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校級神經醫學研究中心

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轉譯影像研究中心
TMU TRANSLATIONAL IMAGING RESEARCH CENTER

Analysis of Functional Magnetic Resonance Imaging (fMRI)

Image Preprocessing

李宜恬 Yi-Tien Li, Ph.D.

TMU Neuroscience Research Center, Taipei Medical University
Translational Imaging Research Center, Taipei Medical University Hospital
angela810727@tmu.edu.tw

Jan. 27th , 2021

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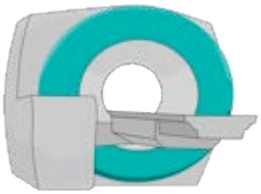
Employed Software

- **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)

DICOM
Digital Imaging and Communications in Medicine
http://dicom.nema.org/

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

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

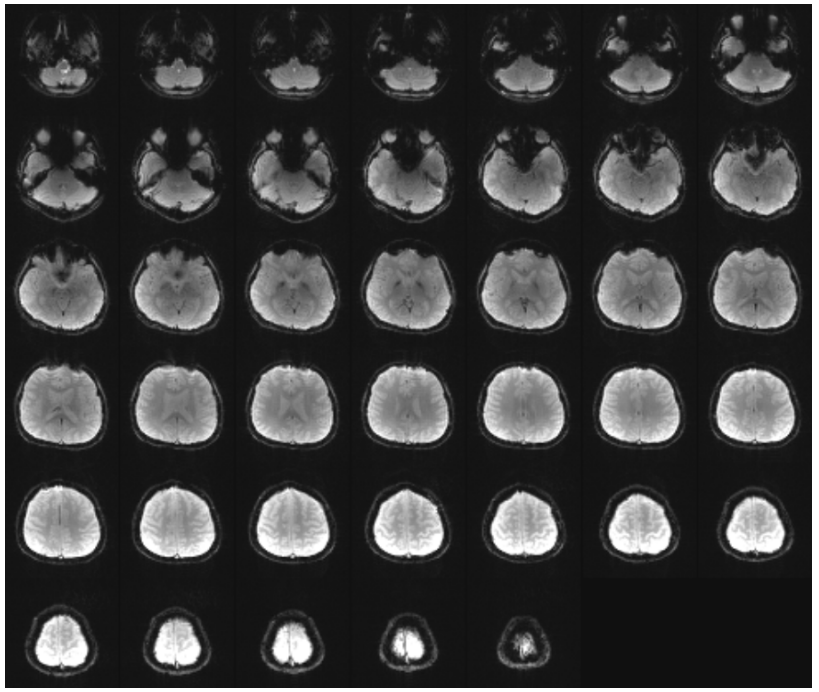
DICOM Tags (H:\我的雲端硬碟\#Presentation\20210127_fMRIcourse\fMRI_example_data\HC0...

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

Find text... Close

DICOM tags (header)

+



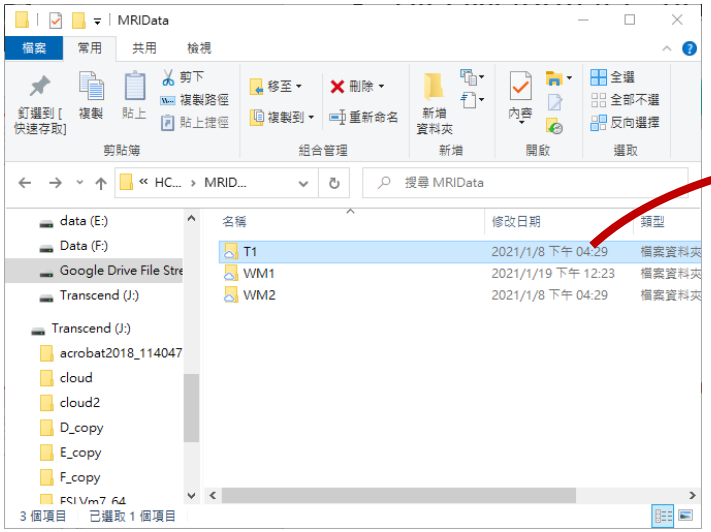
DICOM images

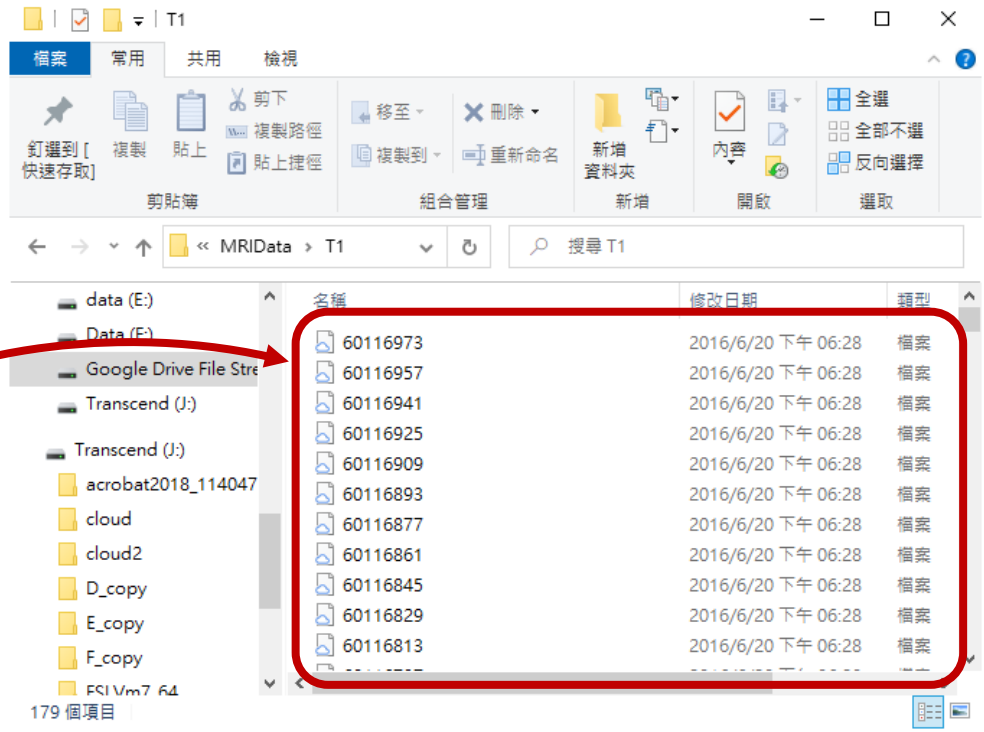
DICOM Import

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

DICOM image folder

Compressed DICOM

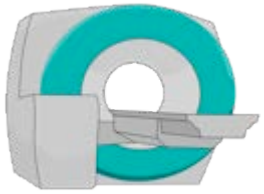




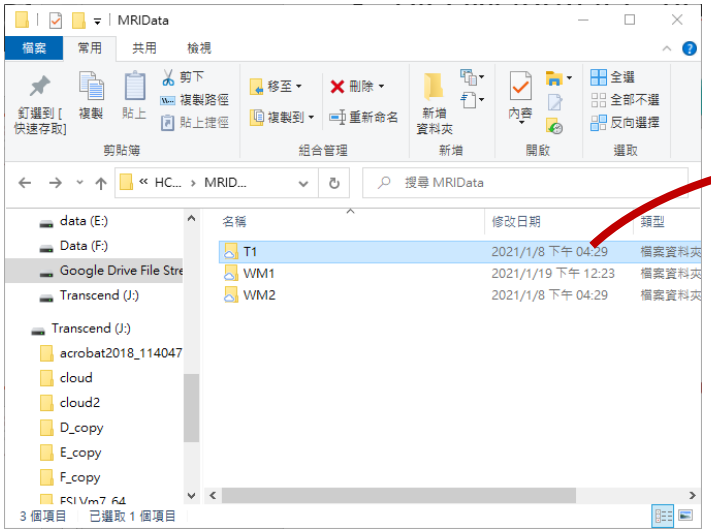
DICOM Import

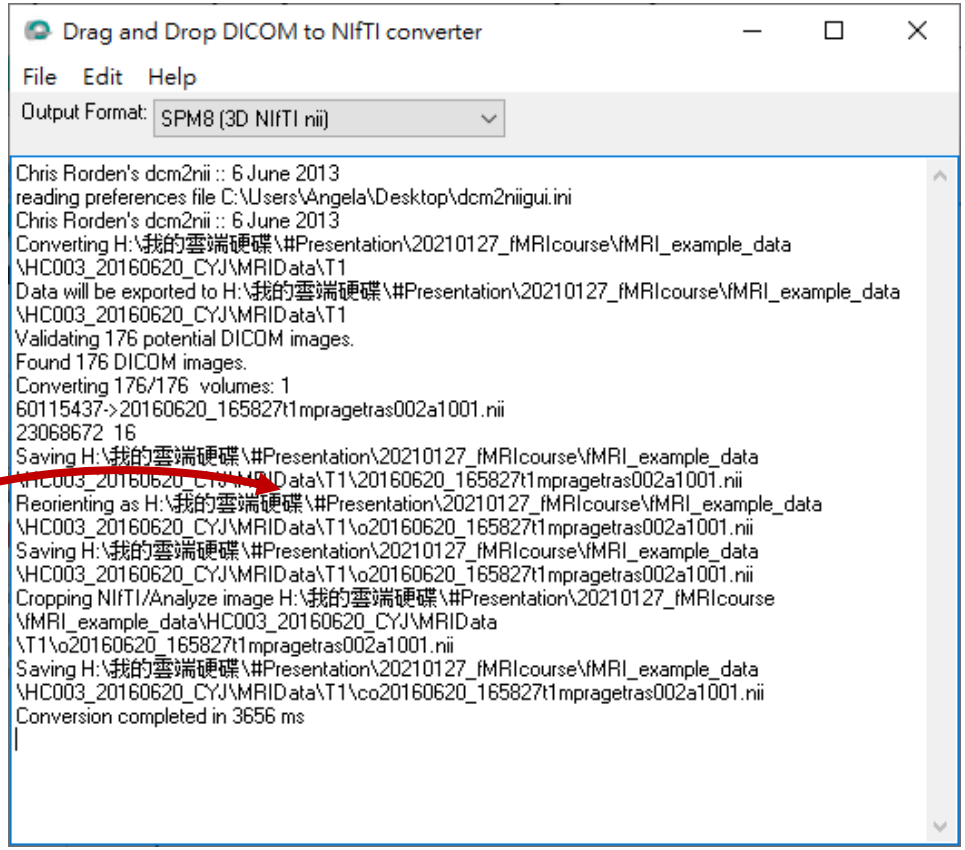
- DICOM format (*.dcm, *.ima, *.) → NIfTI (*.nii)

DICOM image folder



dcm2niigui

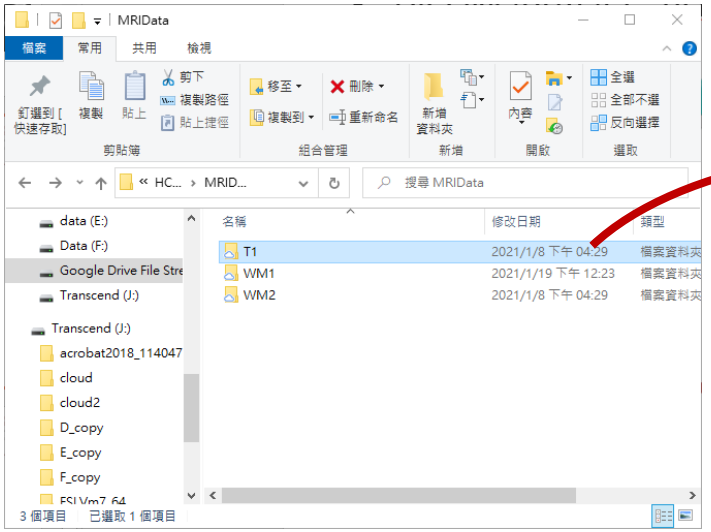


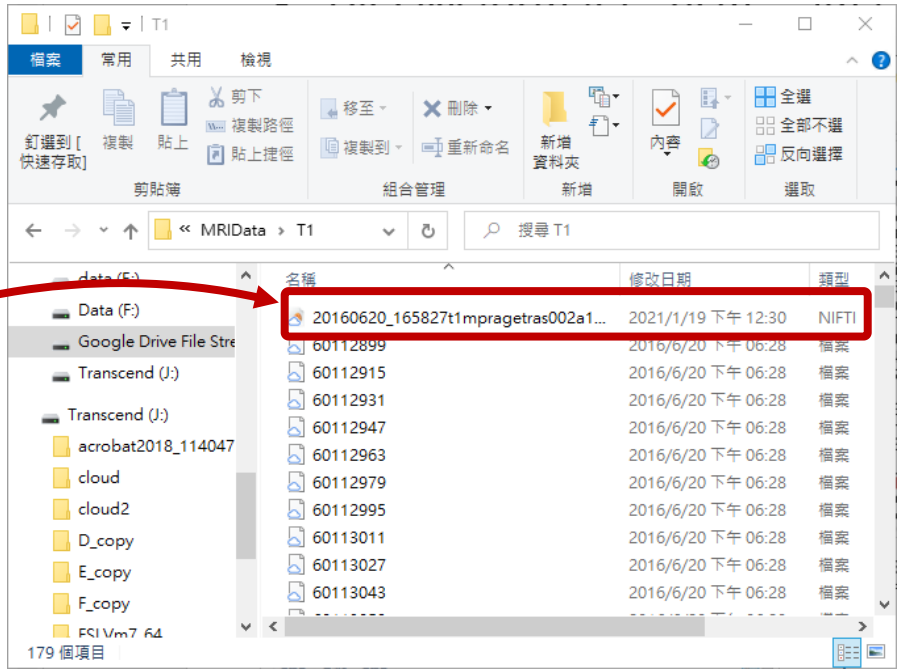


DICOM Import

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

DICOM image folder

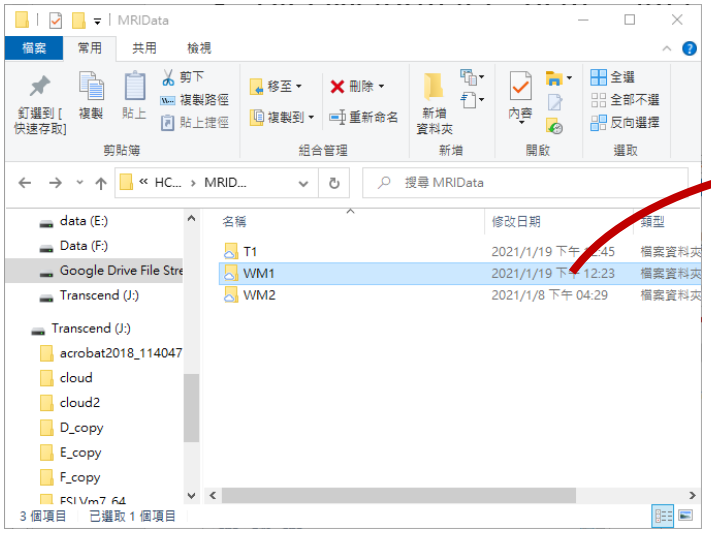


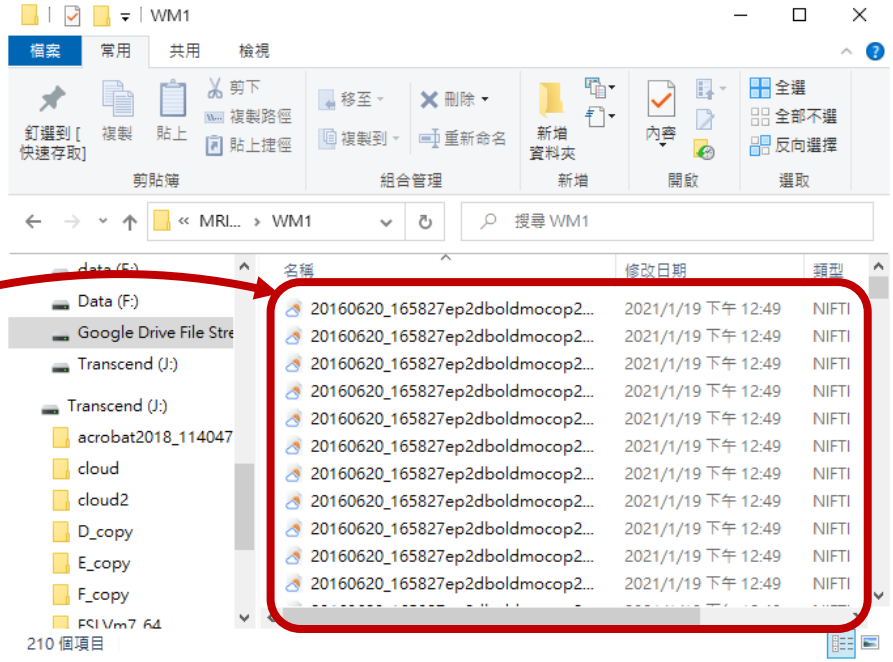


DICOM Import

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

DICOM image folder

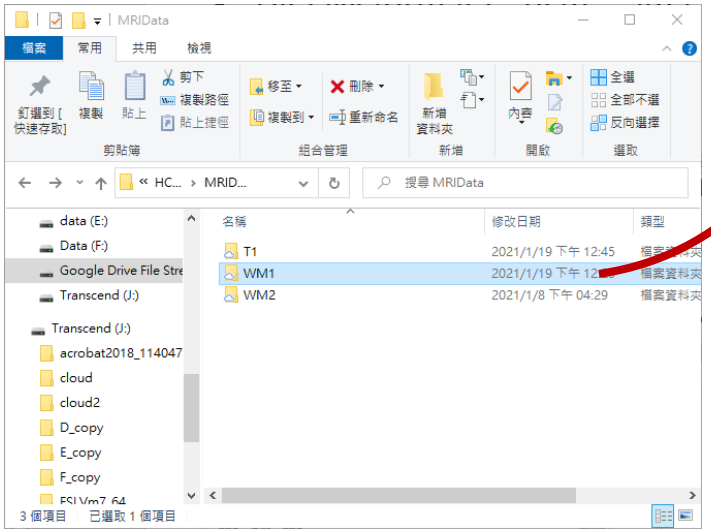


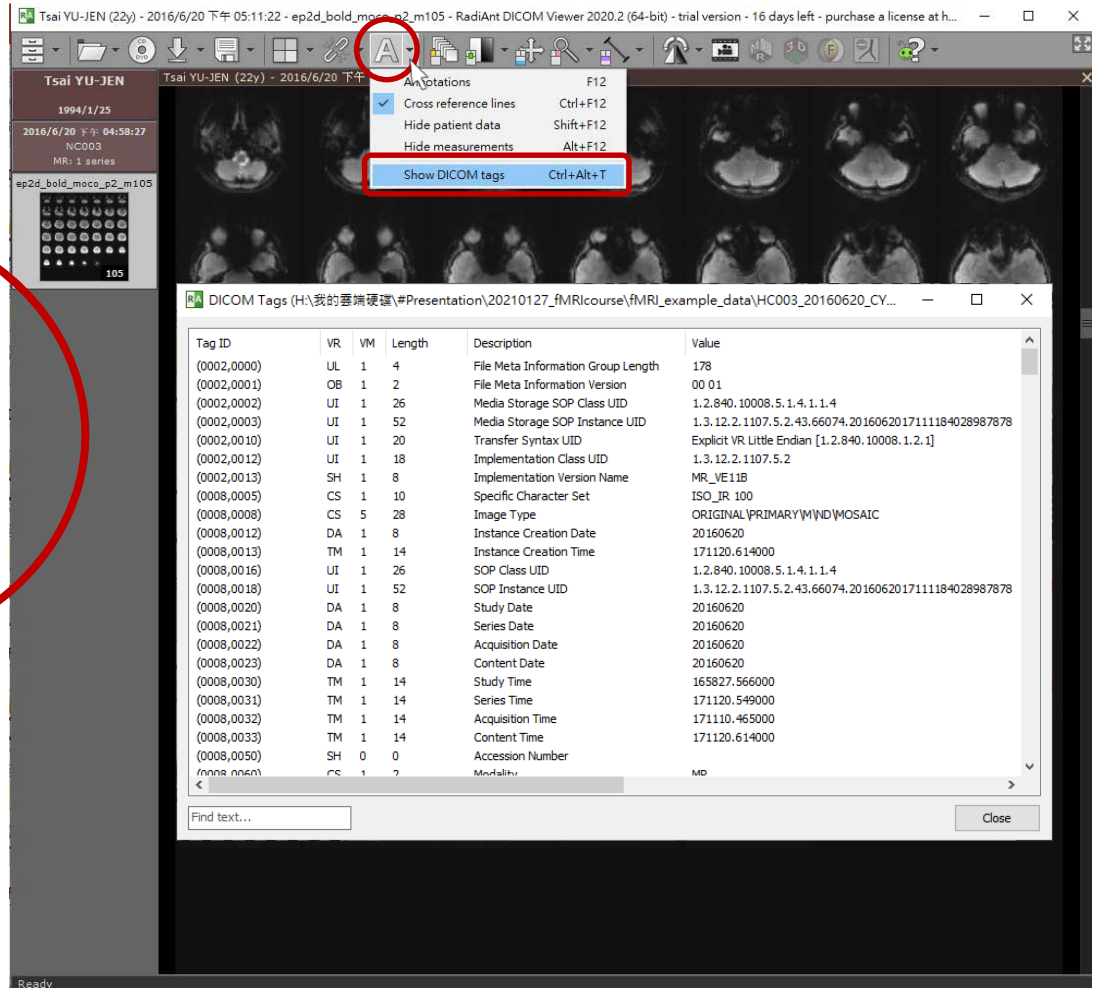


fMRI Protocol (see DICOM tags)

