

Analysis of Functional Magnetic Resonance Imaging (fMRI) Brain Activation – General Linear Model I

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Teaching Materials

- http://www.ym.edu.tw/~cflu/CFLu_course_fMRIana.html

- **Week 7: Brain Activation – General Linear Model I**

<Handout> [Lesson7_slides.pdf](#)

<Materials> [fMRIana07_materials.zip](#)

- **The same fMRI data in Week 6**

<Materials> [fMRIana06_materials.zip](#)

Employed Software

- MRICro

- <https://people.cas.sc.edu/rorden/mricro/mricro.html#Installation>
- <https://www.mccauslandcenter.sc.edu/crnl/mricro>

- Statistical Parametric Mapping (SPM 12)

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

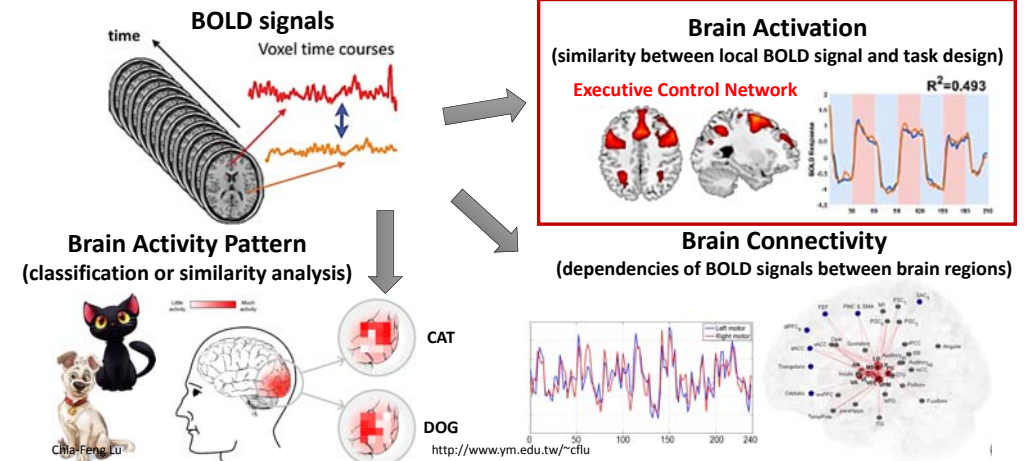


- xjView (A viewing program for SPM)

- <http://www.alivelearn.net/xjview/download/>

[Caution] File name\path contains Chinese character or space may cause error!

fMRI Analysis

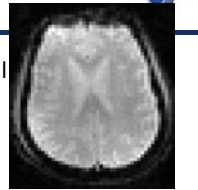


Parameter Setup of SPM Batch

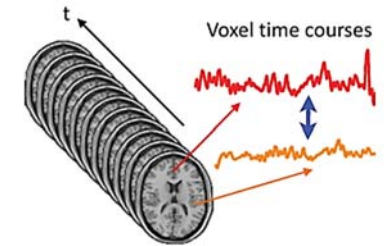
fMRI Preprocessing

fMRI Protocol

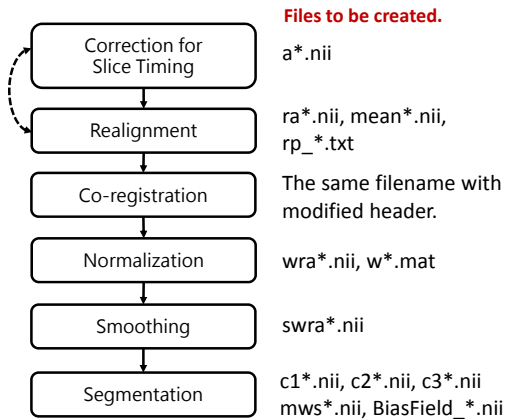
- Siemens 3T MAGNETOM Trio Scanner @ NYMU, 32-channel head coil
- Single-Shot 2D EPI (GRE-EPI), T2* weighting
- Repetition Time = 2000 ms
- Echo Time = 20 ms
- Flip Angle = 70~90°
- NEX = 1
- Slice thickness = 3.4 mm
- Field of View = 220 x 220 mm²
- Matrix size = 64 x 64
- Slice number = 40
- Volume number (**depends on experiment design**)



