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校級神經醫學研究中心



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TMU TRANSLATIONAL IMAGING RESEARCH CENTER



Analysis of Functional Magnetic Resonance Imaging (fMRI) Image Preprocessing

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Employed Software

- RadiAnt DICOM Viewer

- <https://www.radiantviewer.com/>



- Statistical Parametric Mapping (SPM 12)

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



- dcm2niigui

- https://drive.google.com/file/d/1vNBcJnIVMgXBfSIndNf0bEDT7_Z5yRQf/view?usp=sharing



DICOM (1993)



NEMA, Suite 1752
1300 North 17th Street
Rosslyn, VA 22209
Ph: (703) 841-3285
<http://dicom.nema.org>



- **D**igital **I**maging and **CO**mmunication in **M**edicine
 - The common language of medical equipment
 - Retrieve of subject/imaging information

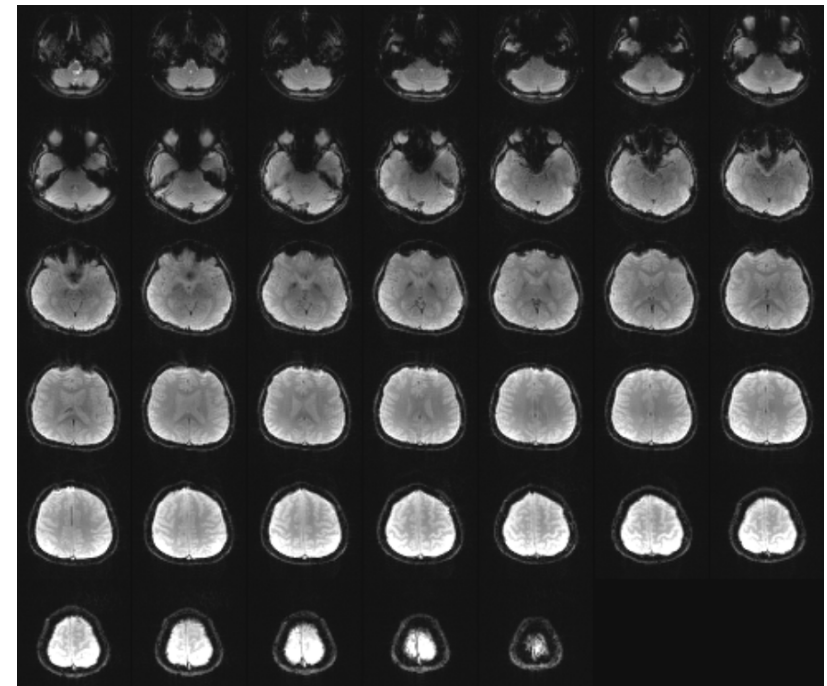
DICOM Tags (H:\我的雲端硬碟\#Presentation\20210127_fmri\course\fmri_example_data\HC0...

Tag ID	VR	VM	Length	Description	Value
(0018,0080)	DS	1	4	Repetition Time	2050
(0018,0081)	DS	1	2	Echo Time	20
(0018,0083)	DS	1	2	Number of Averages	1
(0018,0084)	DS	1	10	Imaging Frequency	123.262425
(0018,0085)	SH	1	2	Imaged Nucleus	1H
(0018,0086)	IS	1	2	Echo Number(s)	1
(0018,0087)	DS	1	2	Magnetic Field Strength	3
(0018,0088)	DS	1	4	Spacing Between Slices	3.5
(0018,0089)	IS	1	2	Number of Phase Encoding Steps	70
(0018,0091)	IS	1	2	Echo Train Length	35
(0018,0093)	DS	1	4	Percent Sampling	100
(0018,0094)	DS	1	4	Percent Phase Field of View	100
(0018,0095)	DS	1	4	Pixel Bandwidth	2305
(0018,1000)	LO	1	6	Device Serial Number	66074
(0018,1020)	LO	1	12	Software Versions	syngo MR E11
(0018,1030)	LO	1	22	Protocol Name	ep2d_bold_moco_p2_m105
(0018,1251)	SH	1	4	Transmit Coil Name	Body
(0018,1310)	US	4	8	Acquisition Matrix	70 0 0 70
(0018,1312)	CS	1	4	In-plane Phase Encoding Direction	COL
(0018,1314)	DS	1	2	Flip Angle	90
(0018,1315)	CS	1	2	Variable Flip Angle Flag	N
(0018,1316)	DS	1	16	SAR	0.14219583517408
(0018,1318)	DS	1	2	dB (1st)	0

Find text... Close

DICOM tags (header)

+



DICOM images

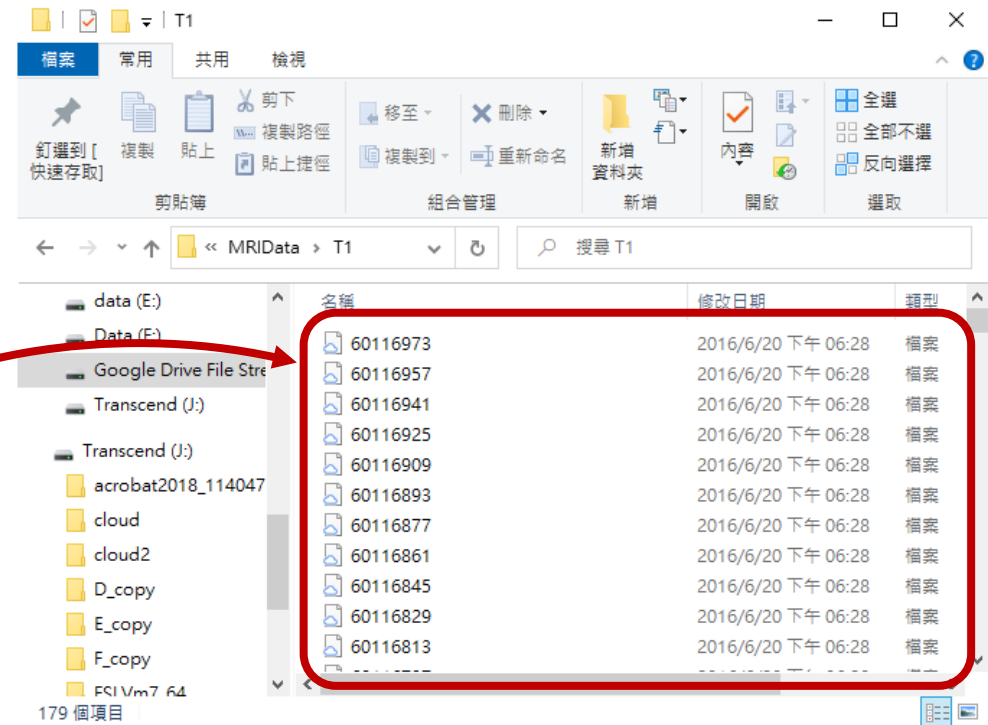
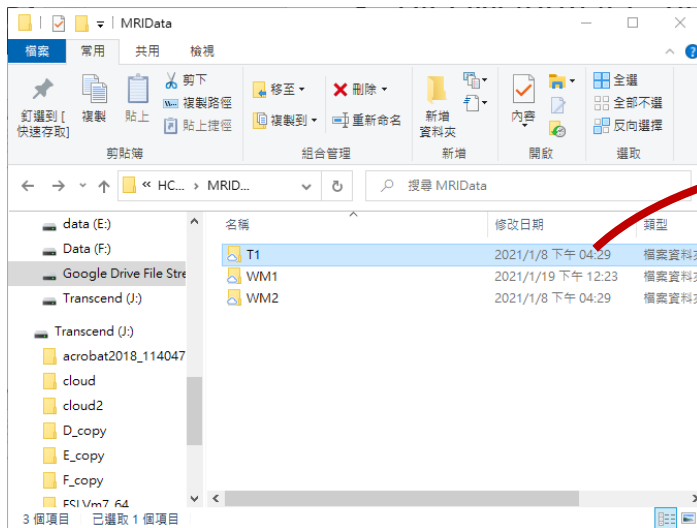
DICOM Import

- DICOM format (*.dcm, *.ima, *.) → NIfTI (*.nii)



DICOM image folder

Compressed DICOM

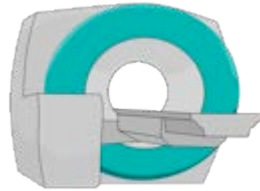


DICOM Import

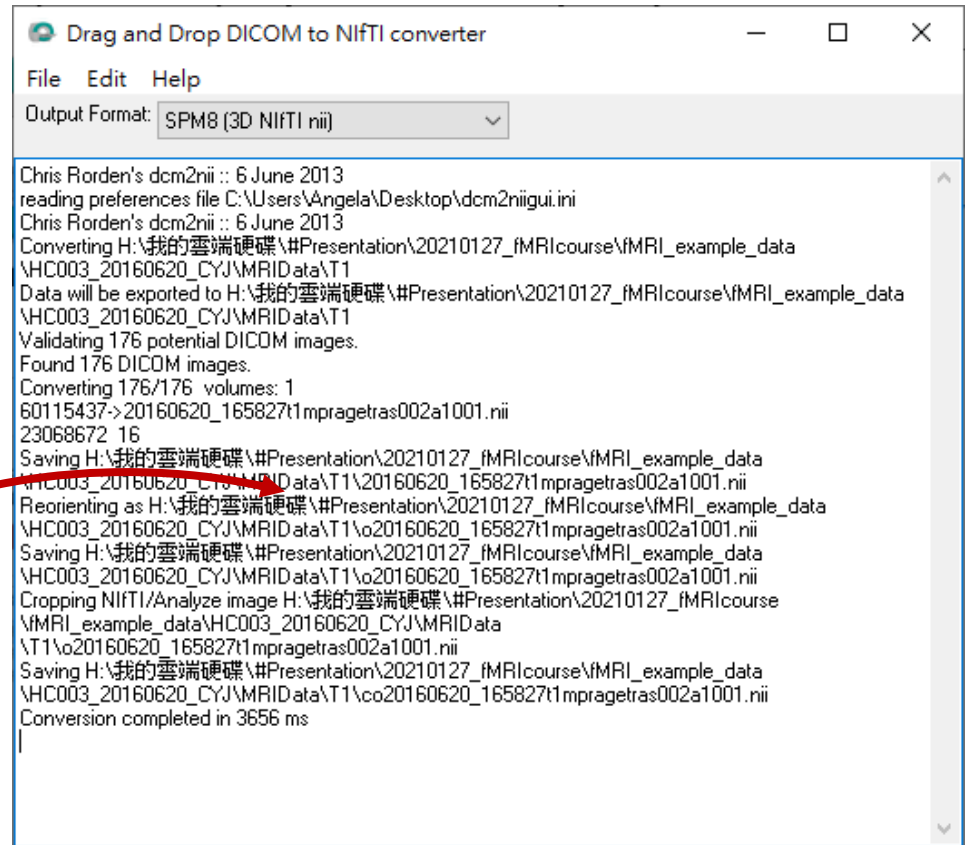
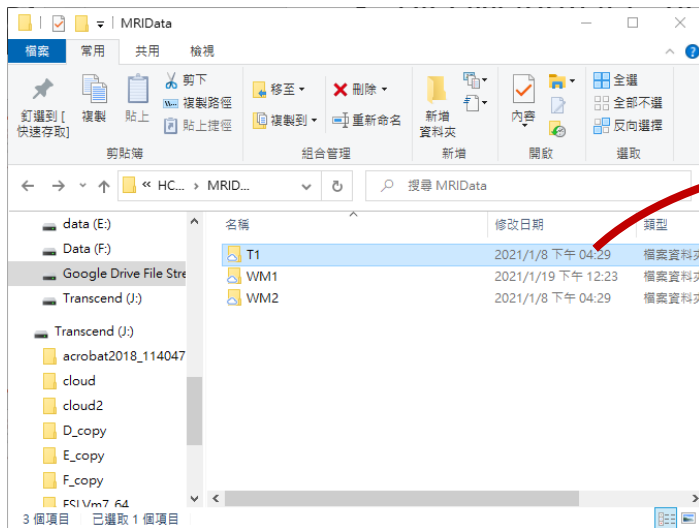
- DICOM format (*.dcm, *.ima, *.) → NIfTI (*.nii)



DICOM image folder



dcm2niiGUI

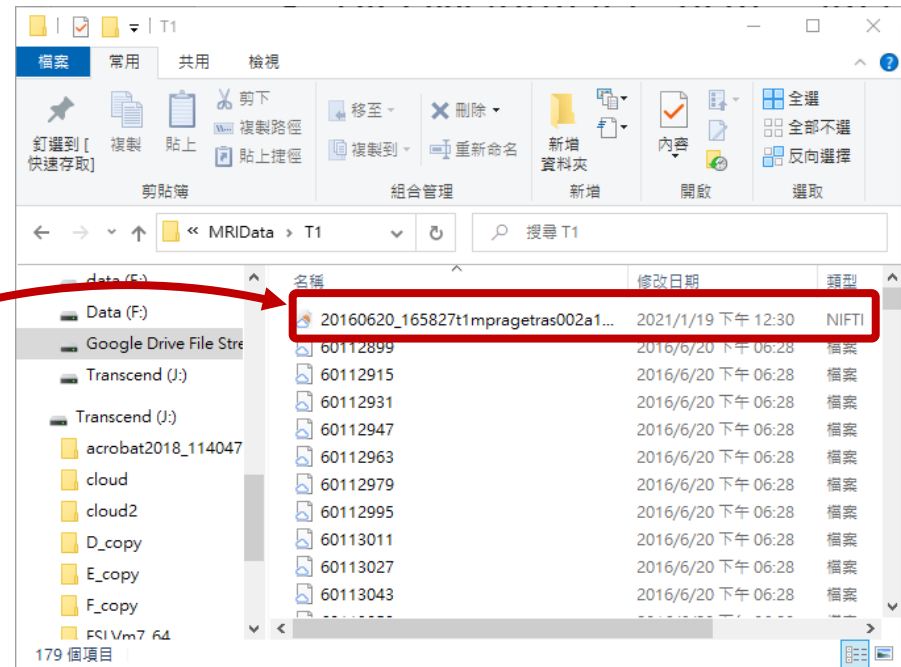
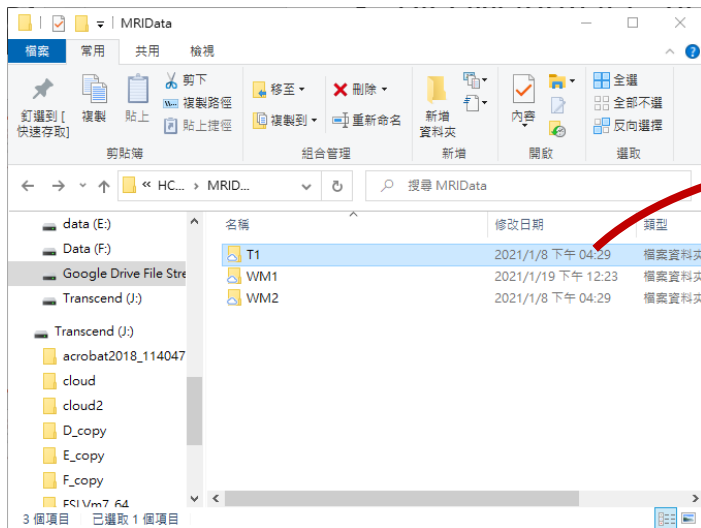


DICOM Import

- DICOM format (*.dcm, *.ima, *.) → **NIfTI (*.nii)**



DICOM image folder

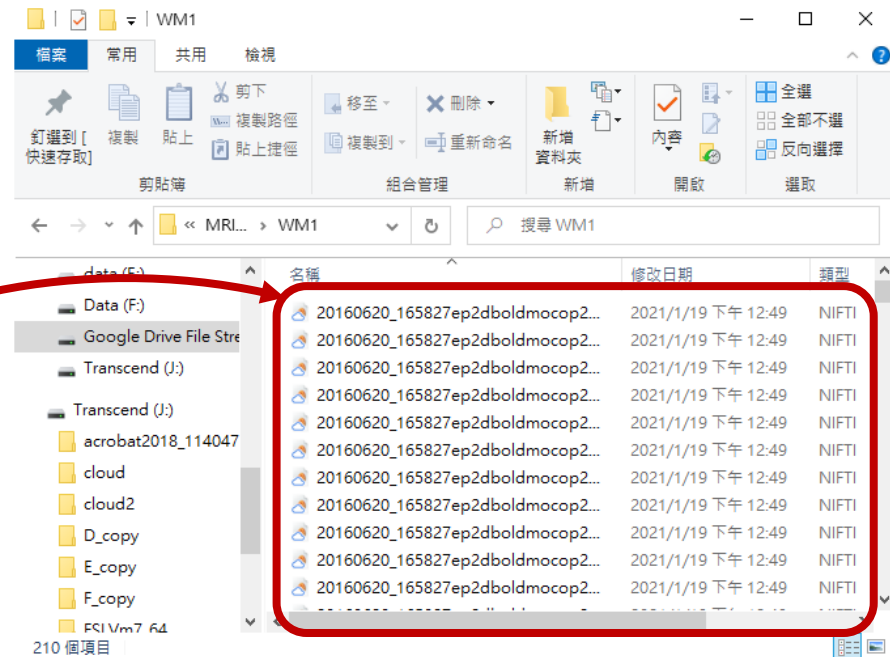
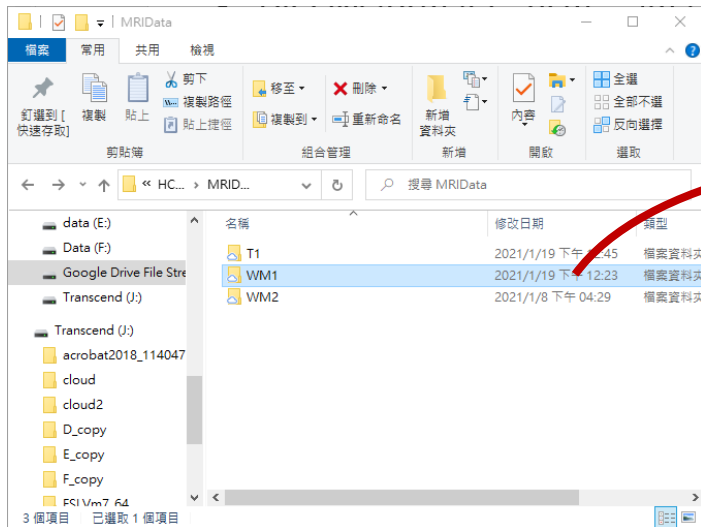


DICOM Import

- DICOM format (*.dcm, *.ima, *.) → **NIFTI (*.nii)**



DICOM image folder



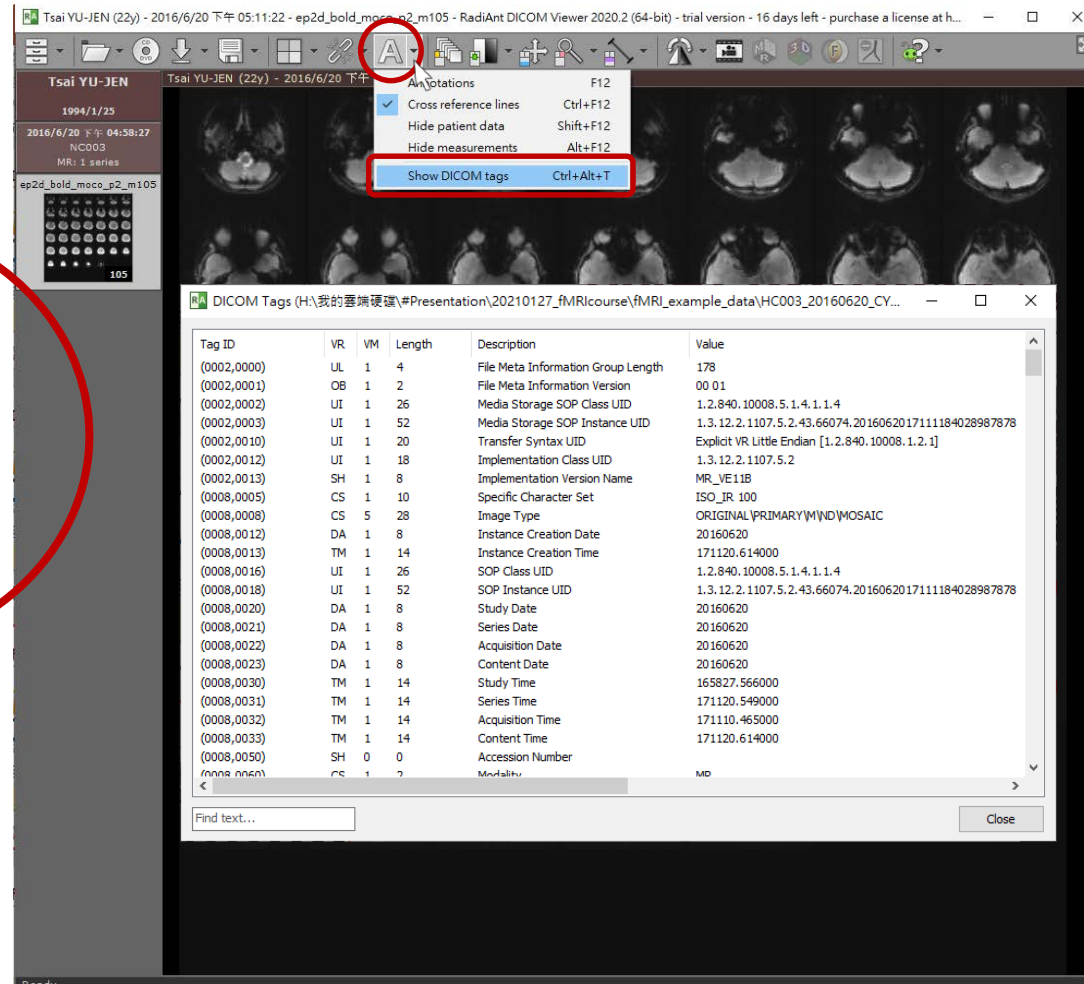
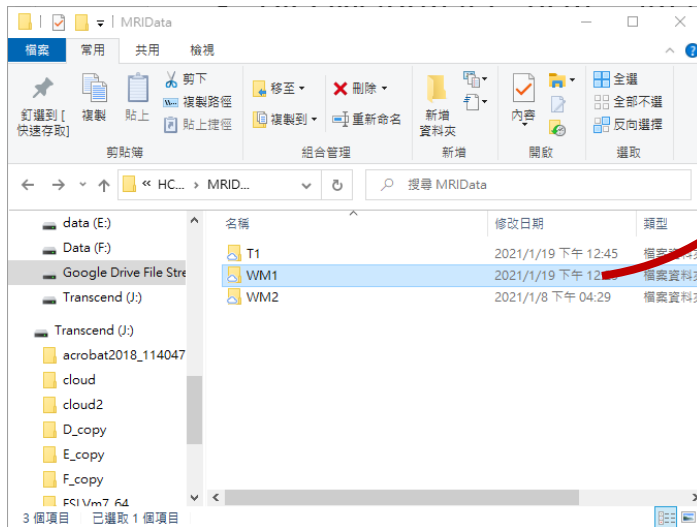
fMRI Protocol (see DICOM tags)



DICOM image folder



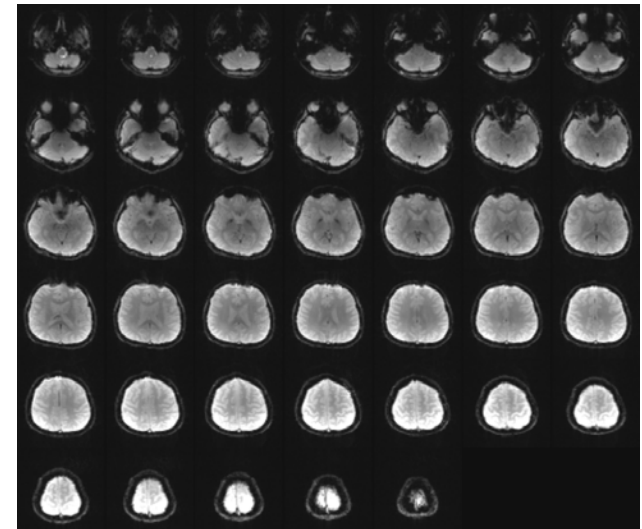
RadiANT DICOM Viewer (64-bit)



fMRI Protocol (see DICOM tags)

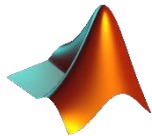
- (0008,0070) Manufacturer : SIEMENS
- (0018,0087) Magnetic Field Strength : 3 (T)
- (0008,1090) Manufacturer's Model Name : Prisma
- (0018,0024) Sequence Name : *epfid2d1_70 → 2D GRE EPI
- (0018,0080) Repetition Time : 2000 (ms)
- (0018,0081) Echo Time : 20 (ms)
- (0018,1314) Flip Angle : 90 (°)
- (0028,0030) Pixel Spacing : 3\3 (mm)
- (0028,0010) Rows : 64
- (0028,0011) Column : 64
- (0018,0088) Spacing Between Slices : 3.5 (mm)
- (0018,0050) Slice Thickness : 3.5 (mm)
- (0019,100A) Number of Image in Mosaic : 40 (slices)

BOLD fMRI images (Moisaics)