DICOM image folder

RadiANT DICOM Viewer (64-bit)

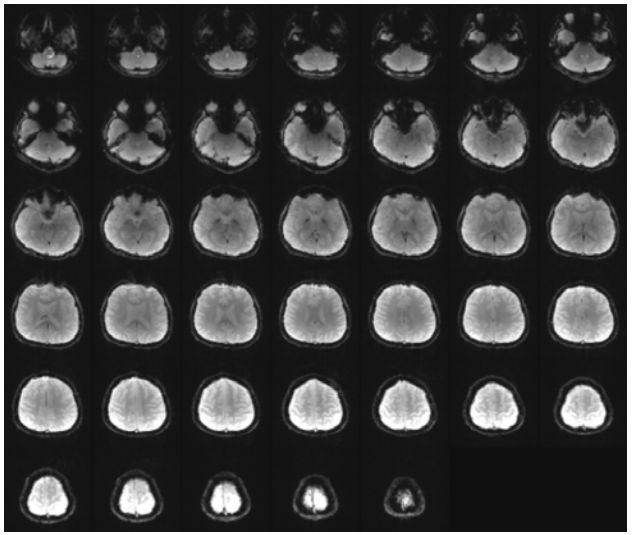




fMRI Protocol (see DICOM tags)

- (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)

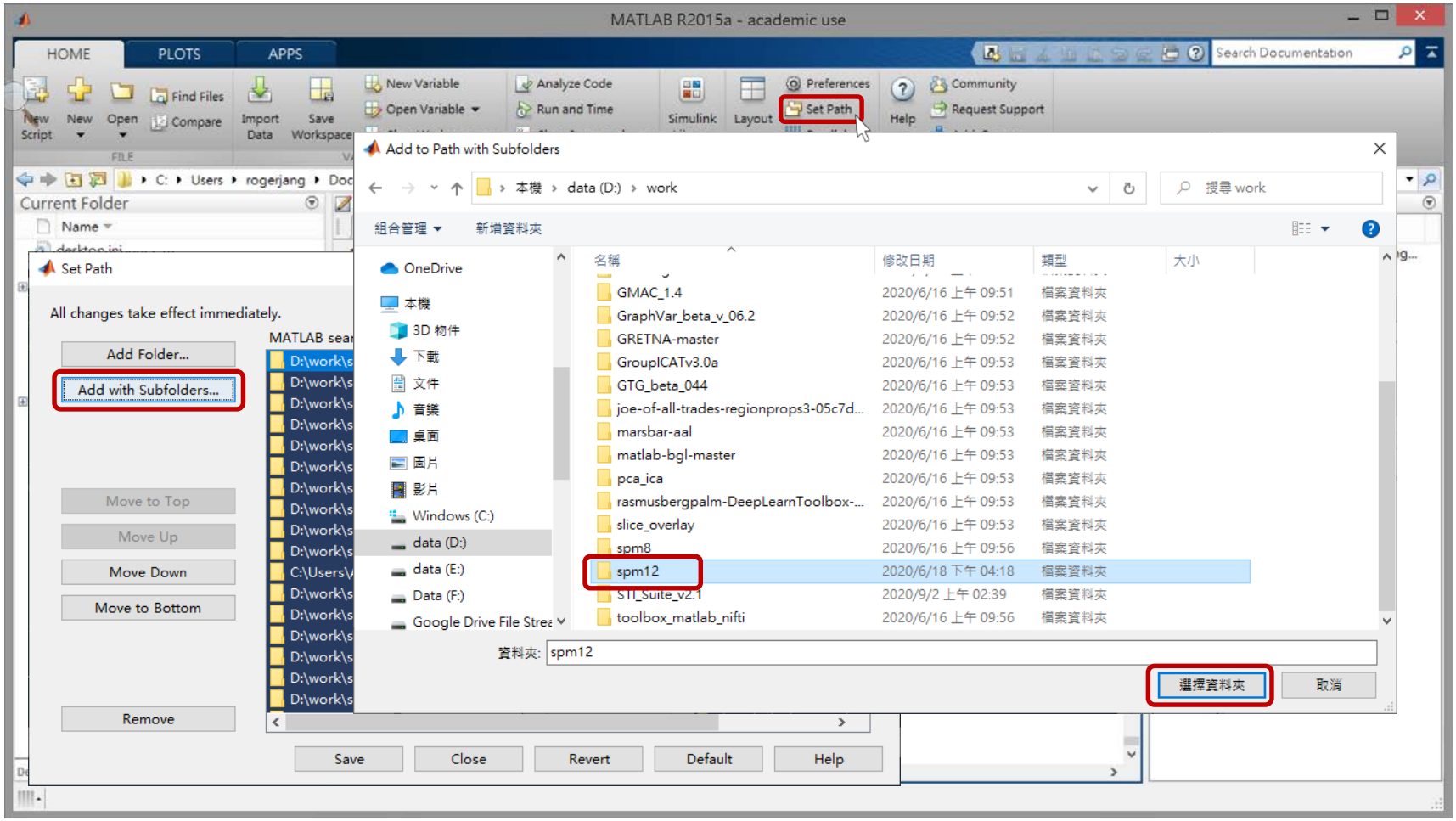
BOLD fMRI images (Moisaics)



Set up

Matlab R2020a

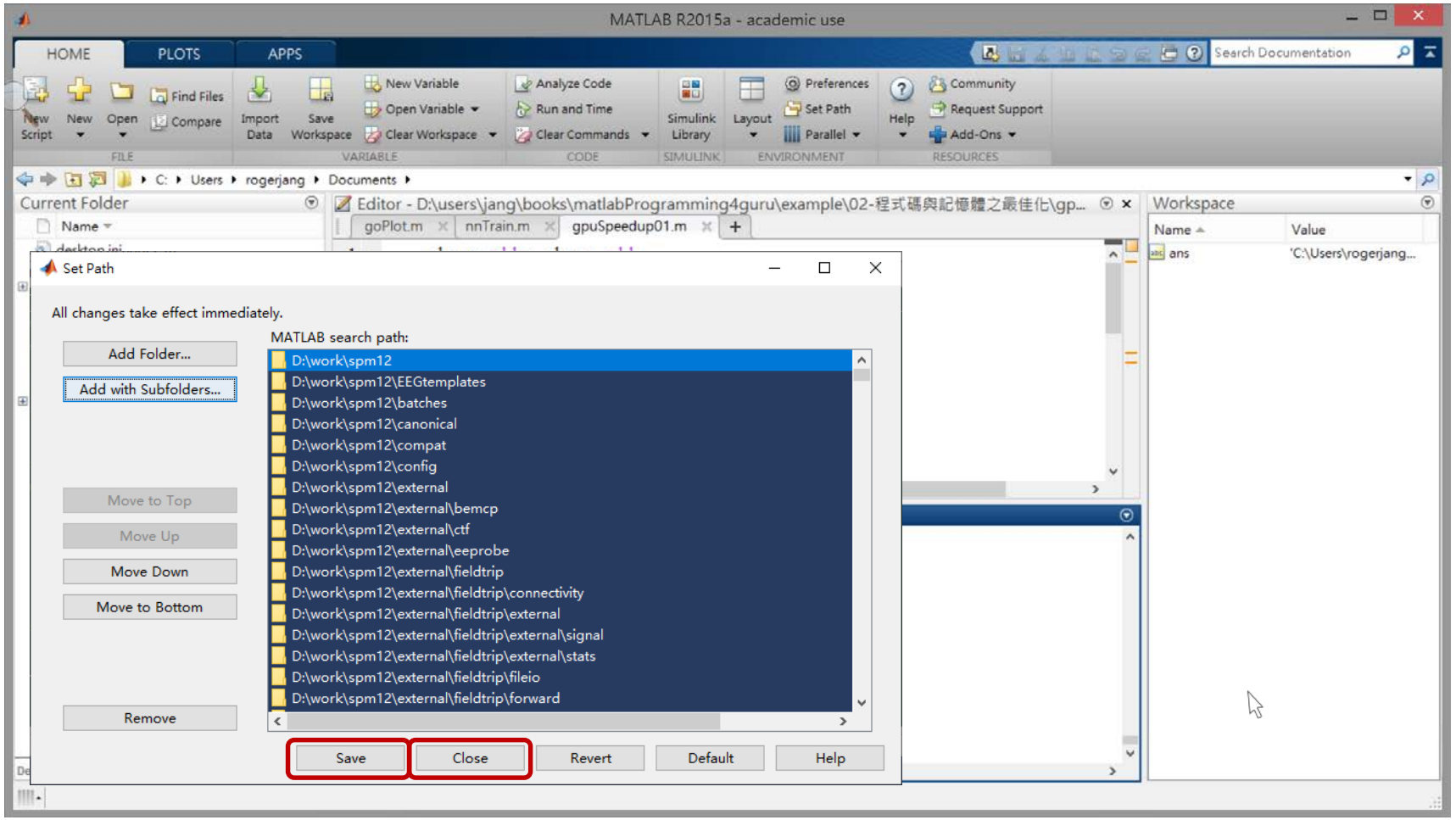
Set Path > Add with Subfolders… > spm12 > 選擇資料夾



Set up

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

Matlab R2020a



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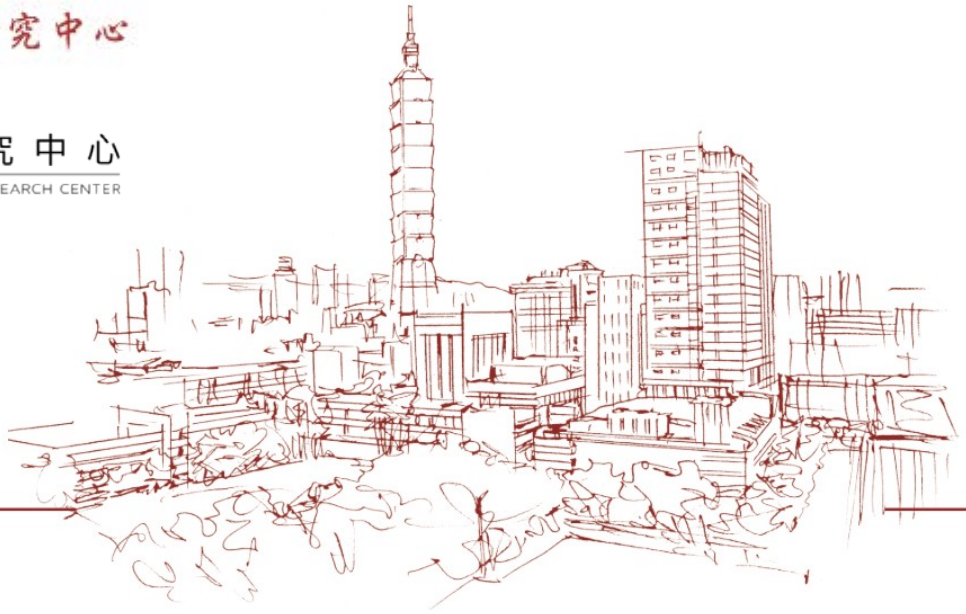

Analysis of Functional Magnetic Resonance Imaging (fMRI)

Set up SPM12 Batch Parameters

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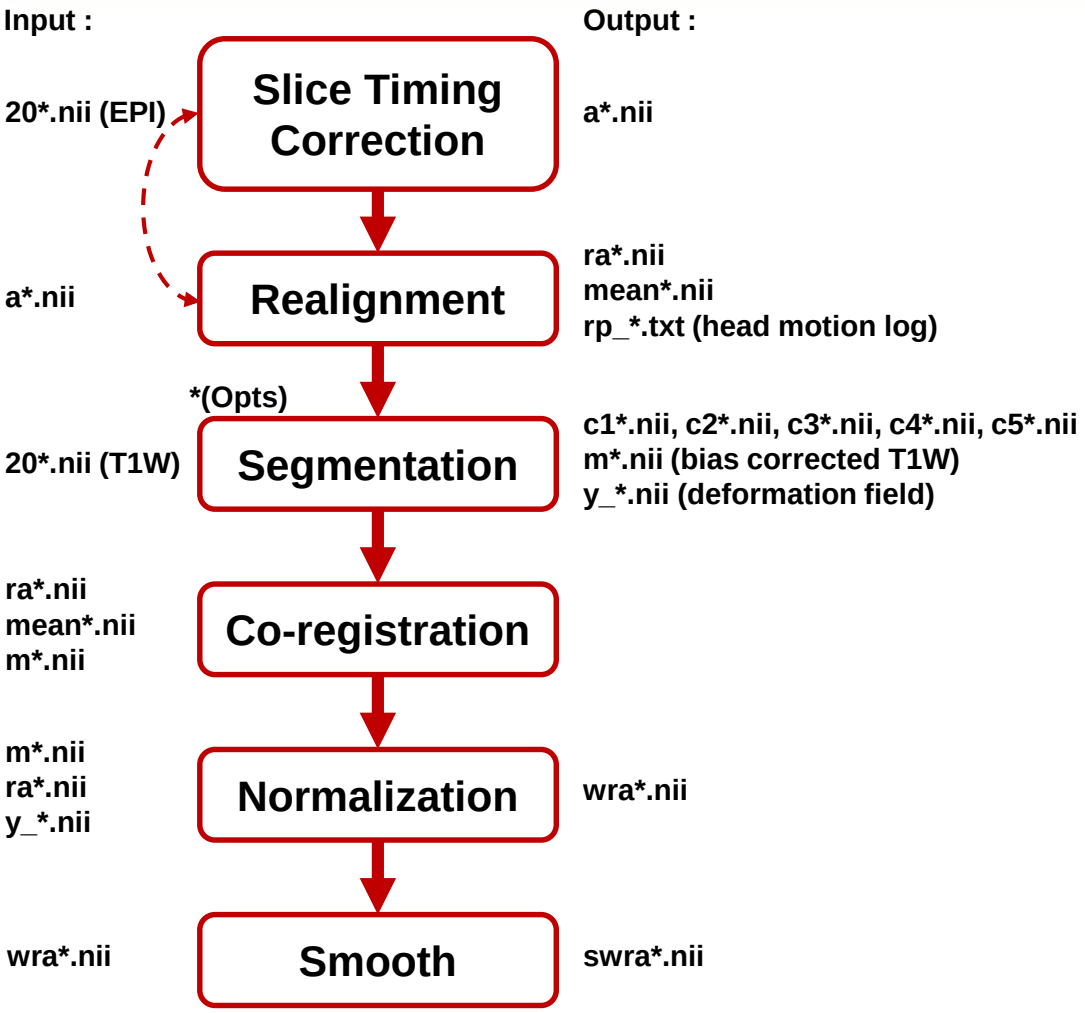
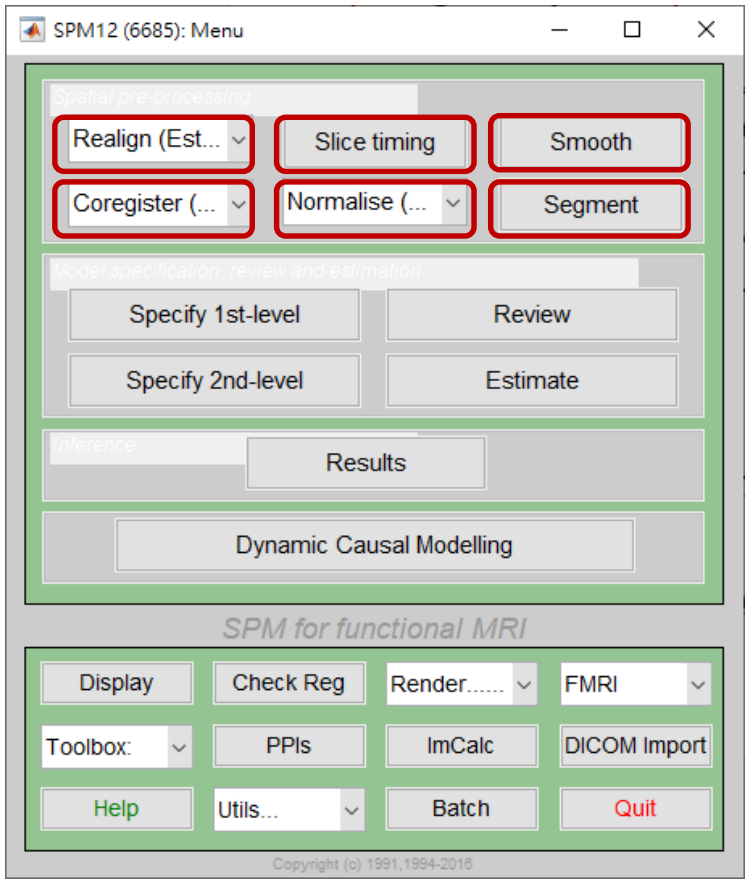
Preprocessing Procedure

