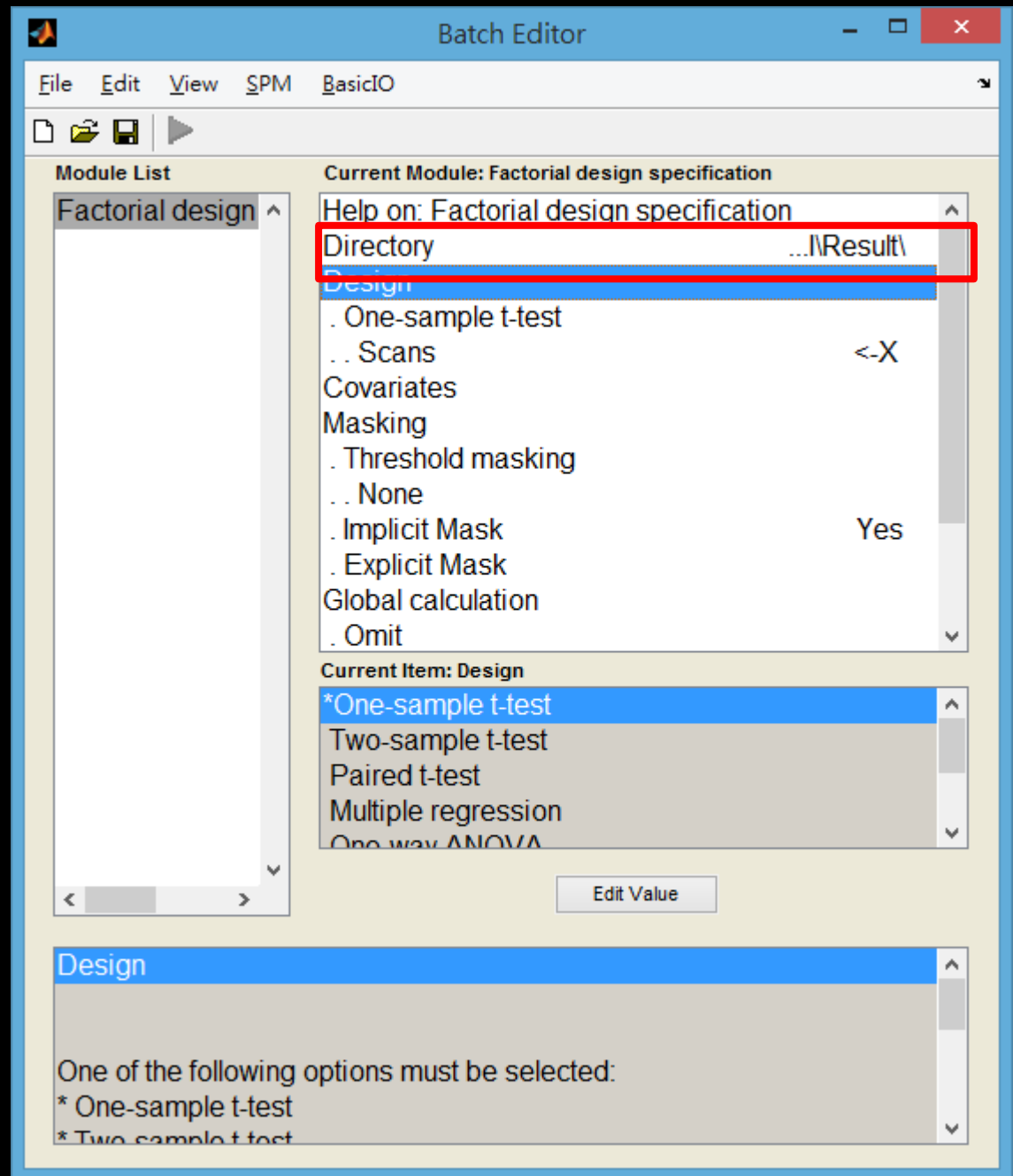
Multiple Regression



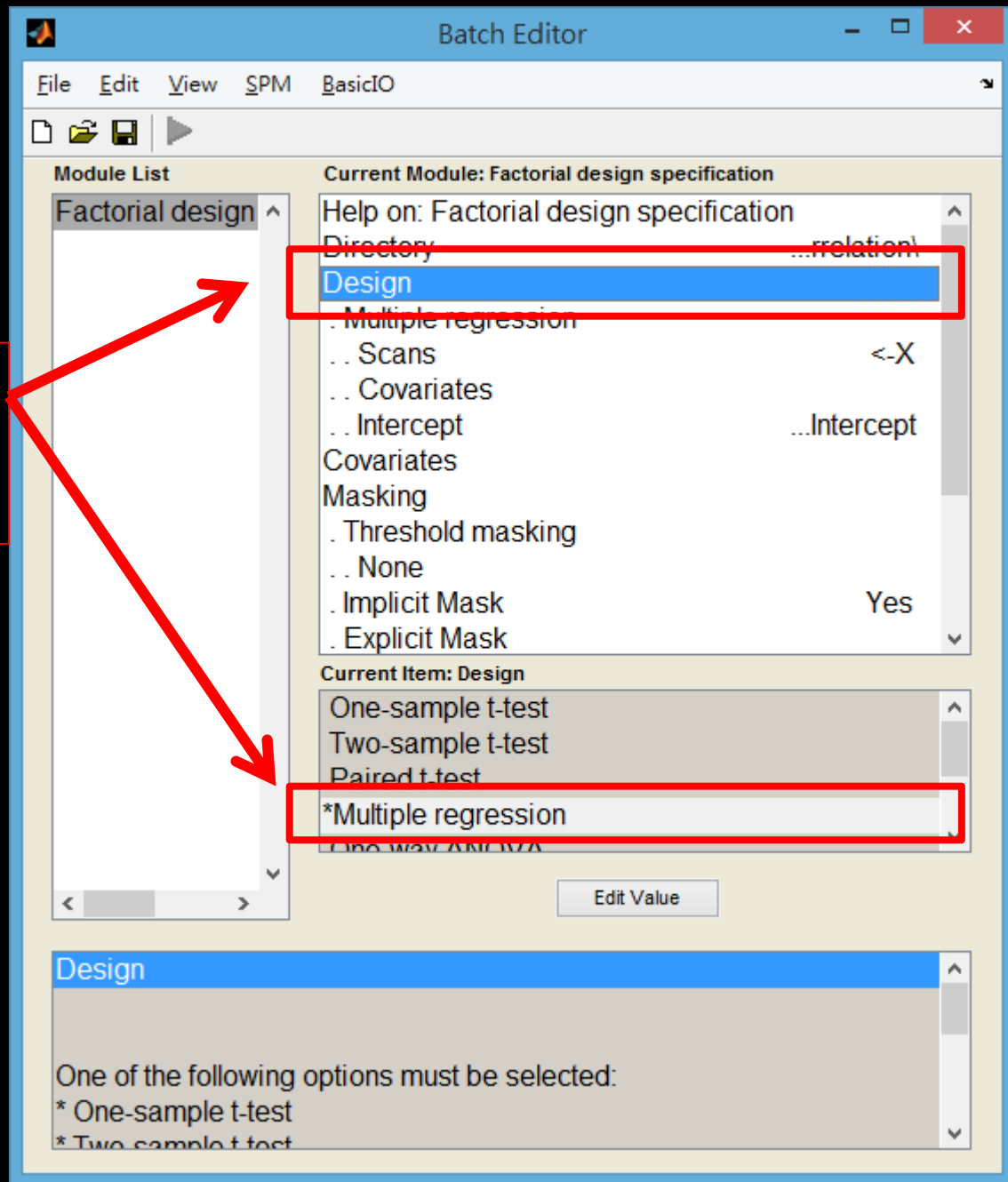
選Specify
2nd-level



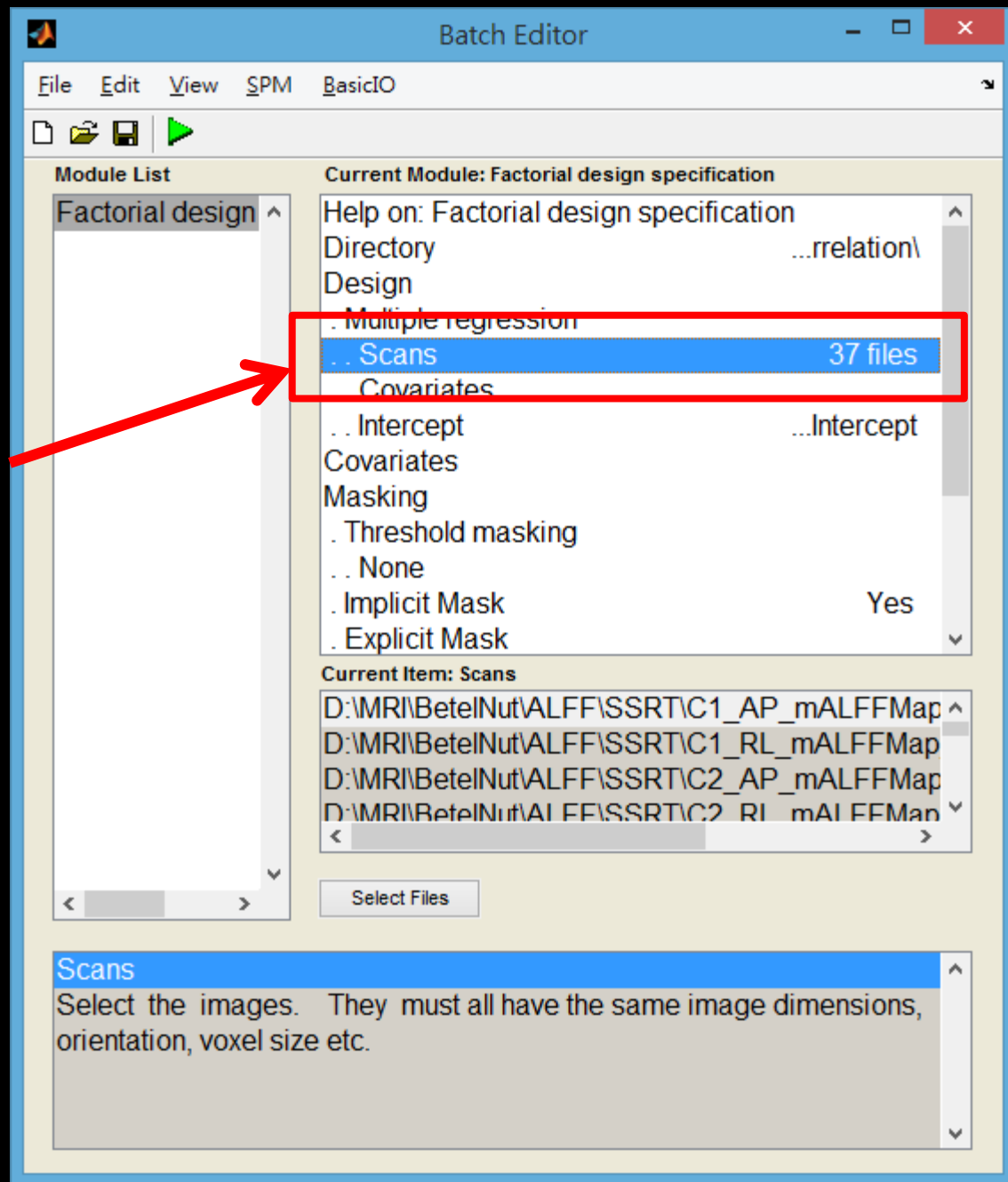
Directory 選擇檔案輸出位置



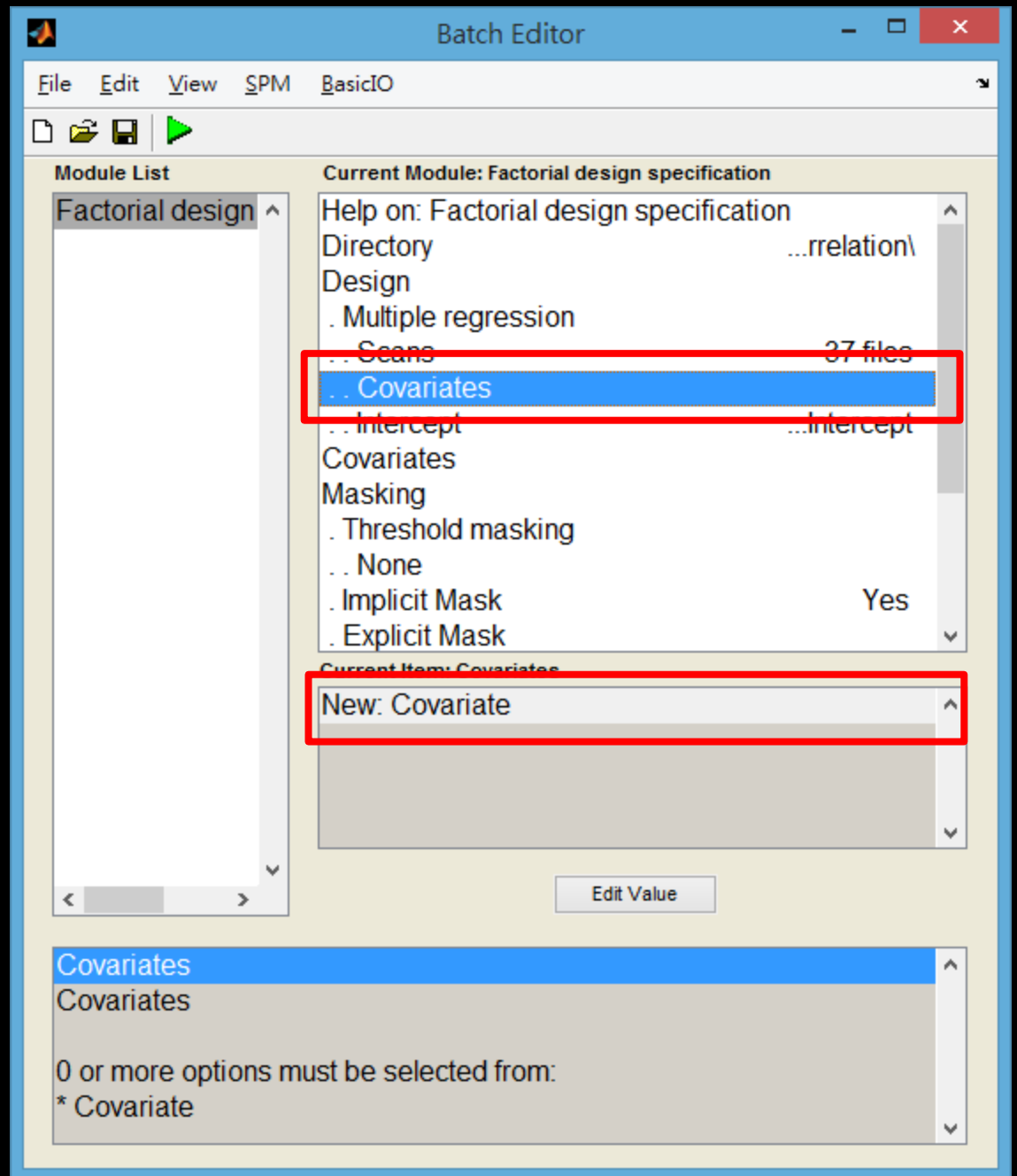
Design去選
Multiple regression

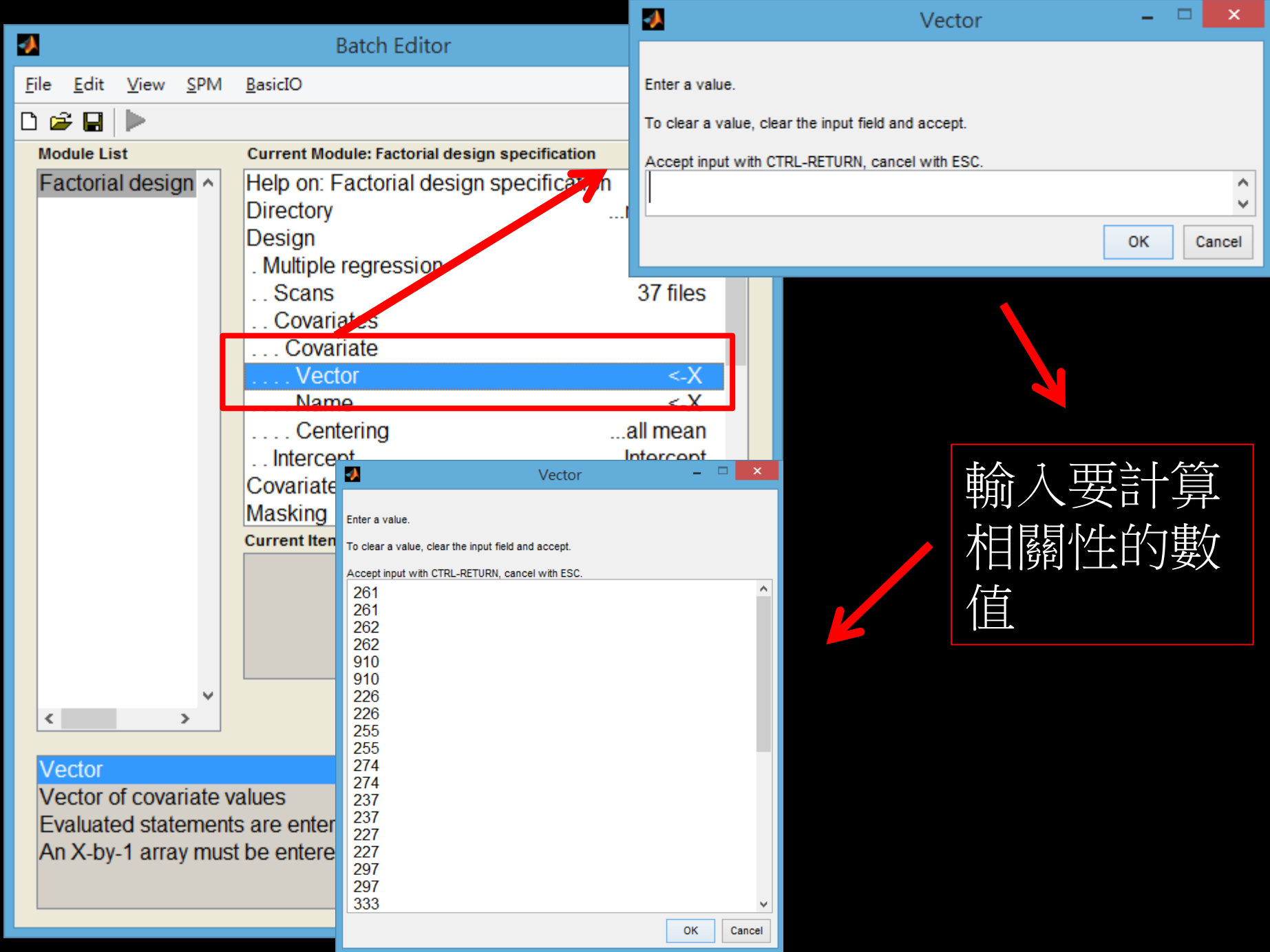


選擇要計算相關性的檔案



點選Covariates
並選New:Covariate





輸入要計算
相關性的數
值

輸入名稱

The screenshot shows the 'Batch Editor' window with the 'Current Module: Factorial design specification' selected. The 'Module List' on the left shows 'Factorial design' expanded. The main panel displays a tree view of the current module's settings. A red box highlights the 'Name' item under the 'Covariate' section, which is currently set to 'SSRT'. Below this, the 'Current Item: Name' section shows the value 'SSRT' in a text field. At the bottom, a detailed description for the 'Name' item is shown: 'Name of covariate', 'A String is entered.', and 'The string must have at least 1 characters.' An 'Edit Value' button is located below the 'Current Item' section.

Batch Editor

File Edit View SPM BasicIO

Module List

Factorial design

Current Module: Factorial design specification

- . Multiple regression
- .. Scans 37 files
- .. Covariates
 - ... Covariate
 - Vector ... 1 double
 - Name SSRT
 - Centering ... all mean
 - .. Intercept ... Intercept
- Covariates
- Masking
 - . Threshold masking
 - .. None
 - . Implicit Mask Yes