3.44 x 3.44 x 3.40 mm³



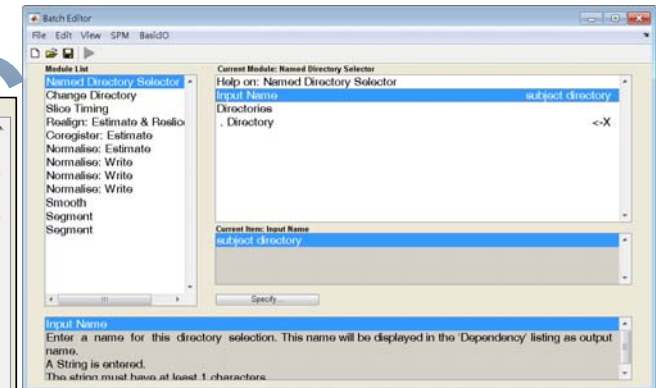
Preprocessing Procedure



Batch of SPM fMRI preprocessing

>> spm_fmri → Batch
Batch_fmriprep.mat

Module List	
Named Directory Selector	<-X
Change Directory	DEP
Slice Timing	<-X
Realign: Estimate & Reslice	DEP
Coregister: Estimate	<-X
Normalise: Estimate	DEP
Normalise: Write	DEP
Normalise: Write	DEP
Normalise: Write	DEP
Smooth	DEP
Segment	DEP
Segment	DEP



Please select the proper file path of SPM Tissue Probability Map (TPM.nii) before running batch.

Correction for Slice Timing

Module List

- Named Directory Selector <-X
- Change Directory DEP
- Slice Timing <-X
- Realign: Estimate & Reslice DEP
- Coregister: Estimate <-X
- Normalise: Estimate DEP
- Normalise: Write DEP
- Normalise: Write DEP
- Normalise: Write DEP
- Smooth DEP
- Segment DEP
- Segment DEP

Current Module: Slice Timing

Help on: Slice Timing

Data

- . Session <-X
- Number of Slices 40
- TR 2
- TA 1.95
- Slice order 1x40 double
- Reference Slice 1
- Filename Prefix a

Slice order:

2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40

1 3 5 7 9 11 13 15 17 19 21 23 25 27 29 31 33 35 37 39

Information Panel: Slice Timing
Correct differences in image acquisition time between slices.
Slice-time corrected files are prepended with an 'a'.

Realignment of head motion

Module List

- Named Directory Selector <-X
- Change Directory DEP
- Slice Timing <-X
- Realign: Estimate & Reslice DEP
- Coregister: Estimate <-X
- Normalise: Estimate DEP
- Normalise: Write DEP
- Normalise: Write DEP
- Normalise: Write DEP
- Smooth DEP
- Segment DEP
- Segment DEP

Current Module: Realign: Estimate & Reslice

Help on: Realign: Estimate & Reslice

Data

- . Session ...ing Corr. Images (Sess 1)

Estimation Options Data dependency

- . Quality 0.9
- . Separation 4
- . Smoothing (FWHM) 5
- . Num Passes Register to mean
- . Interpolation 2nd Degree B-Spline
- . Wrapping No wrap
- . Weighting

Reslice Options All Images + Mean Image

- . Interpolation 4th Degree B-Spline
- . Wrapping No wrap
- . Masking Mask images
- . Filename Prefix r

Realign: Estimate & Reslice
Realign a time-series of images acquired from the same subject using a least squares approach and a 6 parameter (rigid body) spatial transformation.

Co-registration

- Align structural (T1W) images to fMRI (EPI) data.