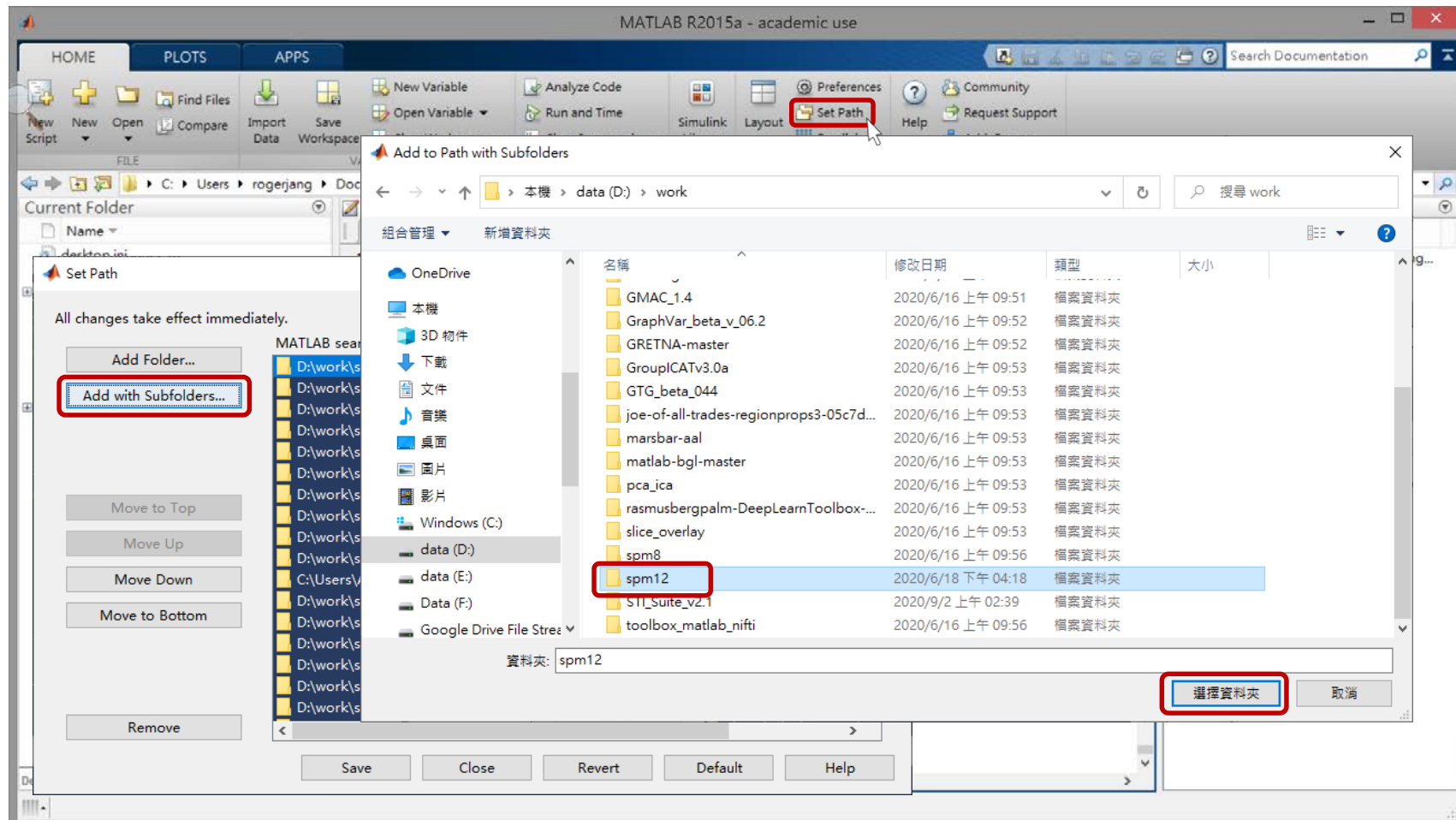


Set up

Set Path > Add with Subfolders... > spm12 > 選擇資料夾

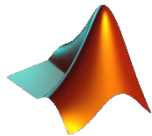


Matlab
R2020a

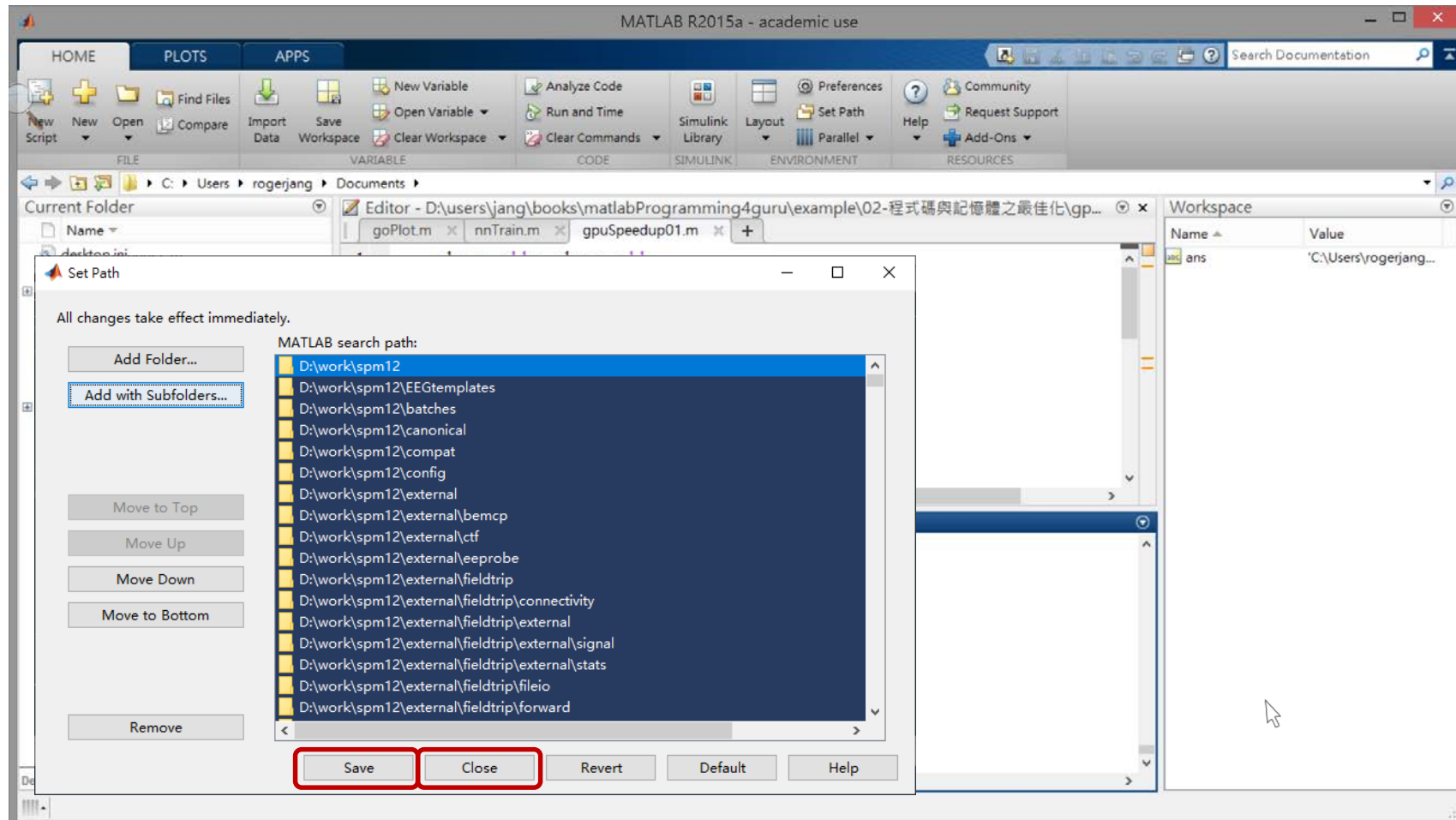


Set up

Set Path > Add with Subfolders... > spm12 > 選擇資料夾 > Save > Close



Matlab
R2020a

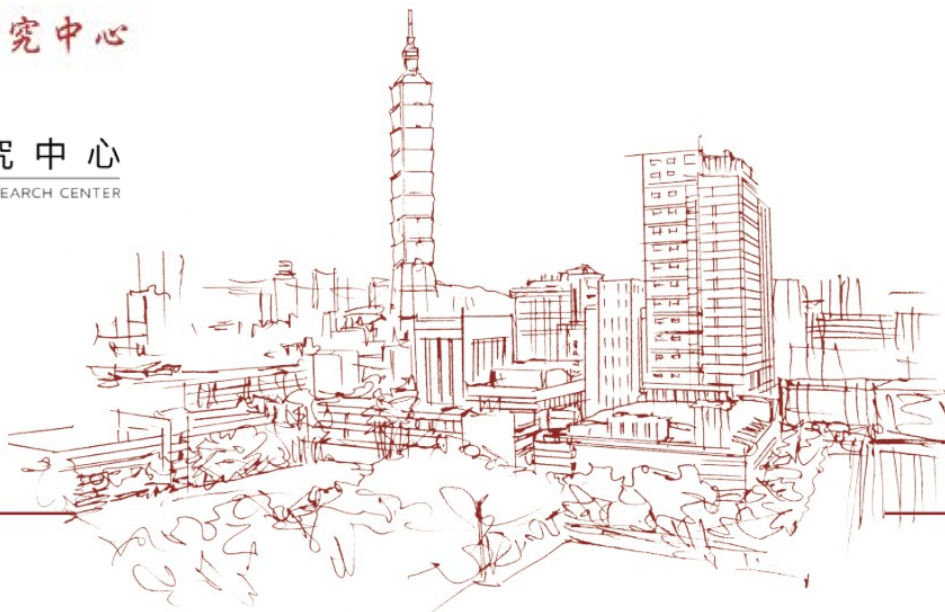




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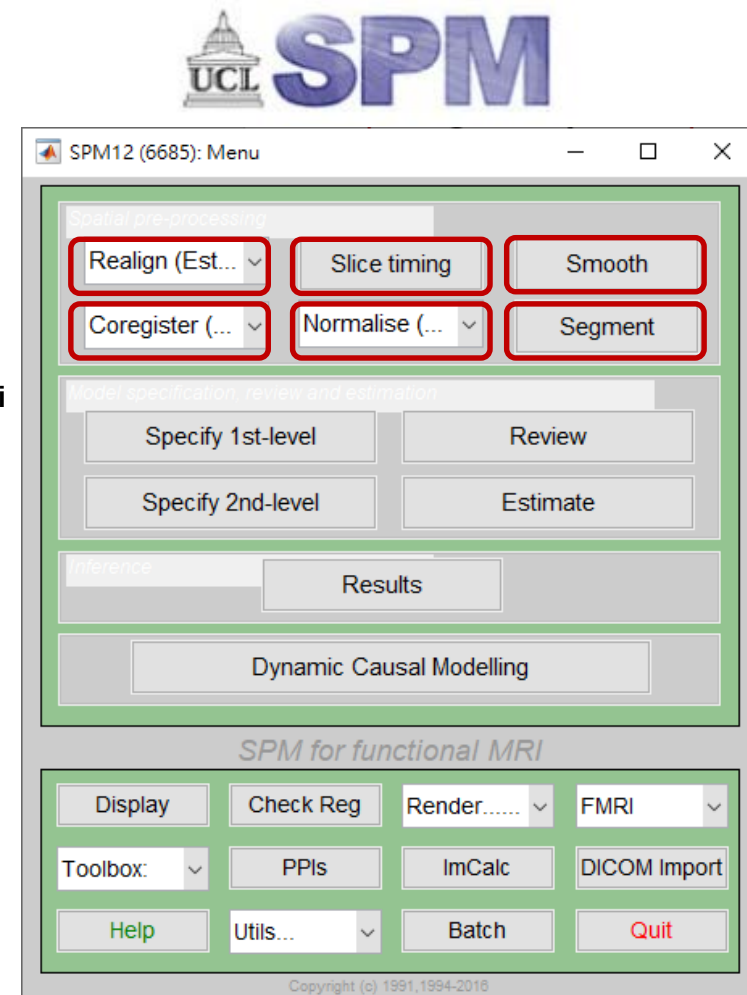
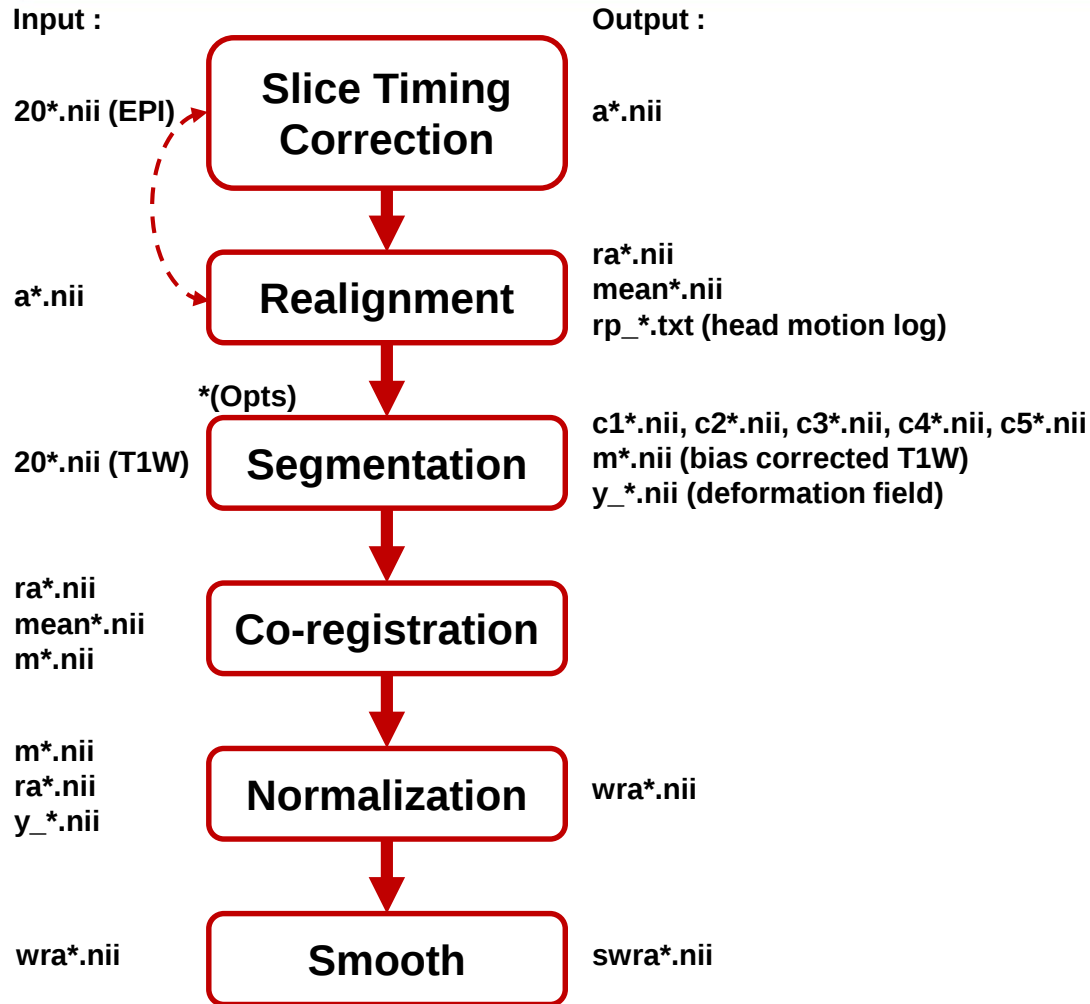


Analysis of Functional Magnetic Resonance Imaging (fMRI) Set up SPM12 Batch Parameters



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Preprocessing Procedure



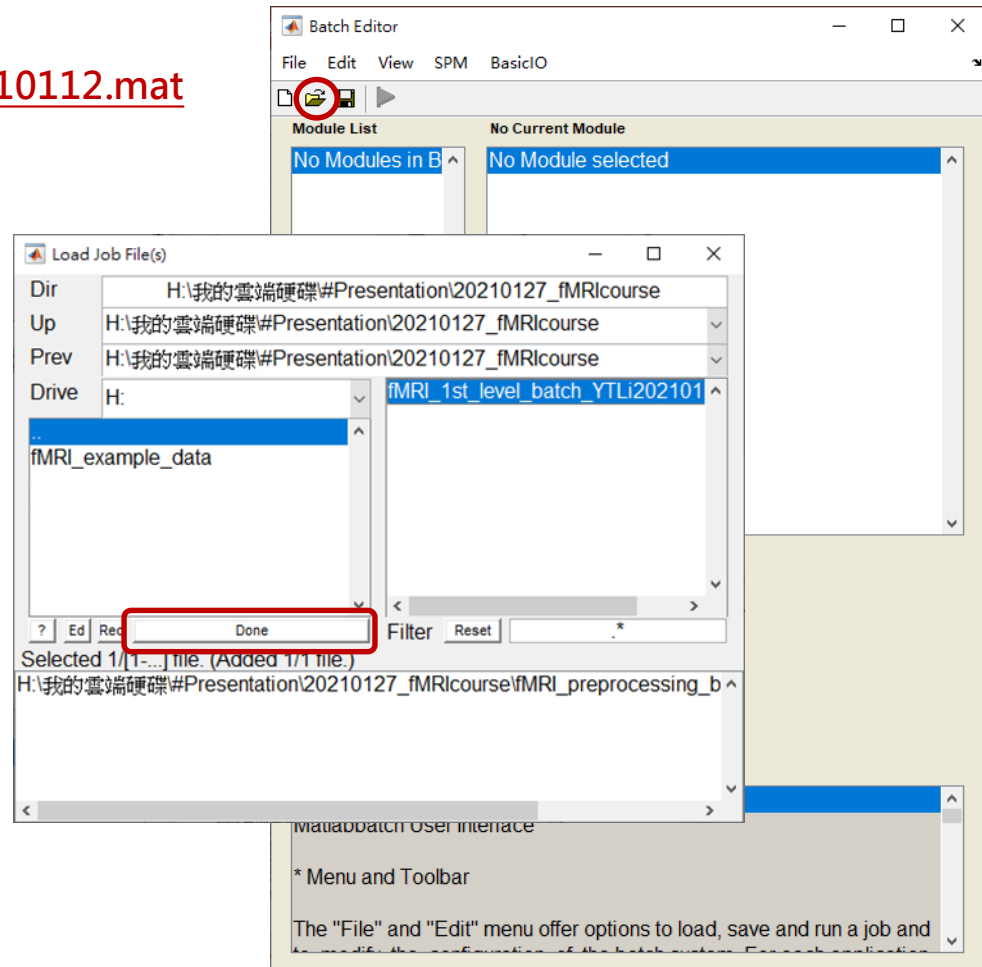
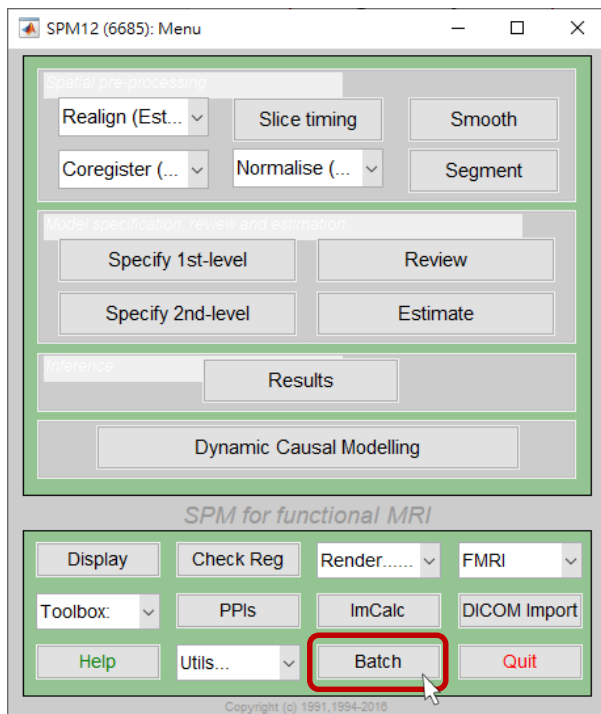
Batch of fMRI preprocessing

>> spm fmri

> Batch

> fMRI_preprocessing_batch_YTLi20210112.mat

> Done



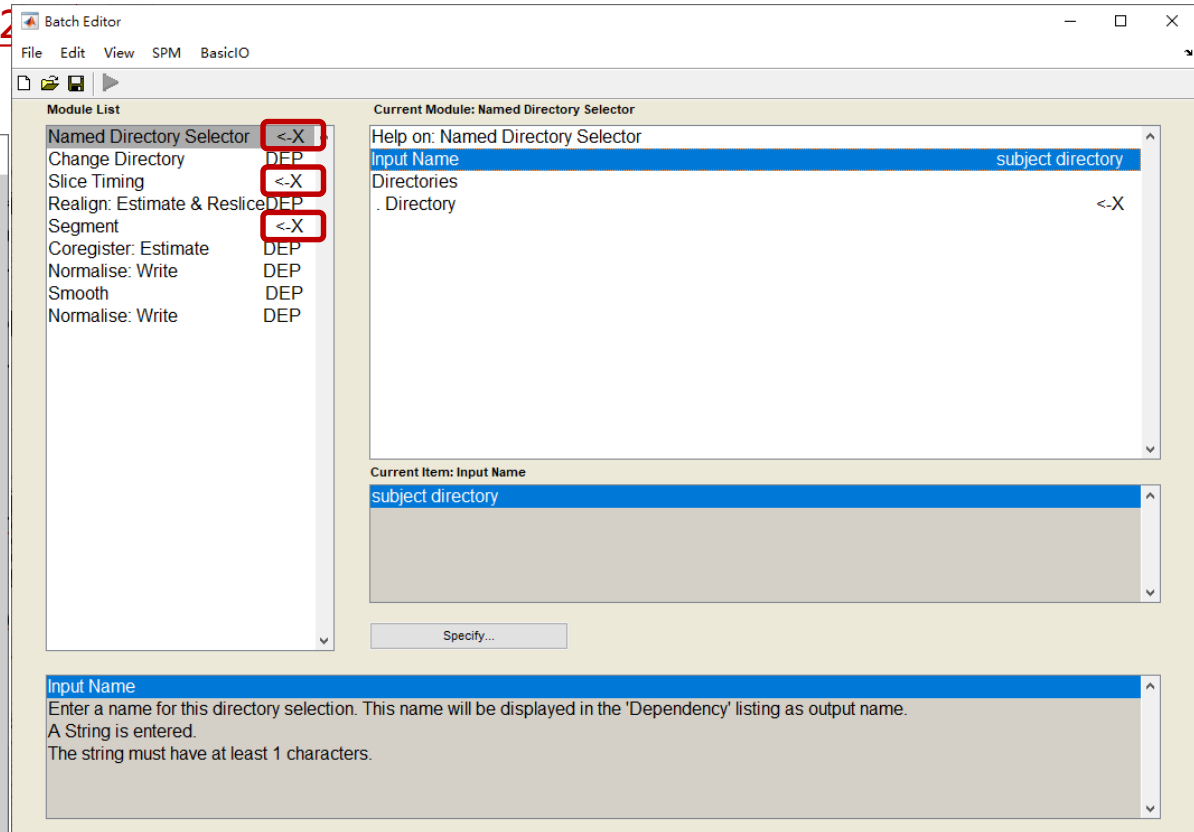
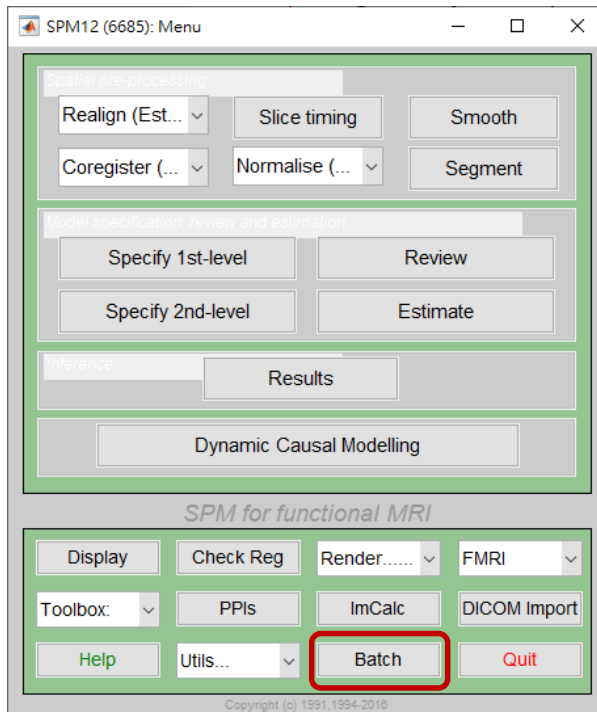
Batch of fMRI preprocessing

>> spm fmri

> Batch

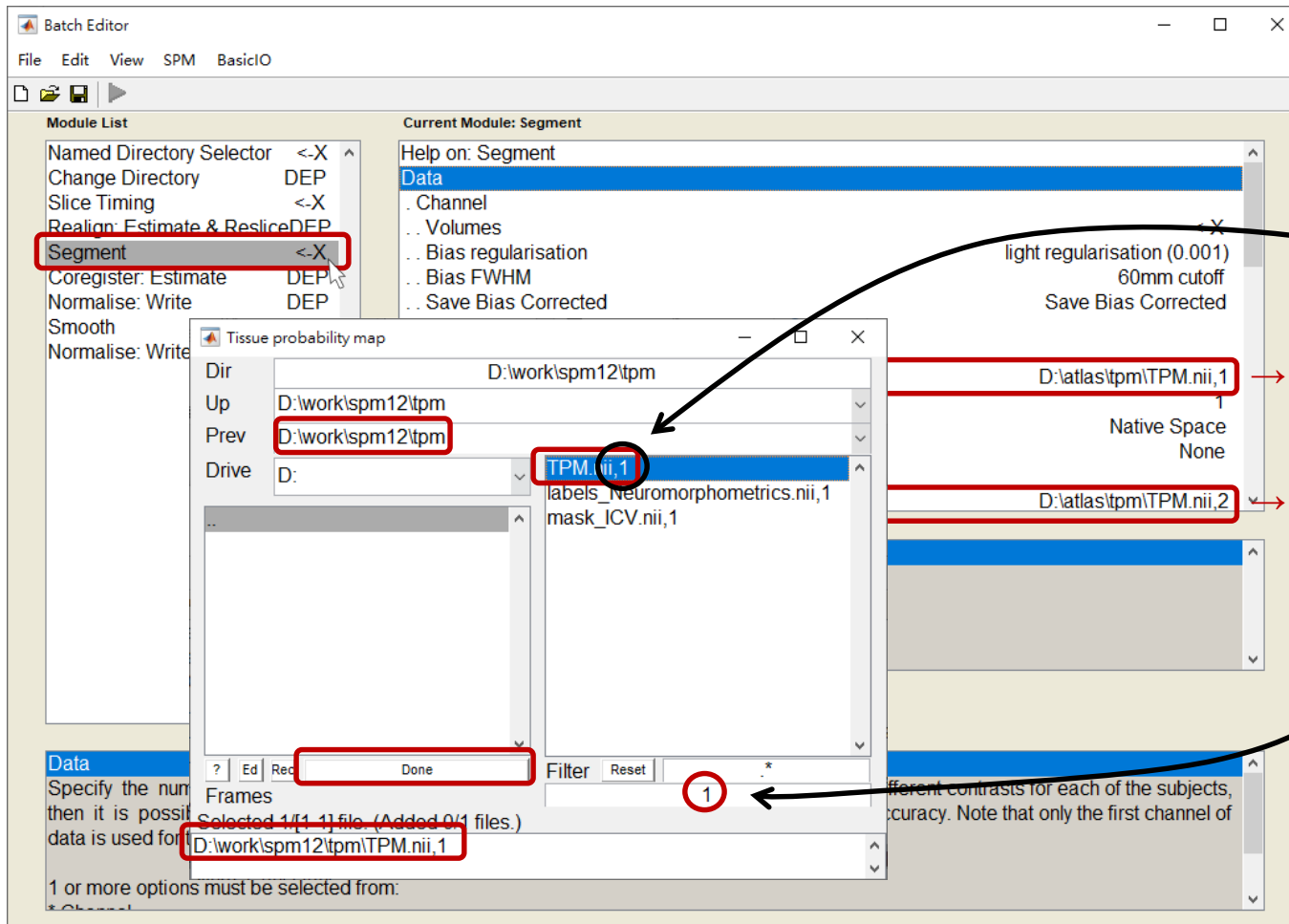
> fMRI_preprocessing_batch_YTLi2

> Done



Batch of fMRI preprocessing

> Select the SPM Tissue Probability Map (~\spm12\TPM.nii)