Current Item: Name

SSRT

Edit Value

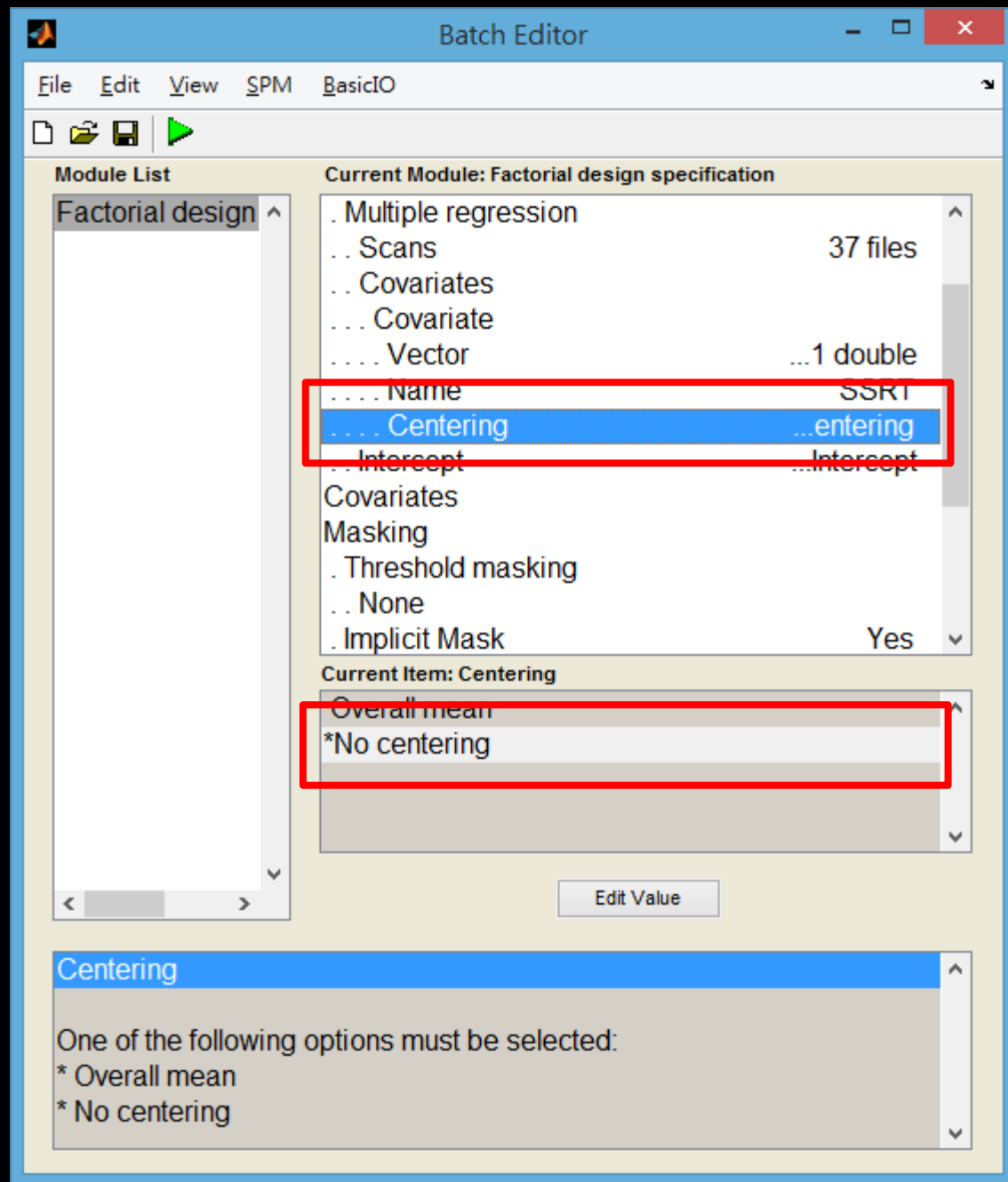
Name

Name of covariate

A String is entered.

The string must have at least 1 characters.

選No centering
才不會做多餘的
計算



點選下面(不包含在
multiple regression裡面)
的Covariates
並選New:Covariate

The screenshot shows the Batch Editor window with the following components:

- Module List:** A list on the left containing "Factorial design".
- Current Module: Factorial design specification:** A large list of parameters on the right. The "Covariates" parameter is highlighted in blue and enclosed in a red box. Below it, a sub-list for "Current Item: Covariates" is also enclosed in a red box, containing "New: Covariate", "Replicate: Covariate (1)", and "Delete: Covariate (1)".
- Buttons:** An "Edit Value" button is located at the bottom right of the parameter list.
- Help Panel:** At the bottom of the window, a help panel for "Covariates" is visible, providing a detailed explanation of the option.

Covariates
This option allows for the specification of covariates and nuisance variables. Unlike SPM94/5/6, where the design was partitioned into effects of interest and nuisance effects for the computation of adjusted data and the F-statistic (which was used to thresh out voxels where there appeared to be no effects of interest), SPM does not partition the

Batch Editor

File Edit View SPM BasicIO

Module List

Current Module: Factorial design specification

- .. Intercept
- Covariates
- .. Covariate
- .. Vector
- .. Name
- .. Interactions
- .. Centering
- .. Covariate
- .. Vector
- .. Name
- .. Interactions
- .. Centering
- Masking

Current Item: Centering

Centering

The appropriate centering option for the interaction chosen, and ensure that the factor aren't affected by the covariate option, unless you have other modules



Vector

Enter a value.

To clear a value, clear the input field and accept.

Accept input with CTRL-RETURN, cancel with ESC.

OK Cancel



輸入要排除
共變數的數
值



Vector

Enter a value.

To clear a value, clear the input field and accept.

Accept input with CTRL-RETURN, cancel with ESC.