Module List

- Named Directory Selector <-X
- Change Directory DEP
- Slice Timing <-X
- Realign: Estimate & Reslice DEP
- Coregister: Estimate <-X
- Normalise: Estimate DEP
- Normalise: Write DEP
- Normalise: Write DEP
- Normalise: Write DEP
- Smooth DEP
- Segment DEP
- Segment DEP

Current Module: Coregister: Estimate

Help on: Coregister: Estimate

- Reference Image DEP Realign: Estimate & Reslice: Mean Image
- Source Image <-X
- Other Images

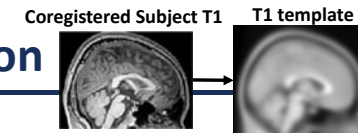
Estimation Options

- . Objective Function Normalised Mutual Information
- . Separation [4 2]
- . Tolerances 1x12 double
- . Histogram Smoothing [7 7]

X1 = -0.000*X -0.006*Y -0.291*Z +62.039
Y1 = -0.290*X +0.025*Y -0.000*Z +61.678
Z1 = 0.025*X +0.293*Y -0.006*Z -31.516

To acquire the transformation matrix for image co-registration.

Spatial Normalization



Module List

- Named Directory Selector <-X
- Change Directory DEP
- Slice Timing <-X
- Realign: Estimate & Reslice DEP
- Coregister: Estimate <-X
- Normalise: Estimate DEP
- Normalise: Write DEP
- Normalise: Write DEP
- Normalise: Write DEP
- Smooth DEP
- Segment DEP
- Segment DEP

Current Module: Normalise: Estimate

Help on: Normalise: Estimate

Data

- . Subject
- . Image to Align DEP Coregister: Estimate: Coregistered Images

Estimation Options

- . Bias regularisation very light regularisation (0.0001)
- . Bias FWHM 60mm cutoff
- . Tissue probability map D:\softwares\spm12\spm12\tpm\TPM.nii
- . Affine Regularisation ICBM space template - East Asian brains
- . Warping Regularisation 1x5 double
- . Smoothness 0
- . Sampling distance 3

To acquire the transformation matrix for spatial normalization.

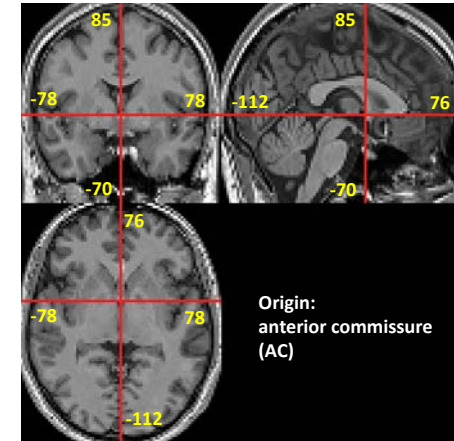
Spatial Normalization

Apply the estimated transformation matrix to fMRI and coregistered T1W.

Module List		Current Module: Normalise: Write	
Named Directory Selector	<-X	Help on: Normalise: Write	
Change Directory	DEP	Data	
Slice Timing	<-X	. Subject	
Realign: Estimate & Reslice	DEP	. . Deformation Field	DEP Normalise: Estimate: Deformation (Subj 1)
Coregister: Estimate	<-X	. . Images to Write	DEP Coregister: Estimate: Coregistered Images
Normalise: Estimate	DEP	Writing Options	
Normalise: Write	DEP	. Bounding box	2x3 double
Normalise: Write	DEP	. Voxel sizes	[2 2 2]
Normalise: Write	DEP	. Interpolation	4th Degree B-Spline
Smooth	DEP	. Filename Prefix	w
Segment	DEP		
Segment	DEP		

Spatial Normalization

- **Bounding Box (in mm)**
[-78 -112 -70
78 76 85]
- **Voxel sizes [2 2 2] (in mm)**



Gaussian Spatial Smoothing

- Each voxel becomes weighted average of surrounding voxels.