Batch of fMRI preprocessing

> Select the SPM Tissue Probability Map (~\spm12\TPM.nii)

Batch Editor

File Edit View SPM BasicIO

Module List

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

Current Module: Segment

Tissue

- Tissue probability map D:\atlas\tpm\TPM.nii,4
- Num. Gaussians 3
- Native Tissue Native Space
- Warped Tissue None
- Tissue
- Tissue probability map D:\atlas\tpm\TPM.nii,5
- Native Space 4
- Native Space None
- D:\atlas\tpm\TPM.nii,6
- None
- None

Tissue probability map

Dir D:\work\spm12\tpm

Up D:\work\spm12\tpm

Prev D:\work\spm12\tpm

Drive D:

TPM.nii,6

Done

Filter Reset

6

D:\work\spm12\tpm\TPM.nii,6

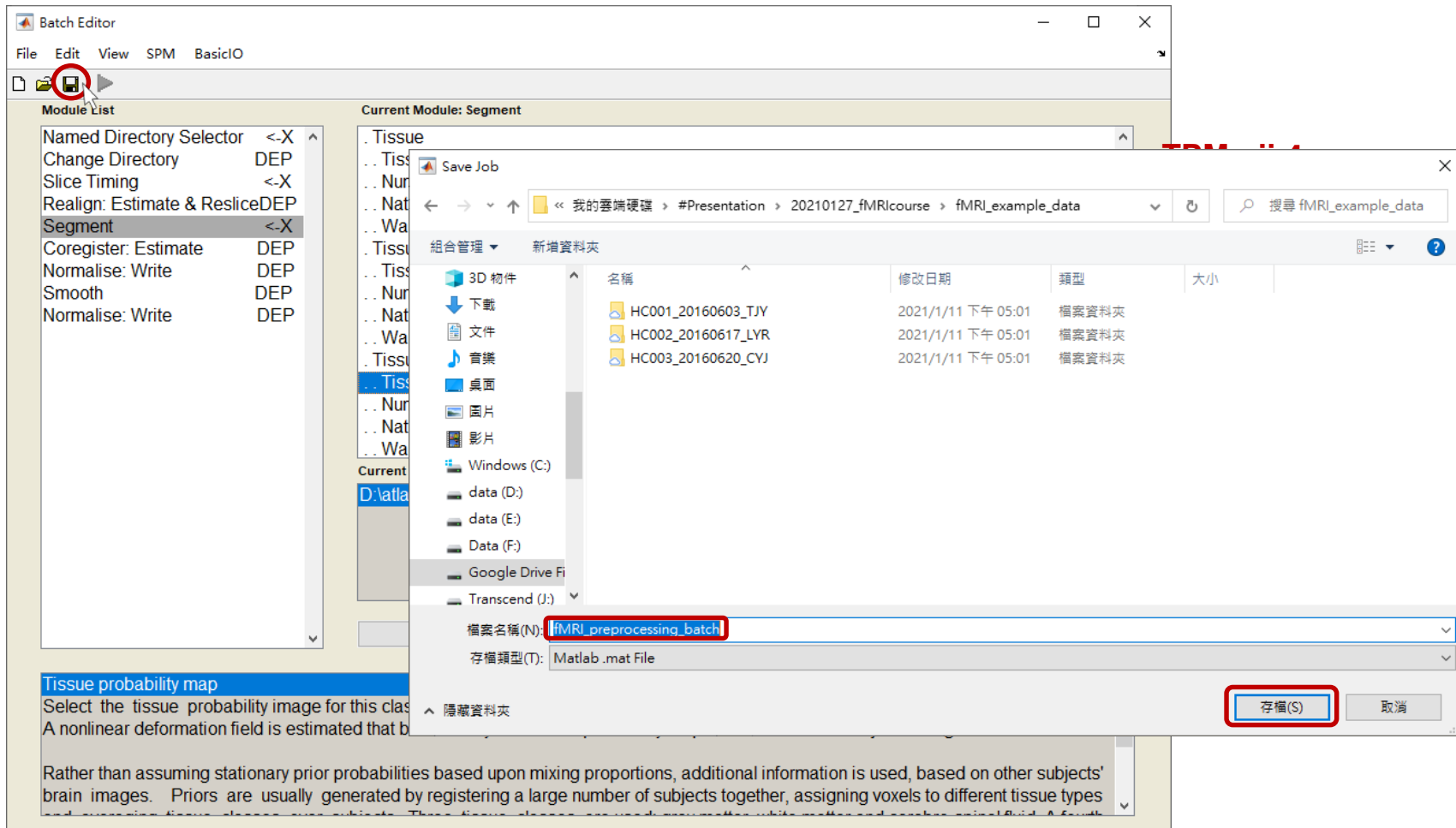
TPM.nii,4

TPM.nii,5

TPM.nii,6

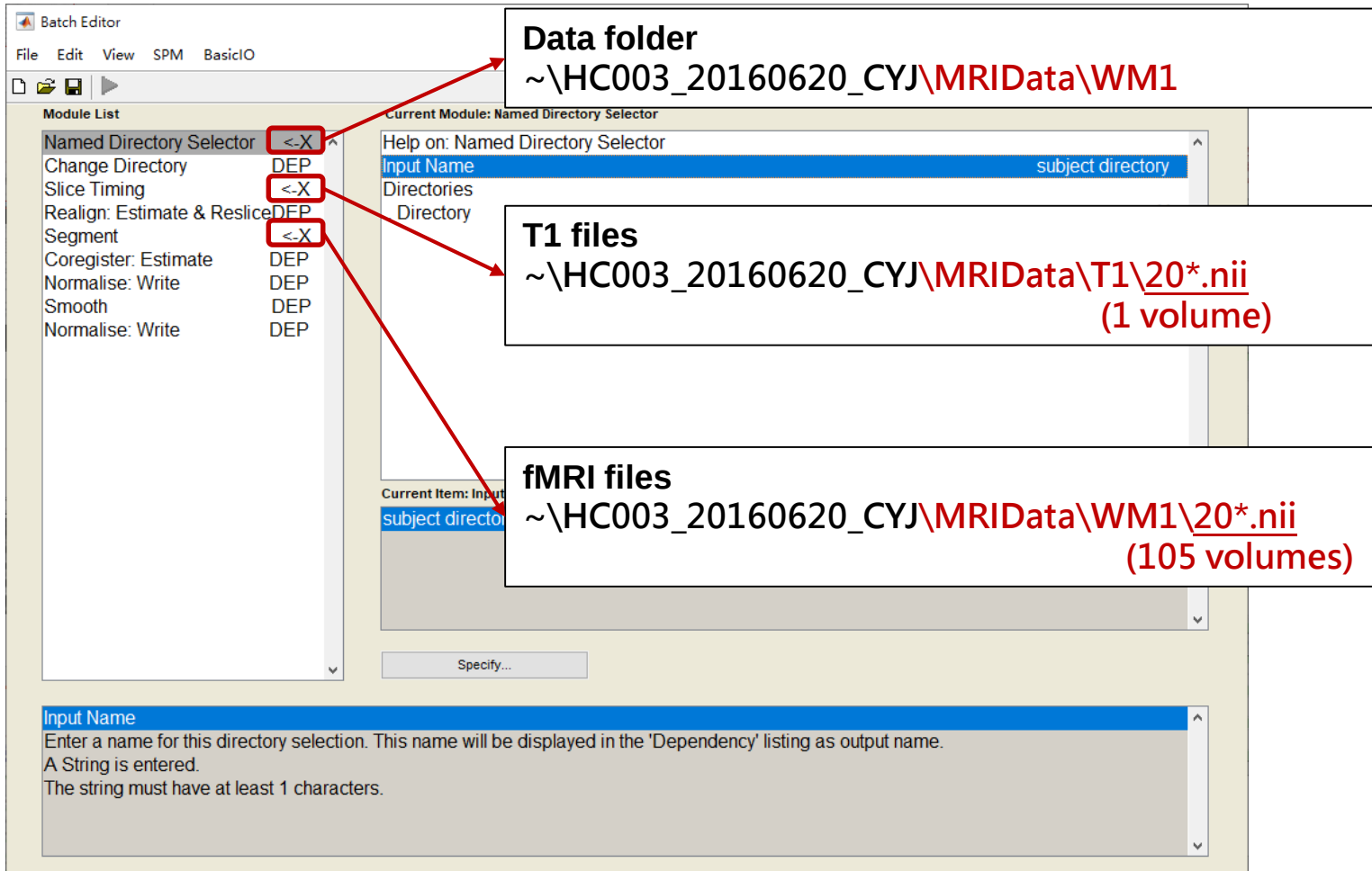
Batch of fMRI preprocessing

> Save new batch file



Batch of fMRI preprocessing

> Select files for preprocessing



Batch Editor
File Edit View SPM BasicIO

Module List

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

Current Module: Named Directory Selector

Help on: Named Directory Selector

Input Name: subject directory

Directories: Directory

Data folder
~\HC003_20160620_CYJ\MRIData\WM1

T1 files
~\HC003_20160620_CYJ\MRIData\T1\20*.nii
(1 volume)

fMRI files
~\HC003_20160620_CYJ\MRIData\WM1\20*.nii
(105 volumes)

Current Item: Input
subject director

Specify...

Input Name
Enter a name for this directory selection. This name will be displayed in the 'Dependency' listing as output name.
A String is entered.
The string must have at least 1 characters.

Slice Timing Correction

Slice Timing Correction

Realignment

Segmentation

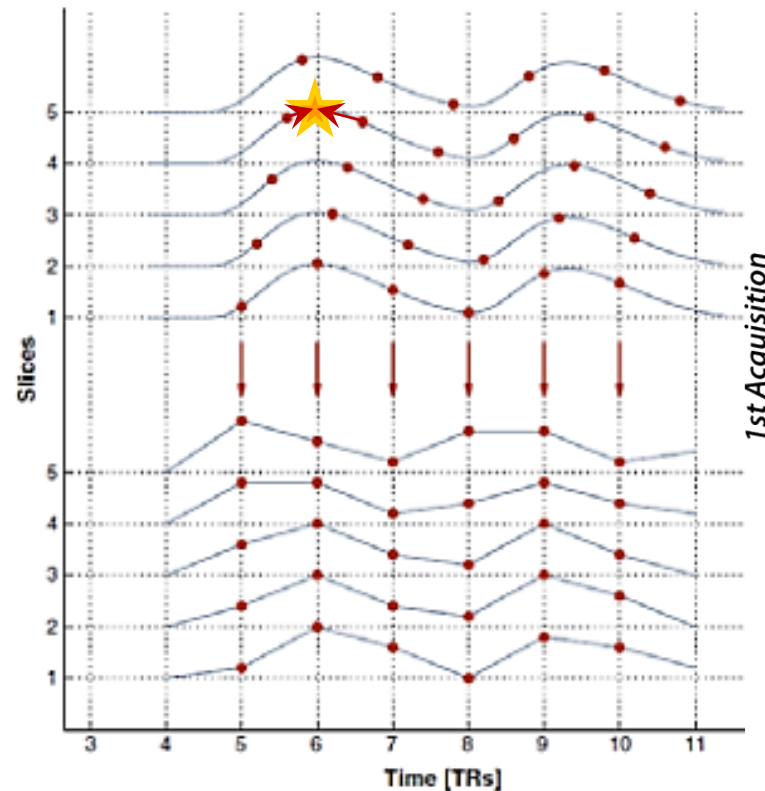
Co-registration

Normalization

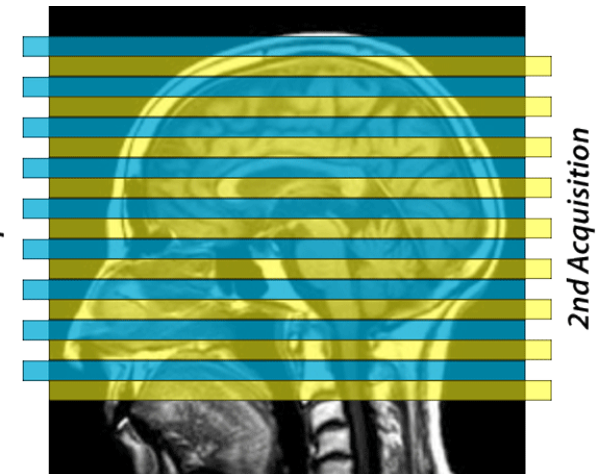
Smooth

Correct for temporal offset between slices for multi-slice acquisition

temporal interpolation



Interleaved Acquisition



Slice Timing Correction

Slice Timing Correction

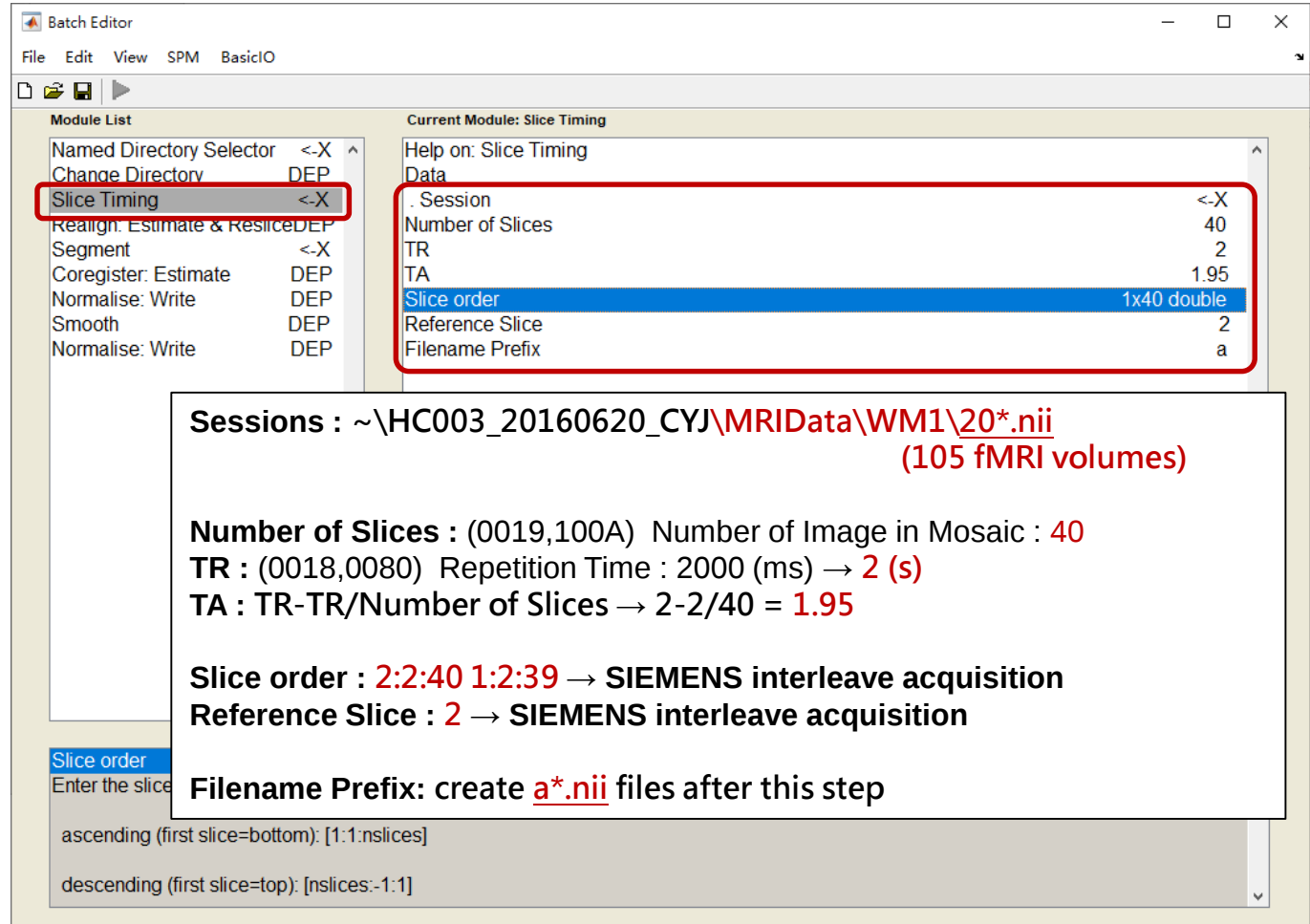
Realignment

Segmentation

Co-registration

Normalization

Smooth



The screenshot shows the Batch Editor window with the 'Slice Timing' module selected in the 'Module List' on the left. The 'Current Module: Slice Timing' panel on the right displays the following parameters:

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

Below the parameter list, a text box provides session and acquisition details:

Sessions : ~\HC003_20160620_CYJ\MRIData\WM1\20*.nii
(105 fMRI volumes)

Number of Slices : (0019,100A) **Number of Image in Mosaic :** 40
TR : (0018,0080) **Repetition Time :** 2000 (ms) → **2 (s)**
TA : TR-TR/Number of Slices → 2-2/40 = **1.95**

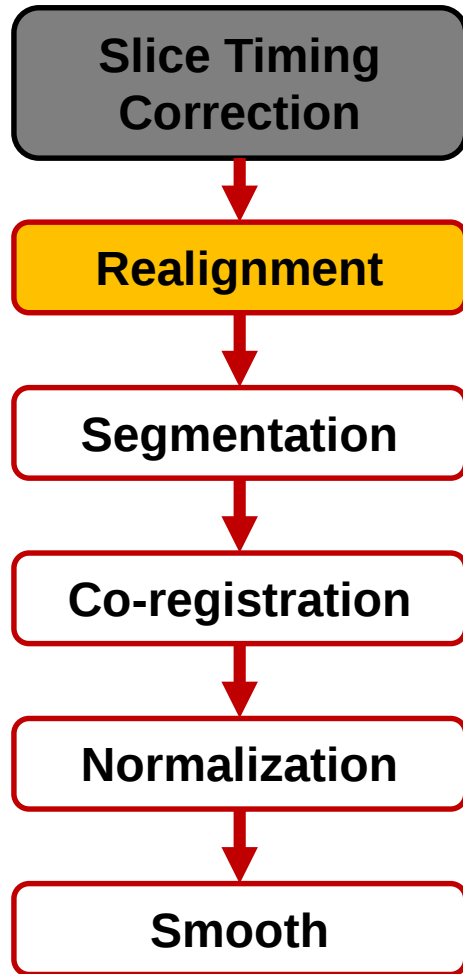
Slice order : 2:2:40 1:2:39 → **SIEMENS** interleave acquisition
Reference Slice : 2 → **SIEMENS** interleave acquisition

Filename Prefix: create a*.nii files after this step

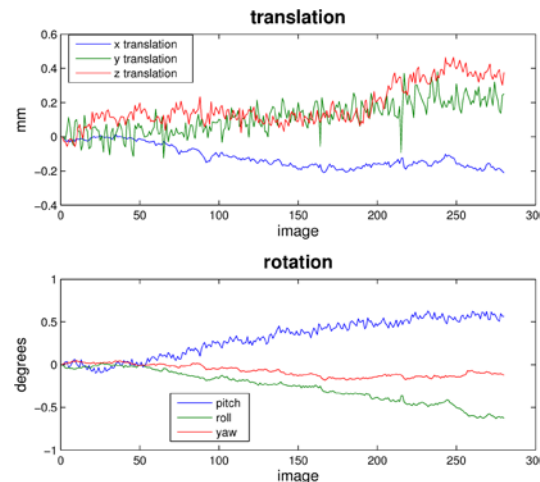
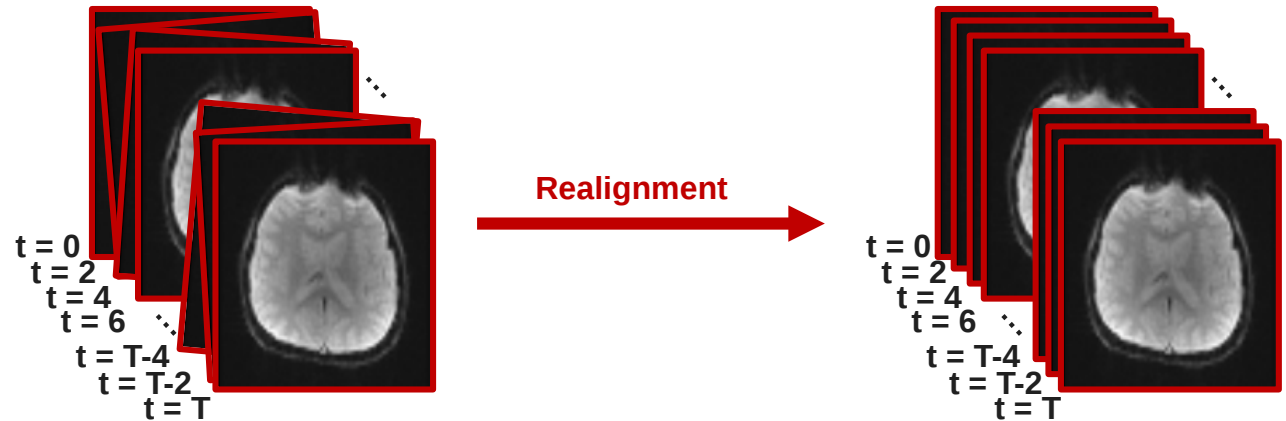
At the bottom, options for slice order are listed:

- ascending (first slice=bottom): [1:1:nslices]
- descending (first slice=top): [nslices:-1:1]

Realignment (Head motion correction)

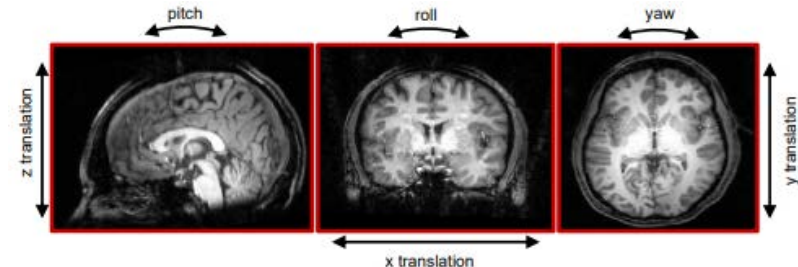


The signal variation from head movement is much **larger** than hemodynamic response.

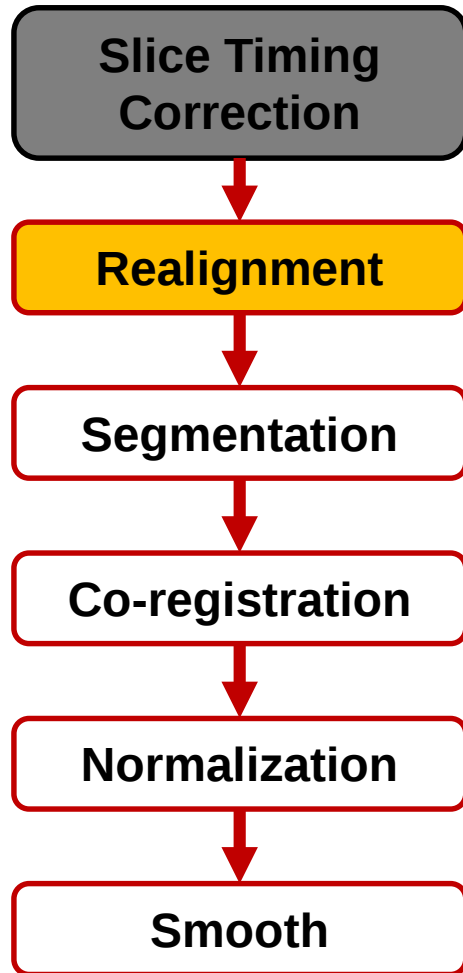


6-parameter rigid body registration & transformation
(Realign to the 1st volume)

→ 6 motion-related co-variables for fMRI analysis



Realignment (Head motion correction)



Batch Editor

File Edit View SPM BasicIO

Module List

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

Current Module: Realign: Estimate & Reslice

Help on: Realign: Estimate & Reslice

Data dependency

Session DEP Slice Timing: Slice Timing Corr. Images (Sess 1)

Estimation Options

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

Volumes : EPI volumes after slice timing correction (a*.nii)

- . Resliced Images All Images + mean image
- . Interpolation 4th Degree B-Spline
- . Wrapping No wrap

Current Item: Session

Reference from

Slice Timing: Slice Timing Corr. Images (Sess 1)

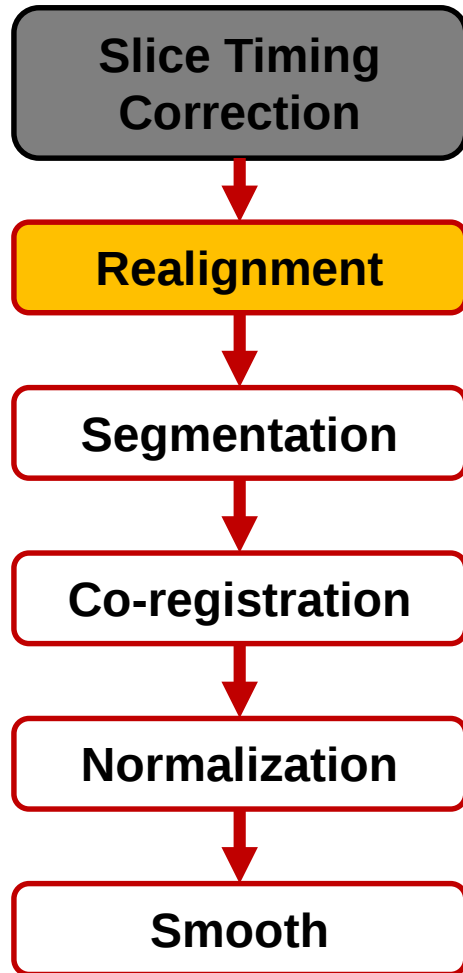
Specify...

Dependency

Session

Select scans for this session. In the coregistration step, the sessions are first realigned to each other, by aligning the first scan from each session to the first scan of the first session. Then the images within each session are aligned to the first image of the session. The parameter estimation is performed this way because it is assumed (rightly or not) that there may be systematic differences in the images between sessions.