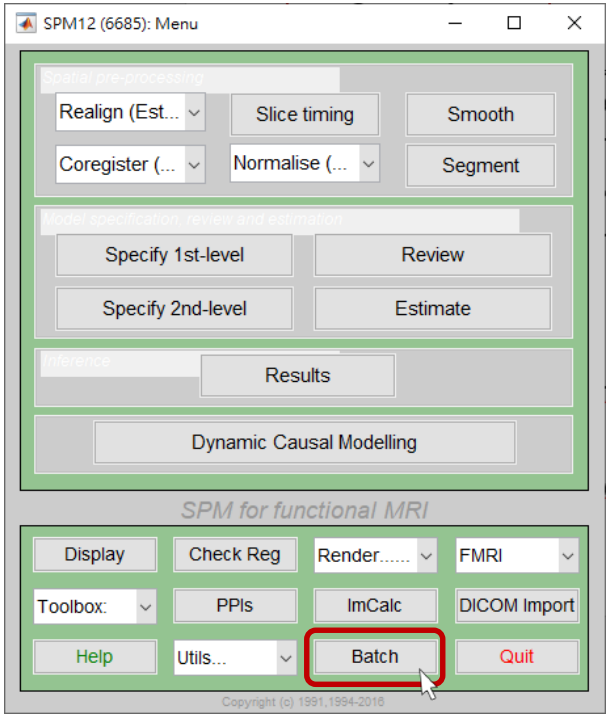


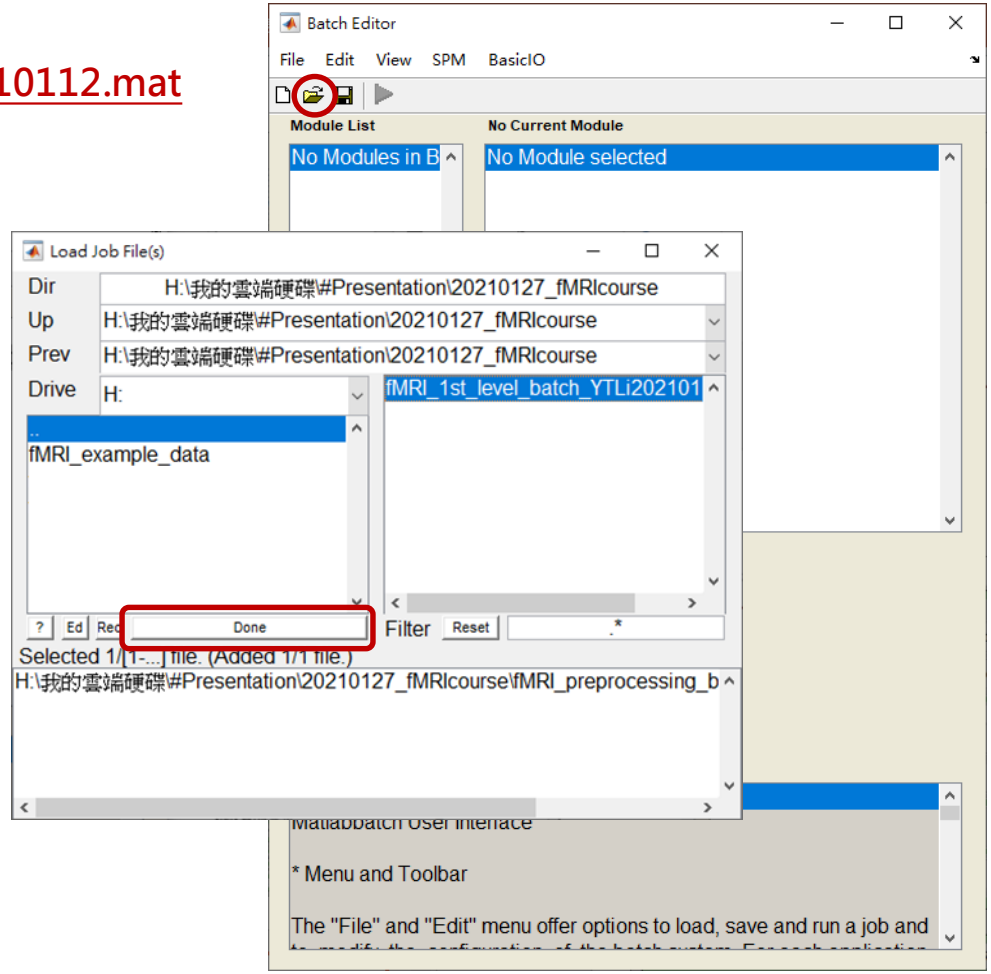


Batch of fMRI preprocessing

>> spm fmri

> Batch
> fMRI_preprocessing_batch_YTLi20210112.mat
> Done

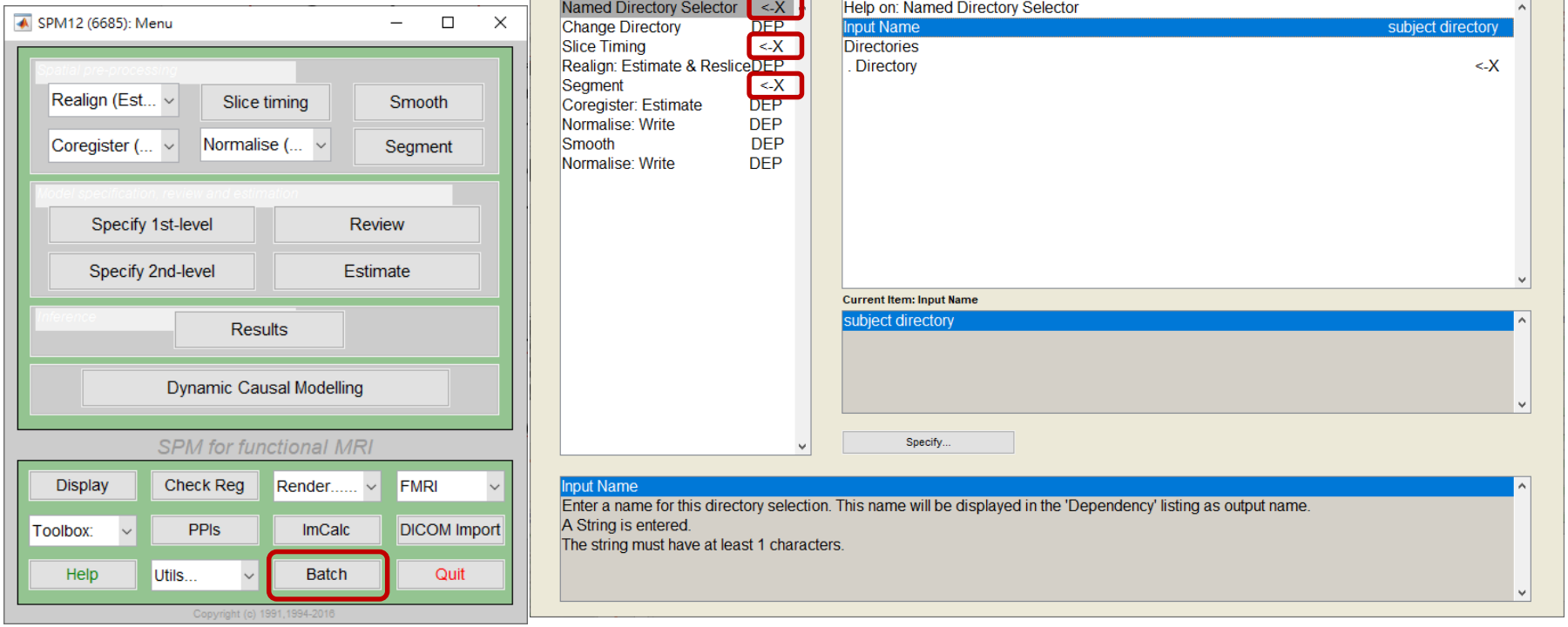




Batch of fMRI preprocessing

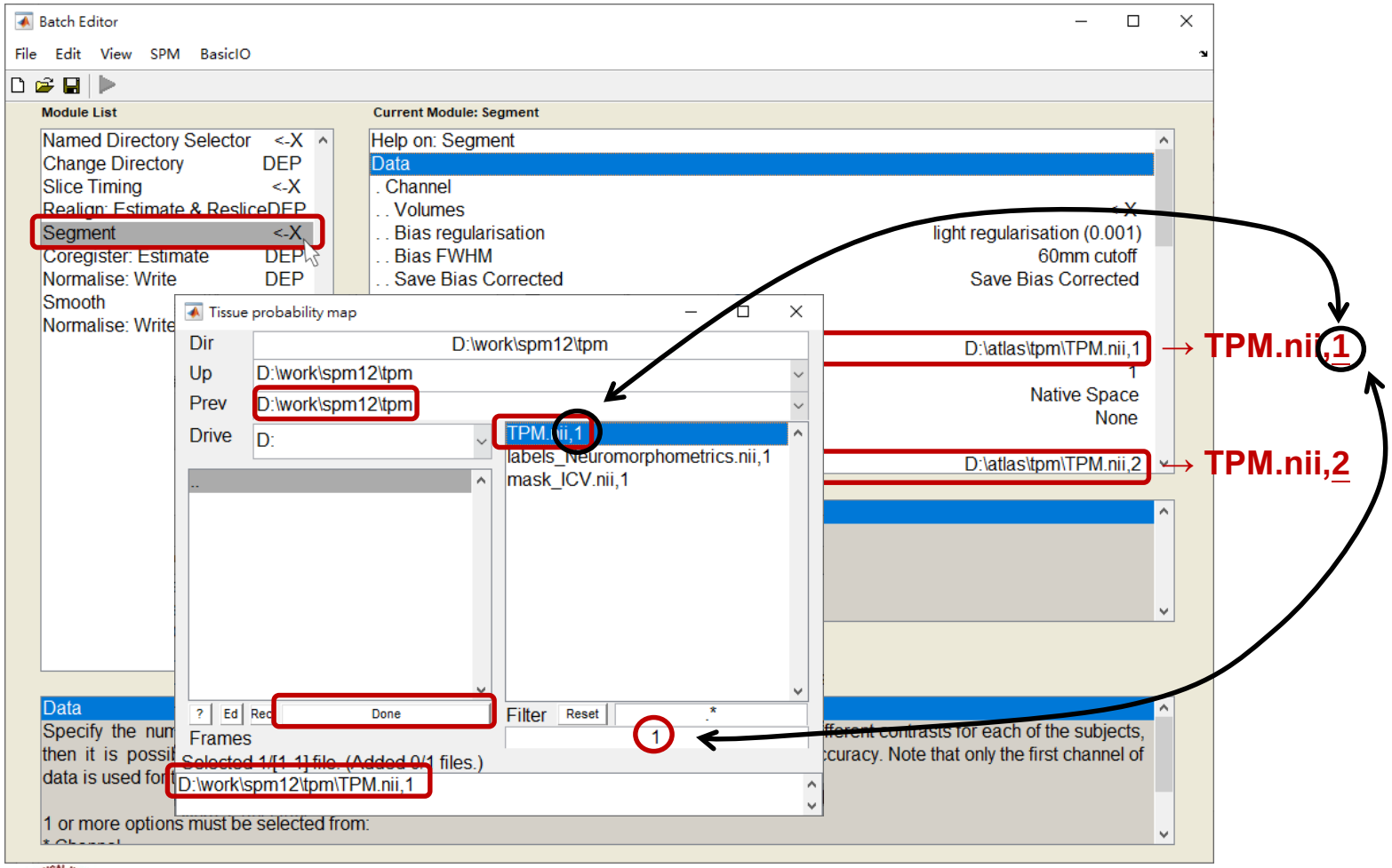
>> spm fmri

> Batch
> fMRI_preprocessing_batch_YTLi2
> Done



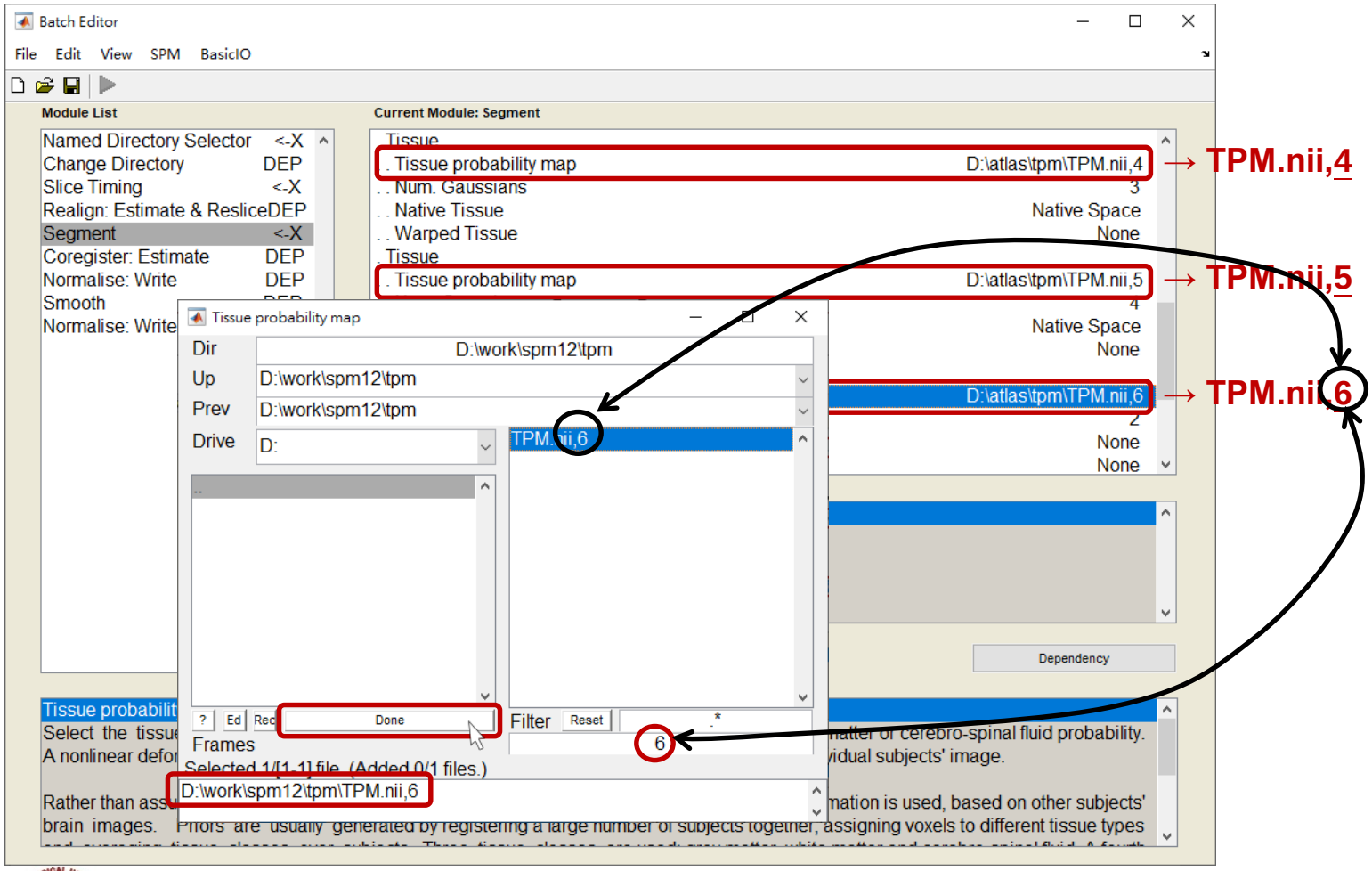
Batch of fMRI preprocessing

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



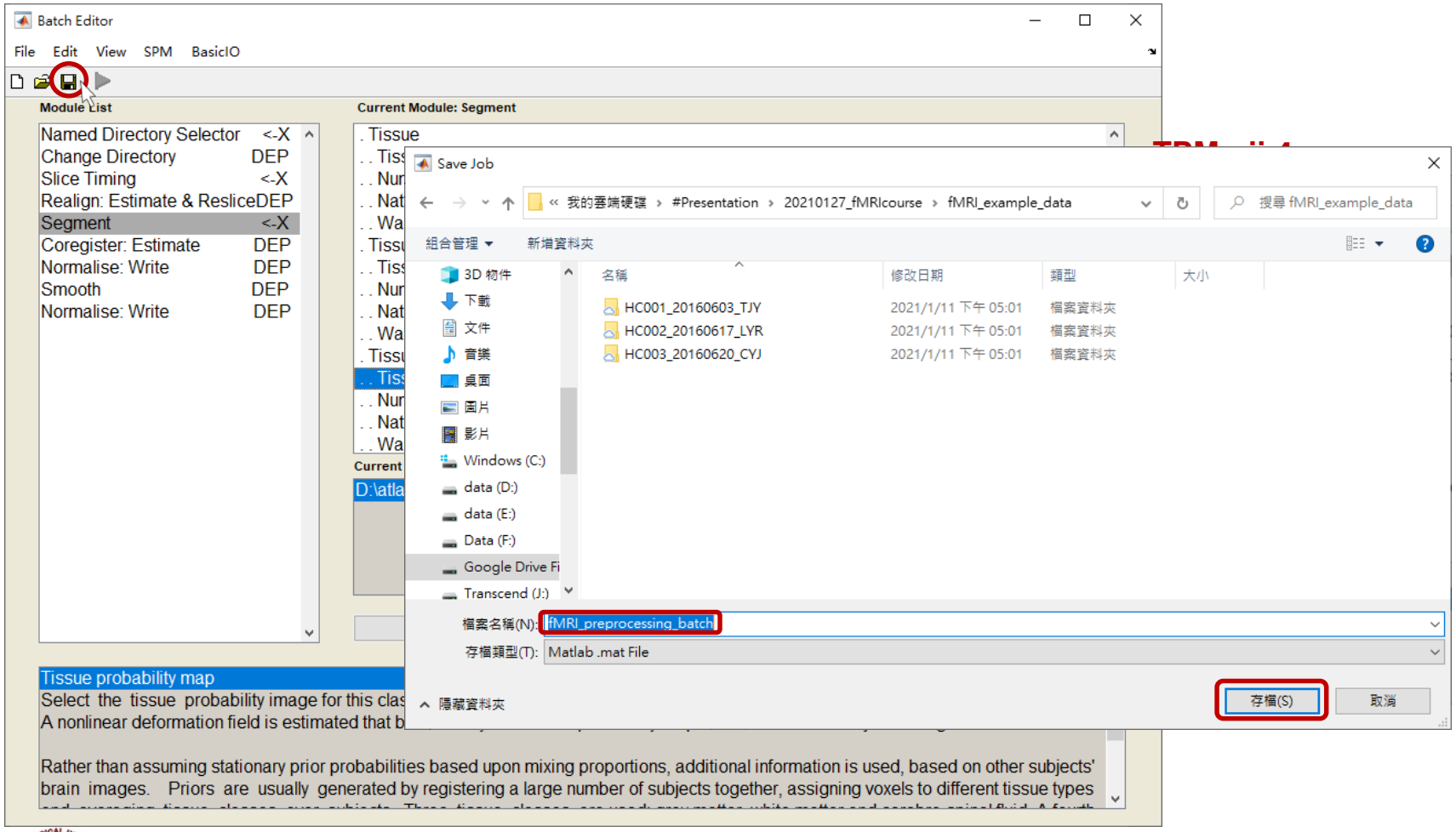
Batch of fMRI preprocessing

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



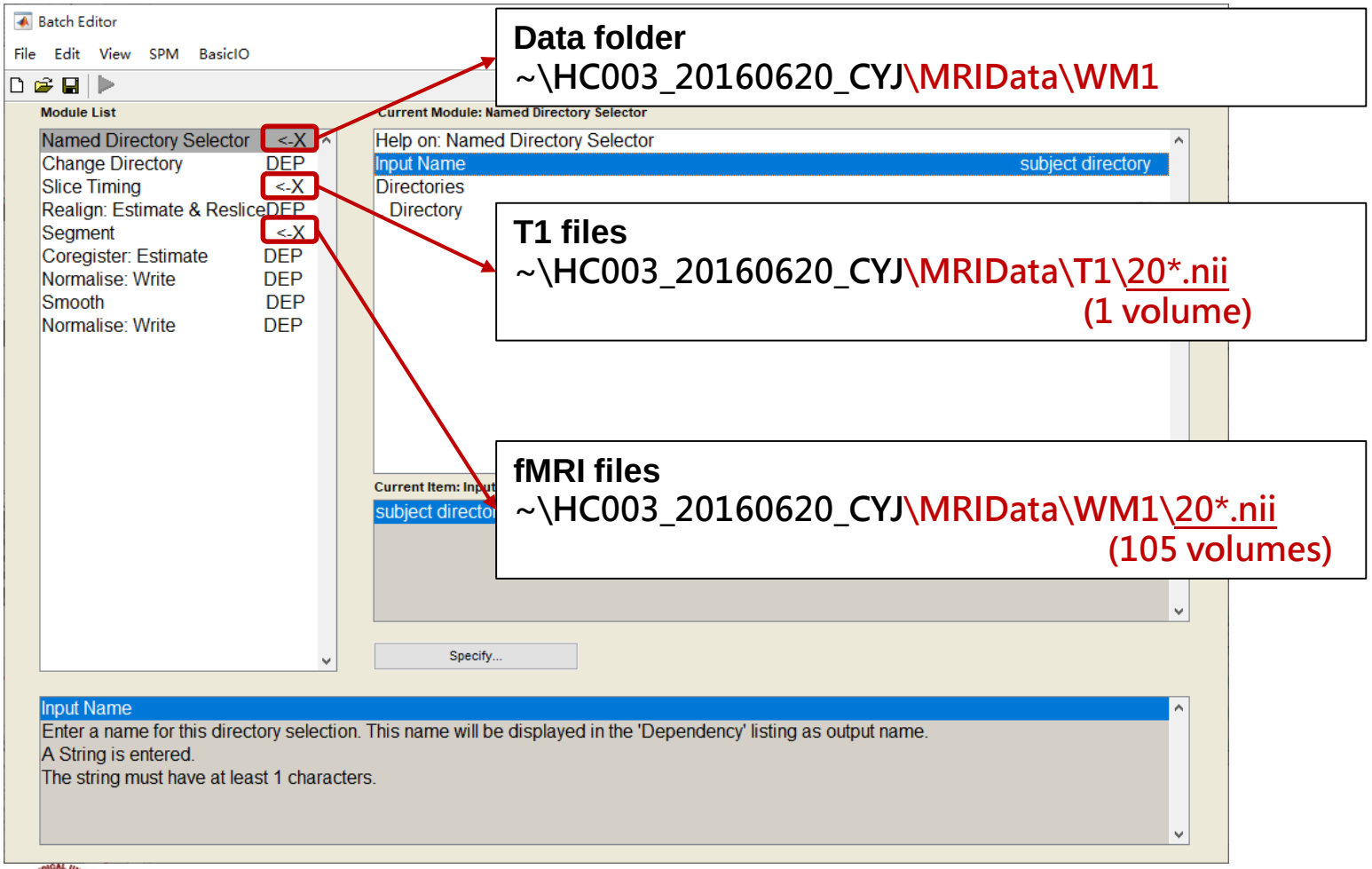
Batch of fMRI preprocessing

> **Save** new batch file



Batch of fMRI preprocessing

> Select files for preprocessing



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)

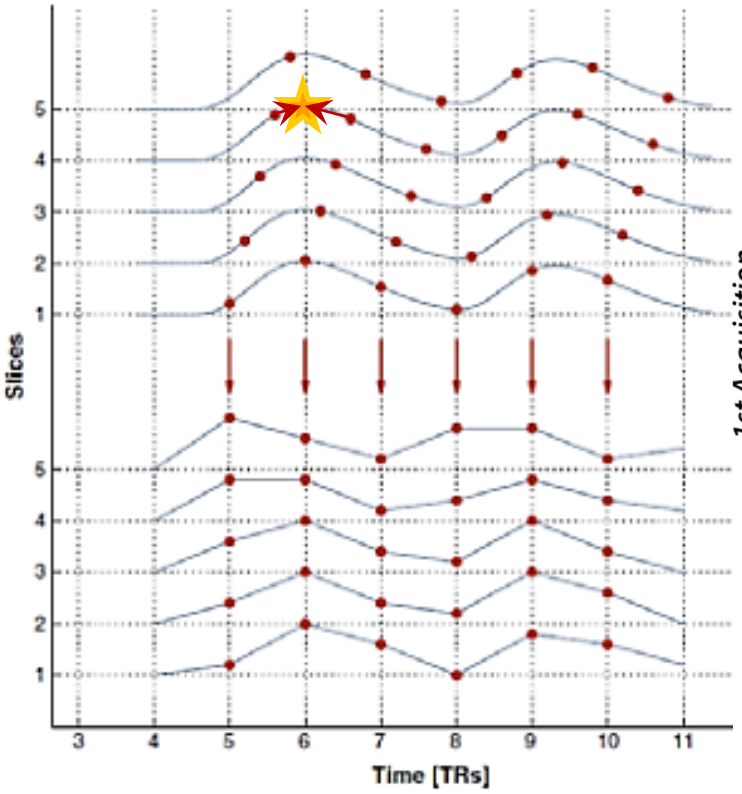
Slice Timing Correction

Slice Timing Correction

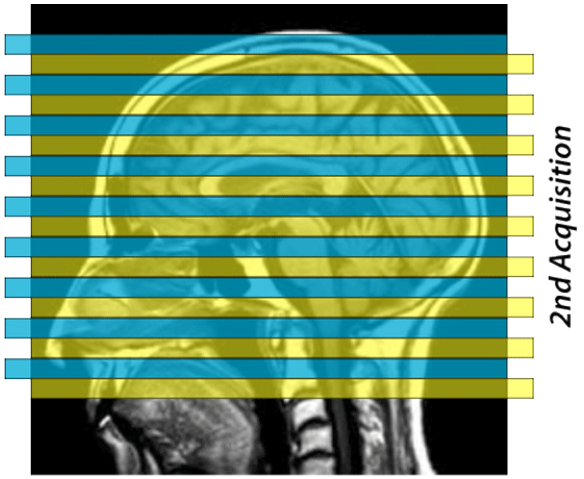
- Realignment
- Segmentation
- Co-registration
- Normalization
- Smooth