Module List		Current Module: Smooth	
Named Directory Selector	<-X	Help on: Smooth	
Change Directory	DEP	Images to smooth	DEP (2 outputs)
Slice Timing	<-X	FWHM	[8 8 8]
Realign: Estimate & Reslice	DEP	Data Type	SAME
Coregister: Estimate	<-X	Implicit masking	No
Normalise: Estimate	DEP	Filename prefix	s
Normalise: Write	DEP		
Normalise: Write	DEP		
Normalise: Write	DEP		
Smooth	DEP		
Segment	DEP		
Segment	DEP		

Full width at half maximum (FWHM) of the Gaussian smoothing kernel in mm.


Tissue Segmentation

Module List		Current Module: Segment	
Named Directory Selector	<-X	Help on: Segment	
Change Directory	DEP	Data	
Slice Timing	<-X	. Channel	
Realign: Estimate & Reslice	DEP	. . Volumes	DEP Normalise: Write: Normalised Images (Subj 1)
Coregister: Estimate	<-X	. . Bias regularisation	light regularisation (0.001)
Normalise: Estimate	DEP	. . Bias FWHM	60mm cutoff
Normalise: Write	DEP	. . Save Bias Corrected	Save Field and Corrected
Normalise: Write	DEP	Tissues	
Normalise: Write	DEP	. Tissue	
Smooth	DEP	. . Tissue probability map	D:\softwares\spm12\spm12\tpm\TPM.nii,1
Segment	DEP	. . Num. Gaussians	1
Segment	DEP	. . Native Tissue	Native Space
		. . Warped Tissue	None
		. Tissue	
		. . Tissue probability map	D:\softwares\spm12\spm12\tpm\TPM.nii,2
		. . Num. Gaussians	1
		. . Native Tissue	Native Space
		. . Warped Tissue	None
		. Tissue	


GM map
(c1*.nii)



WM map
(c2*.nii)

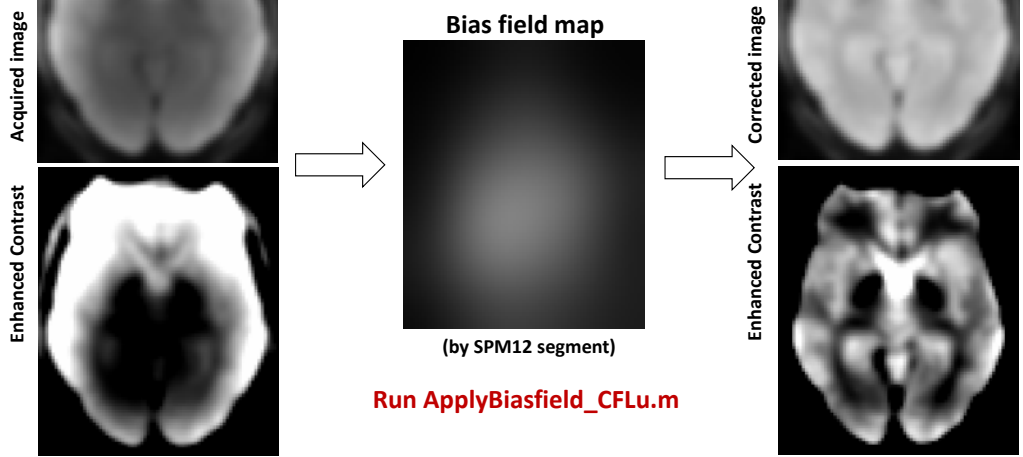


CSF map
(c3*.nii)