261
261
262
262
910
910
226
226
255
255
274
274
237
237
227
227
297
297
333

OK Cancel

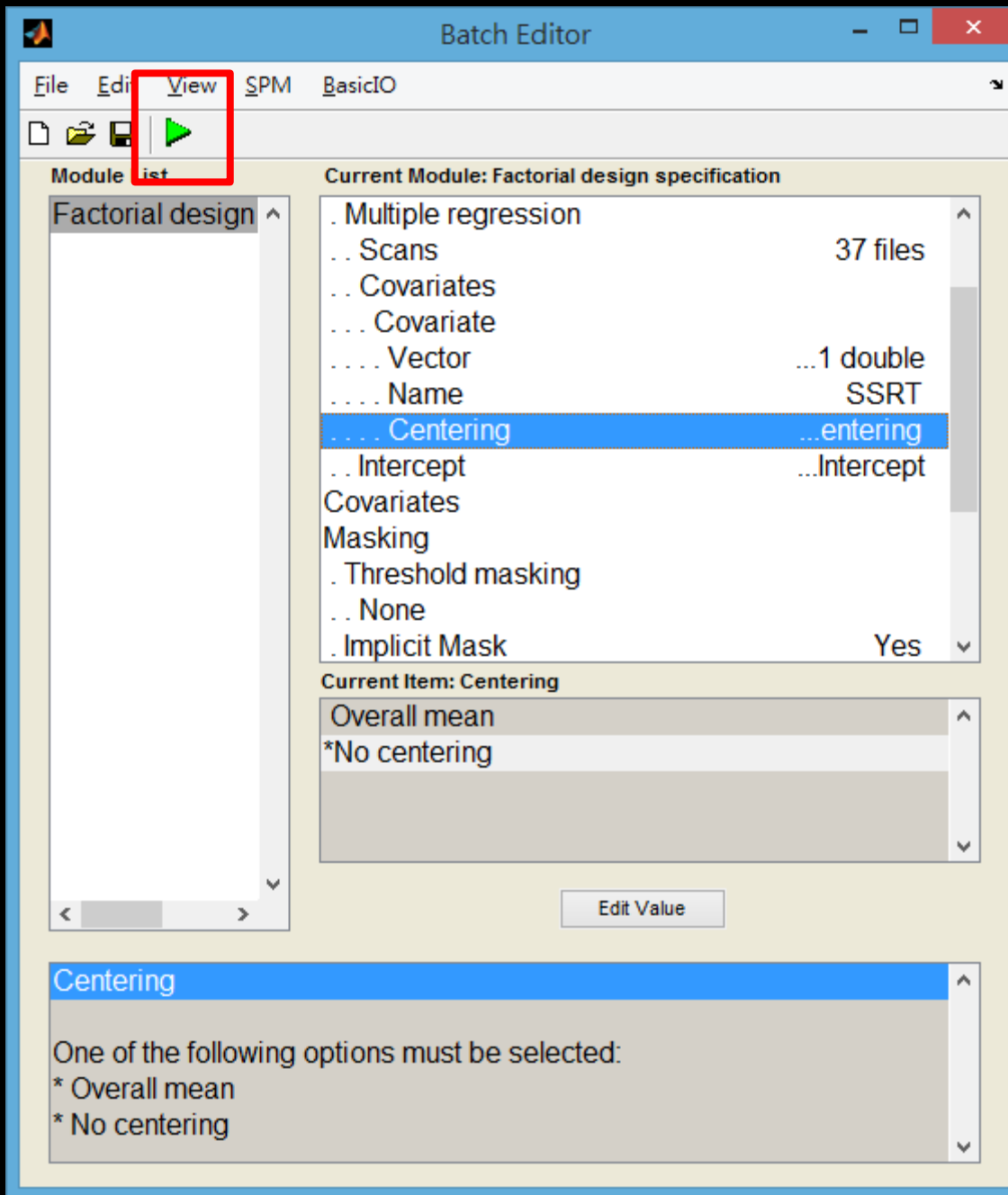
選No centering
才不會做多餘的
計算

The screenshot shows the 'Batch Editor' window with the 'Current Module: Factorial design specification' selected. The 'Module List' on the left shows 'Factorial design' expanded. The main area displays a list of design specifications with the following items highlighted by red boxes:

- .. Interactions: None
- .. Centering: ...entering
- .. Centering: ...entering
- *No centering

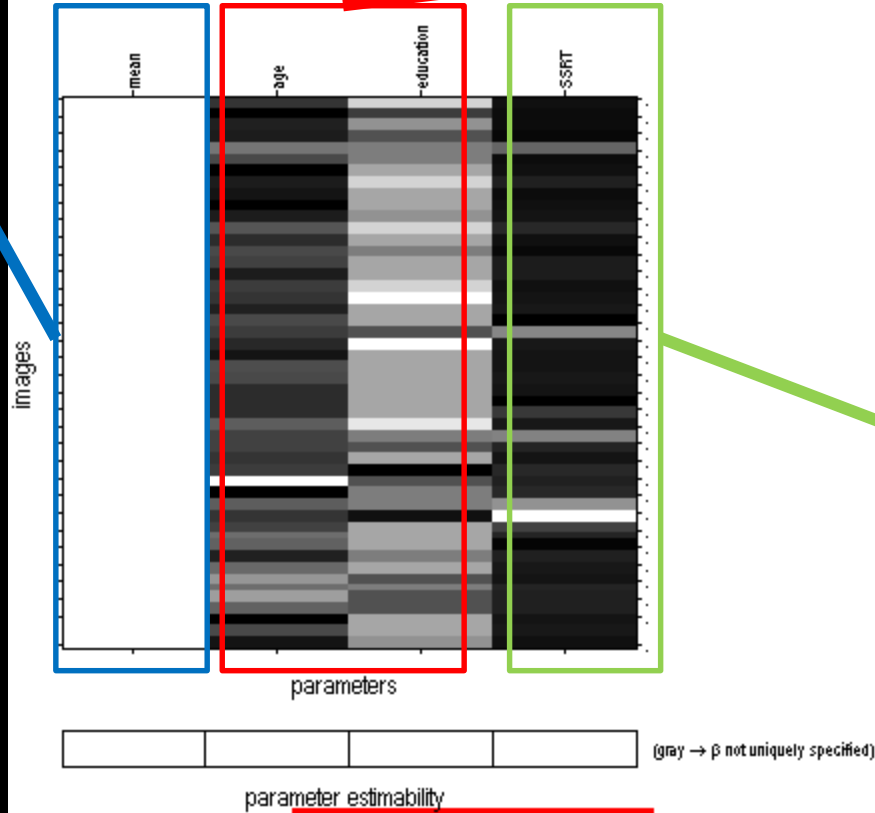
The 'Current Item: Centering' section shows a list of options: Overall mean, Factor 1 mean, Factor 2 mean, Factor 3 mean, and *No centering. The '*No centering' option is selected and highlighted by a red box. An 'Edit Value' button is visible below the list.

Centering
The appropriate centering option is usually the one that corresponds to the interaction chosen, and ensures that main effects of the interacting factor aren't affected by the covariate. You are advised to choose this option, unless you have other modelling considerations.