Correct for temporal offset between slices for multi-slice acquisition

temporal interpolation



Interleaved Acquisition



Slice Timing Correction

Slice Timing Correction

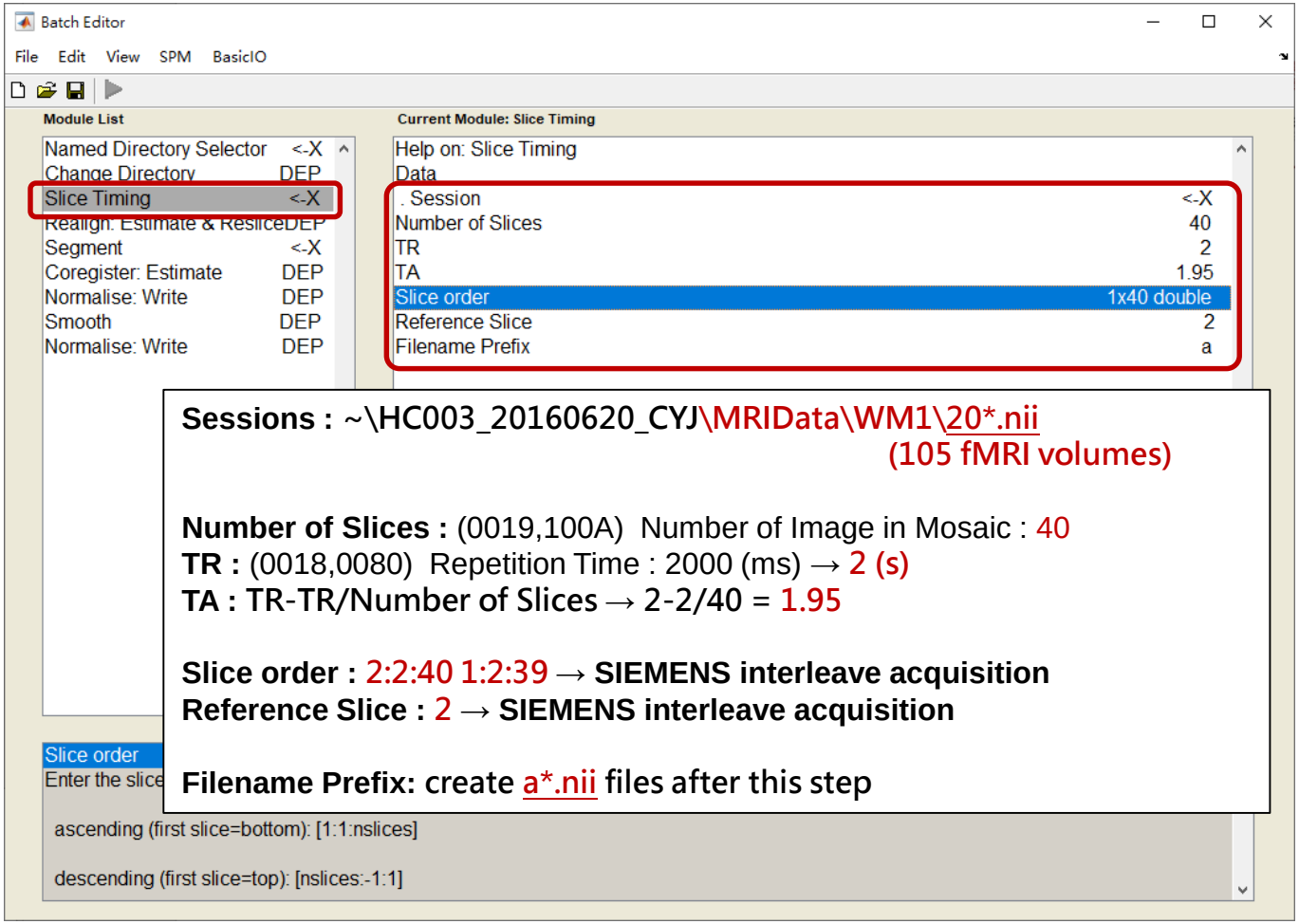
Realignment

Segmentation

Co-registration

Normalization

Smooth



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

Realignment (Head motion correction)

Slice Timing Correction

Realignment

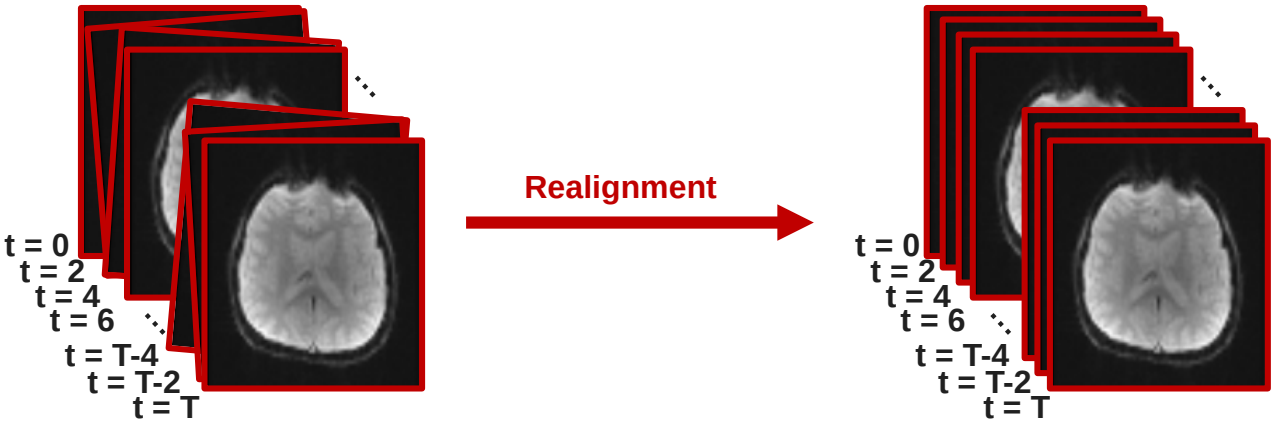
Segmentation

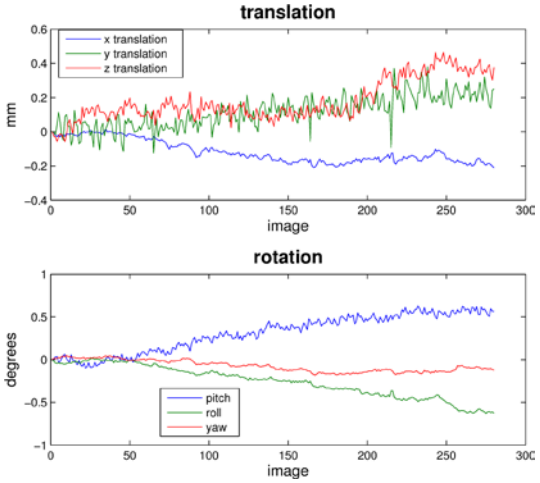
Co-registration

Normalization

Smooth

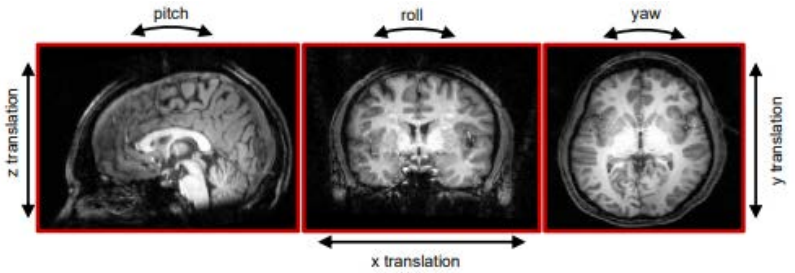
The signal variation from head movement is much larger than hemodynamic response.





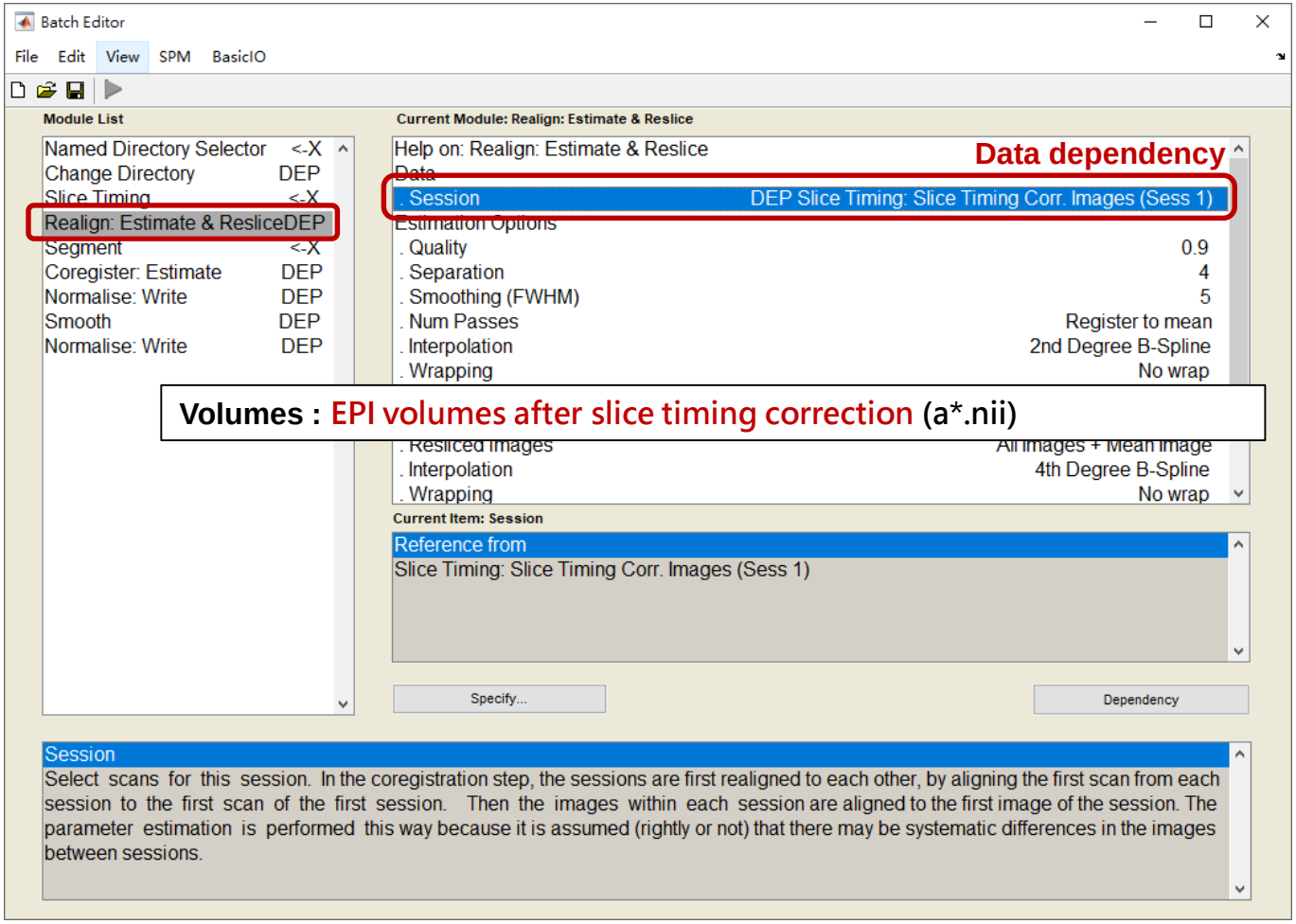
6-parameter rigid body registration & transformation (Realign to the 1st volume)

→ 6 motion-related co-variates for fMRI analysis



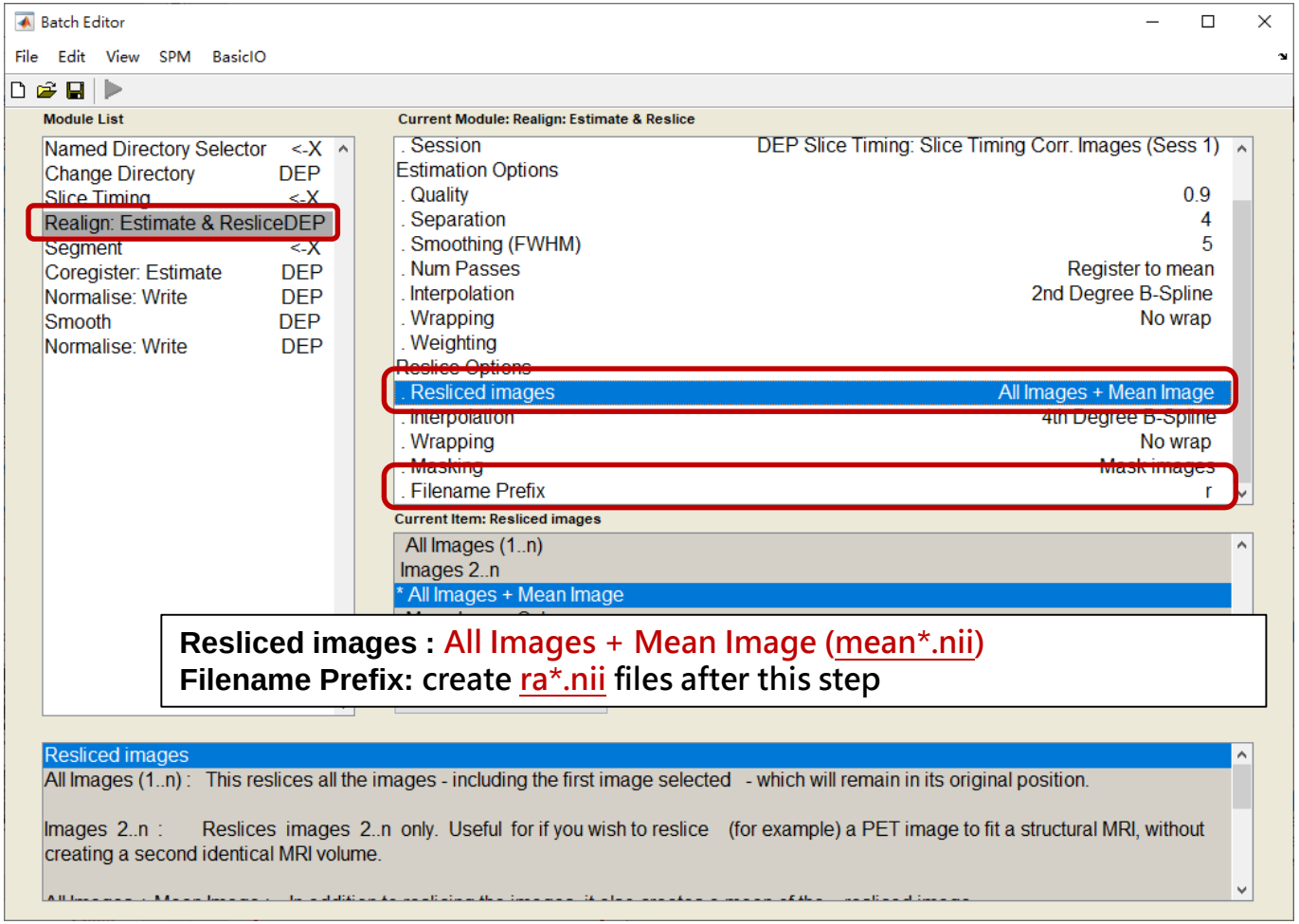
Realignment (Head motion correction)

- Slice Timing Correction
- **Realignment**
- Segmentation
- Co-registration
- Normalization
- Smooth



Realignment (Head motion correction)

- Slice Timing Correction
- **Realignment**
- Segmentation
- Co-registration
- Normalization
- Smooth

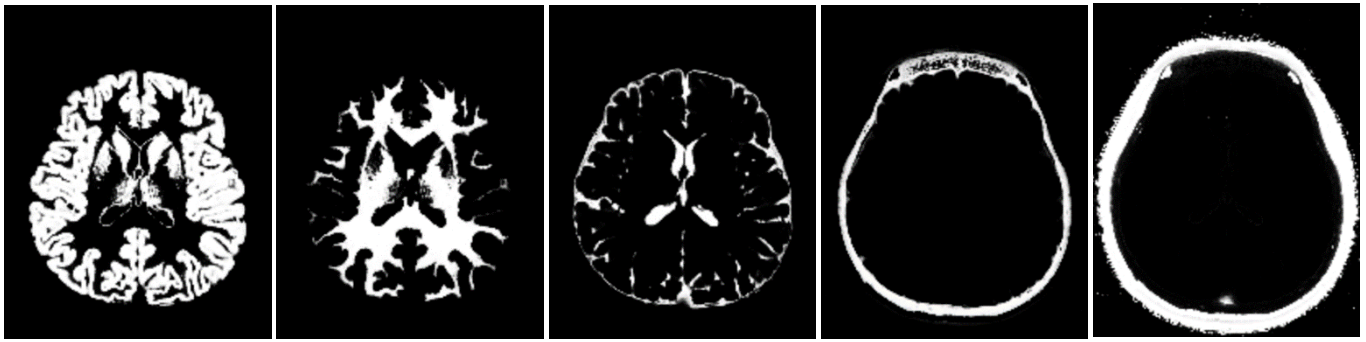


Resliced images : All Images + Mean Image (mean*.nii)
Filename Prefix: create ra*.nii files after this step

Segmentation (Bias field correction)

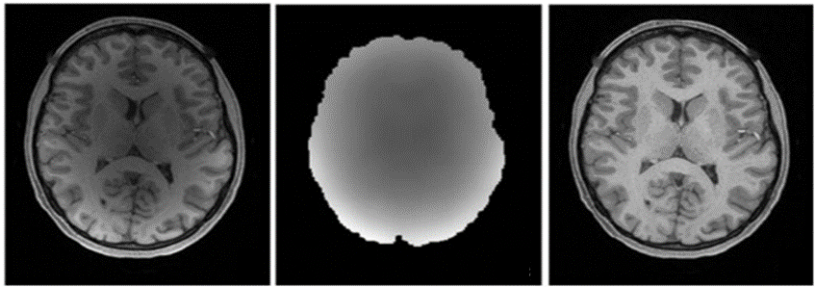
- Slice Timing Correction
- Realignment
- **Segmentation**
- Co-registration
- Normalization
- Smooth

Estimate tissue probability maps for each subject.