Bias Field Correction

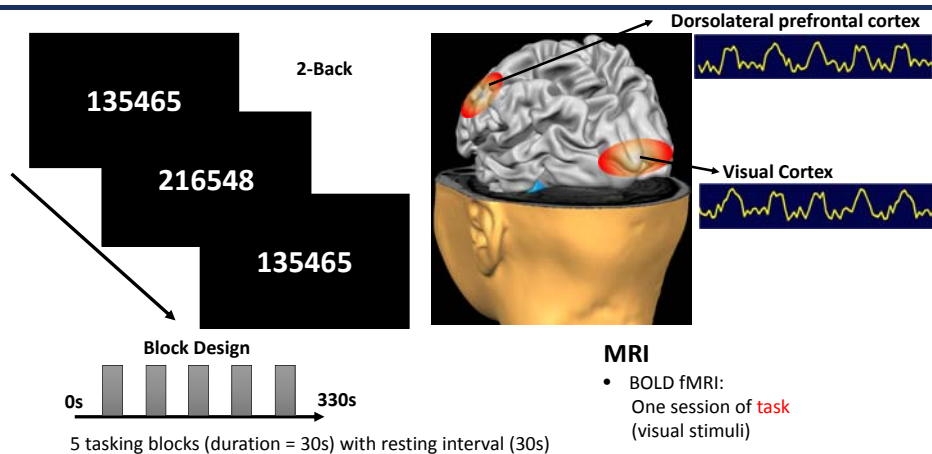
NYMU_32ch_EPI_BOLD



General Linear Model

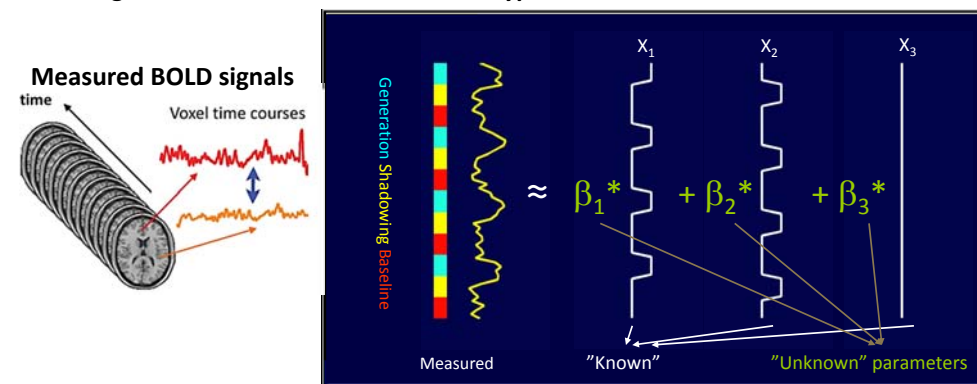
Introduction and Model Construction

N-Back fMRI Data Acquisition



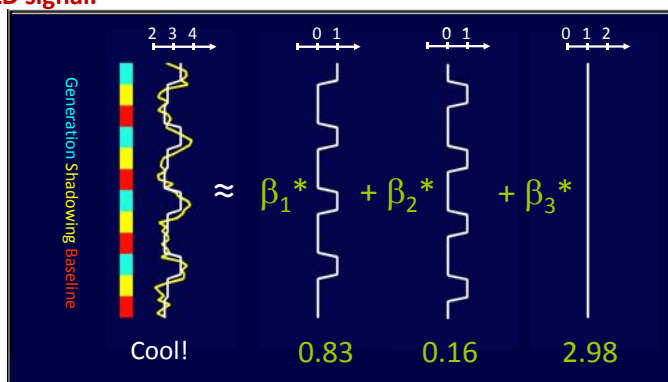
The Model of GLM

Finding the linear combination of these hypothetical time series "best" fits the data.



Parameter Estimation

Beta value represents the association between a condition design and the measured BOLD signal.