Realignment (Head motion correction)



Batch Editor

File Edit View SPM BasicIO

Module List

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

Current Module: Realign: Estimate & Reslice

Session DEP Slice Timing: Slice Timing Corr. Images (Sess 1)

Estimation Options

Quality 0.9

Separation 4

Smoothing (FWHM) 5

Num Passes

Interpolation Register to mean

Wrapping 2nd Degree B-Spline

Weighting No wrap

Reslice Options

Resliced images All Images + Mean Image

Interpolation 4th Degree B-Spline

Wrapping No wrap

Masking Mask images

Filename Prefix r

Current Item: Resliced images

All Images (1..n)

Images 2..n

* All Images + Mean Image

Resliced images : All Images + Mean Image (mean*.nii)

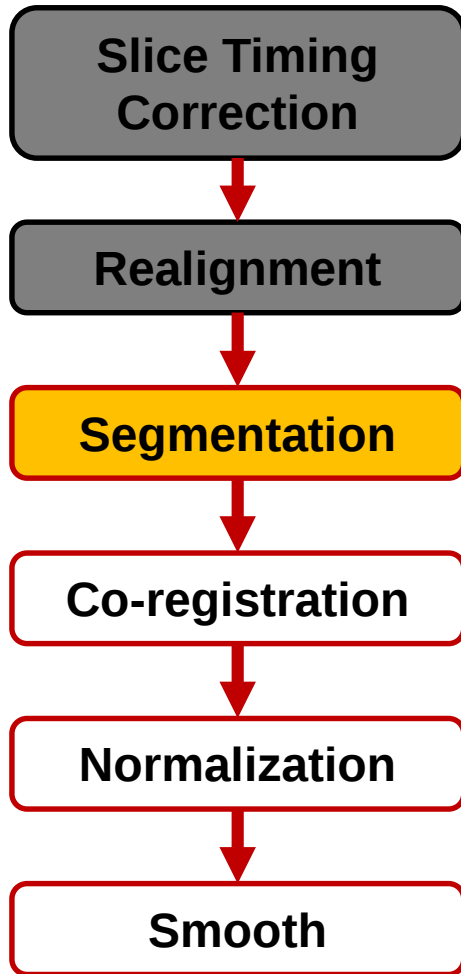
Filename Prefix: create ra*.nii files after this step

Resliced images

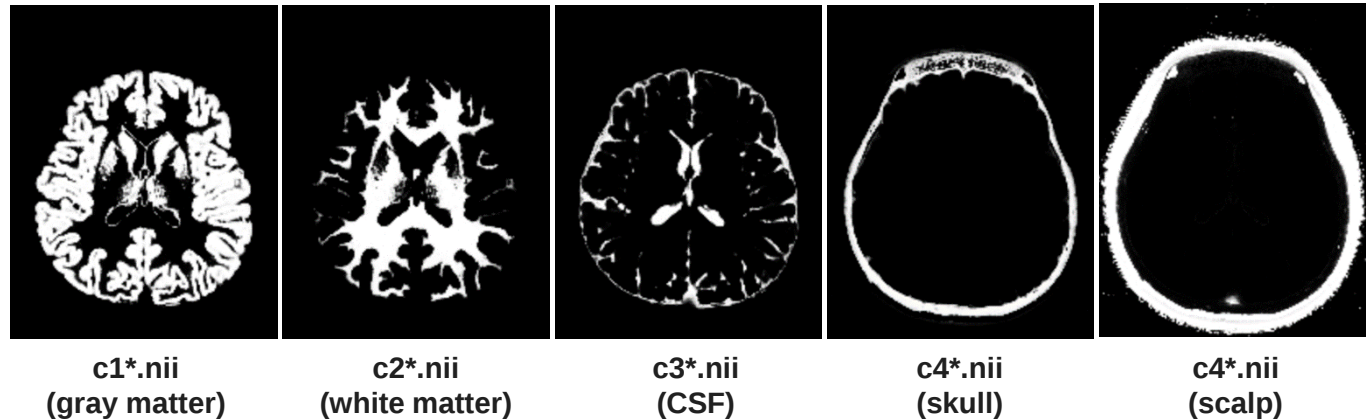
All Images (1..n) : This reslices all the images - including the first image selected - which will remain in its original position.

Images 2..n : Reslices images 2..n only. Useful for if you wish to reslice (for example) a PET image to fit a structural MRI, without creating a second identical MRI volume.

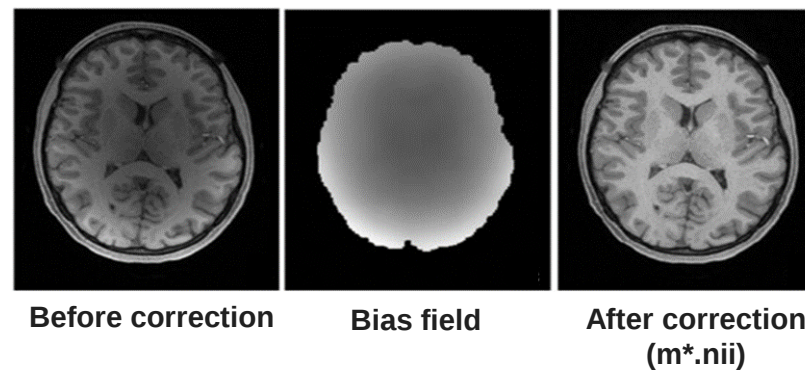
Segmentation (Bias field correction)



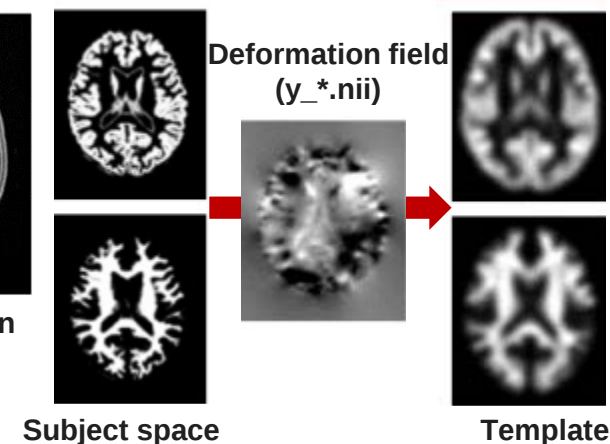
Estimate tissue probability maps for each subject.



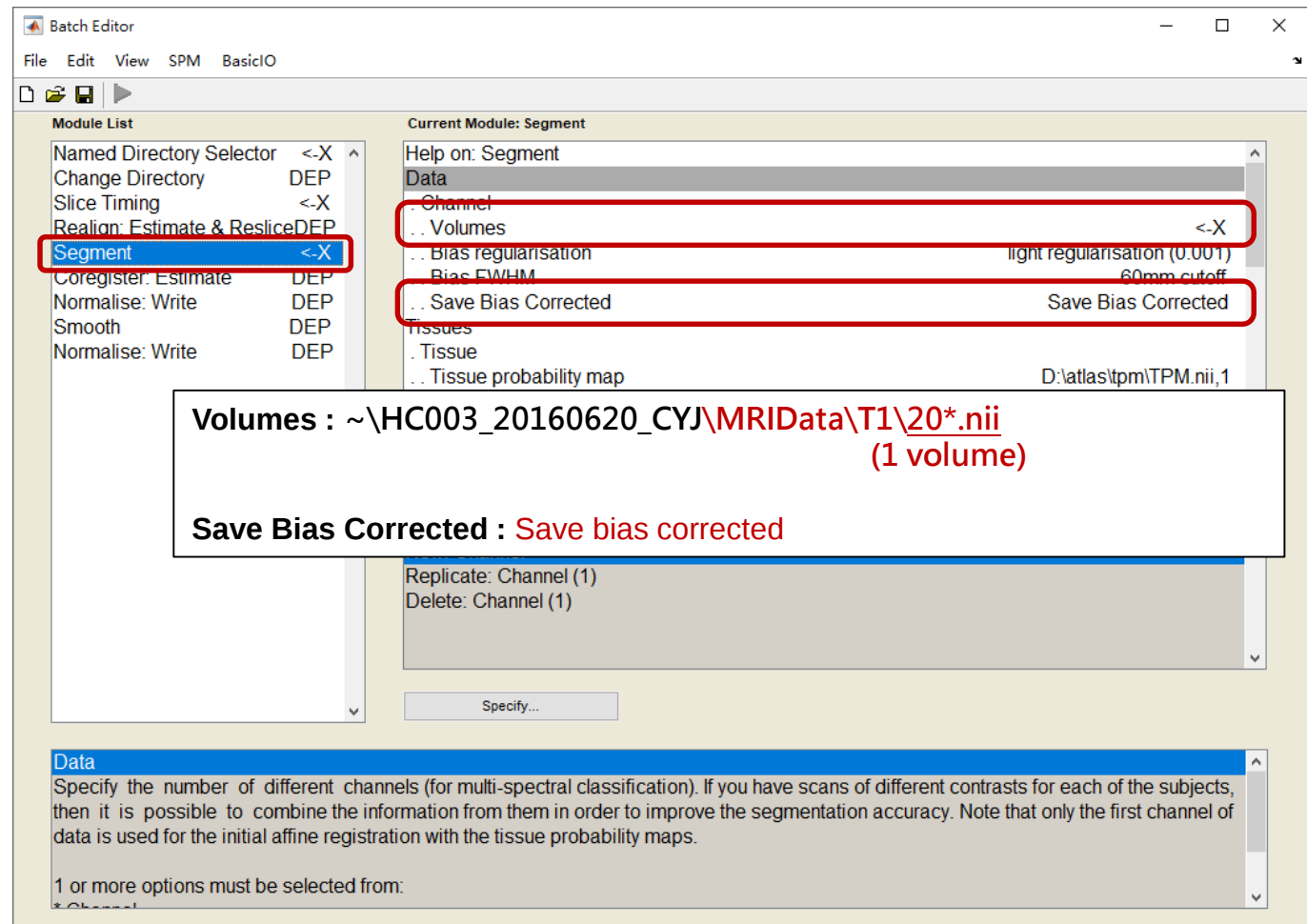
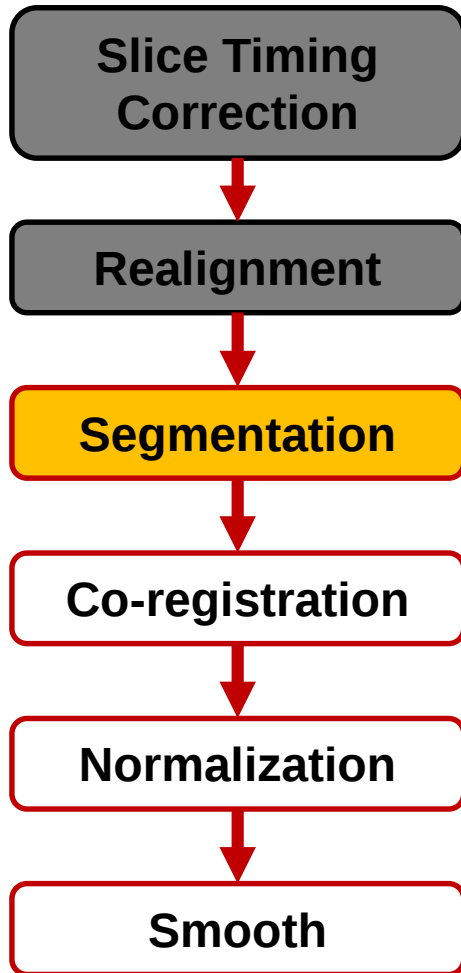
Bias field correction → benefit for registration



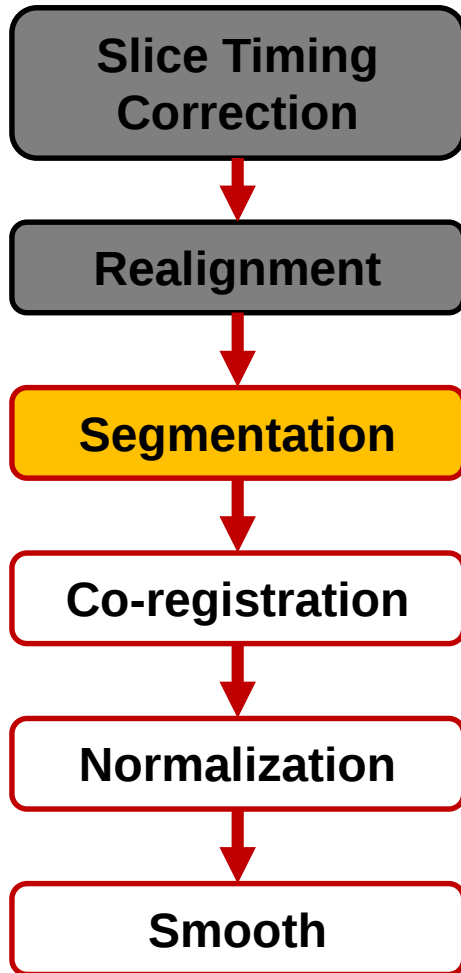
Estimate deformation field



Segmentation (Bias field correction)



Segmentation (Bias field correction)



Batch Editor

File Edit View SPM BasicIO

Module List

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

Current Module: Segment

- Native Tissue Native Space
- Warped Tissue None
- Tissue
- Tissue probability map D:\atlas\tpm\TPM.nii,6
- Num. Gaussians 2
- Native Tissue None
- Warped Tissue None
- Warping & MRF 1
- MRF Parameter Thorough Clean
- Clean Up 1x5 double
- Warping Regularisation
- Affine Regularisation ICBM space template - East Asian brains**
- Smoothness 0
- Sampling distance 3
- Deformation Fields Forward**

Current Item: Affine Regularisation

- No Affine Registration
- ICBM space template - European brains
- ICBM space template - East Asian brains**
- Average sized template
- No regularisation

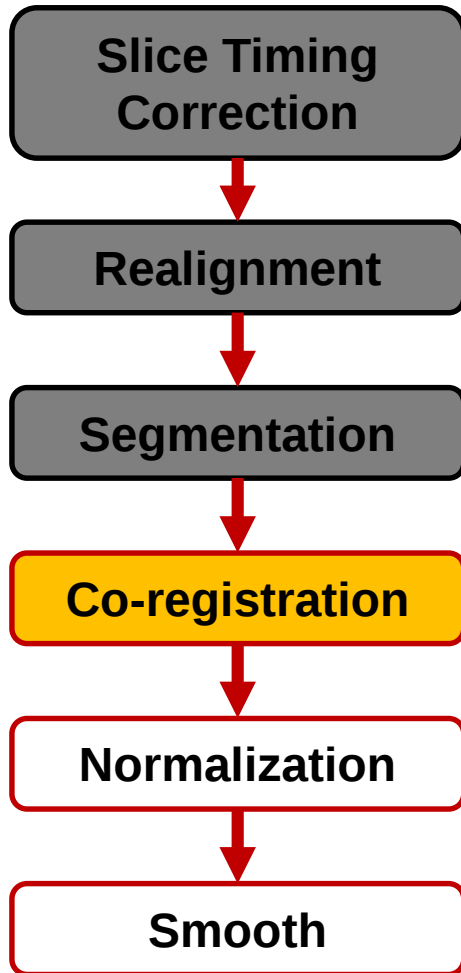
Specify...

Affine Regularisation : ICBM space template – East Asian Brains

Deformation Fields : Forward (subject T1 → template)

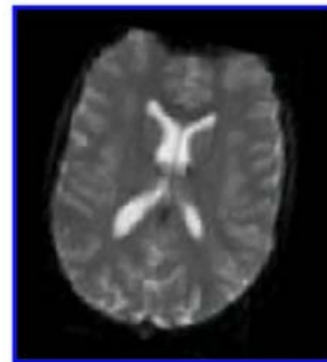
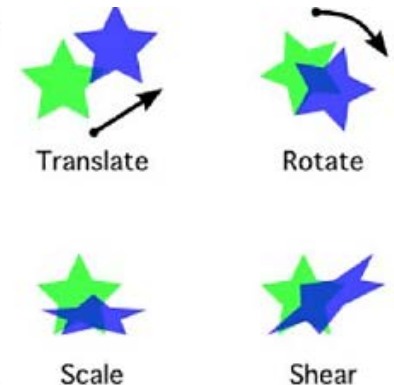
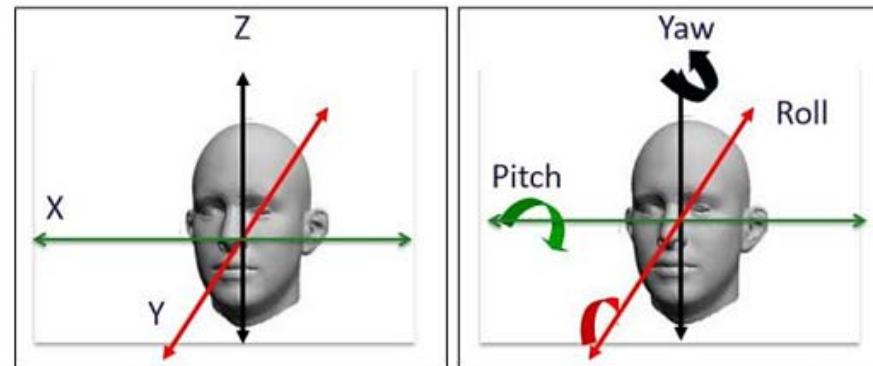
Affine Regularisation
The procedure using the Disal, 2004) is u
that if the procedure is to be initialised with the affine registration, then the data should not be too corrupted with this artifact. If there is a lot of intensity non-uniformity, then manually position your image in order to achieve closer starting estimates, and turn off the affine registration.

Co-registration (cross-modality registration)

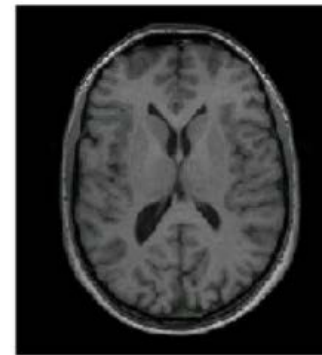


Align fMRI (EPI) data to structural (T1W) image.

- Matching modalities in individual subjects
- Rigid body transformation using mutual information

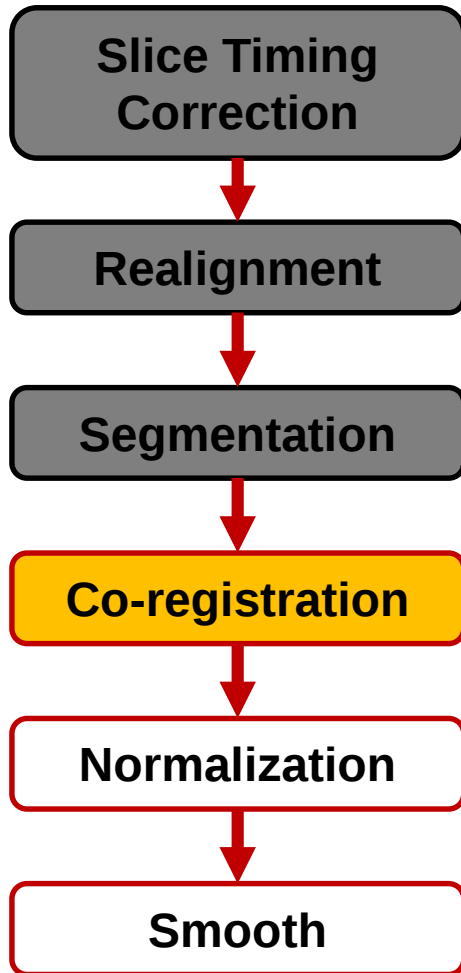


T2*W EPI images
(**low resolution** & poor
structural information)



T1W structural images
(**high resolution**)

Co-registration (cross-modality registration)



Batch Editor

File Edit View SPM BasicIO

Module List

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

Current Module: Coregister: Estimate

Help on: Coregister: Estimate

Data dependency

Reference Image: DEP Segment: Bias Corrected (1)

Source Image: DEP Realign: Estimate & Reslice: Mean Image

Other Images: DEP Realign: Estimate & Reslice: Resliced Images (Sess 1)

Estimation Options

. Objective Function: Normalised Mutual Information

. Separation: [4 2]

. Tolerances: 1x12 double

. Histogram Smoothing: [7 7]

Match to Reference Image

Reference Image : bias corrected T1W images (m*.nii)

Source Image : mean EPI volume (mean*.nii)

Other Images : intra-session realigned EPI volumes (ra*.nii)

* Fitting fMRI data (source image) to T1W structural images (reference image)

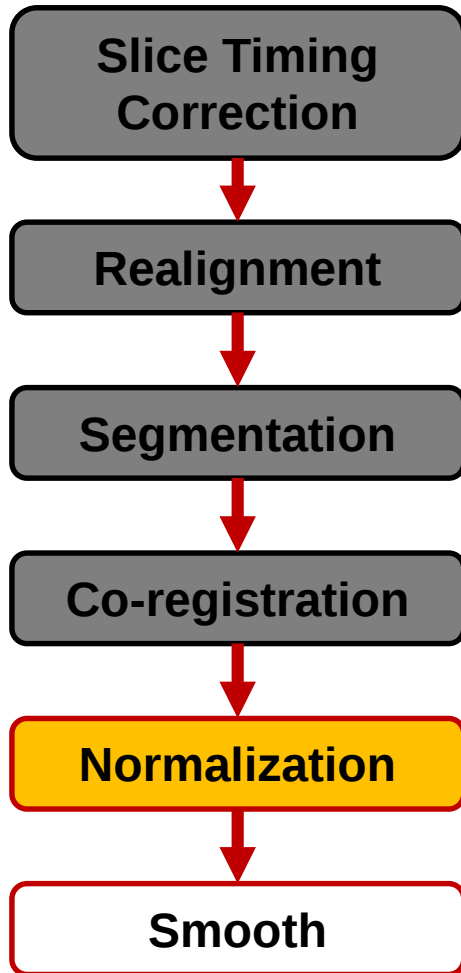
Specify...

Dependency

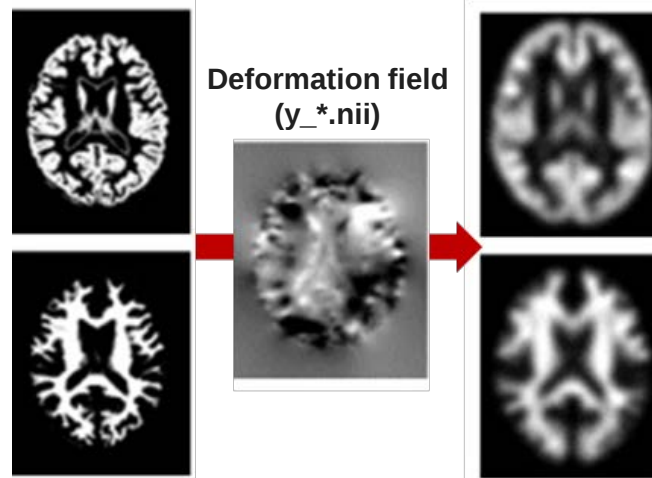
Reference Image

This is the image that is assumed to remain stationary (sometimes known as the target or template image), while the source image is moved to match it.

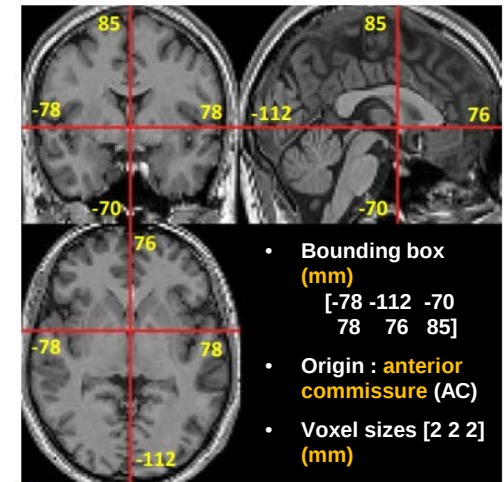
Normalization (native space → standard space)



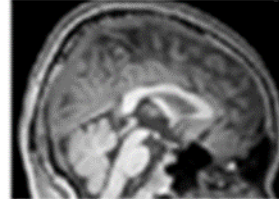
Apply deformation field



Bounding box & origin

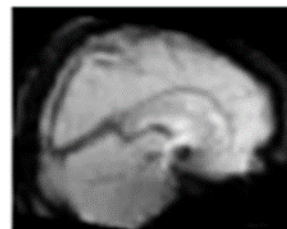
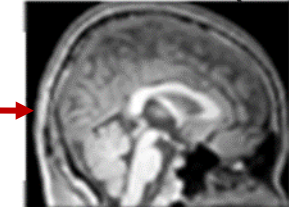


Bias corrected T1 (m*.nii)

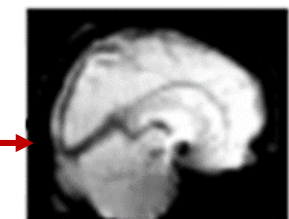


Deformation field (y_*.nii)

Normalized T1 (wm*.nii)



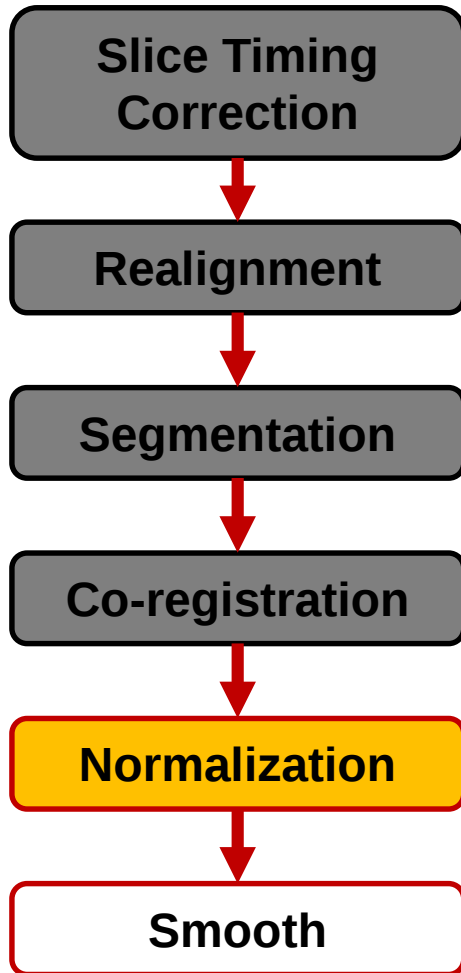
Deformation field (y_*.nii)



Co-registered EPI volumes

Normalized EPI volumes (wra*.nii)

Normalization (native space → standard space)



Batch Editor
File Edit View SPM BasicIO

Module List

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

Current Module: Normalise: Write

Help on: Normalise: Write

Data

Subject

Deformation Field DEP Segment: Forward Deformations

Images to Write DEP Coregister: Estimate: Coregistered Images

Data dependency

Bounding box 2x3 double

Voxel sizes [2 2 2]

Interpolation 4th Degree B-Spline

Filename Prefix W

Current Item: Bounding box

-78 -112 -70

78 76 85

Specify...