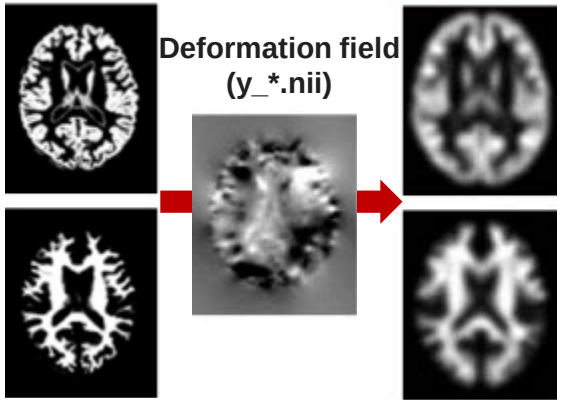
c1*.nii (gray matter) | c2*.nii (white matter) | c3*.nii (CSF) | c4*.nii (skull) | c4*.nii (scalp)

Bias field correction → benefit for registration



Before correction | Bias field | After correction (m*.nii)

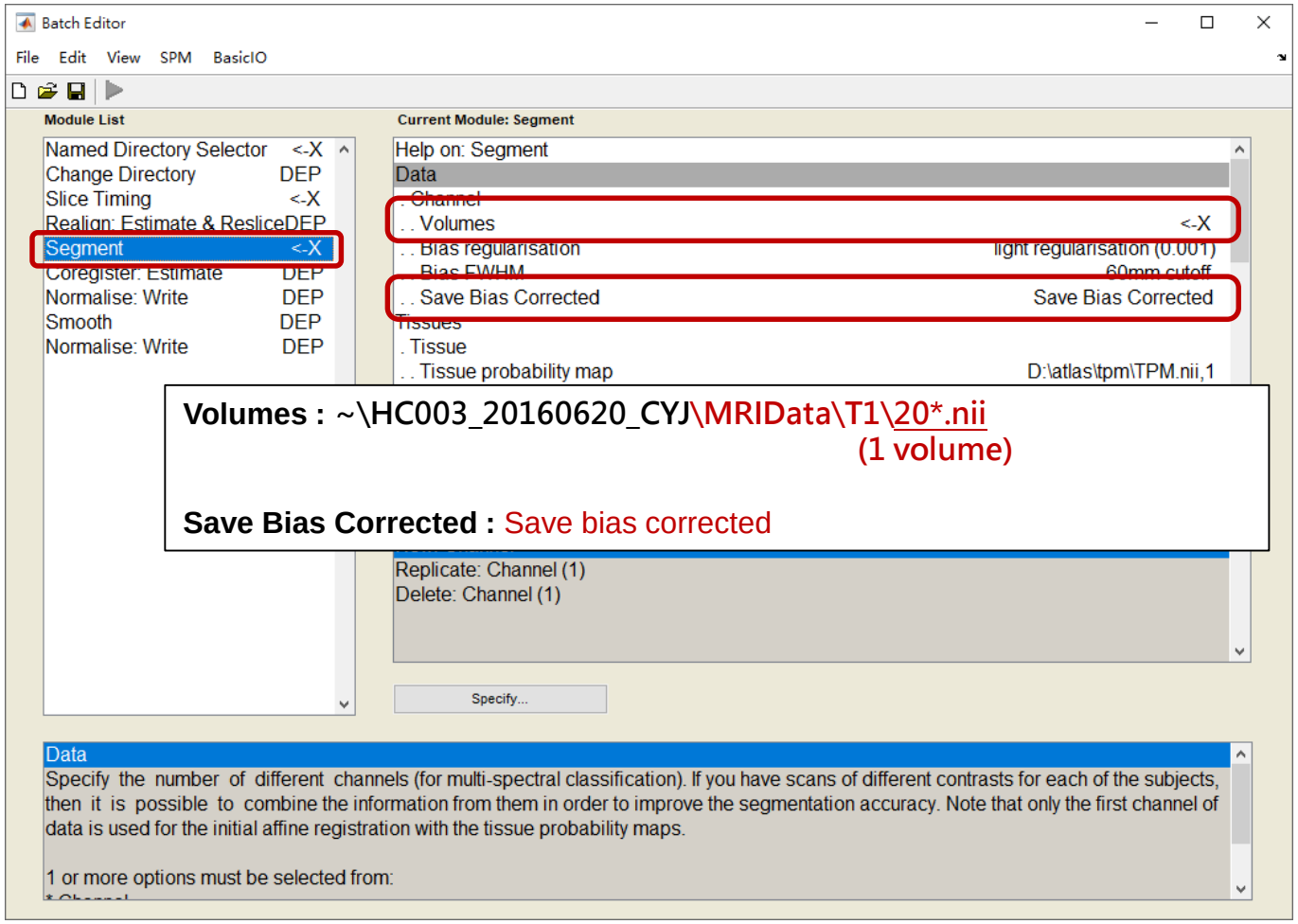
Estimate deformation field



Subject space | Template

Segmentation (Bias field correction)

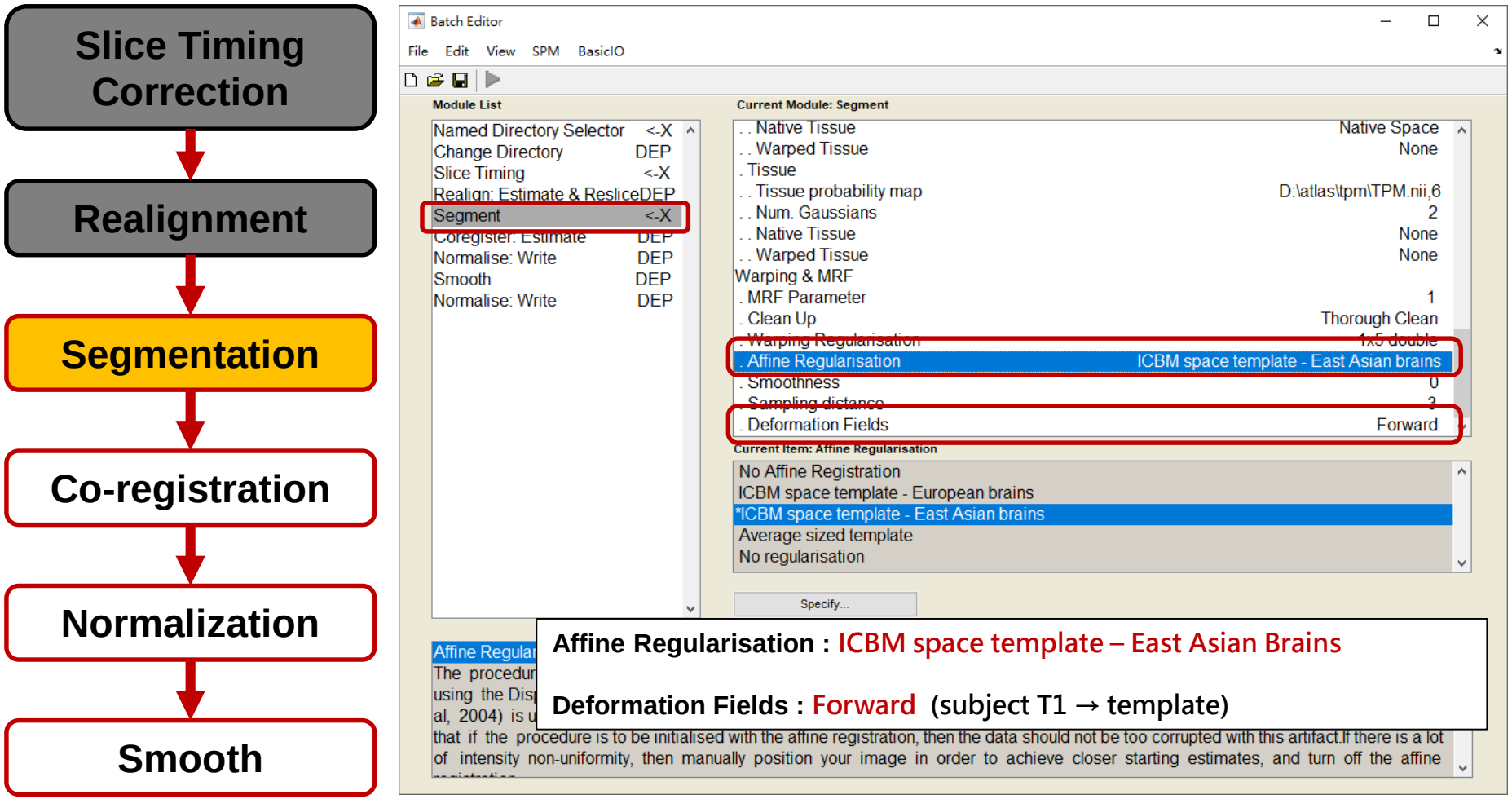
- Slice Timing Correction
- Realignment
- **Segmentation**
- Co-registration
- Normalization
- Smooth



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

Save Bias Corrected : Save bias corrected

Segmentation (Bias field correction)

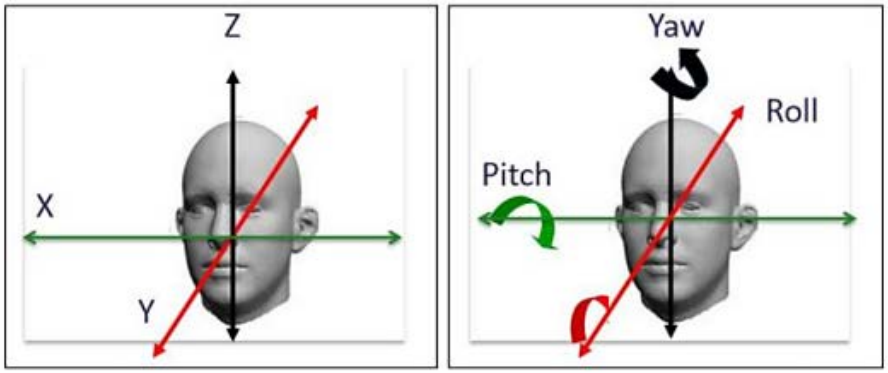


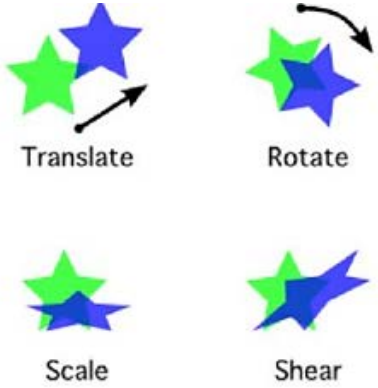
Co-registration (cross-modality registration)

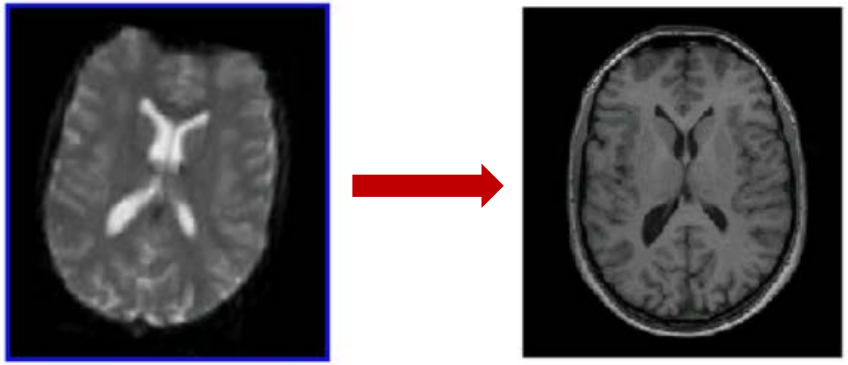
- Slice Timing Correction
- Realignment
- Segmentation
- **Co-registration**
- Normalization
- Smooth

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

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





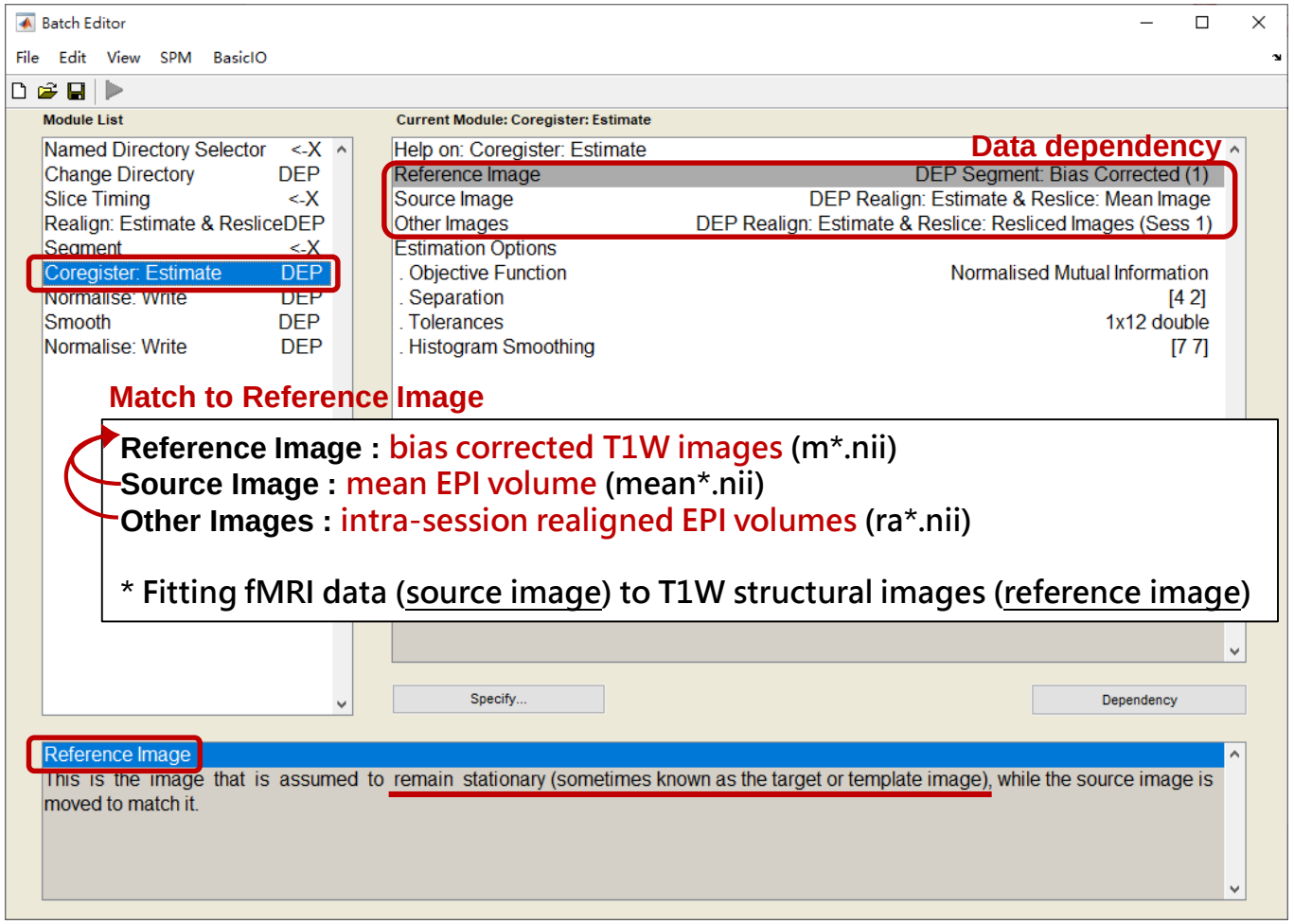


T2*W EPI images (low resolution & poor structural information)

T1W structural images (high resolution)

Co-registration (cross-modality registration)

- Slice Timing Correction
- Realignment
- Segmentation
- **Co-registration**
- Normalization
- Smooth



Normalization (native space → standard space)

Slice Timing Correction

Realignment

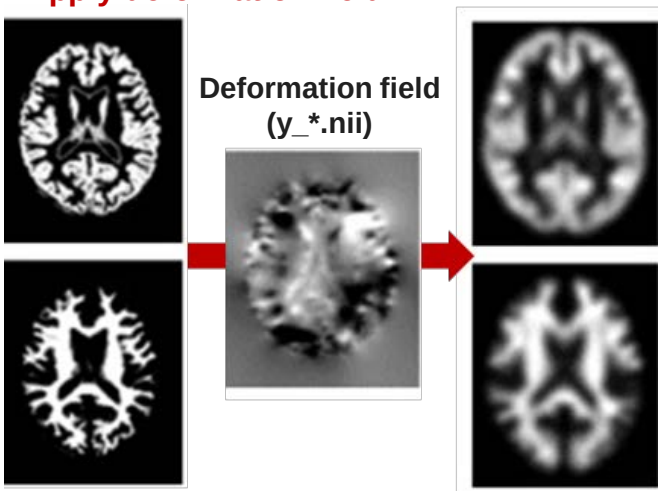
Segmentation

Co-registration

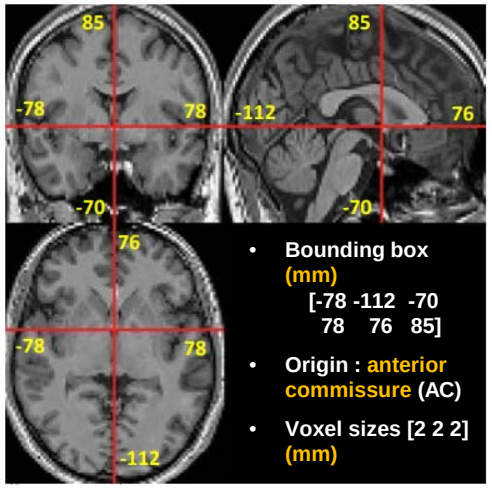
Normalization

Smooth

Apply deformation field



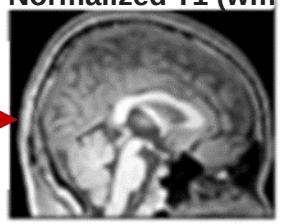
Bounding box & origin

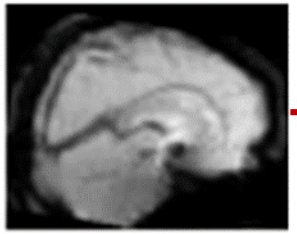


Bias corrected T1 (m*.nii)

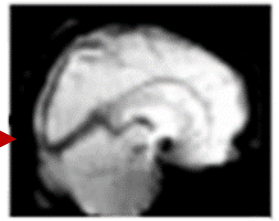
Deformation field
(y_*.nii)

Normalized T1 (wm*.nii)





Deformation field
(y_*.nii)

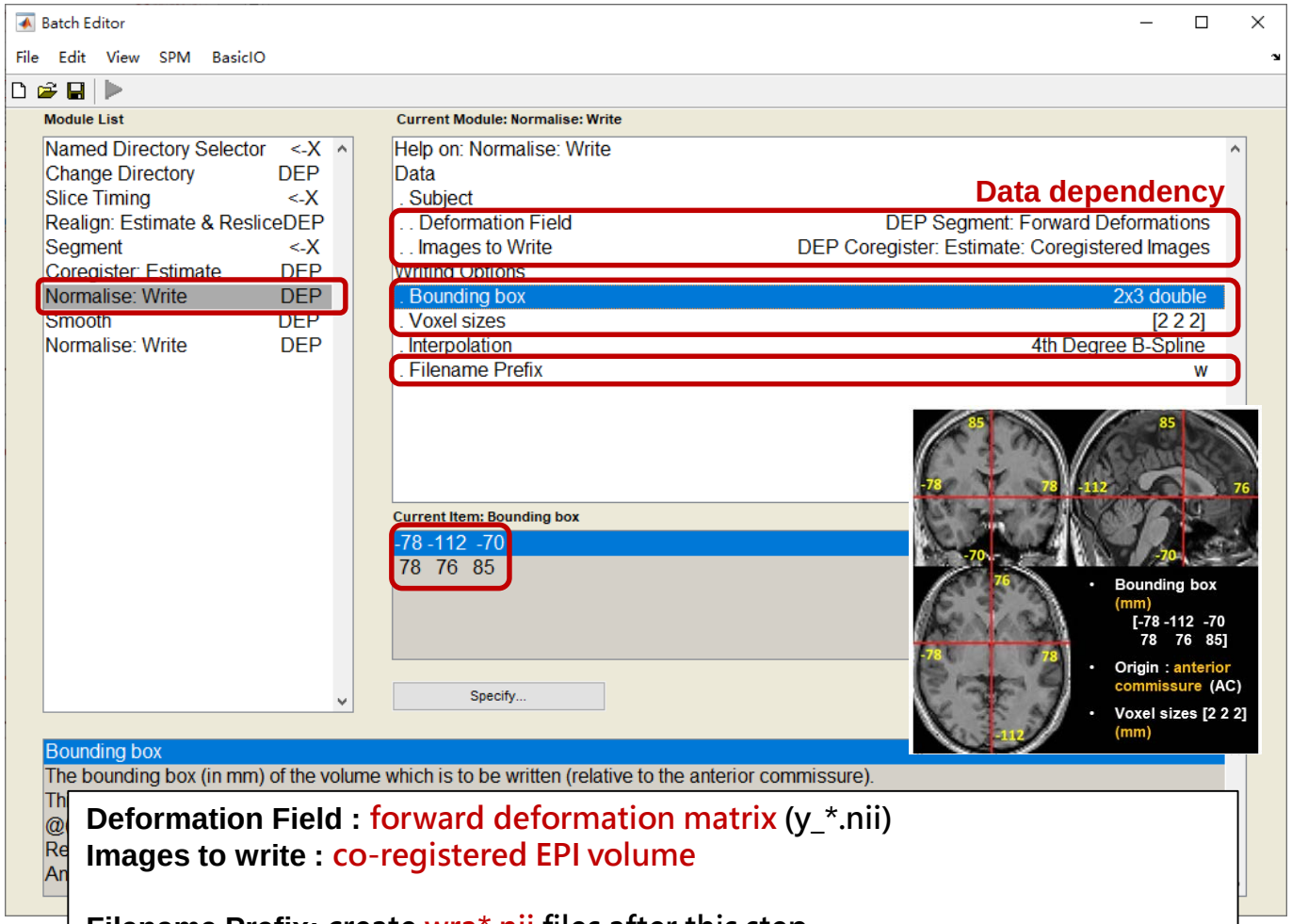


Co-registered EPI volumes

Normalized EPI volumes (wra*.nii)

Normalization (native space → standard space)

- Slice Timing Correction
- Realignment
- Segmentation
- Co-registration
- **Normalization**
- Smooth