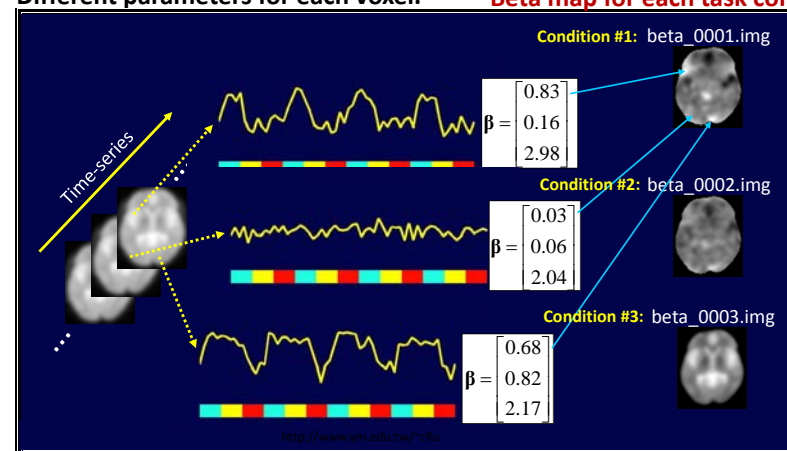


Parameter Estimation

Same model for all voxels.

Different parameters for each voxel.

Beta map for each task condition



Specify 1st-level Model

SPM12 (7219): Menu

Current Module: fMRI model specification

Help on: fMRI model specification

Directory <-X

Timing parameters <-X

- . Units for design <-X
- . Interscan interval <-X
- . Microtime resolution 16
- . Microtime onset 8

Data & Design <-X

Factorial design

Basis Functions

- . Canonical HRF
- . . Model derivatives No derivatives

Model Interactions (Volterra) ...model Interactions

Global normalisation None

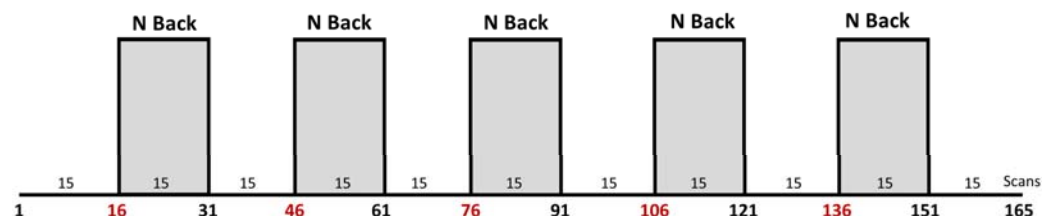
Masking threshold 0.8

Explicit mask

Serial correlations AR(1)

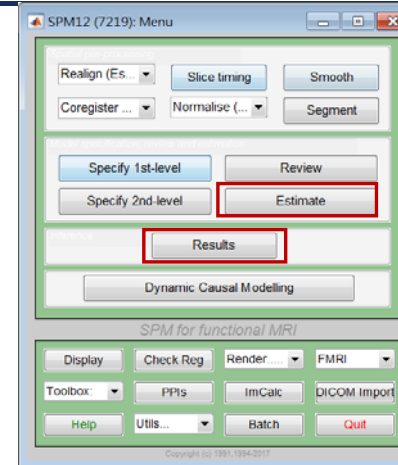
Specify 1st-level Model

- Units for design = Scans
- Interscan interval = 2
- Microtime resolution = 40 (Slice number)
- Microtime onset = 1 (Reference Slice)
- Condition
 - Name = N-Back
 - Onsets = [16 46 76 106 136]
 - Durations = 15
- Multiple regressors (rp_*.txt)