Statistical analysis: Design

影像平均

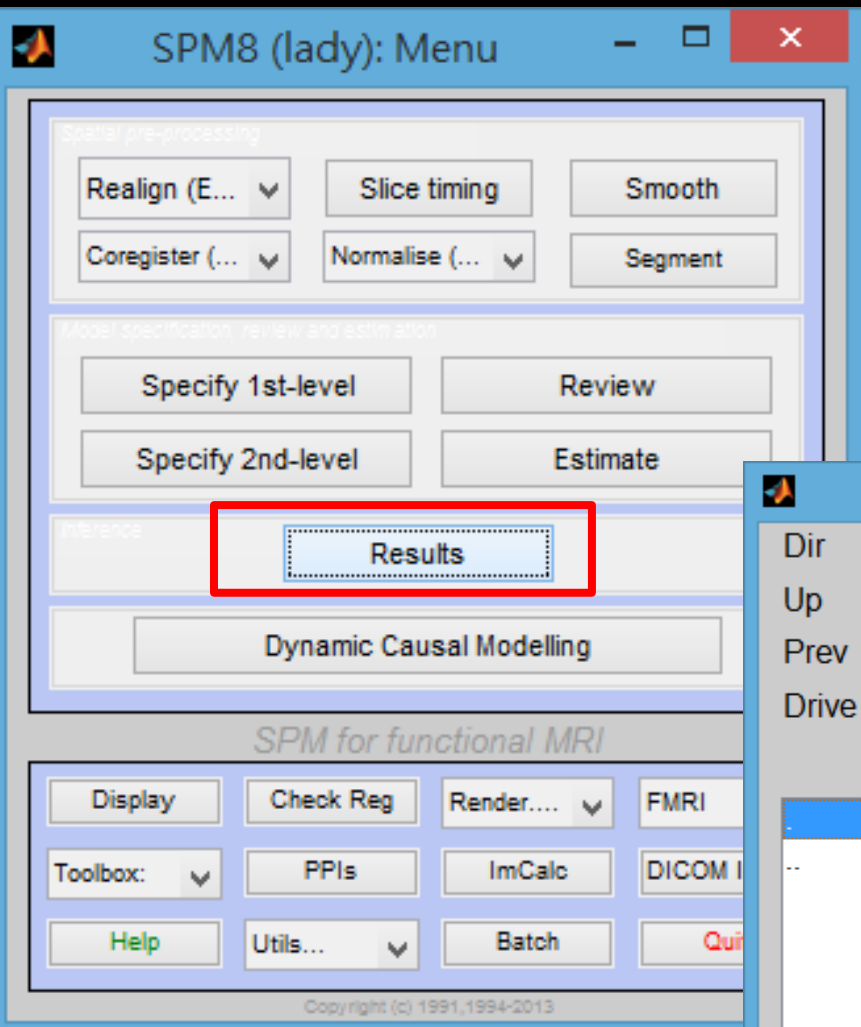


排除的
共變數

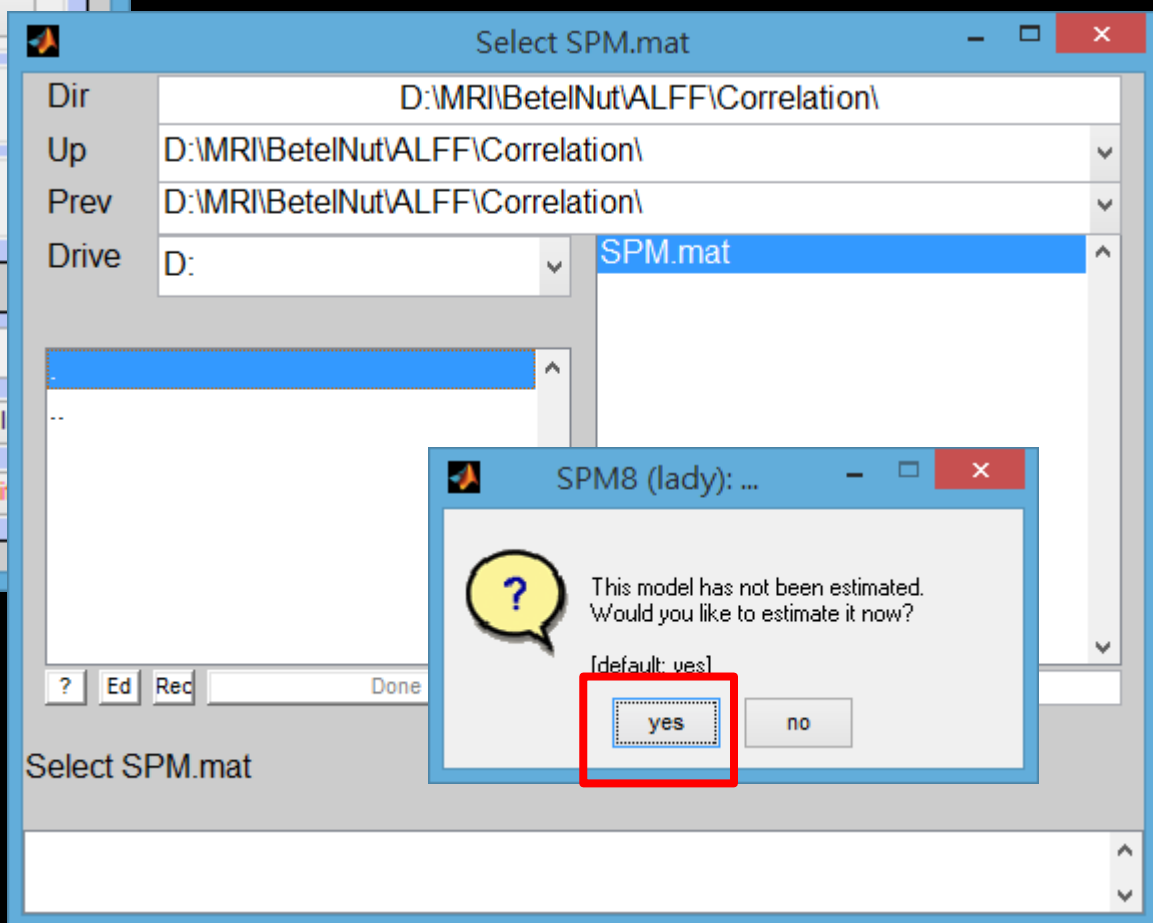
量表或認知
分數等

Design description...

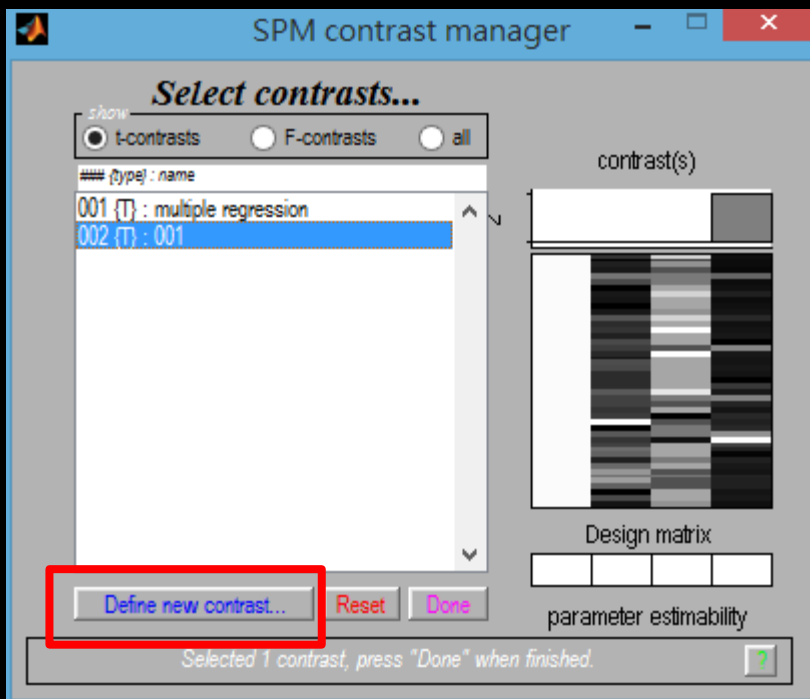
- Design** : Multiple regression
- Global calculation** : omit
- Grand mean scaling** : <no grand Mean scaling>
- Global normalisation** : <no global normalisation>
- Parameters** : 1 condition, +3 covariate, +0 block, +0 nuisance
4 total, having 4 degrees of freedom
leaving 92 degrees of freedom from 96 images



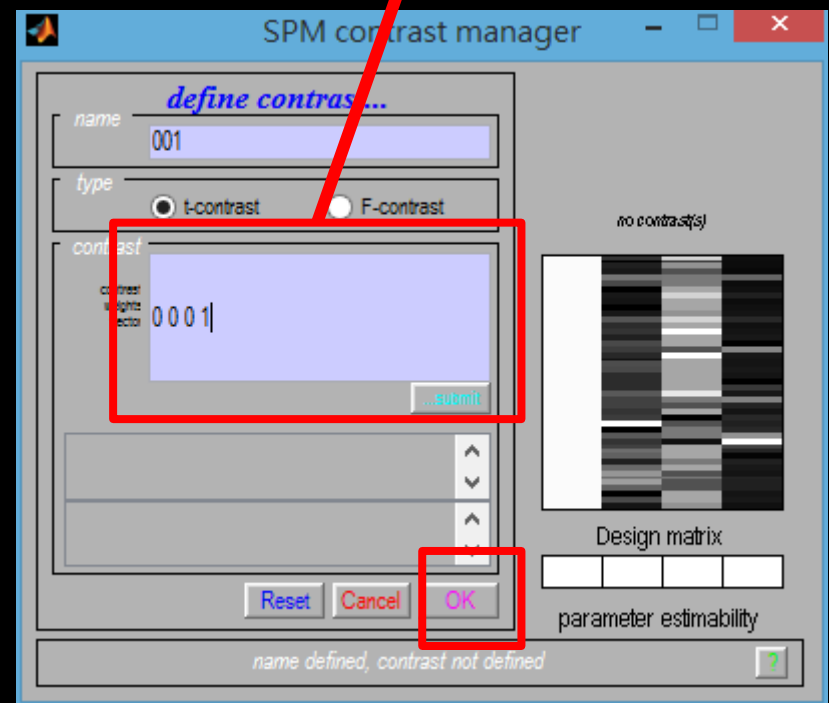
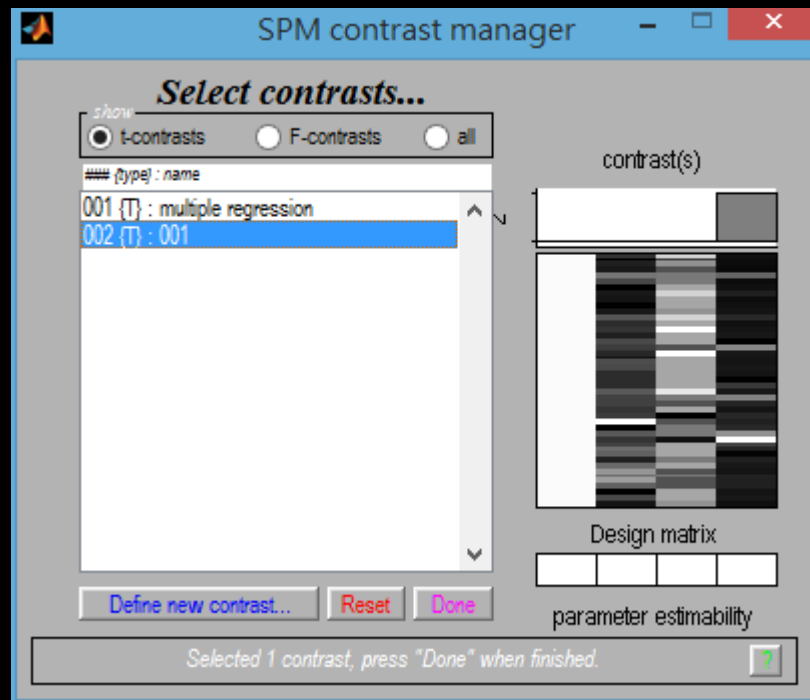
選擇前面計算出來的檔案