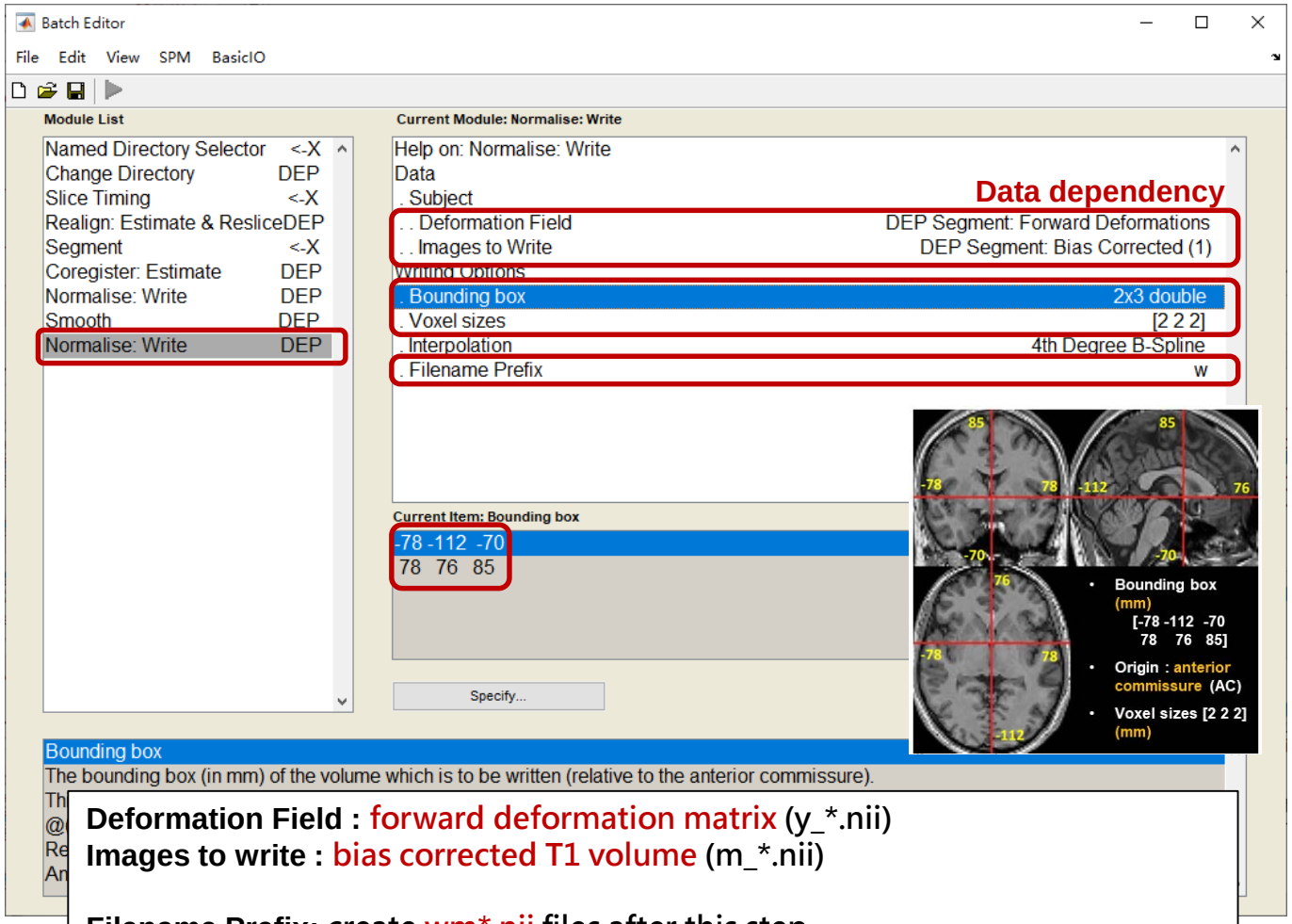


Deformation Field : forward deformation matrix (y_*.nii)
Images to write : co-registered EPI volume

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

Normalization (native space → standard space)

- Slice Timing Correction
- Realignment
- Segmentation
- Co-registration
- **Normalization**
- Smooth



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

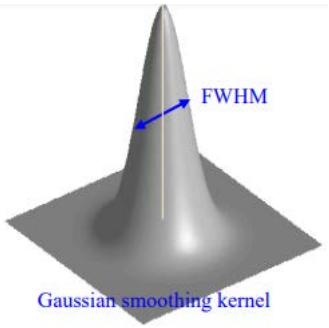
Gaussian Spatial Smoothing

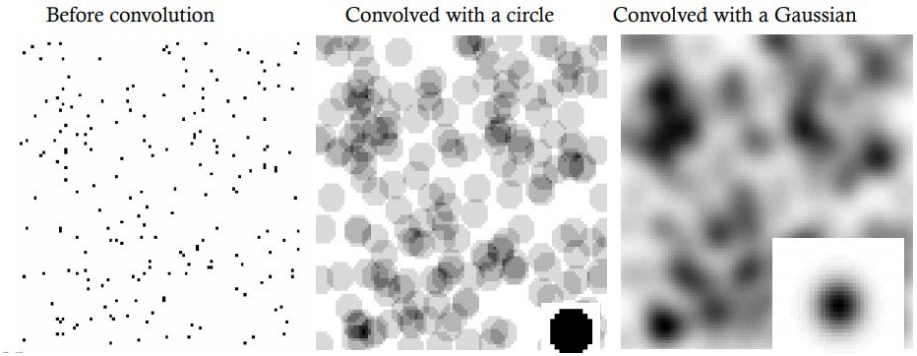
- Slice Timing Correction
- Realignment
- Segmentation
- Co-registration
- Normalization
- **Smooth**

(stamp)

Apply Gaussian kernel smoothing to the normalized EPI volumes

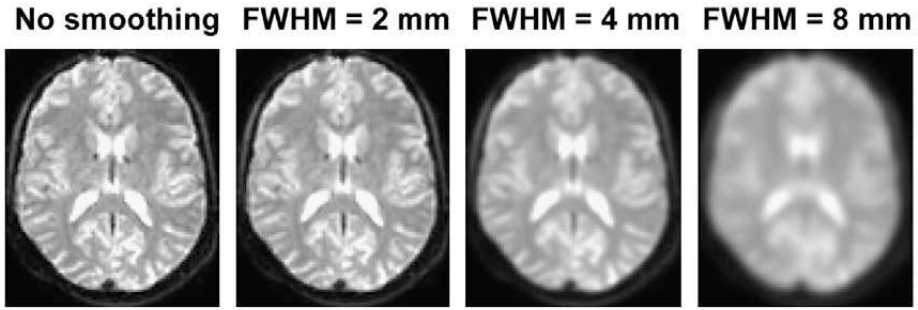
- Each voxel becomes weighted average of surrounding voxels
- Compensate for in accuracies in normalization between individuals
- Increase signal-to-noise ratio (SNR)





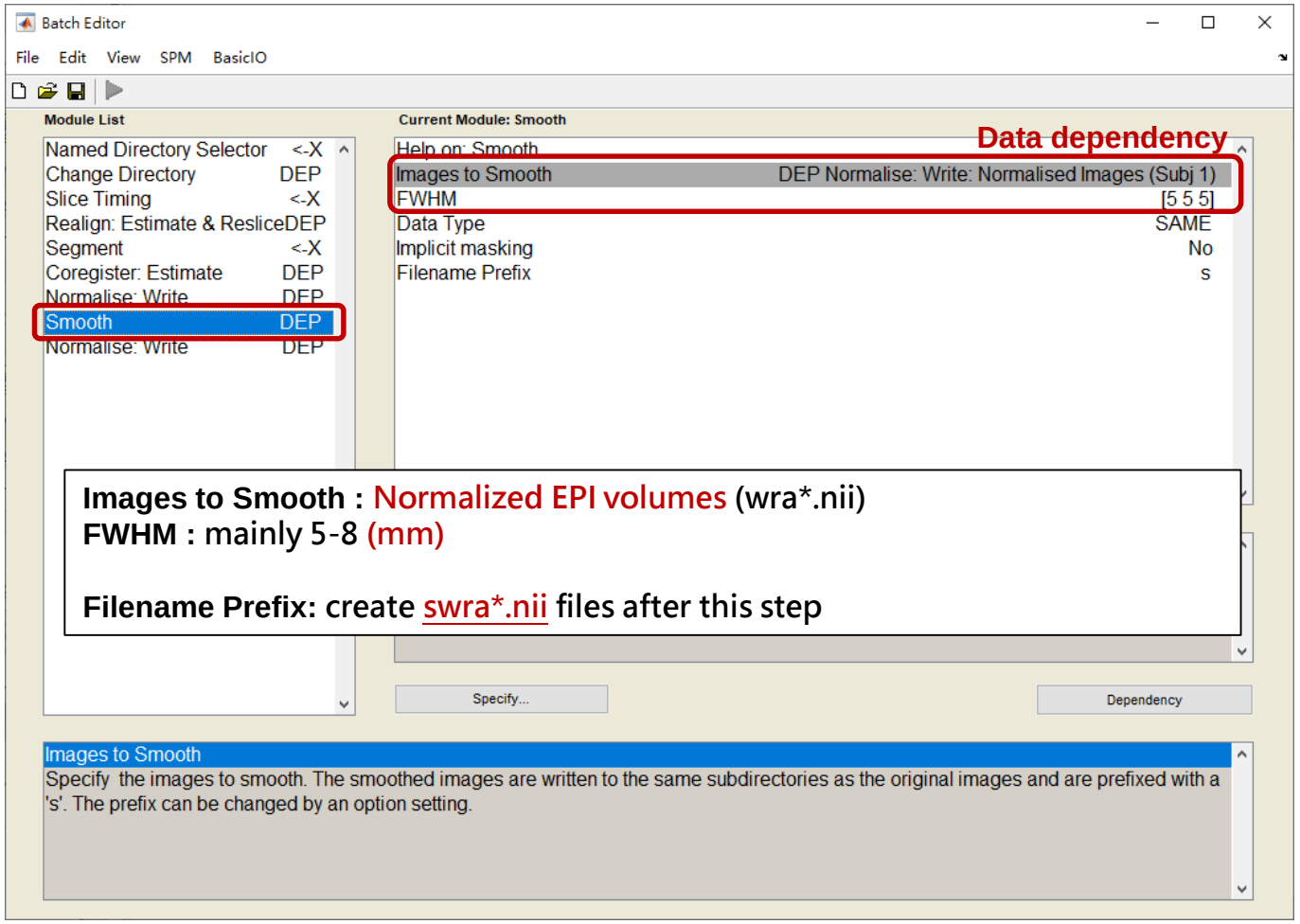
FWHM (full width half maximum)

- 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

- Slice Timing Correction
- Realignment
- Segmentation
- Co-registration
- Normalization
- **Smooth**



Images to Smooth : Normalized EPI volumes (wra*.nii)
FWHM : mainly 5-8 (mm)

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

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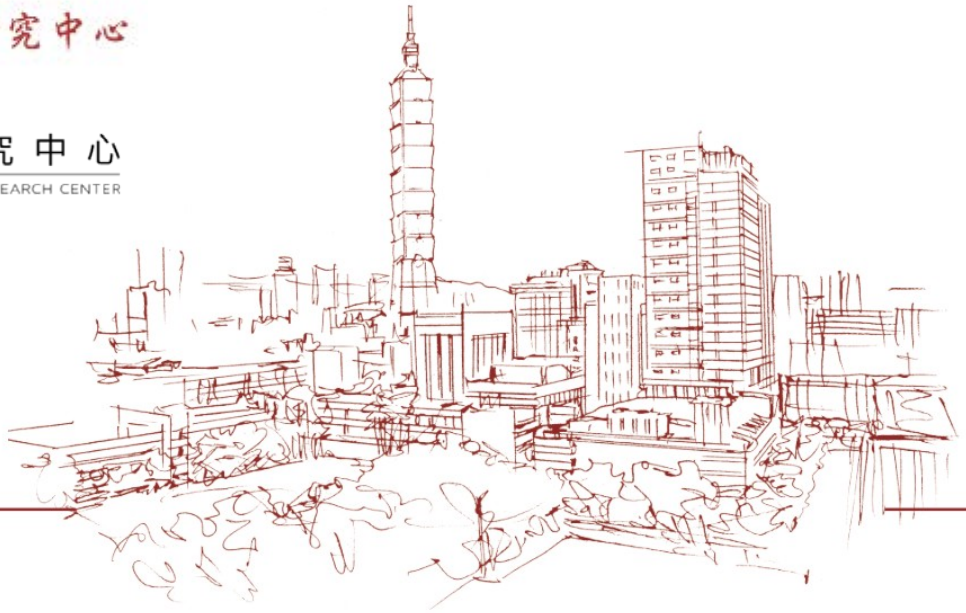
轉譯影像研究中心
TMU TRANSLATIONAL IMAGING RESEARCH CENTER



Analysis of Functional Magnetic Resonance Imaging (fMRI)

Set up SPM Batch Jobs

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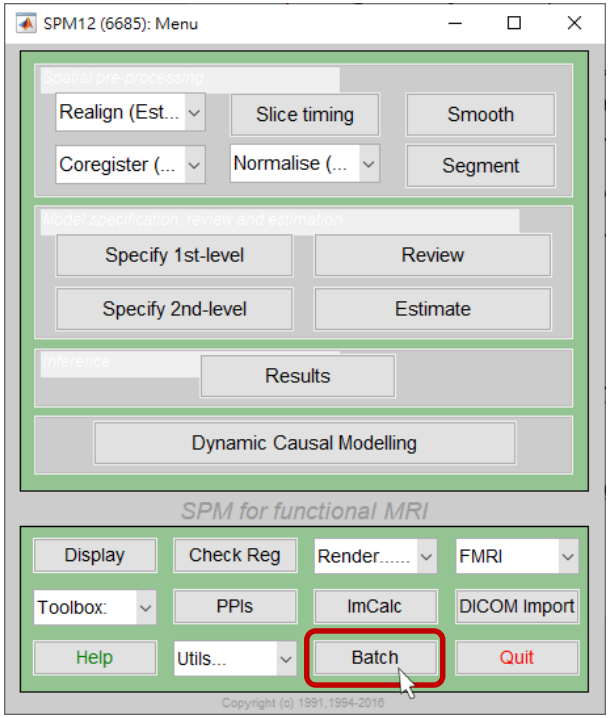
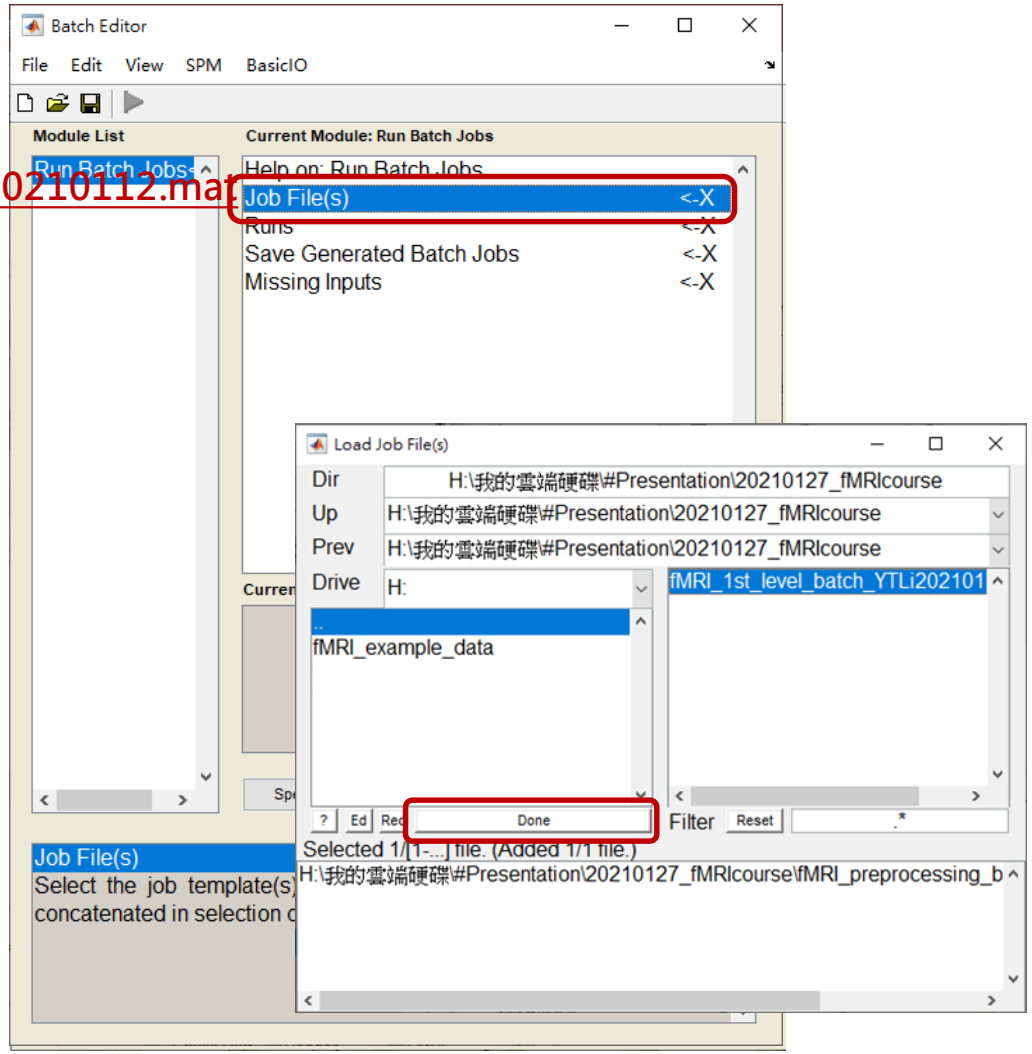
SPM Batch Jobs

>> spm fmri

> Batch
> BasicIO > Run > Run Batch Jobs
> fMRI_preprocessing_batch_YTLi20210112.mat
> Done

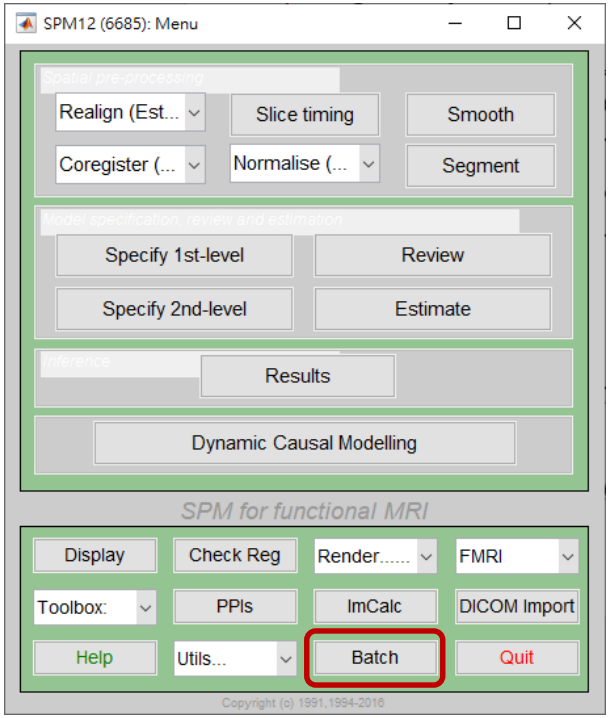


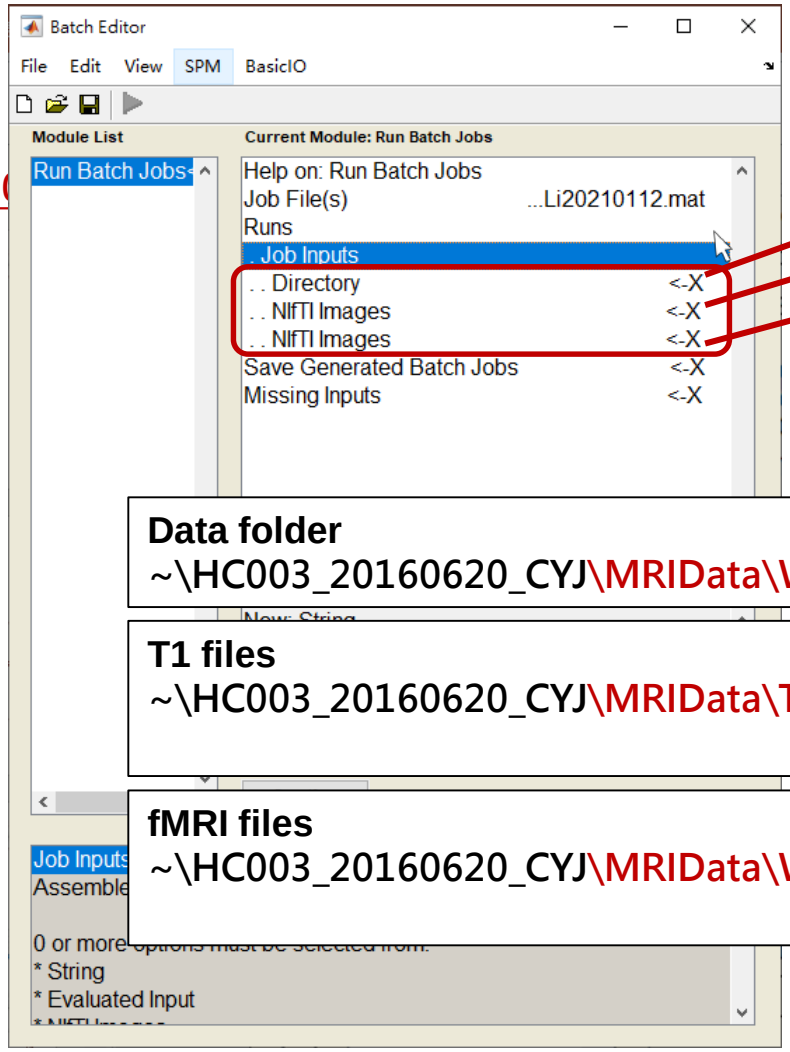


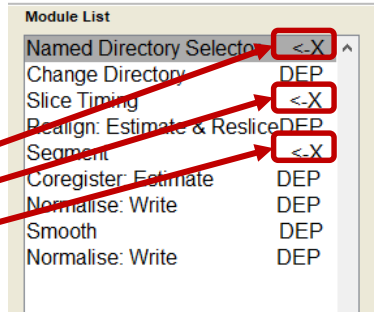
SPM Batch Jobs

>> spm fmri

> Batch
> BasicIO > Run > Run Batch Jobs
> fMRI_preprocessing_batch_YTLi2(
> Done