Bounding box
The bounding box (in mm) of the volume which is to be written (relative to the anterior commissure).

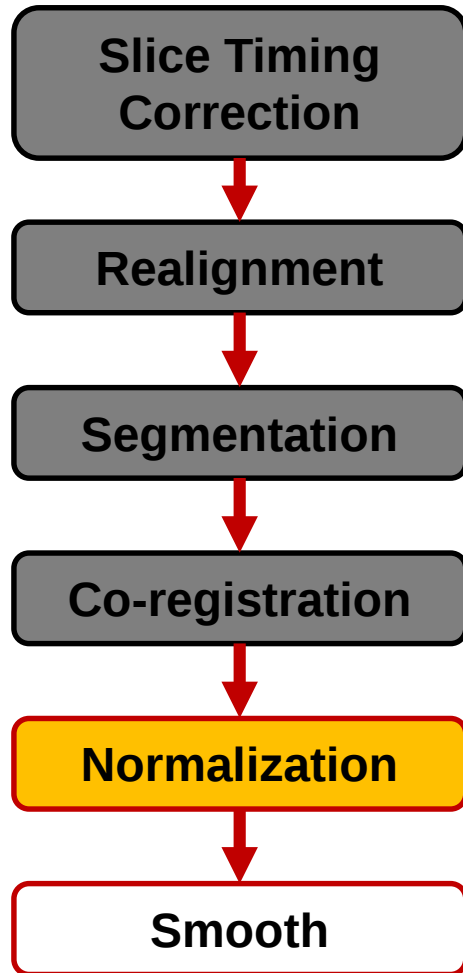
Th
@
Re
An

Deformation Field : forward deformation matrix (y_*.nii)
Images to write : co-registered EPI volume
Filename Prefix: create wra*.nii files after this step

85 85 78 78 -112 -112 -70 -70 76 76

- Bounding box (mm) [-78 -112 -70 78 76 85]
- Origin : anterior commissure (AC)
- Voxel sizes [2 2 2] (mm)

Normalization (native space → standard space)



Batch Editor

File Edit View SPM BasicIO

Module List

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

Current Module: Normalise: Write

Help on: Normalise: Write

Data

. Subject

. Deformation Field DEP Segment: Forward Deformations

. Images to Write DEP Segment: Bias Corrected (1)

Writing Options

. Bounding box 2x3 double

. Voxel sizes [2 2 2]

. Interpolation 4th Degree B-Spline

. Filename Prefix W

Data dependency

Current Item: Bounding box

-78 -112 -70

78 76 85

Specify...

Bounding box

The bounding box (in mm) of the volume which is to be written (relative to the anterior commissure).

Th
@
Re
An

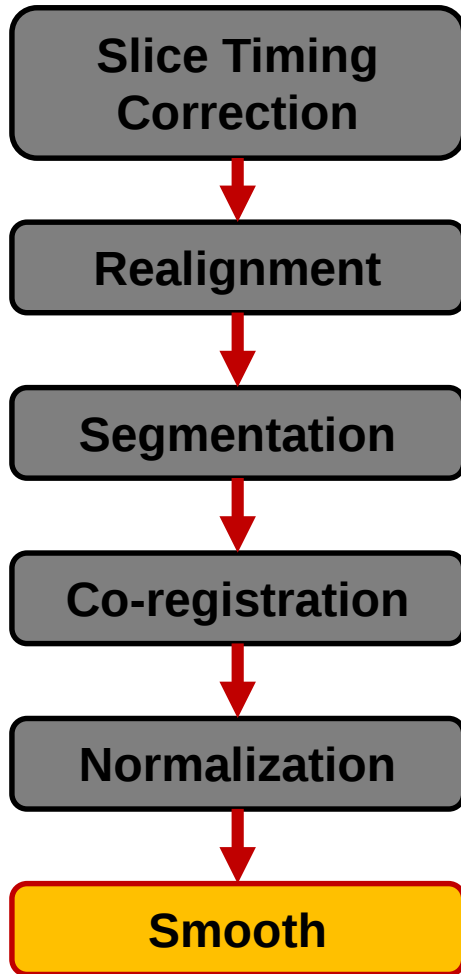
Deformation Field : forward deformation matrix ($y_*.nii$)

Images to write : bias corrected T1 volume ($m_*.nii$)

Filename Prefix: create wm*.nii files after this step

- Bounding box (mm) [-78 -112 -70 78 76 85]
- Origin : anterior commissure (AC)
- Voxel sizes [2 2 2] (mm)

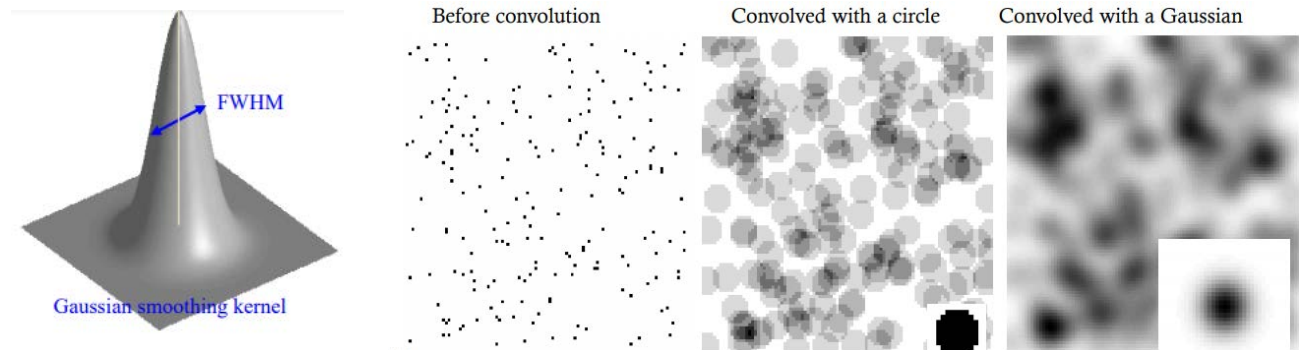
Gaussian Spatial Smoothing



(stamp)

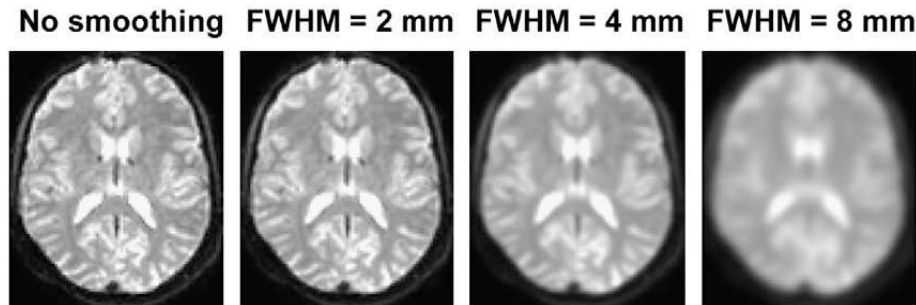
Apply Gaussian kernel smoothing to the normalized EPI volumes

- Each voxel becomes weighted average of surrounding voxels
- Compensate for inaccuracies in normalization between individuals
- Increase signal-to-noise ratio (SNR)

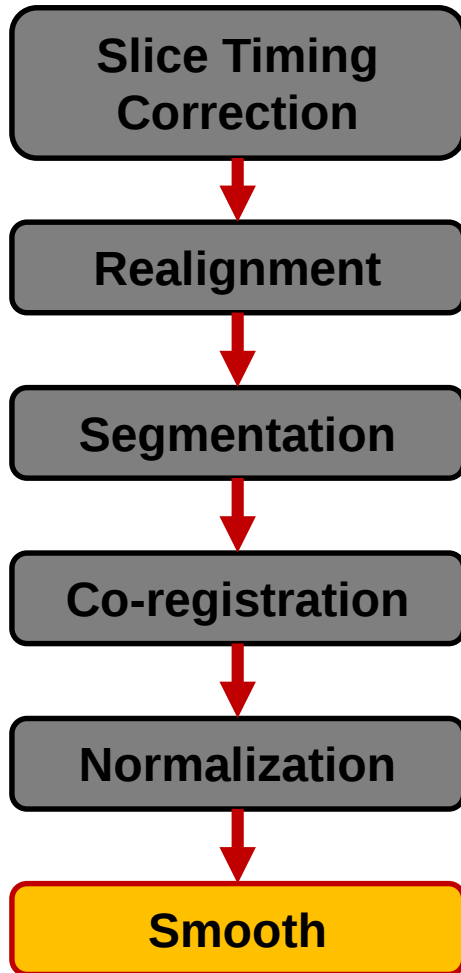


FWHM (full width half maximum)

- Mainly 5-10 mm FWHM (2 to 3 voxels)
- Smoothing process may be skipped when the target brain region is small.
(i.e. amygdala, deep nucleus)



Gaussian Spatial Smoothing



Batch Editor

File Edit View SPM BasicIO

Module List

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

Current Module: Smooth

Help on: Smooth

Images to Smooth DEP Normalise: Write: Normalised Images (Subj 1)

FWHM [5 5 5]

Data Type SAME

Implicit masking No

Filename Prefix s

Data dependency

Images to Smooth : Normalized EPI volumes (wra*.nii)

FWHM : mainly 5-8 (mm)

Filename Prefix: create swra*.nii files after this step

Specify...

Dependency

Images to Smooth

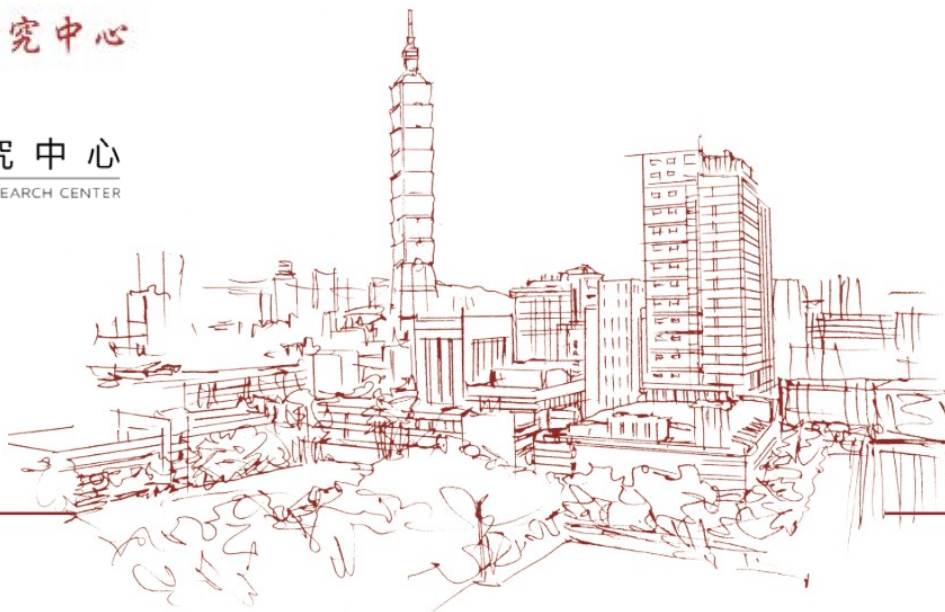
Specify the images to smooth. The smoothed images are written to the same subdirectories as the original images and are prefixed with a 's'. The prefix can be changed by an option setting.



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Analysis of Functional Magnetic Resonance Imaging (fMRI) Set up SPM Batch Jobs



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SPM Batch Jobs

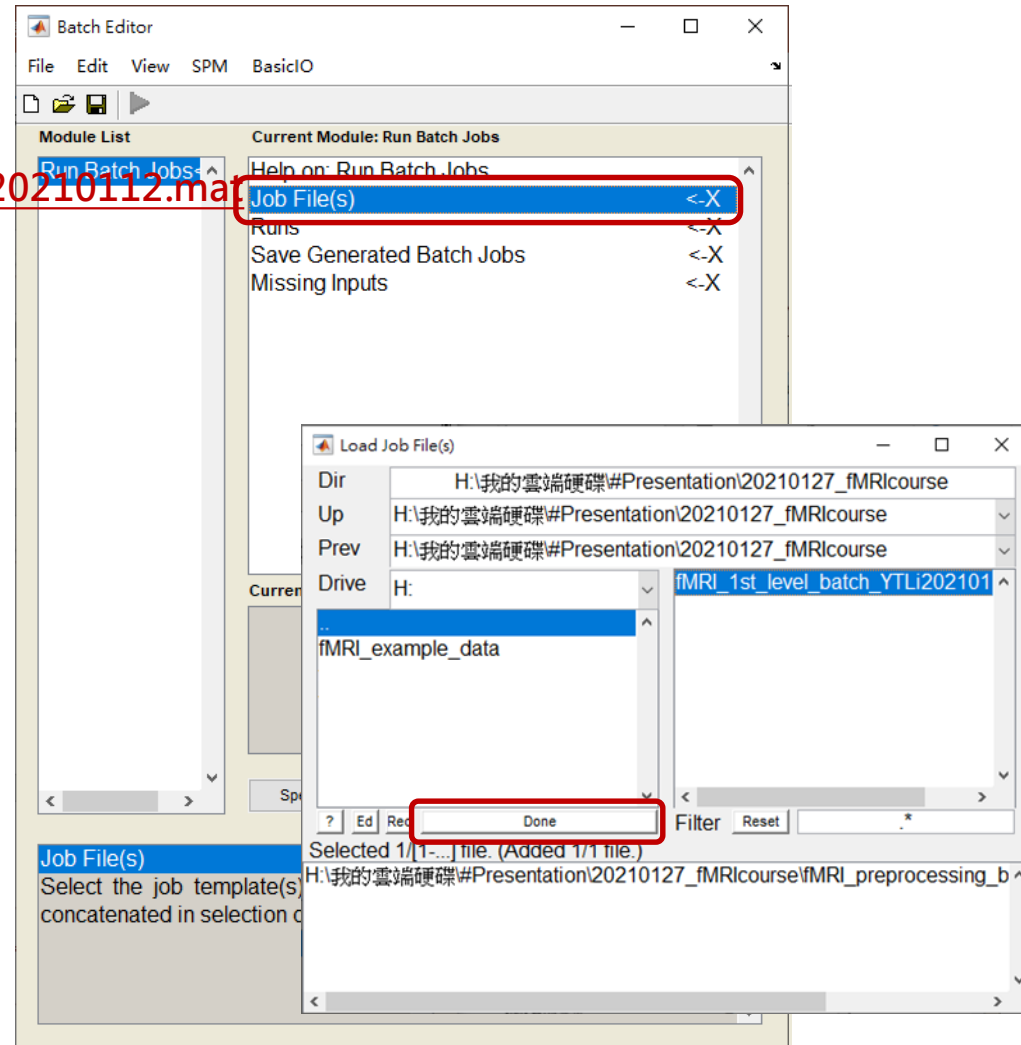
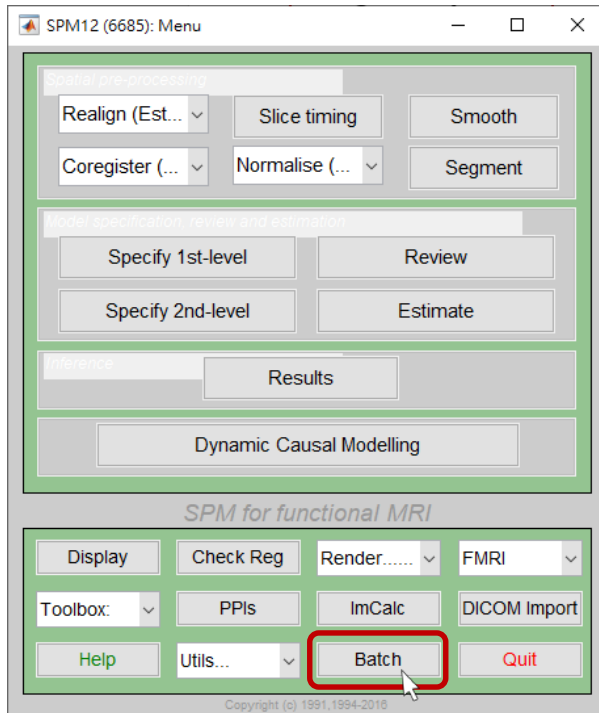
>> spm fmri

> Batch

> BasicIO > Run > Run Batch Jobs

> fMRI_preprocessing_batch_YTLi20210112.mat

> Done



SPM Batch Jobs

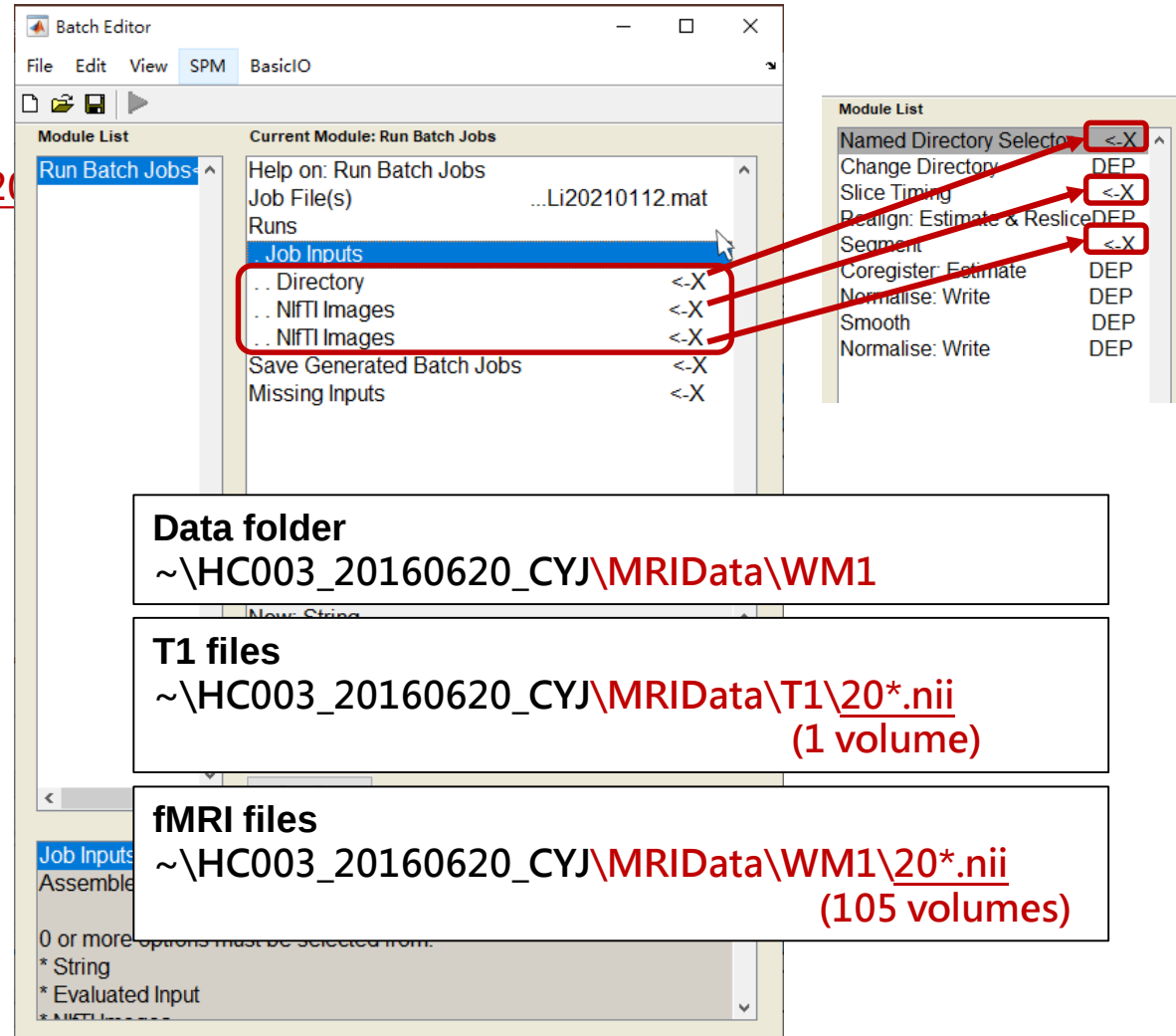
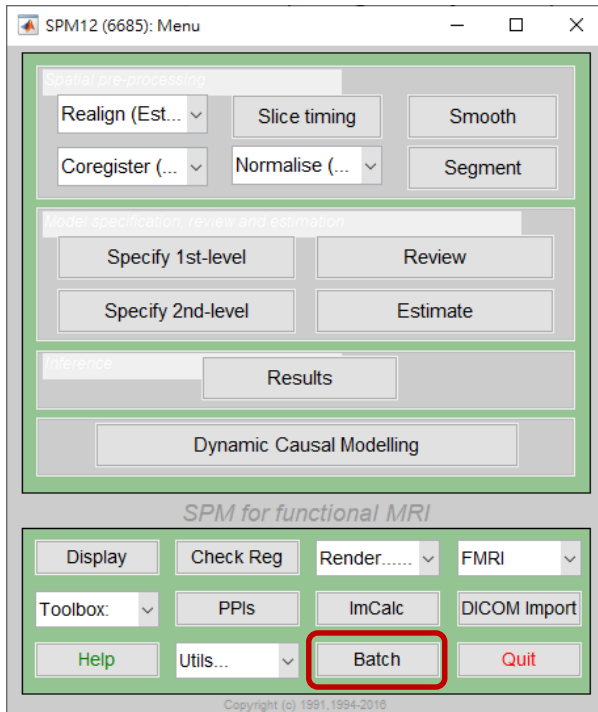
>> spm fmri

> Batch

> BasicIO > Run > Run Batch Jobs

> fMRI_preprocessing_batch_YTLi20160620

> Done



Data folder

~\HC003_20160620_CYJ\MRIData\WM1

T1 files

~\HC003_20160620_CYJ\MRIData\T1\20*.nii
(1 volume)

fMRI files

~\HC003_20160620_CYJ\MRIData\WM1\20*.nii
(105 volumes)

SPM Batch Jobs

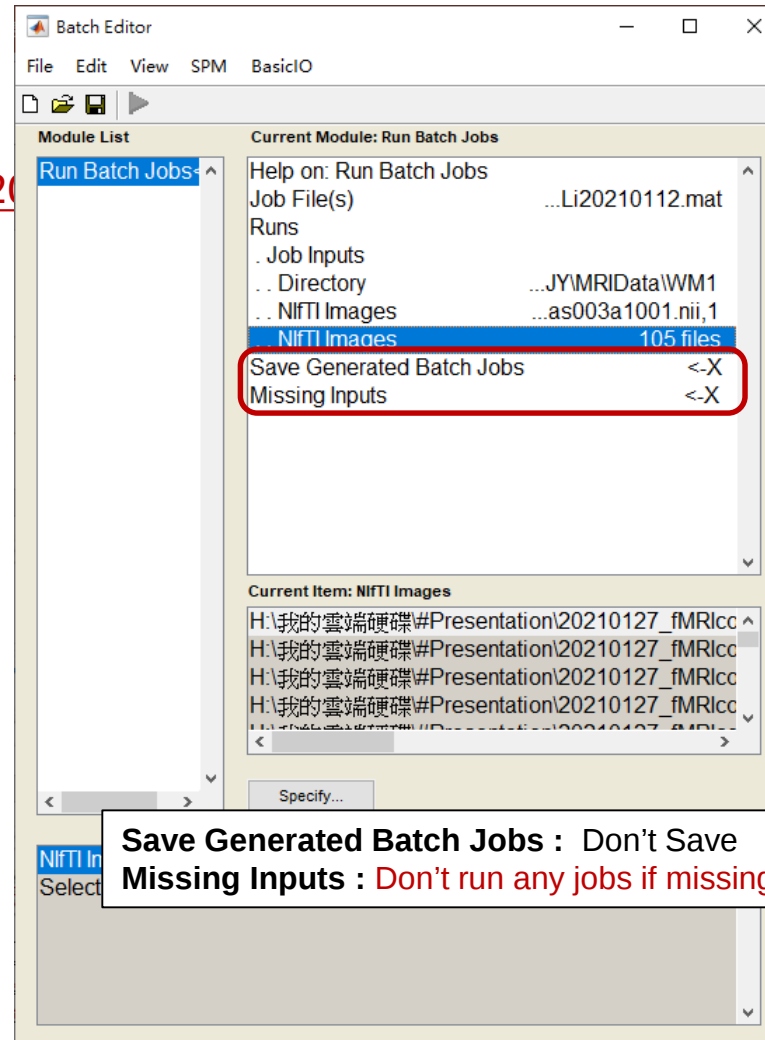
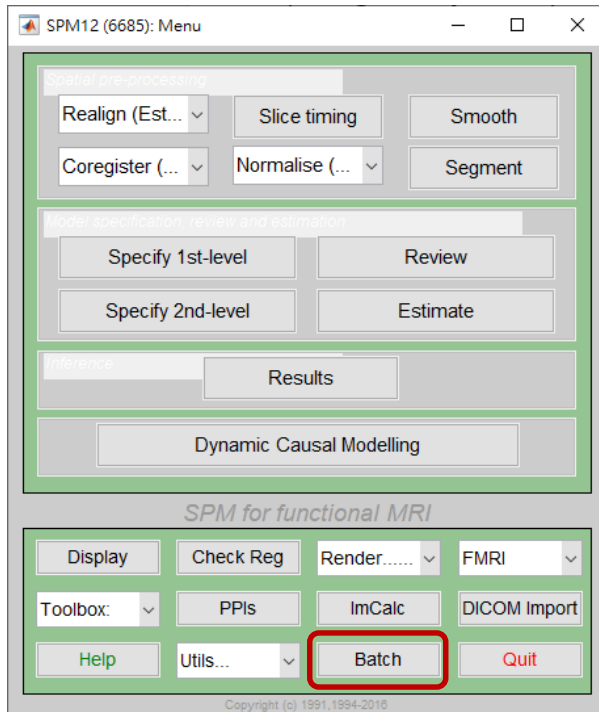
>> spm fmri

> Batch

> BasicIO > Run > Run Batch Jobs

> fMRI_preprocessing_batch_YTLi20

> Done



Save Generated Batch Jobs : Don't Save
Missing Inputs : Don't run any jobs if missing inputs