Load Nback_model.mat

Estimate Model

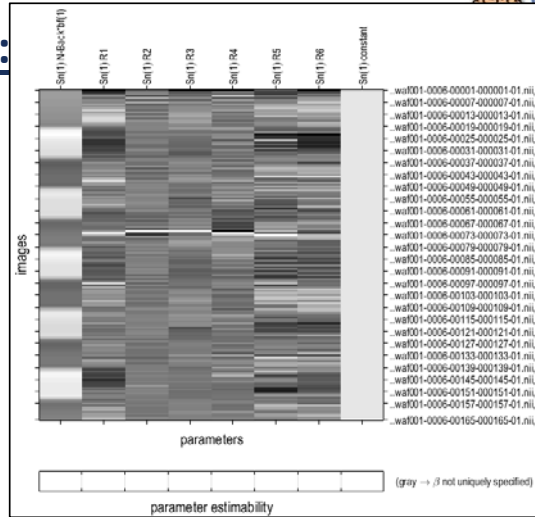


Current Module: Model estimation
 Help on: Model estimation
 Select SPM.mat ...process\2BACK\SPM.mat
 Write residuals No
 Method
 . Classical

http://www.ym.edu.tw/~cfu

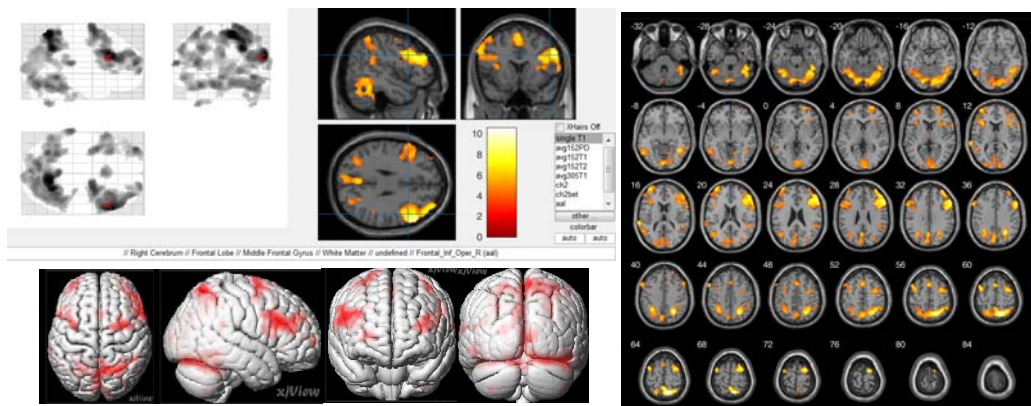
Statistical Analysis: Design

Taking the 2-Back as an example.



http://www.ym.edu.tw/~cfu

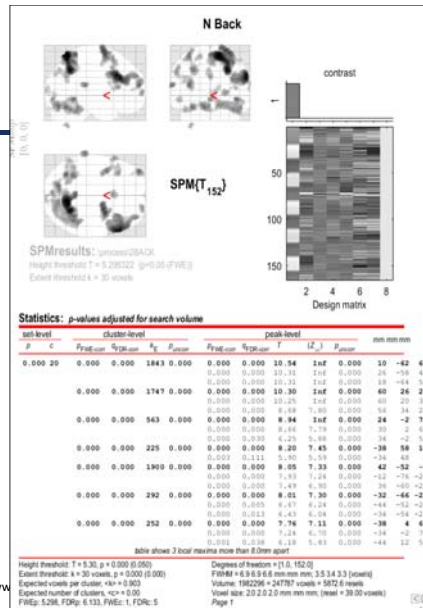
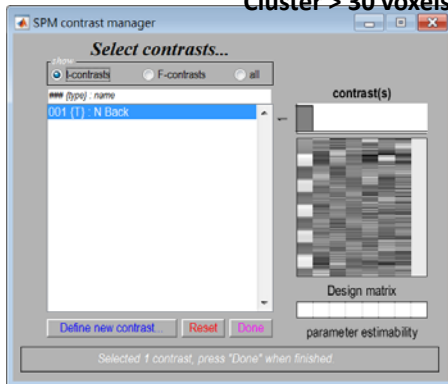
xjview



http://www.ym.edu.tw/~cfu

Review Results

FWE, $p < 0.05$
 Cluster > 30 voxels



http://www



THE END

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Teaching Materials: http://www.ym.edu.tw/~cflu/CFLu_course_fMRIana.html