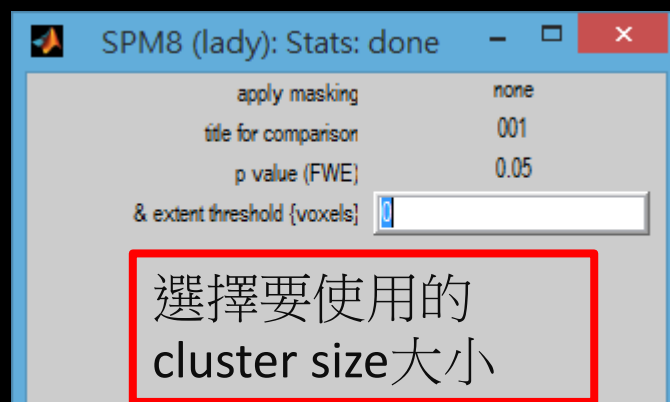
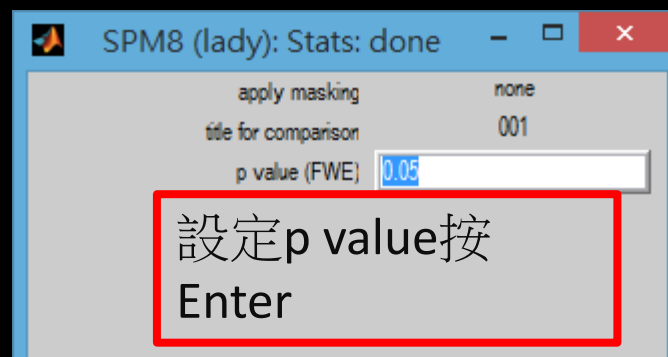
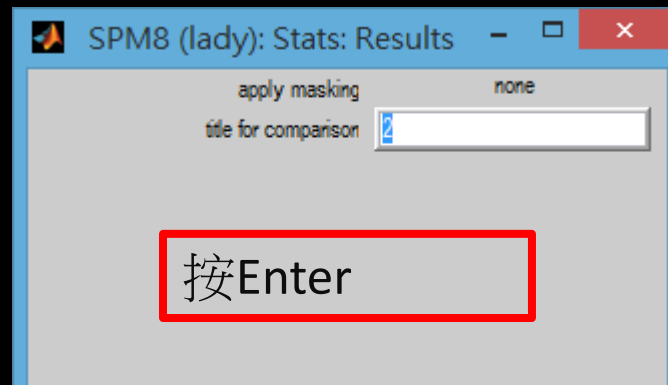
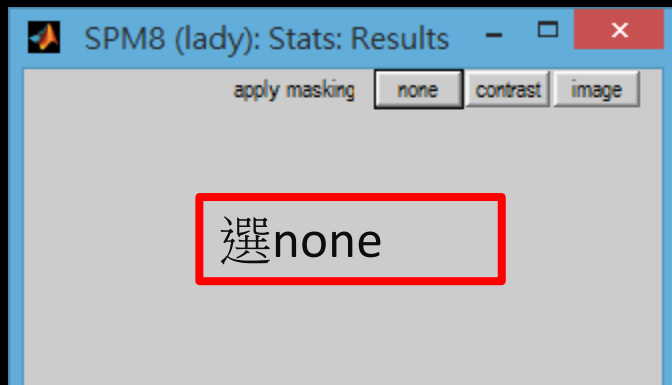