SPM Batch Jobs

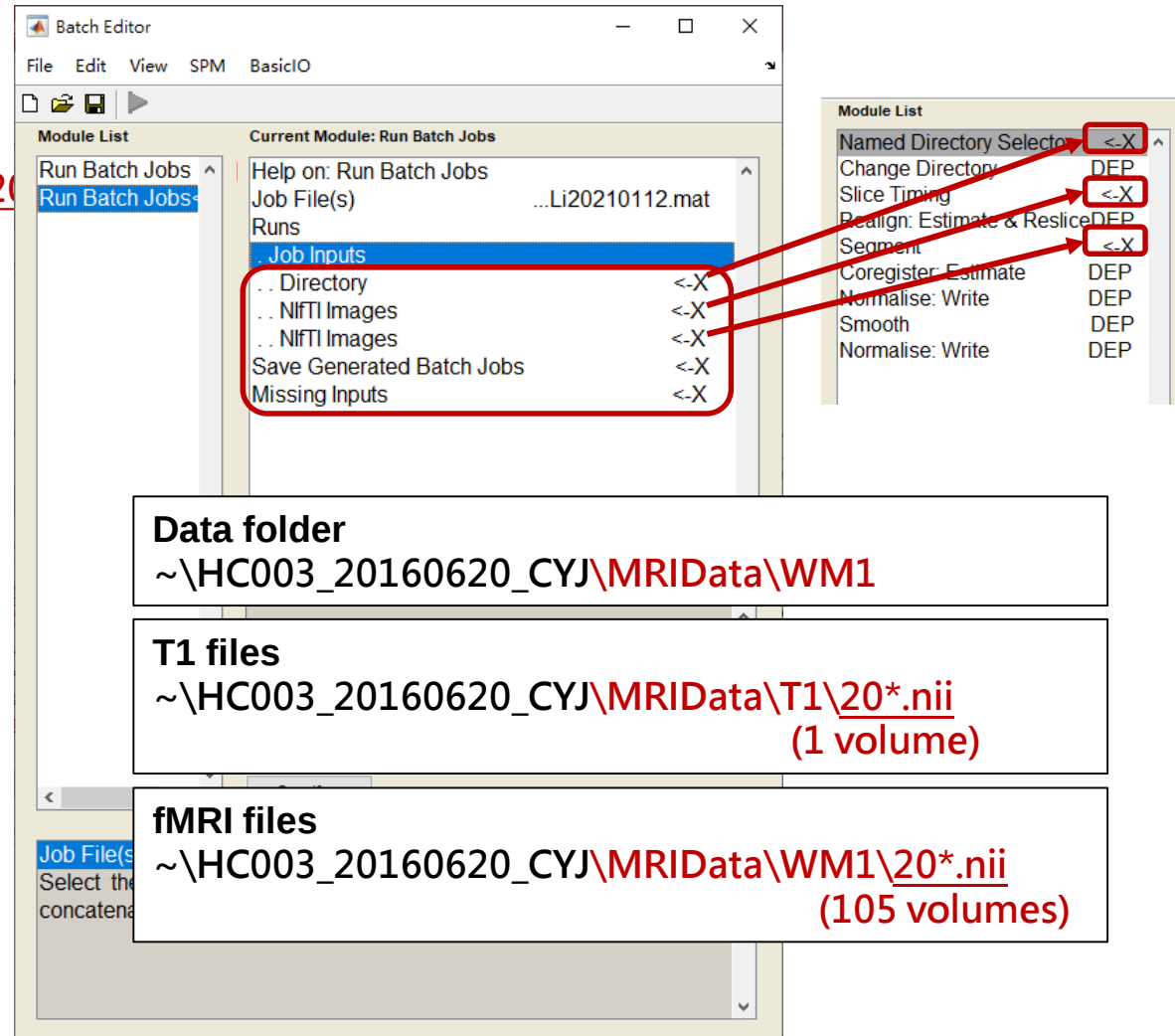
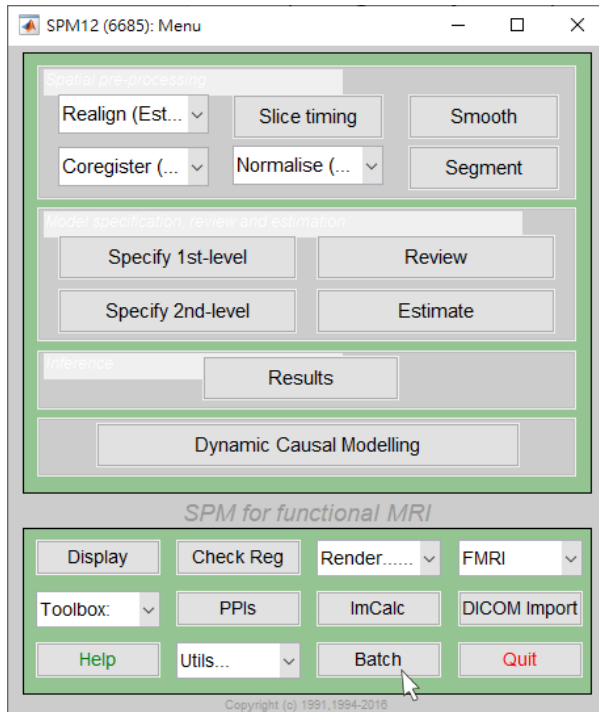
>> spm fmri

> Batch

> BasicIO > Run > Run Batch Jobs

> fMRI_preprocessing_batch_YTLi20160620

> Done



SPM Batch Jobs

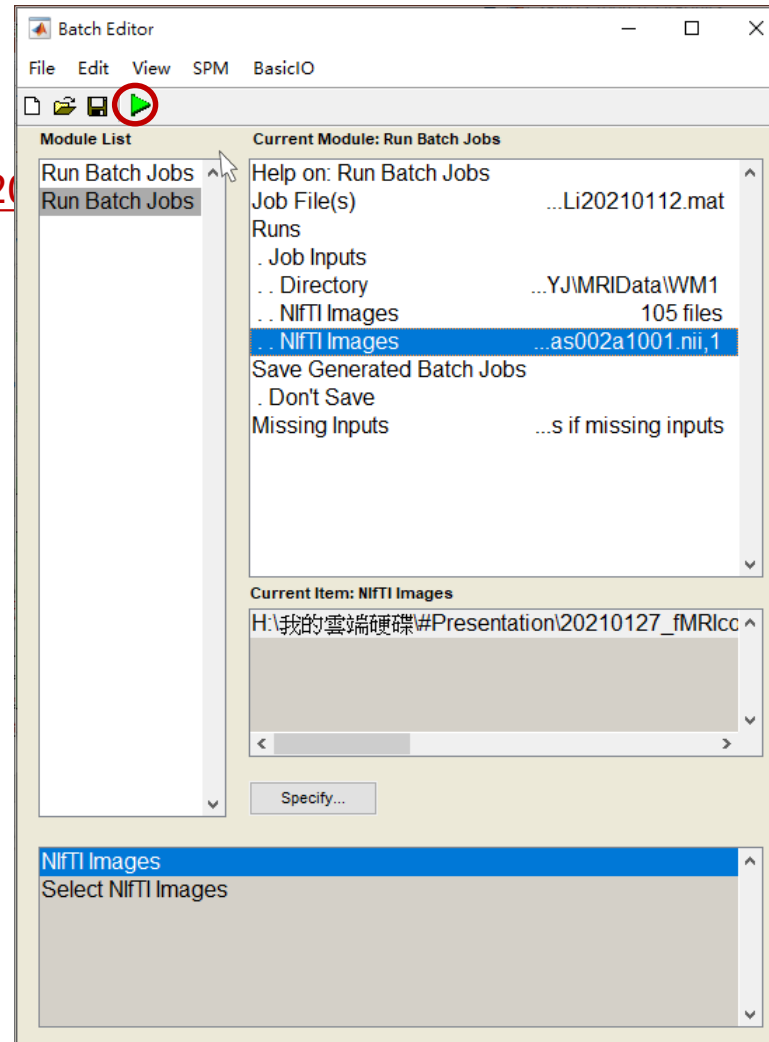
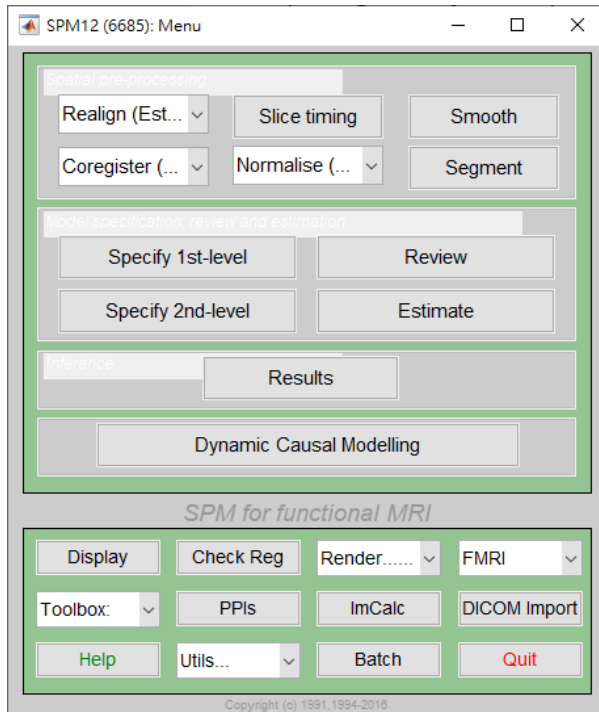
>> spm fmri

> Batch

> BasicIO > Run > Run Batch Jobs

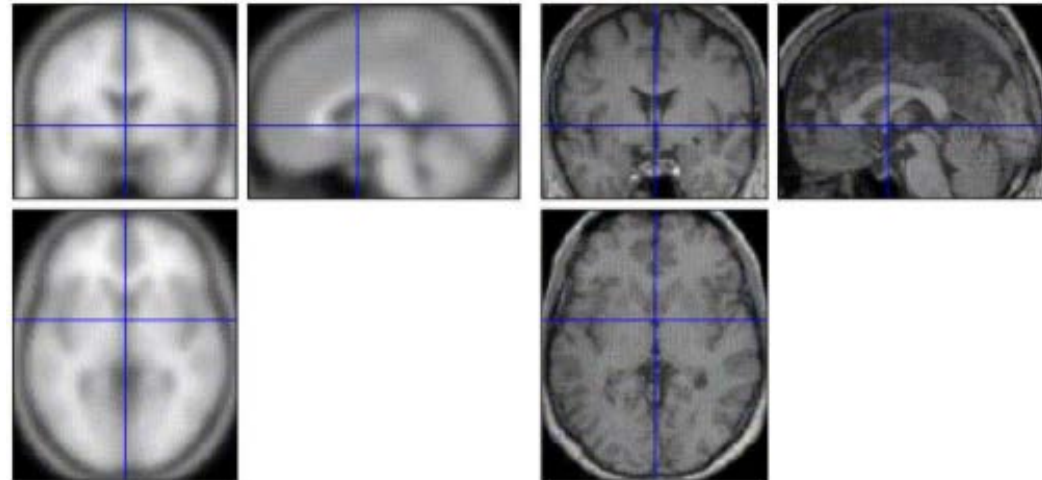
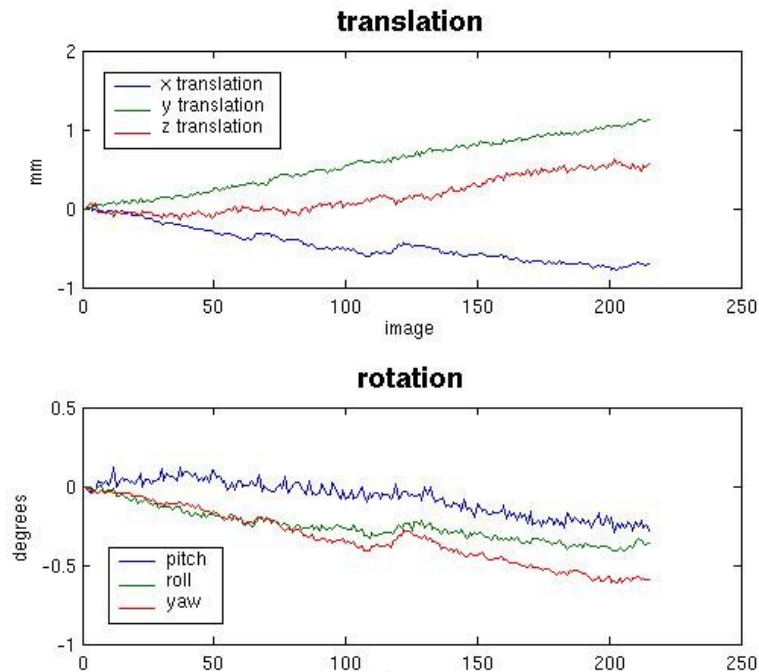
> fMRI_preprocessing_batch_YTLi20

> Done



Check SPM processing logfile

- SPM processing logfile (**spm_Date.ps**)
- Convert *.ps file to *.pdf file (<https://online2pdf.com/convert-ps-to-pdf>)

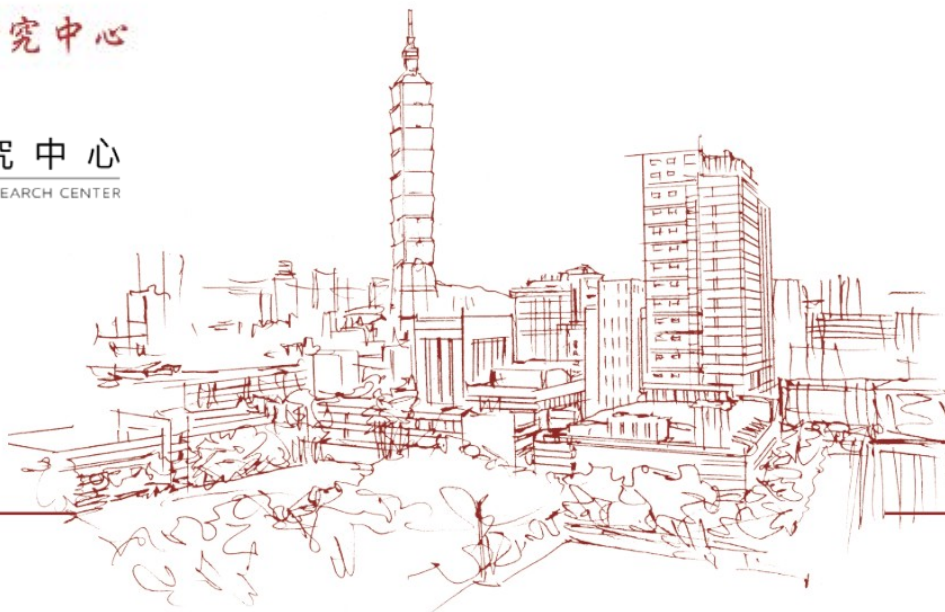




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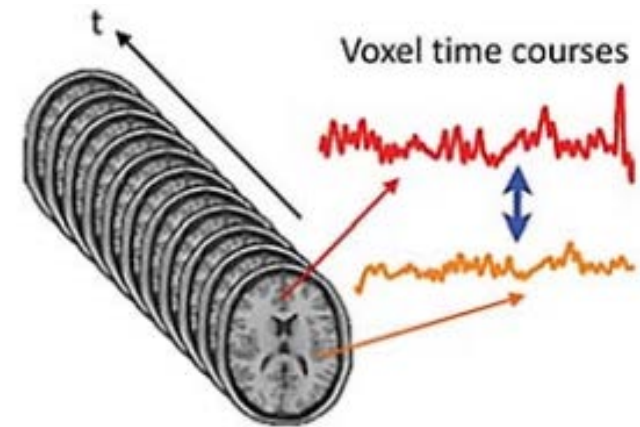
Analysis of Functional Magnetic Resonance Imaging (fMRI) General Linear Model (1st level analysis)



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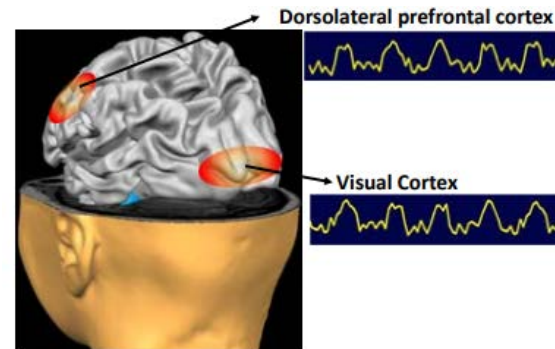
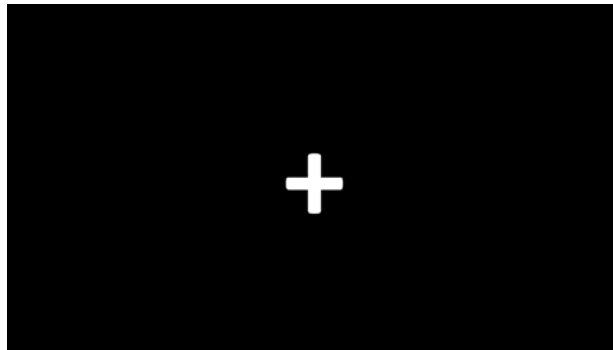
fMRI Protocol (see DICOM tags)

- (0008,0070) Manufacturer : SIEMENS
- (0018,0087) Magnetic Field Strength : 3 (T)
- (0008,1090) Manufacturer's Model Name : Prisma
- (0018,0024) Sequence Name : *epfid2d1_70 → 2D GRE EPI
- (0018,0080) Repetition Time : 2000 (ms)
- (0018,0081) Echo Time : 20 (ms)
- (0018,1314) Flip Angle : 90 (°)
- (0028,0030) Pixel Spacing : 3\3 (mm)
- (0028,0010) Rows : 64
- (0028,0011) Column : 64
- (0018,0088) Spacing Between Slices : 3.5 (mm)
- (0018,0050) Slice Thickness : 3.5 (mm)
- (0019,100A) Number of Image in Mosaic : 40 (slices)



fMRI Protocol (experimental design)

- N-back Verbal Working Memory Task ($N = 1$ or 2)



A. Block design fMRI



B. Visual presentation

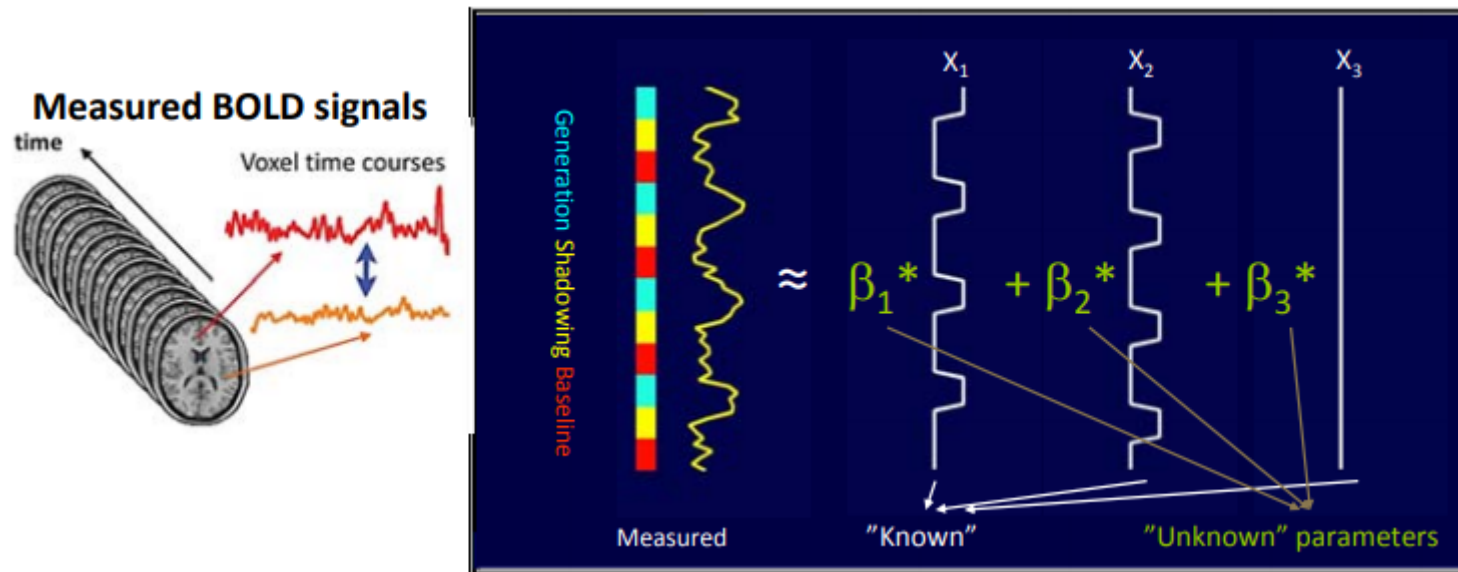


C. Response targets of N-back task



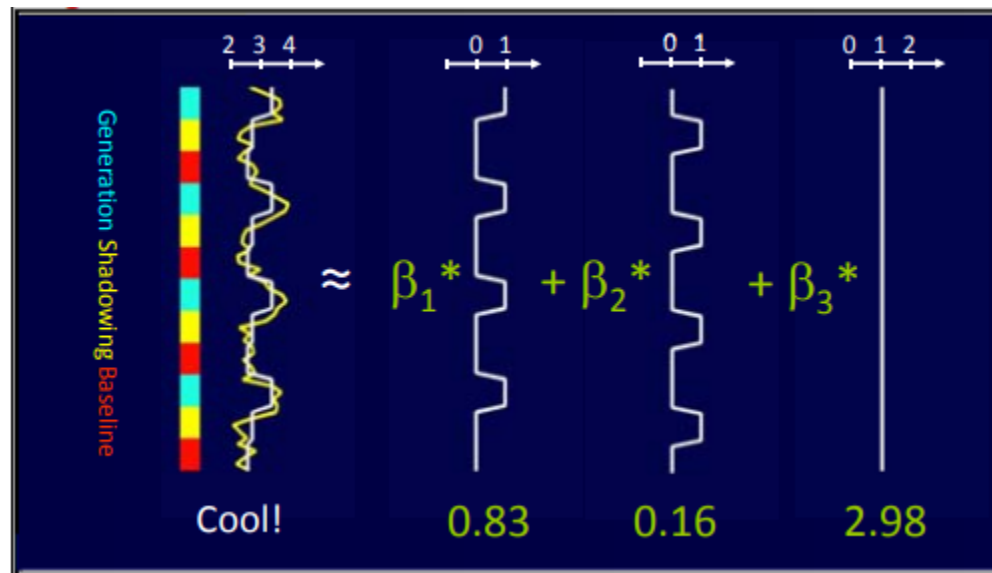
General Linear Model (GLM)

- Finding the linear combination of these hypothetical time series “best” fits the fMRI time series.



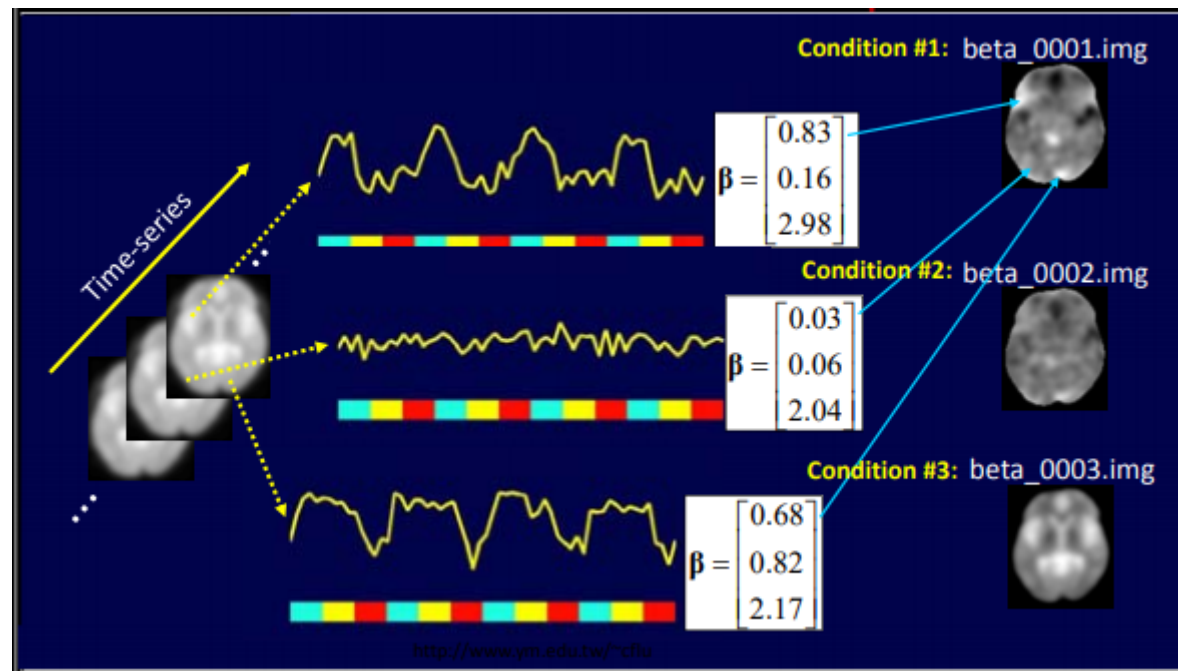
General Linear Model (GLM) parameter estimation

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



General Linear Model (GLM) parameter estimation

- Apply the same model to all voxels.
- Different parameters (beta value) for each voxel.
- Beta map for each task condition.