Data folder
~\HC003_20160620_CYJ\MRIData\WM1

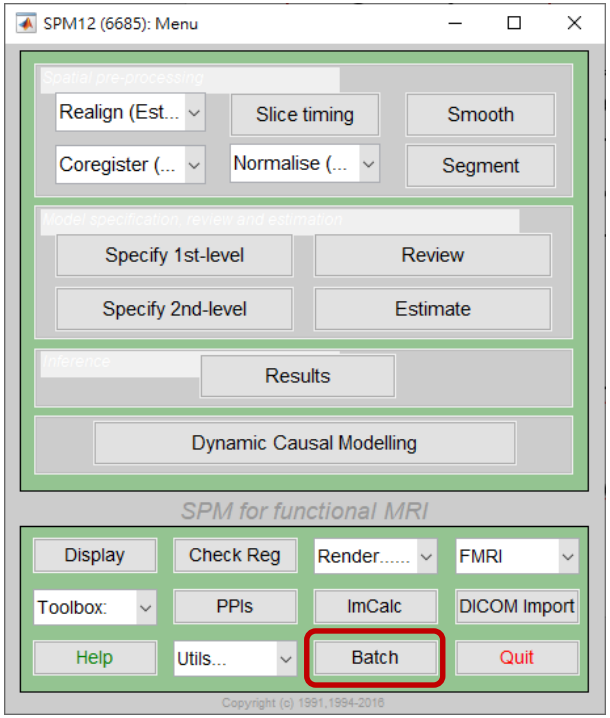
T1 files
~\HC003_20160620_CYJ\MRIData\T1\20*.nii
(1 volume)

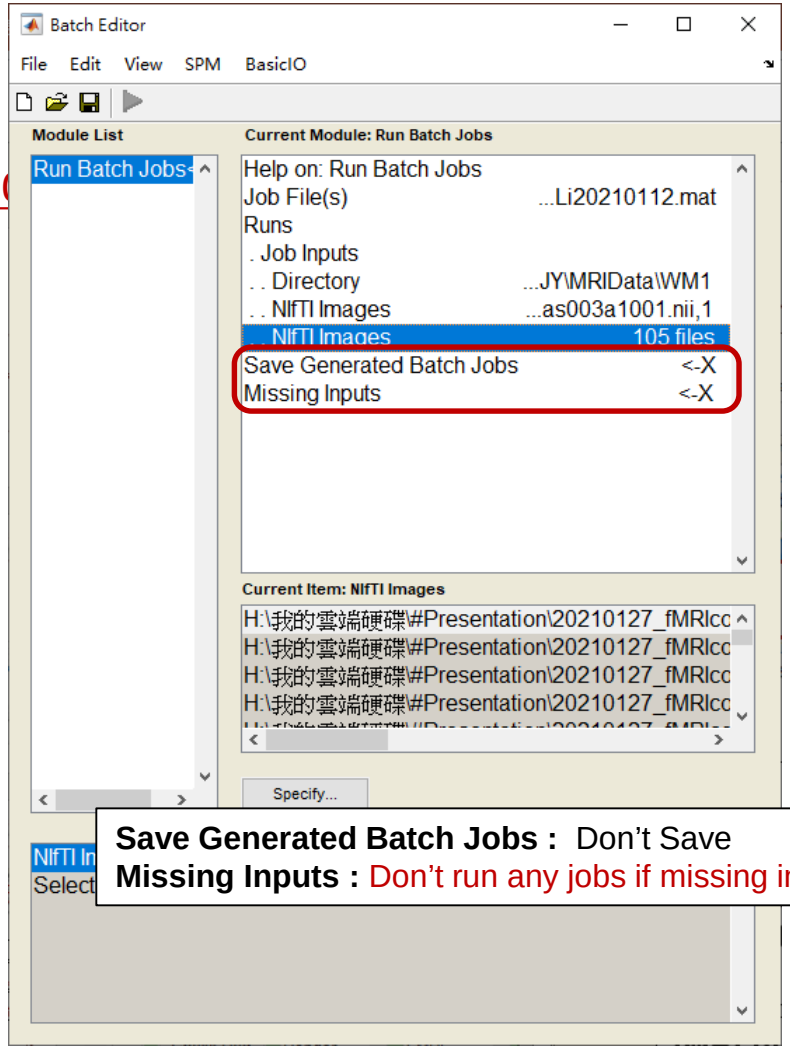
fMRI files
~\HC003_20160620_CYJ\MRIData\WM1\20*.nii
(105 volumes)

SPM Batch Jobs

>> spm fmri

> Batch
> BasicIO > Run > Run Batch Jobs
> fMRI_preprocessing_batch_YTLi2(
> Done



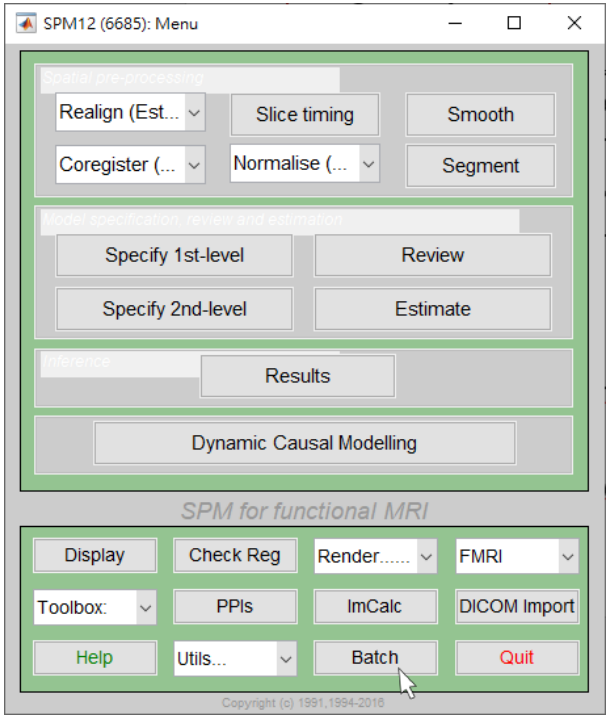


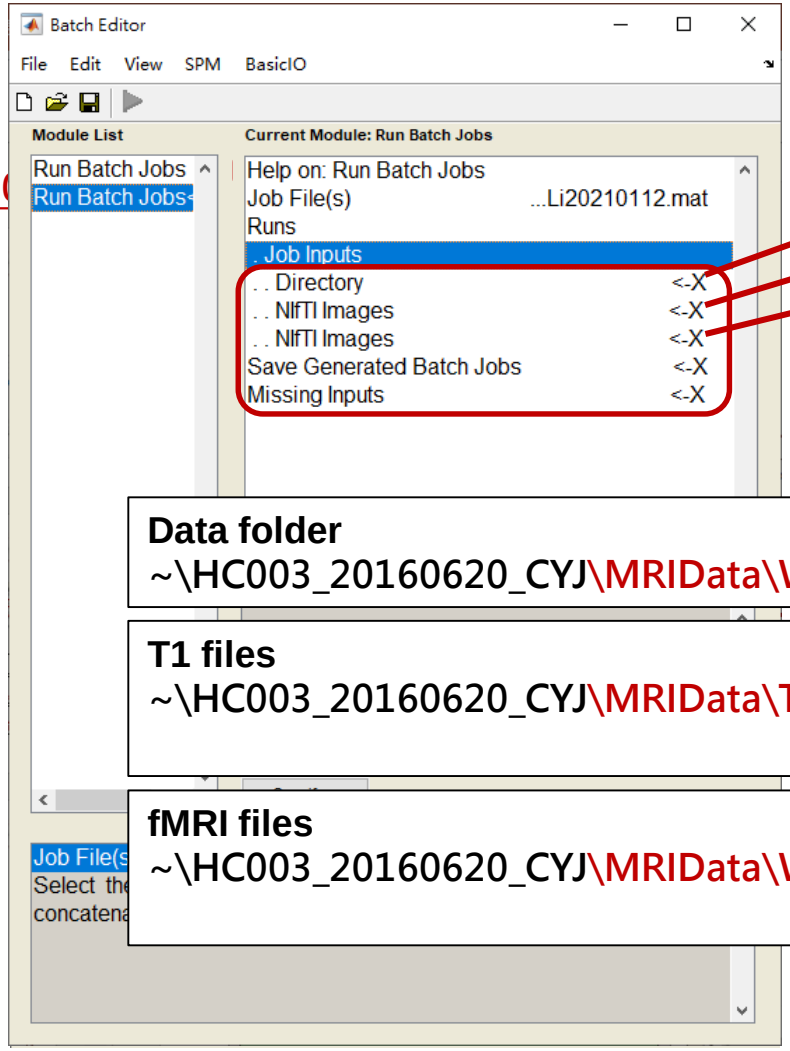
Save Generated Batch Jobs : Don't Save
Missing Inputs : Don't run any jobs if missing inputs

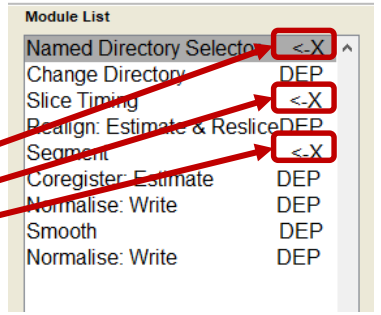
SPM Batch Jobs

>> spm fmri

> Batch
> BasicIO > Run > Run Batch Jobs
> fMRI_preprocessing_batch_YTLi2(
> Done







Data folder
~\HC003_20160620_CYJ\MRIData\WM1

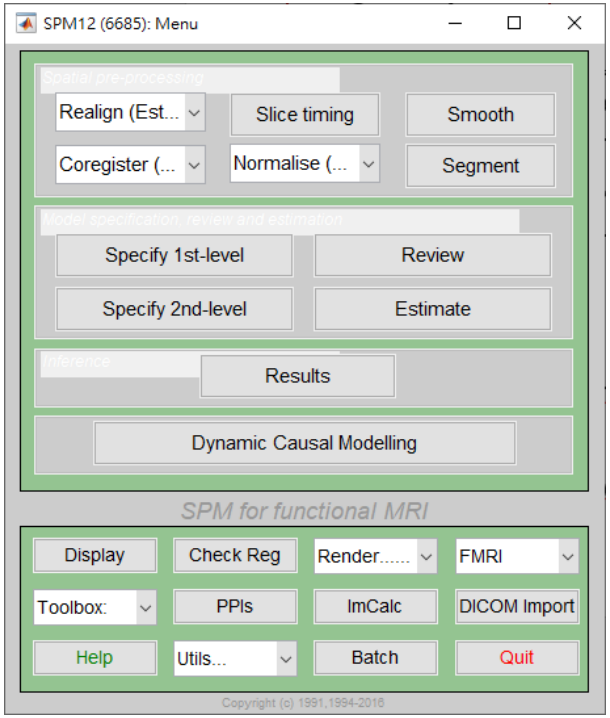
T1 files
~\HC003_20160620_CYJ\MRIData\T1\20*.nii
(1 volume)

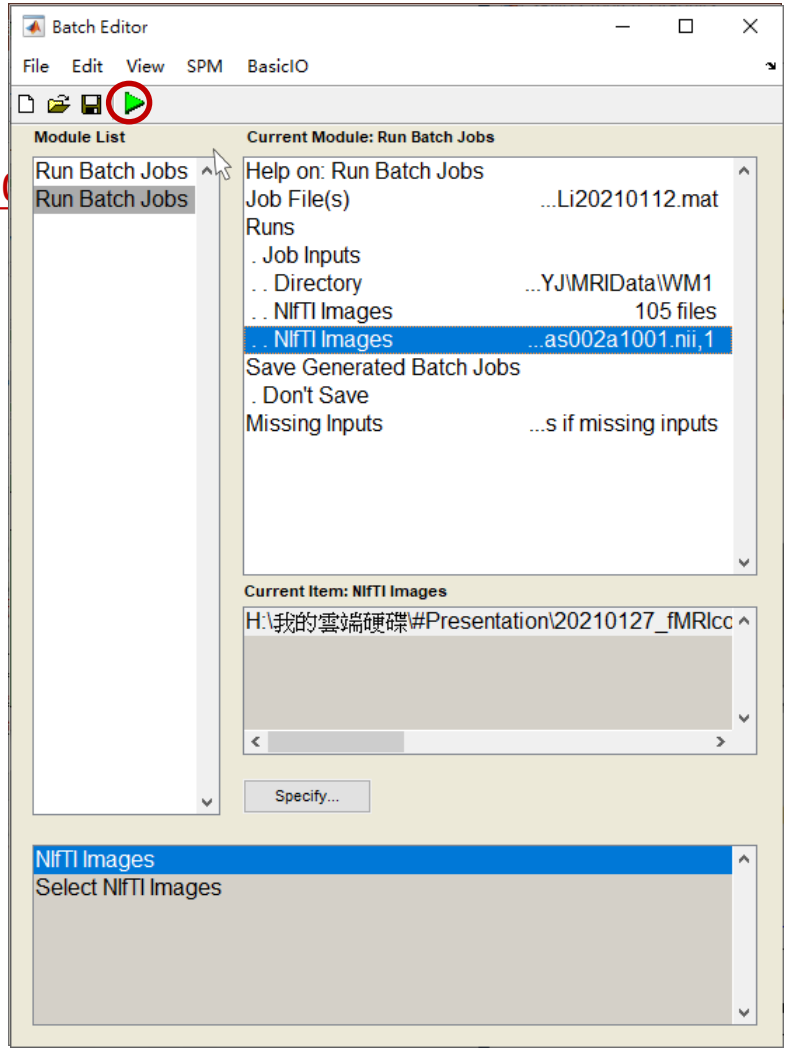
fMRI files
~\HC003_20160620_CYJ\MRIData\WM1\20*.nii
(105 volumes)

SPM Batch Jobs

>> spm fmri

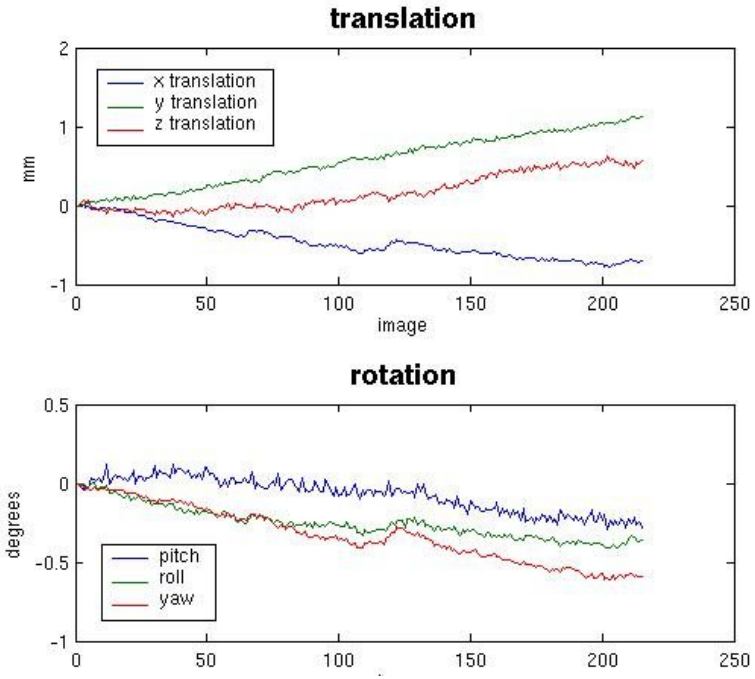
> Batch
> BasicIO > Run > Run Batch Jobs
> fMRI_preprocessing_batch_YTLi2(
> Done

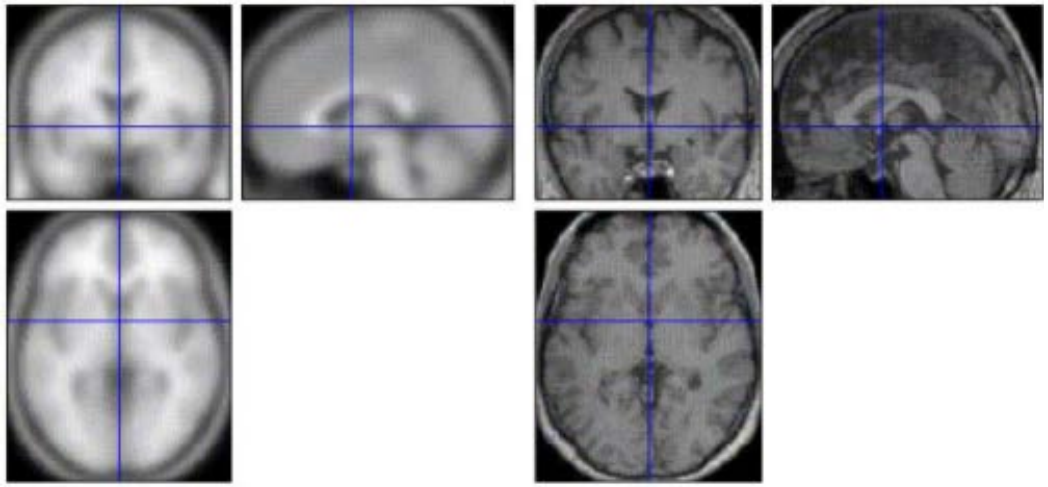




Check SPM processing logfile

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





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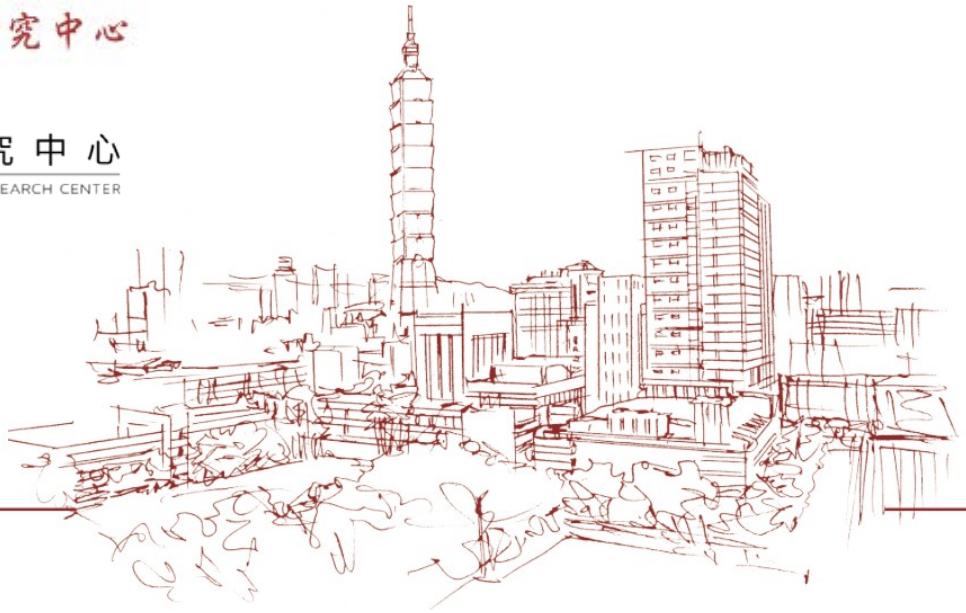
轉譯影像研究中心
TMU TRANSLATIONAL IMAGING RESEARCH CENTER



Analysis of Functional Magnetic Resonance Imaging (fMRI)

General Linear Model
(1st level analysis)