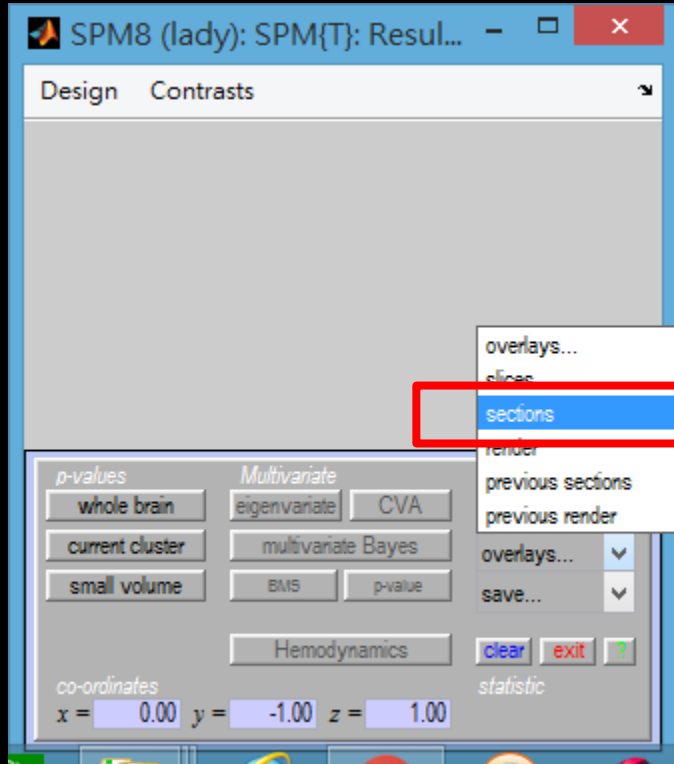
選擇Result



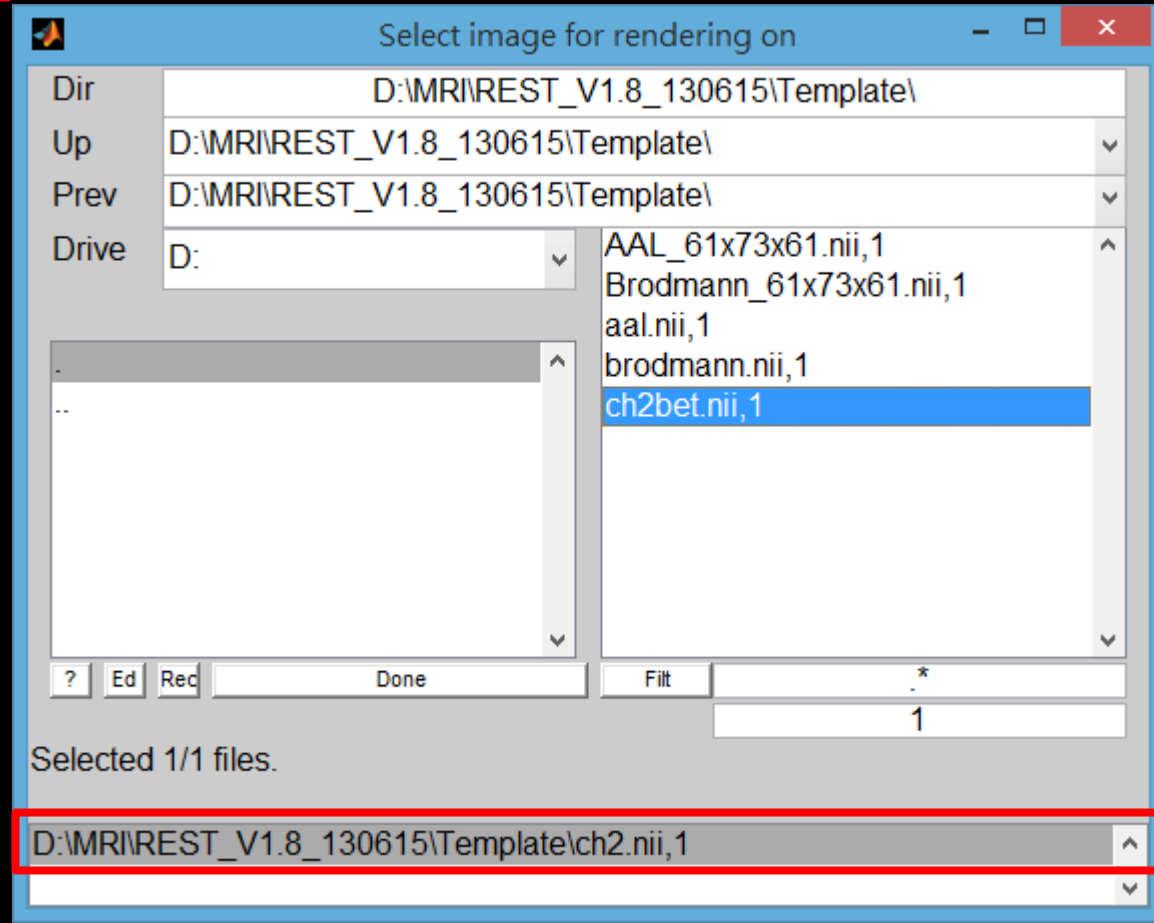
Contrast輸入[0 0 0 1]
可同時看到正相關及負相關
把我們要排除的
covariate 權重設0，量表
分數的權重輸入1



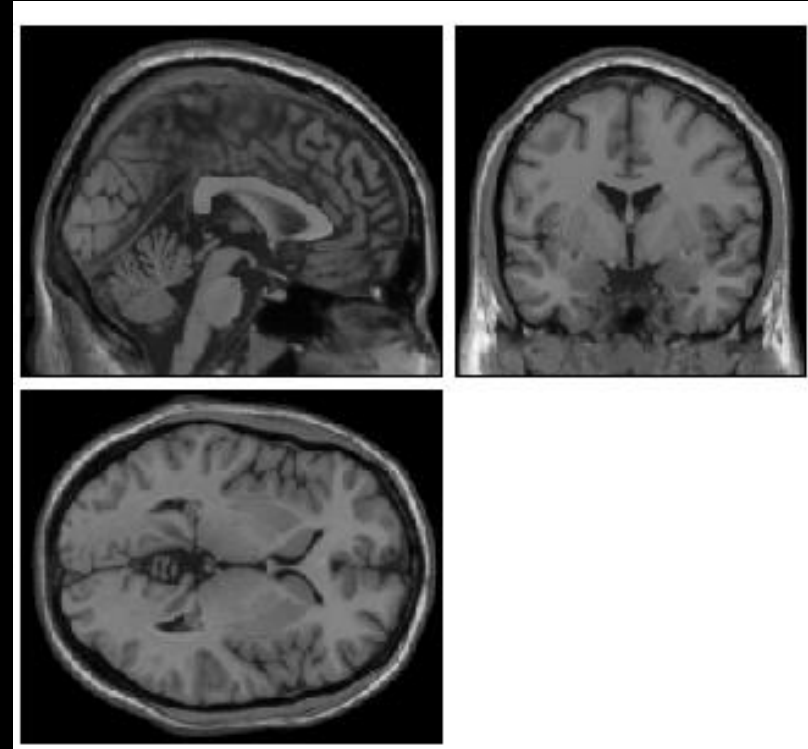
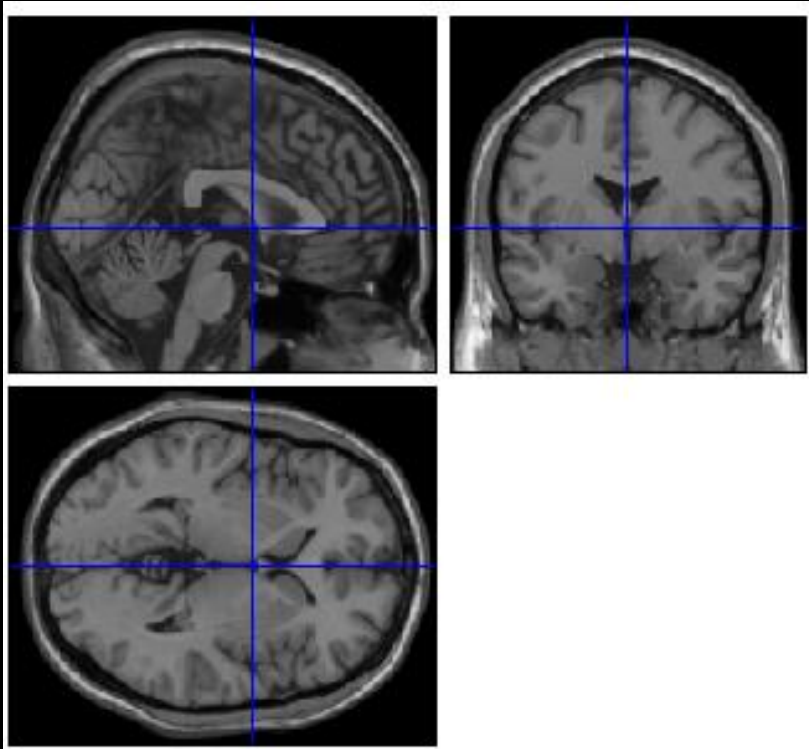




Overlays→sections→
REST→Template→ch2.nii



右鍵→crosshair→Off
把十字拿掉



如果沒結果就用xjview
FDR校正p value