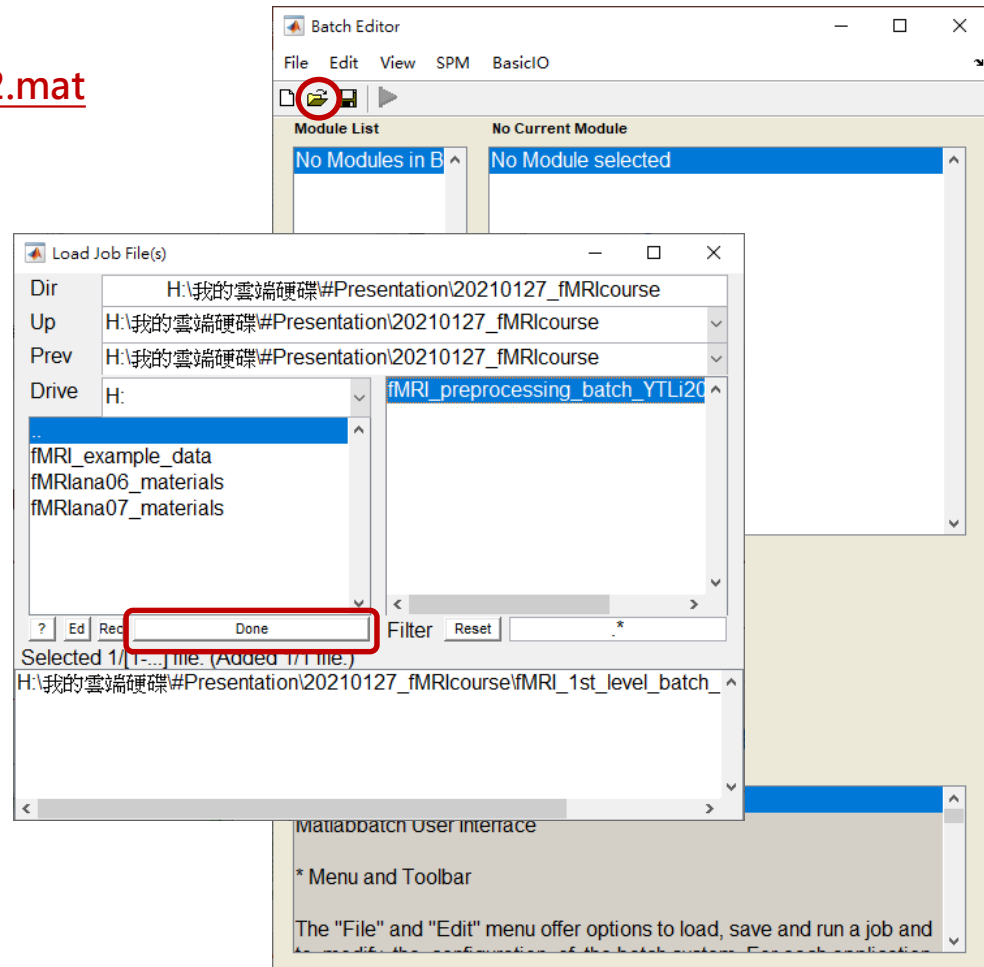
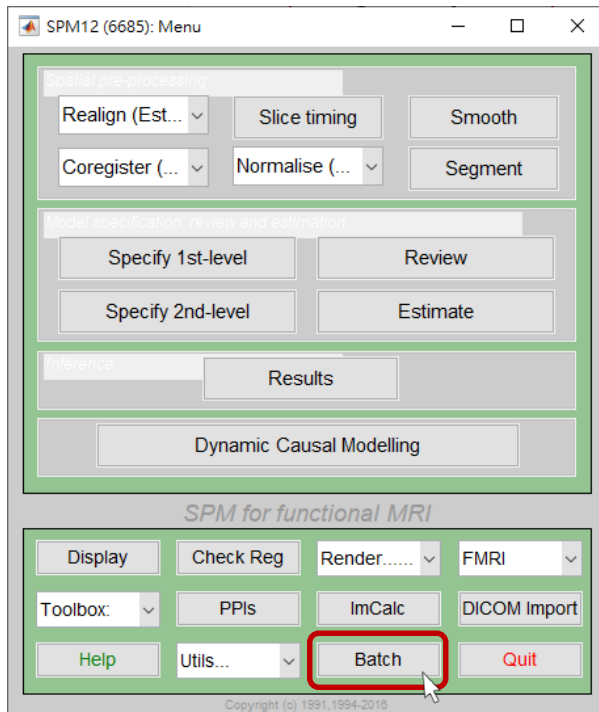
Specify 1st-level Analysis Model

>> spm_fmri

> Batch

> fMRI_1st_level_batch_YTLi20210112.mat

> Done



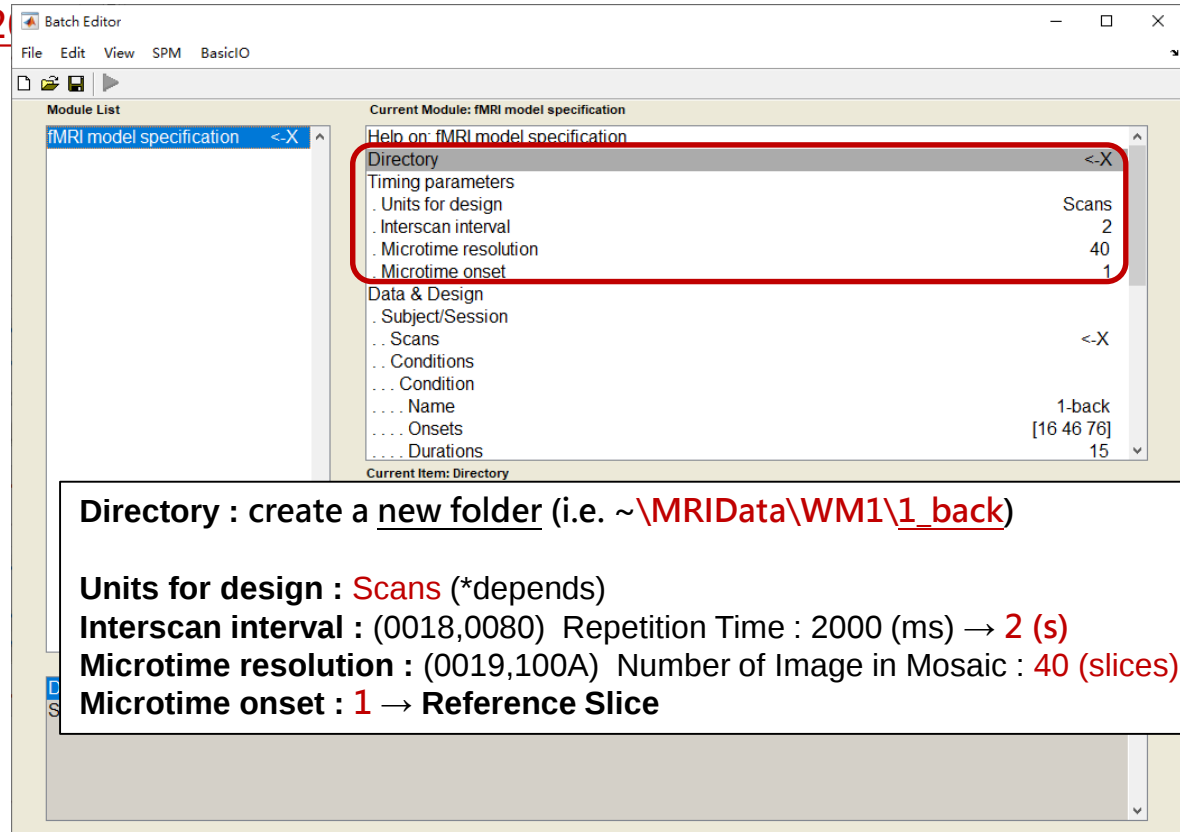
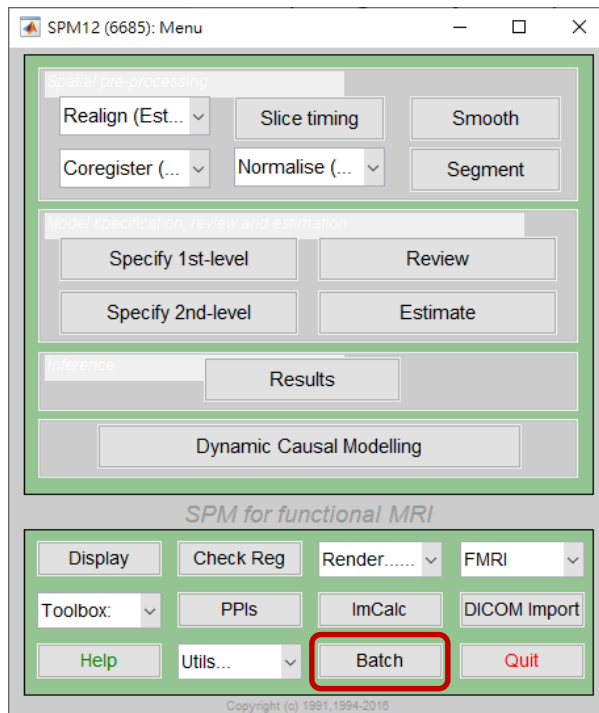
Specify 1st-level Analysis Model

>> spm fmri

> Batch

> fMRI_preprocessing_batch_YTLi2

> Done



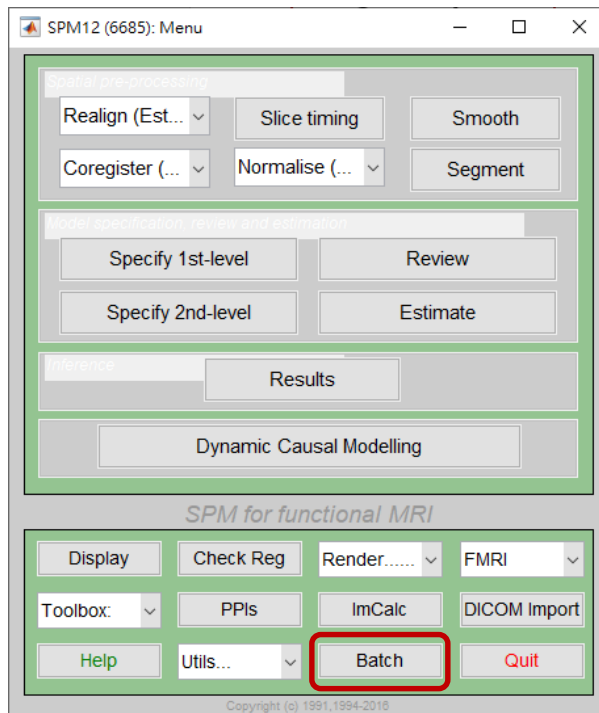
Specify 1st-level Analysis Model

>> spm fmri

> Batch

> fMRI_preprocessing_batch_YTLi2

> Done



A. Block design fMRI

Batch Editor

File Edit View SPM BasicIO

Module List

Current Module: fMRI model specification

Data & Design

Subject/Session

Scans <-X

Conditions

Condition

Name 1-back

Onsets [16 46 76]

Durations 15

Time Modulation No Time Modulation

Parametric Modulations

Orthogonalise modulations Yes

Multiple conditions

Regressors

Multiple regressors <-X

High-pass filter 128

Current Item: Masking threshold

Scans : ~\HC003_20160620_CYJ\MRIData\WM1\swra*.nii
(105 fMRI volumes)

Name : 1-back

Onsets : [16 46 76] (scans → depends on “Units for Design”)

Durations : 15 (scans for a stimulus block → depends on “Units for Design”)

Multiple regressors : head motion log file (r_p*.txt)

Rear numbers are entered.
An 1-by-1 array must be entered.

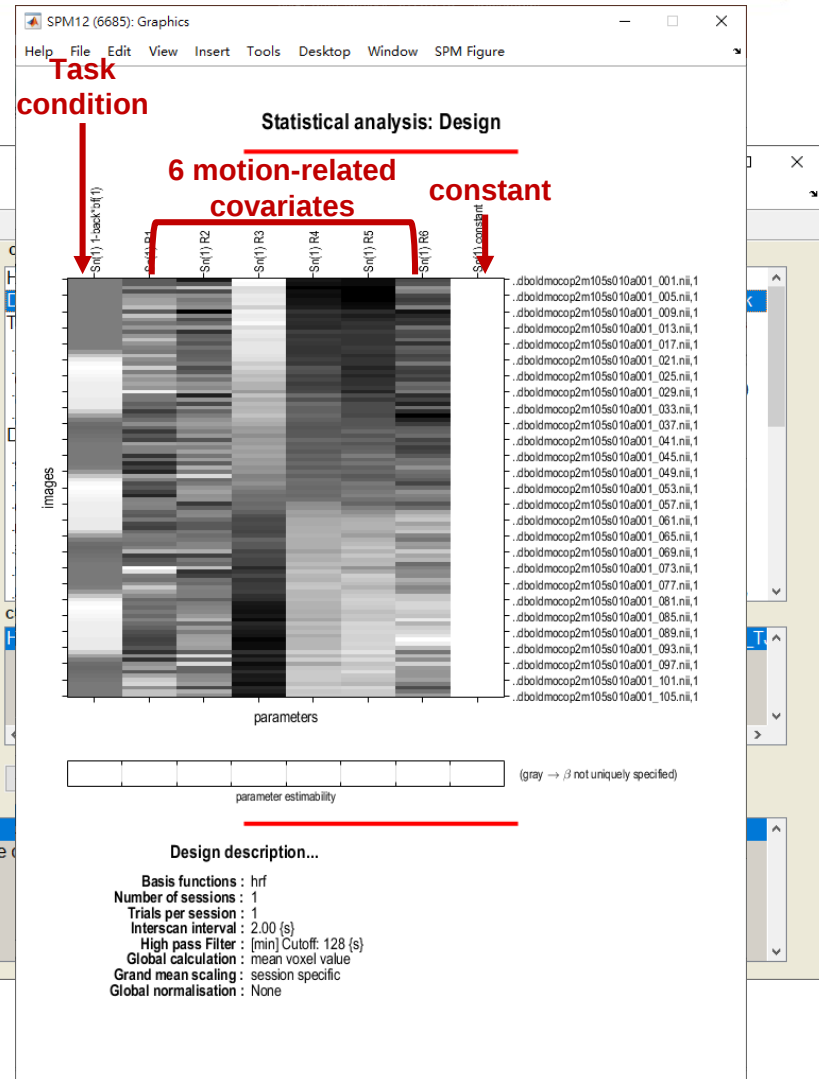
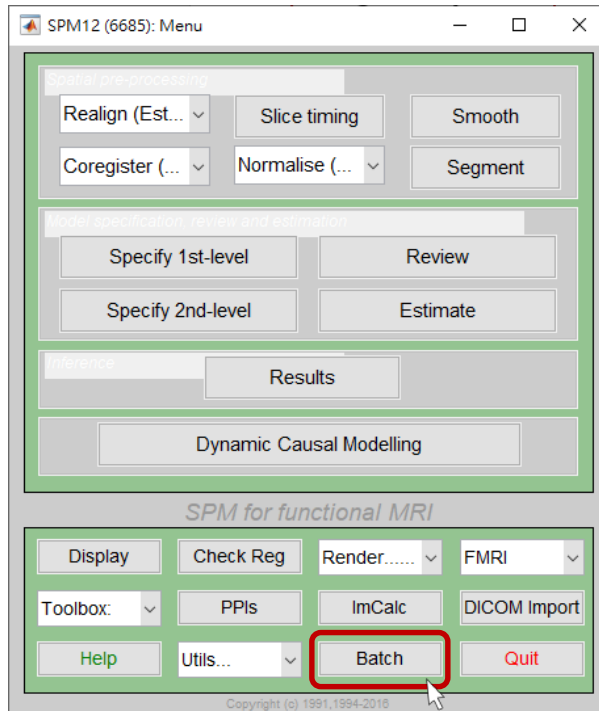
Specify 1st-level Analysis Model

>> spm fmri

> Batch

> fMRI_preprocessing_batch_YTLi2

> Done



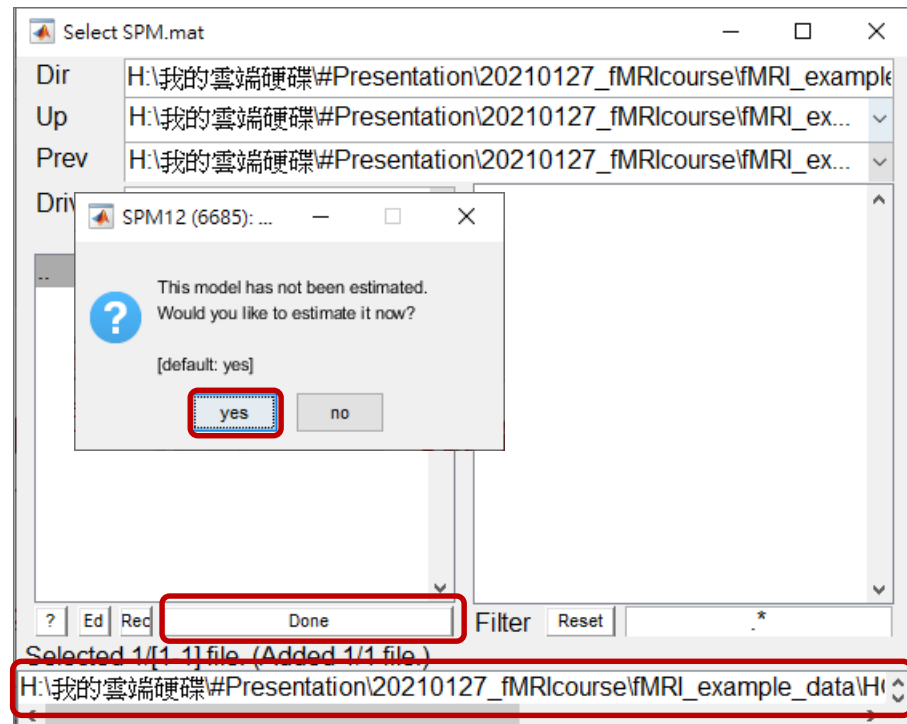
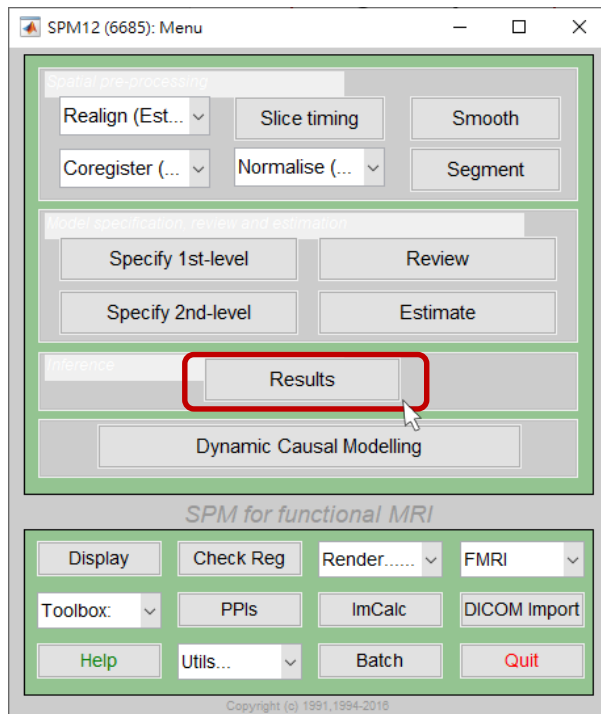
Estimate Model Parameters

>> spm fmri

> Results

> SPM.mat

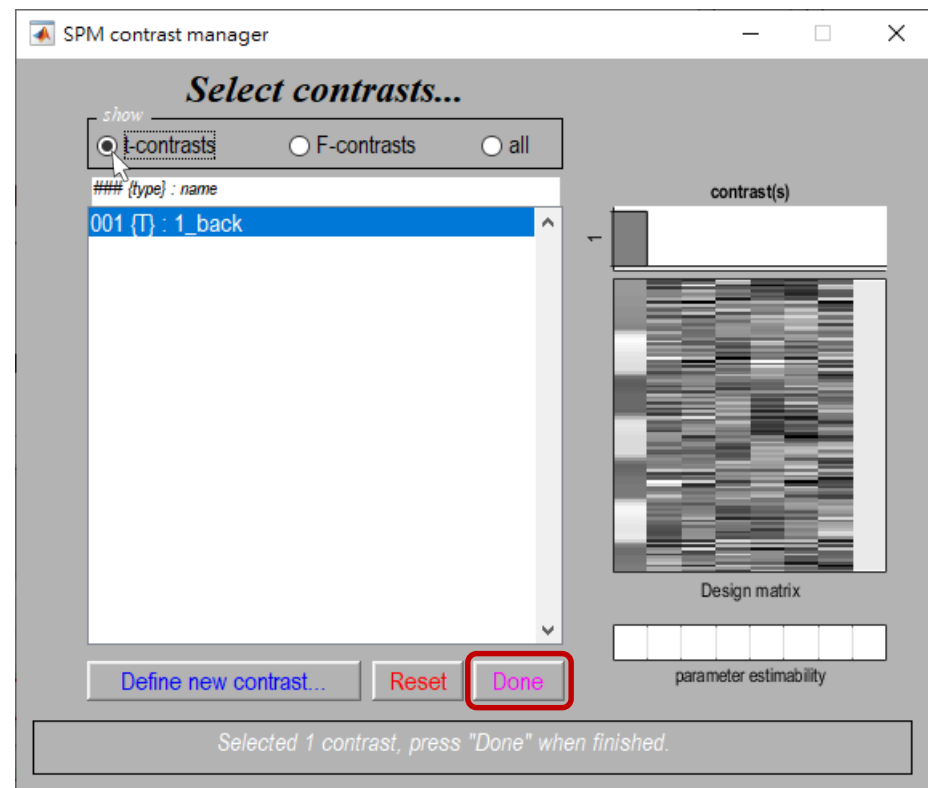
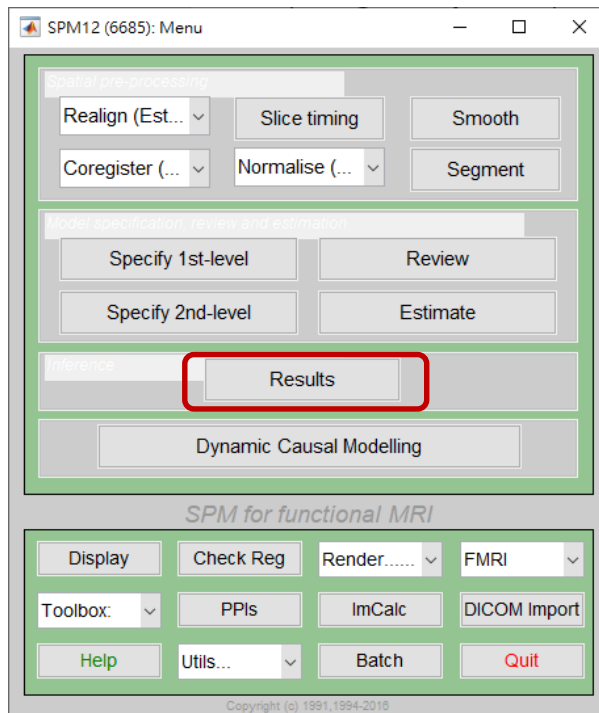
> Done



Estimate Model Parameters

>> spm fmri

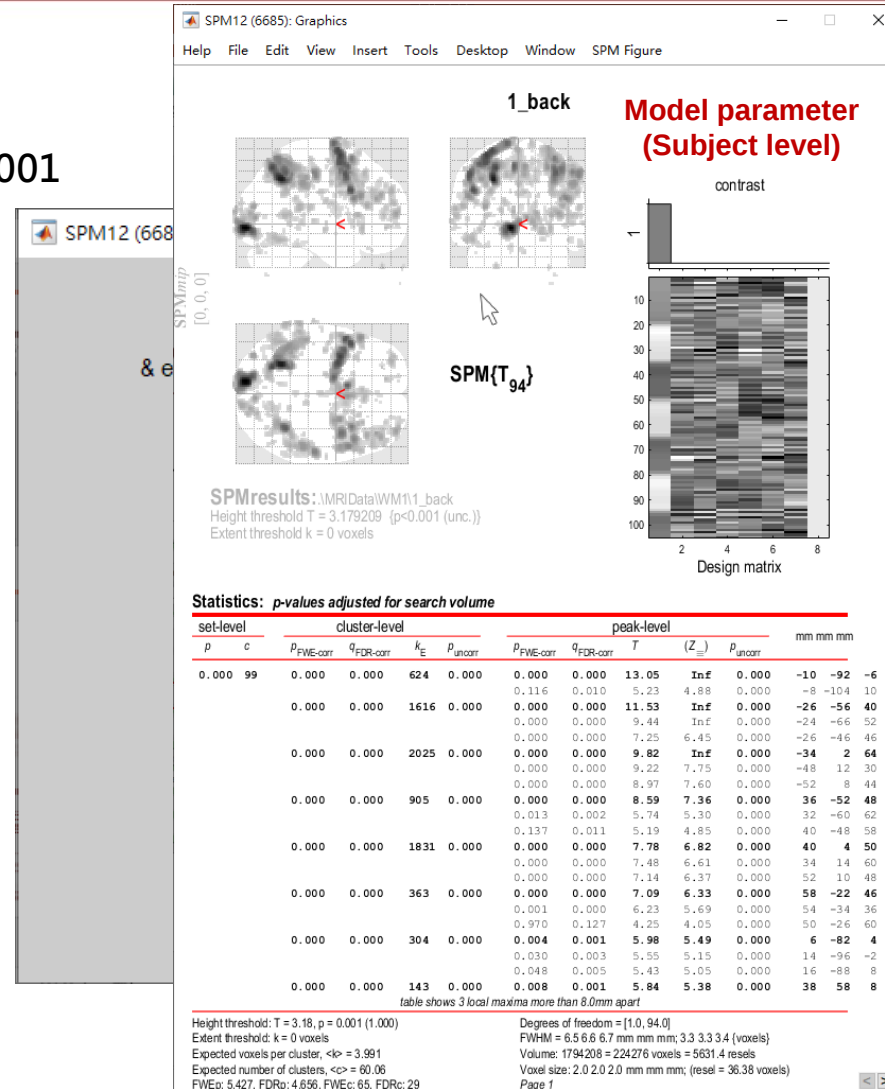
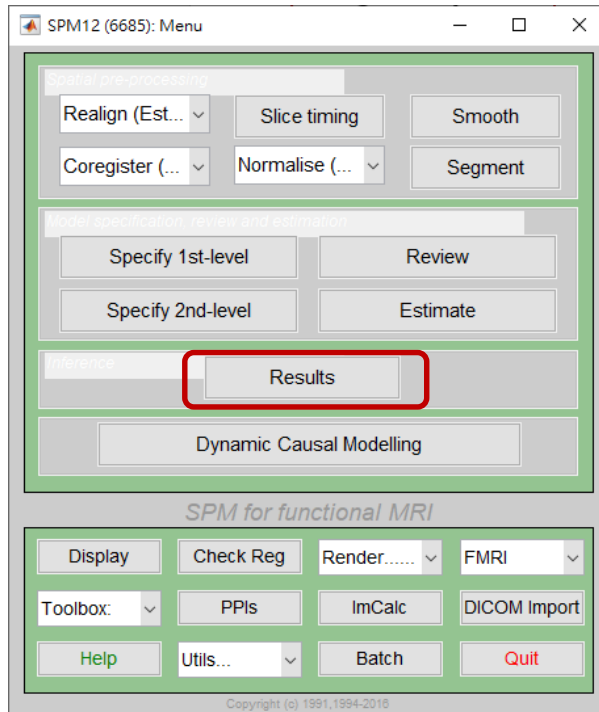
- > t-contrasts
- > Define new contrast...
- > Done



Estimate Model Parameters

>> spm_fmri

- > apply masking : none
- > threshold {T or p value} : none, 0.001
- > & extent threshold {voxels} : 0

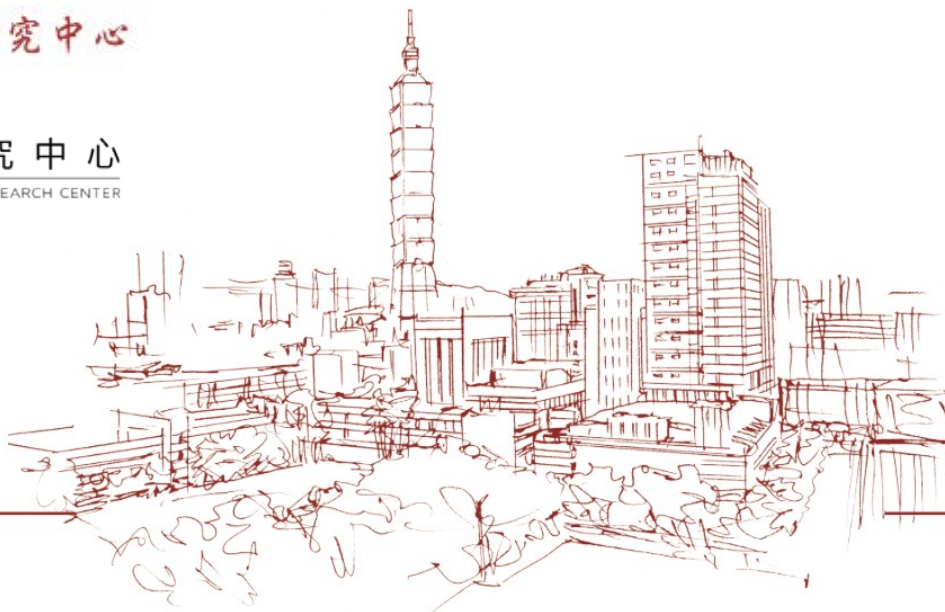




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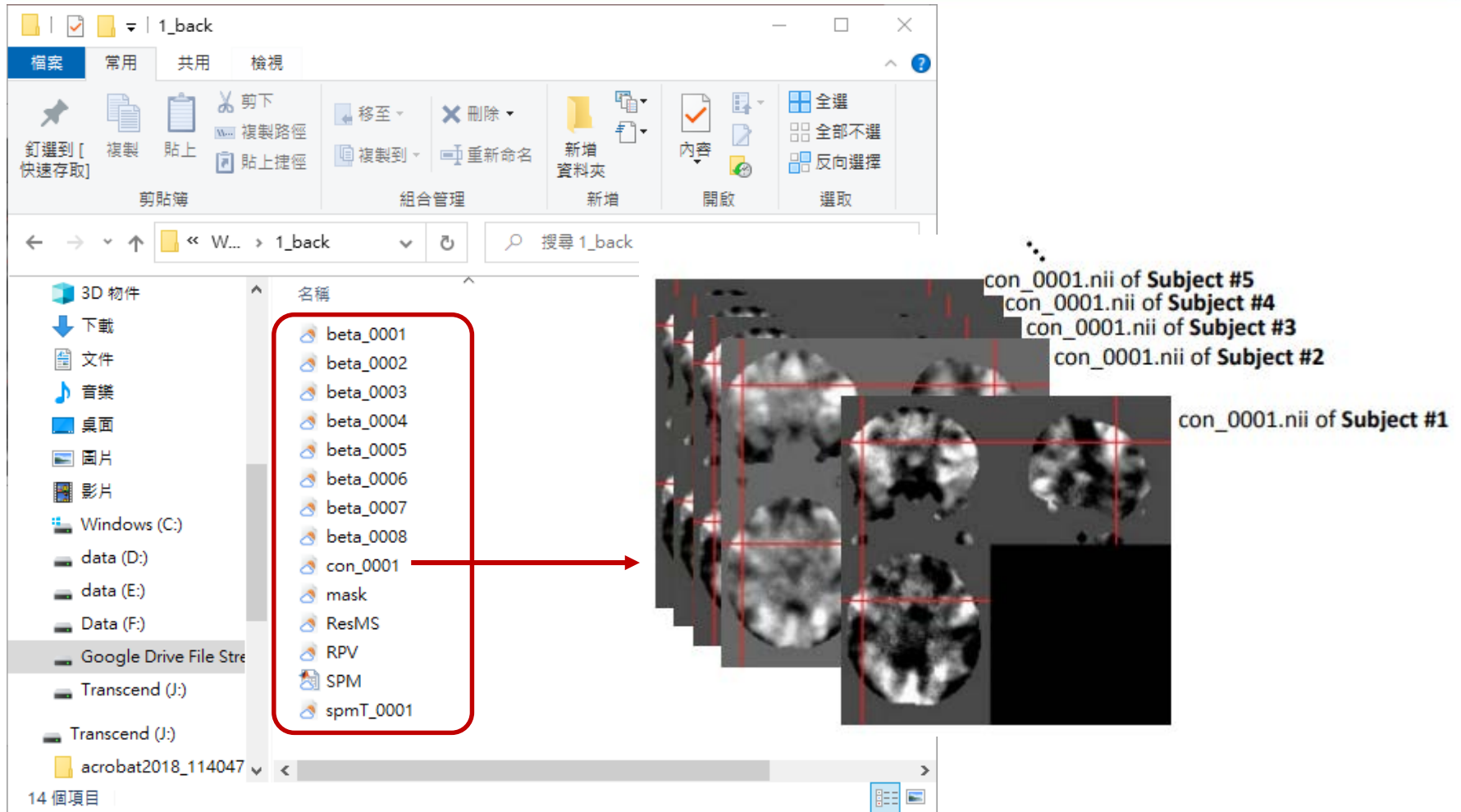


Analysis of Functional Magnetic Resonance Imaging (fMRI) Group-Level Statistical Analysis (2nd level analysis)



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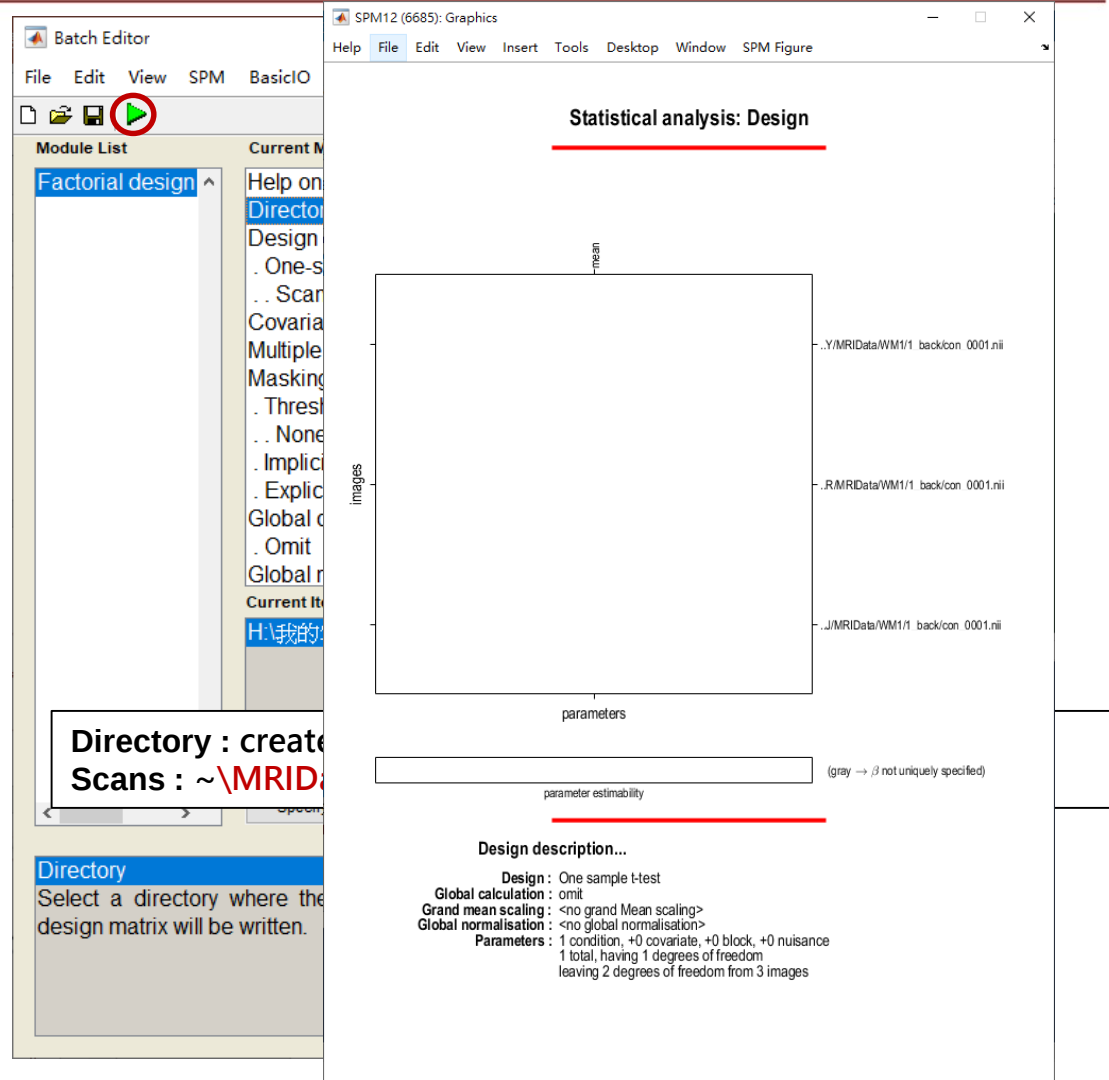
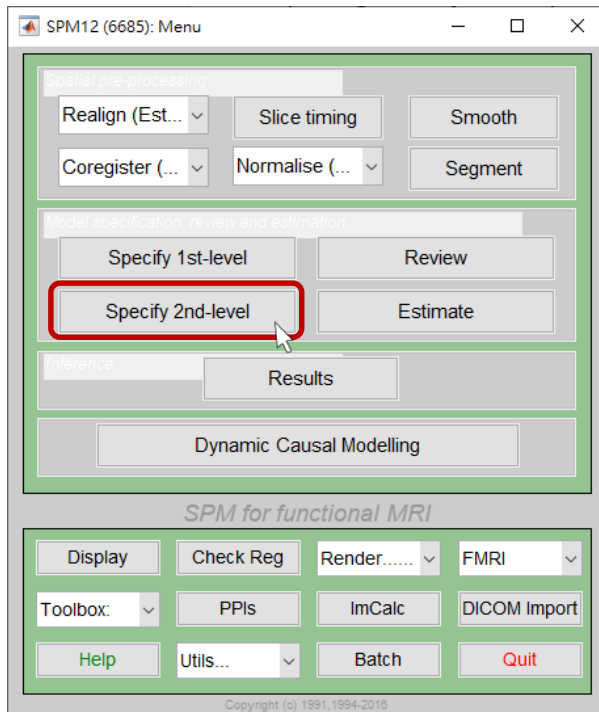
Statistical Inference on Group Data



Specify 2nd-level Analysis Model

>> spm fmri

> Specify 2nd-level



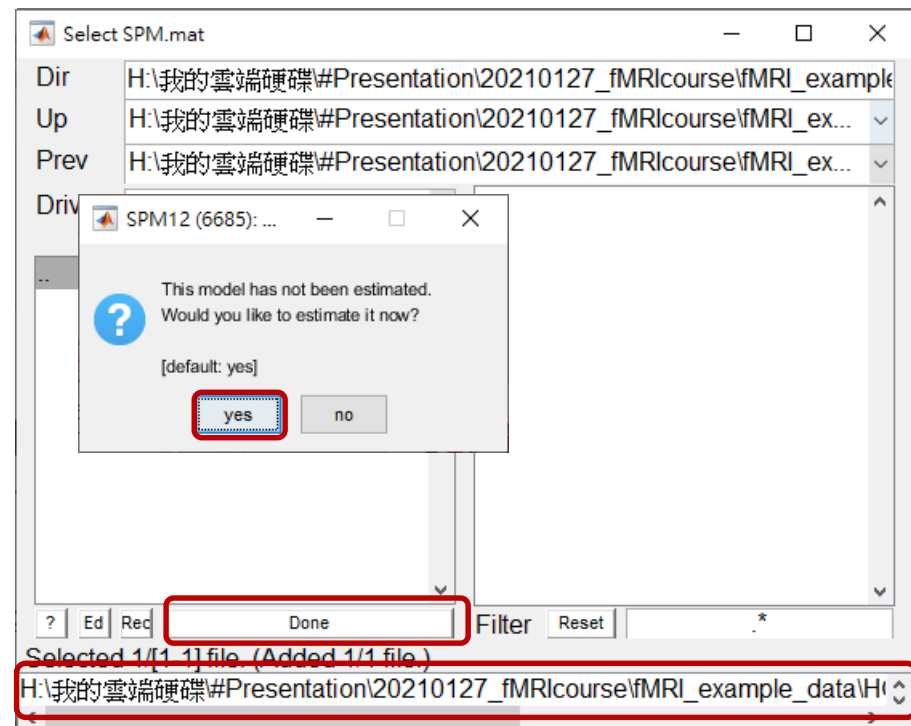
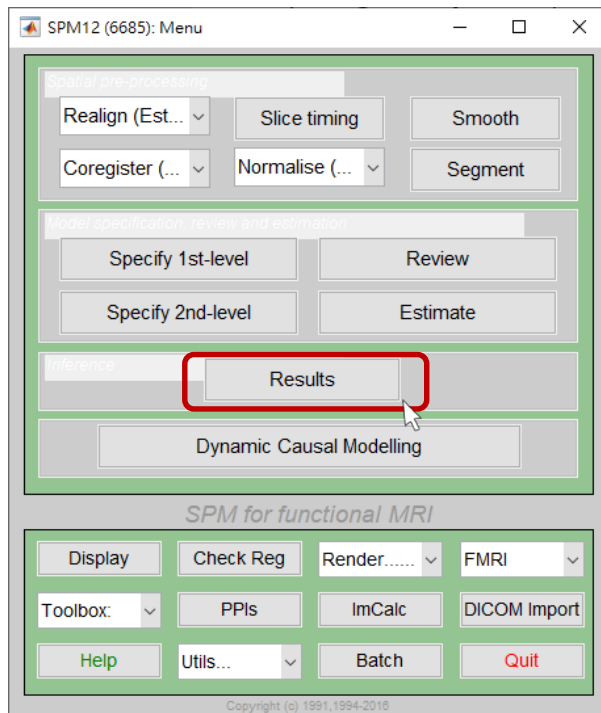
Estimate Model Parameters

>> spm fmri

> Results

> SPM.mat

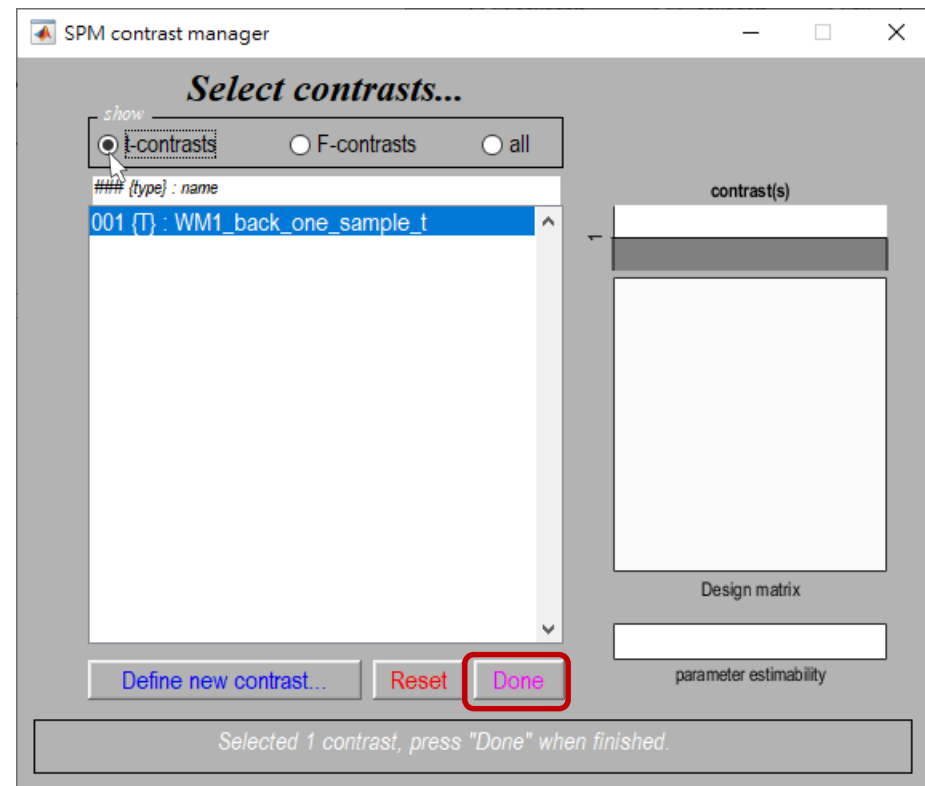
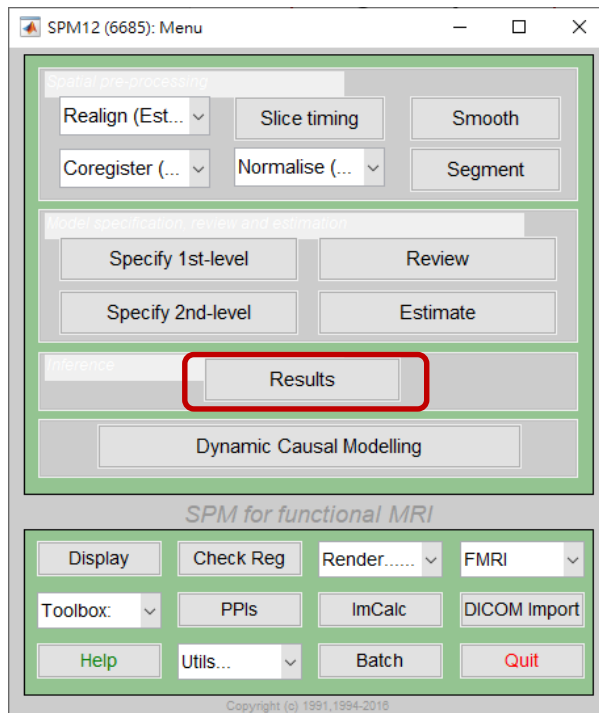
> Done



Estimate Model Parameters

>> spm fmri

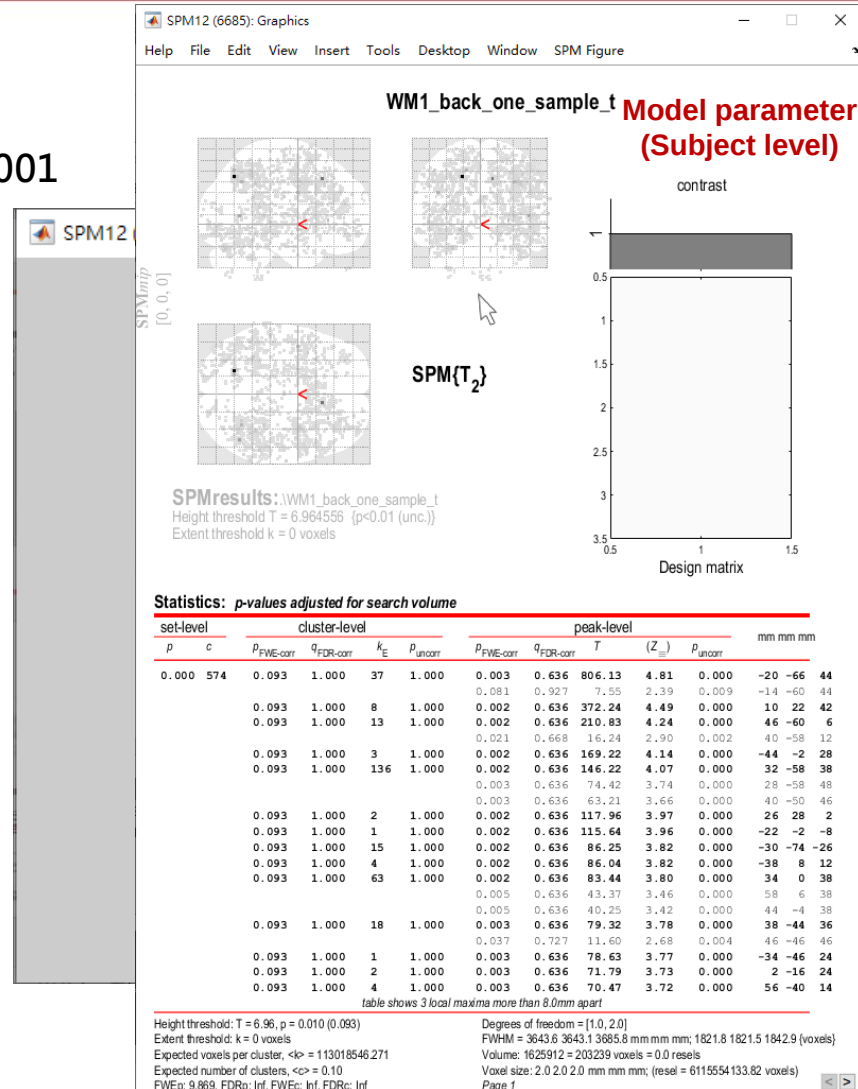
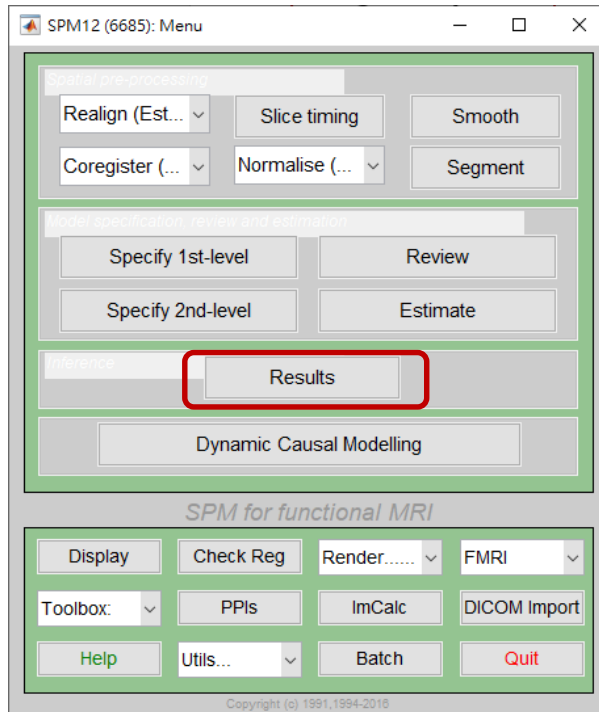
- > t-contrasts
- > Define new contrast...
- > Done



Estimate Model Parameters

>> spm_fmri

- > apply masking : none
- > threshold {T or p value} : none, 0.001
- > & extent threshold {voxels} : 0

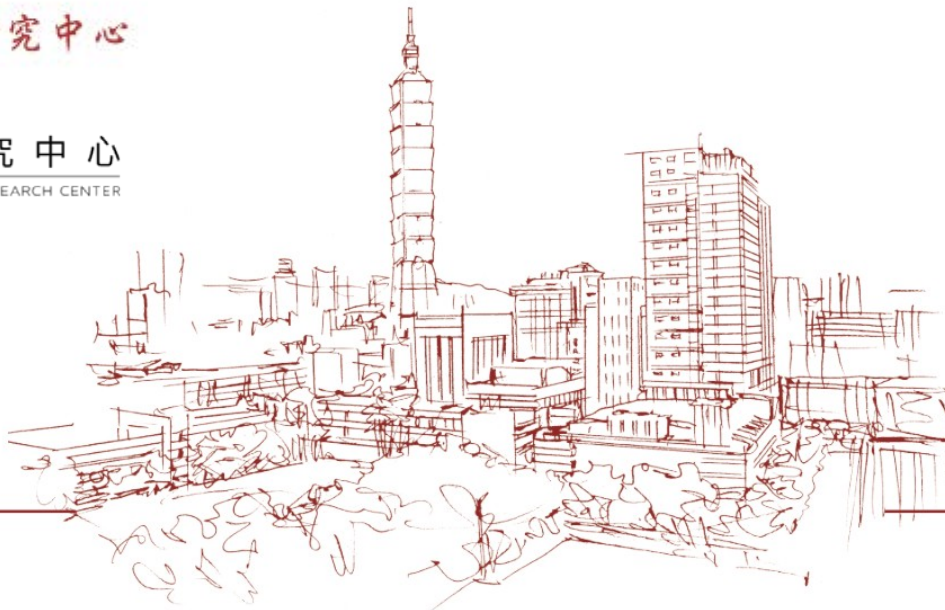




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Analysis of Functional Magnetic Resonance Imaging (fMRI) Data Visualization



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Employed Software

- **Mango**

- <http://ric.uthscsa.edu/mango/download.html>



- **xjview**

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



- **bspmview**

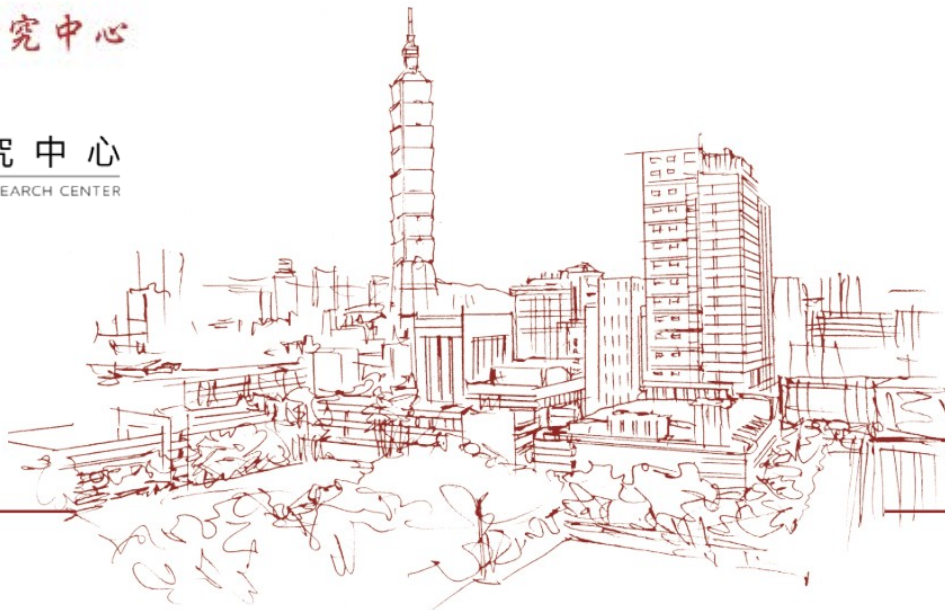
- <https://www.bobspunt.com/software/bspmview/>



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Thanks!

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