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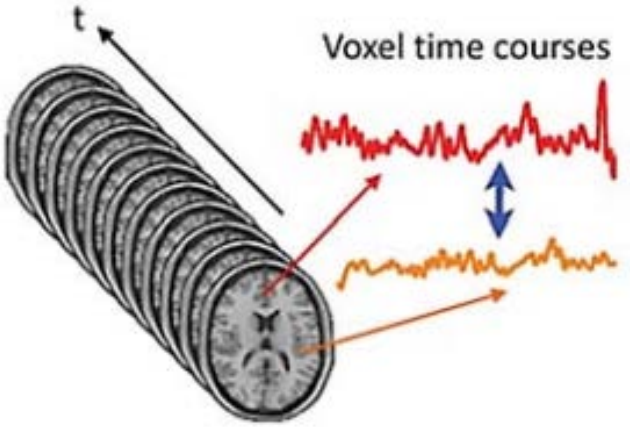
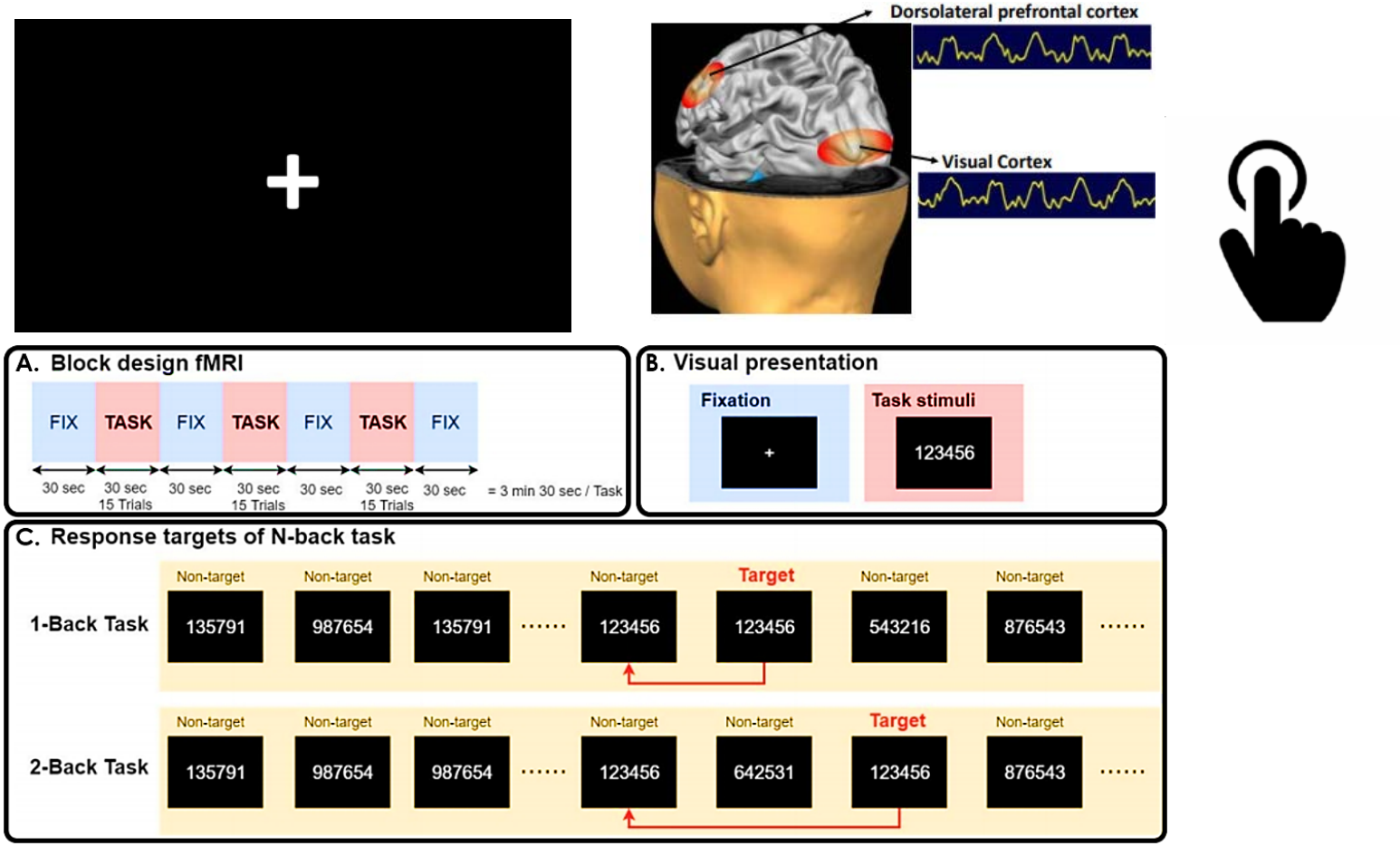
fMRI Protocol (see DICOM tags)

- (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)



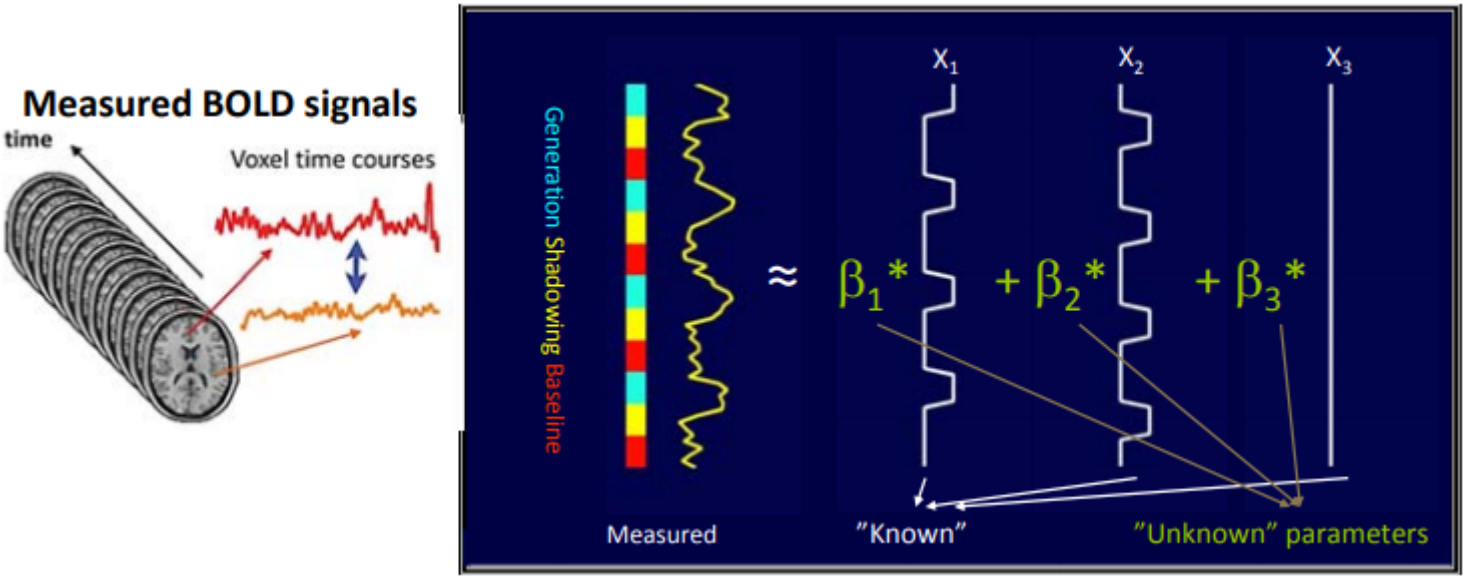
fMRI Protocol (experimental design)

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



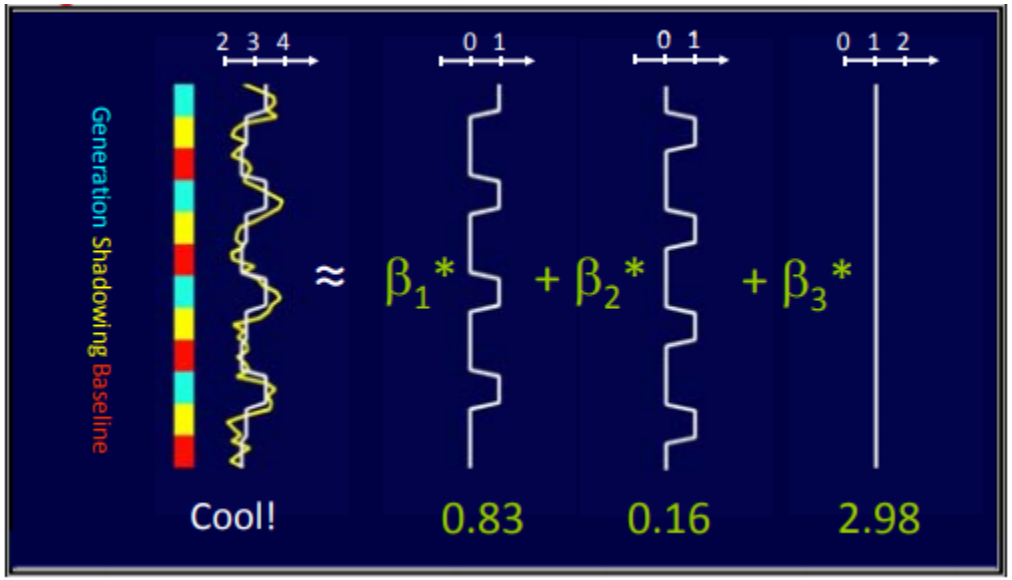
General Linear Model (GLM)

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



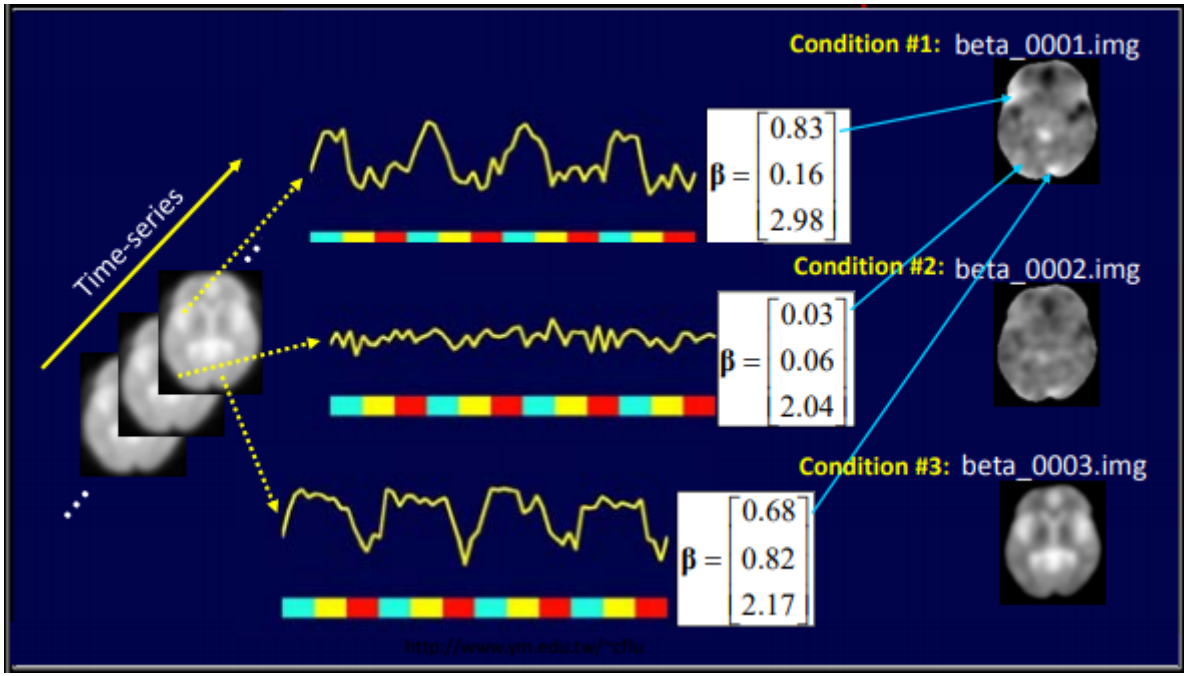
General Linear Model (GLM) parameter estimation

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



General Linear Model (GLM) parameter estimation

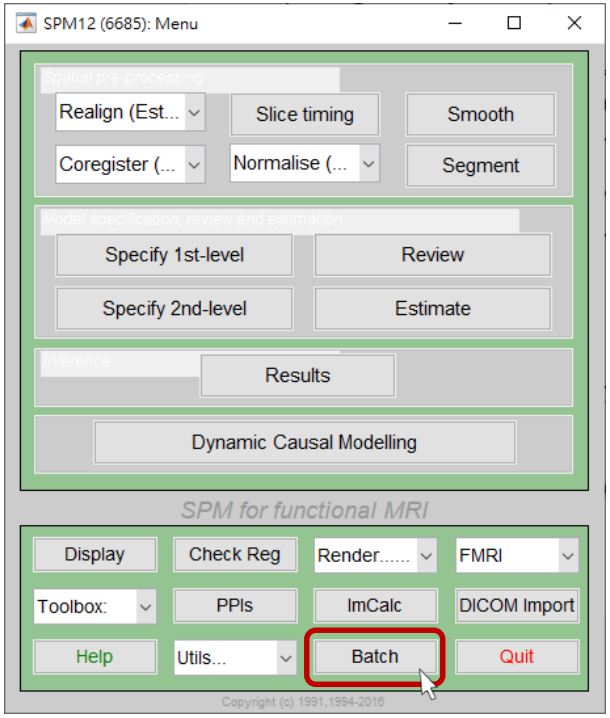
- Apply the same model to all voxels.
- Different parameters (beta value) for each voxel.
- Beta map for each task condition.

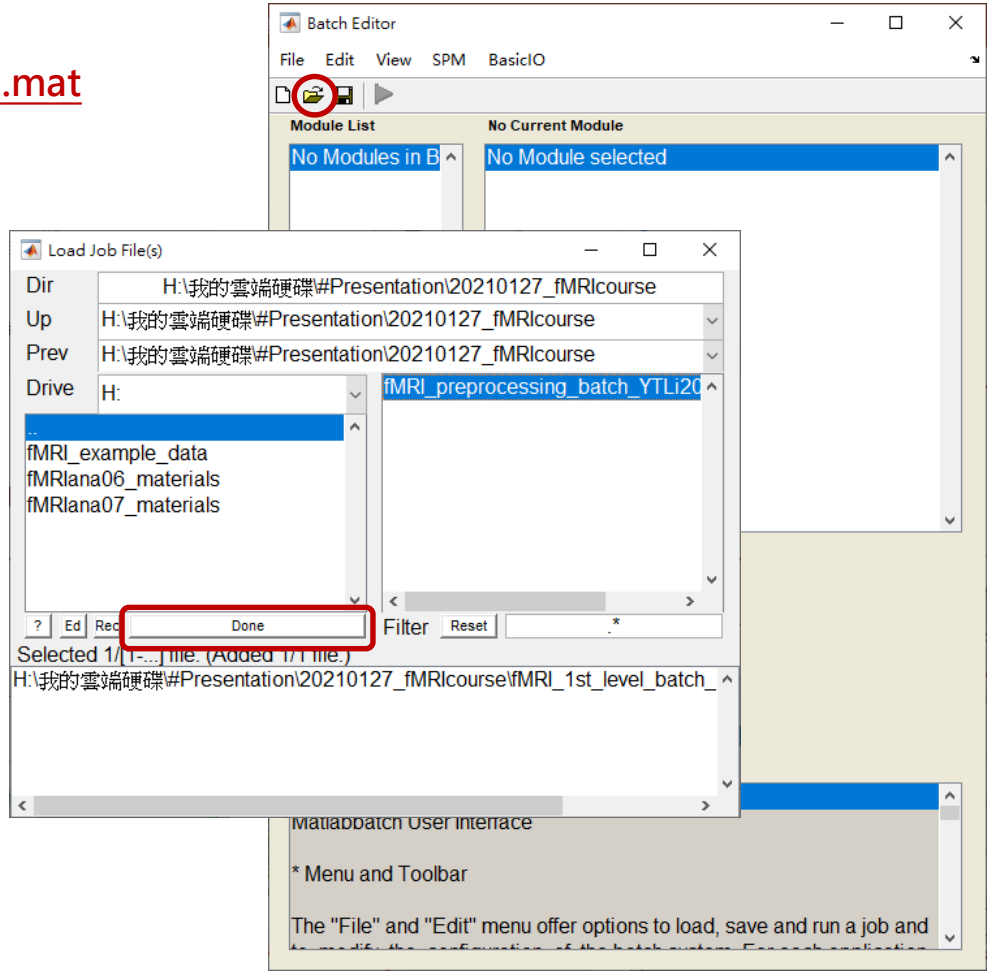


Specify 1st-level Analysis Model

>> spm fmri

> Batch
> fMRI_1st_level_batch_YTLi20210112.mat
> Done

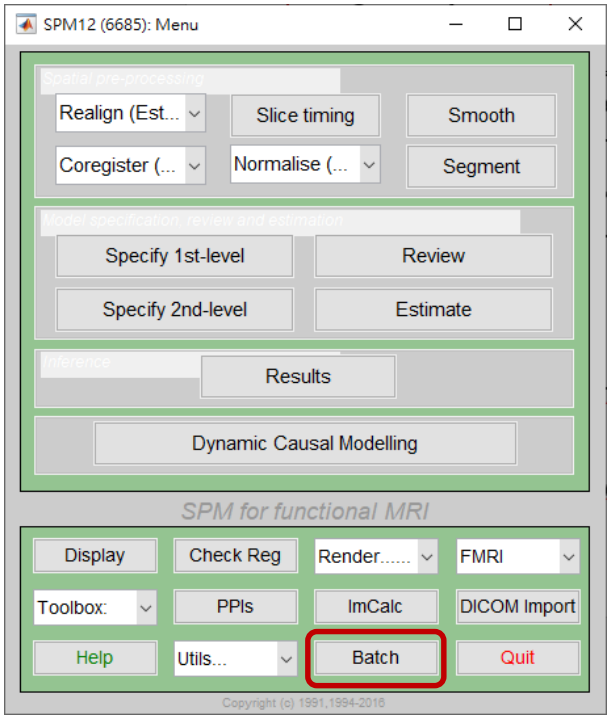


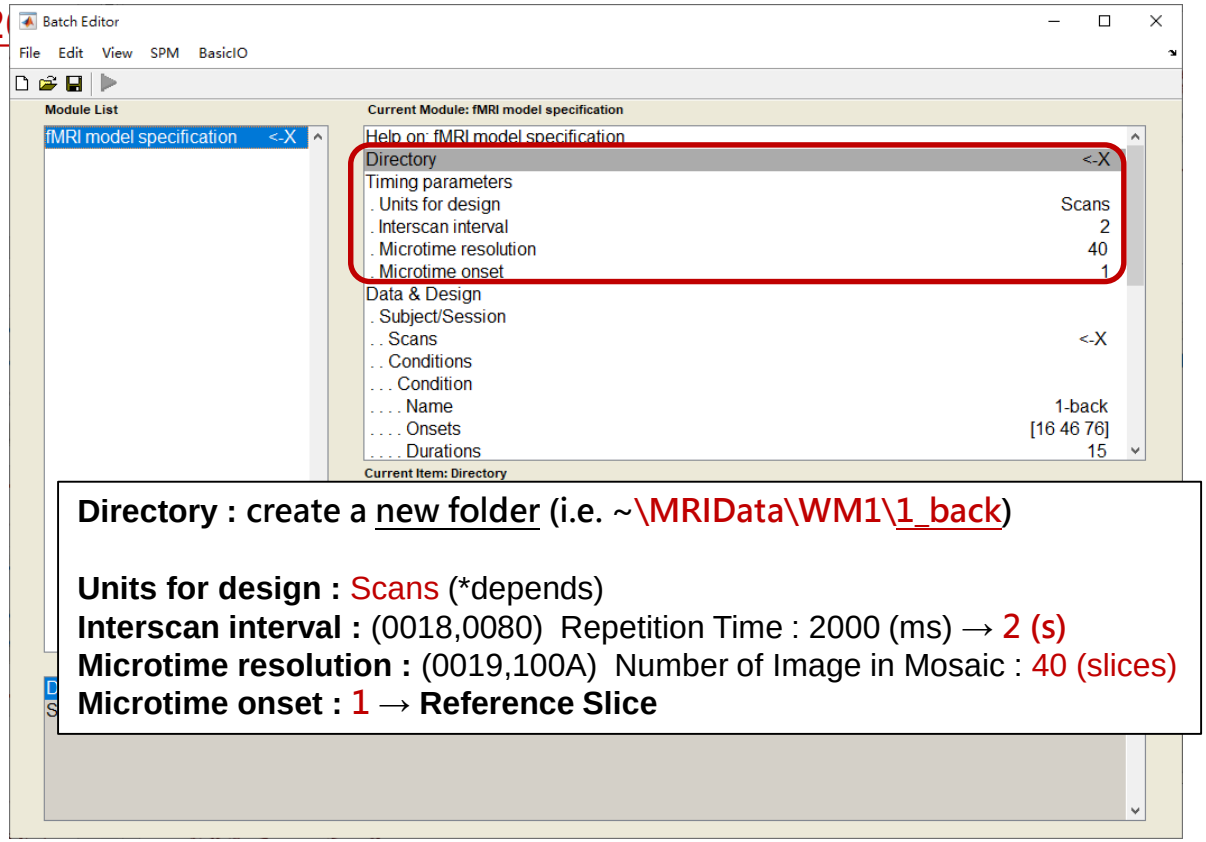


Specify 1st-level Analysis Model

>> spm fmri

> Batch
> fMRI_preprocessing_batch_YTLi2(
> Done





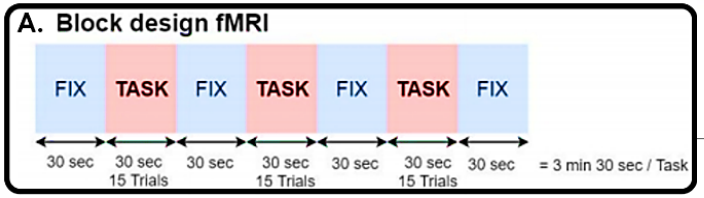
Directory : create a new folder (i.e. ~\MRIData\WM1\1_back)

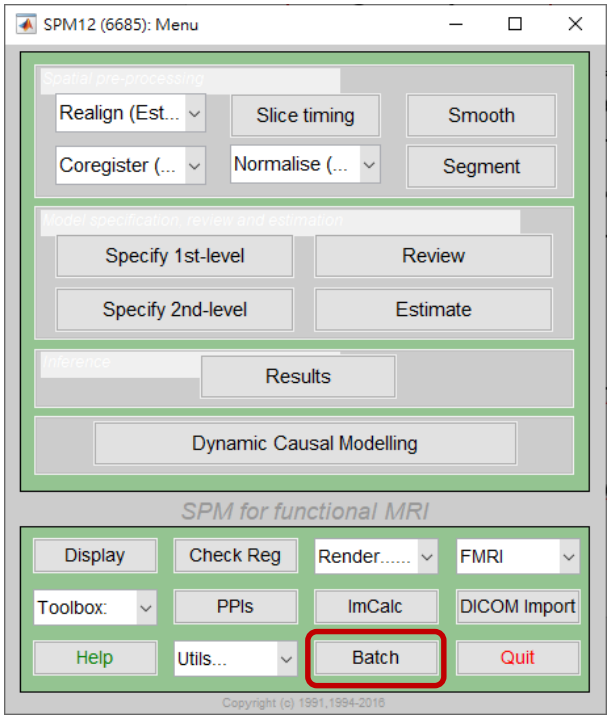
Units for design : Scans (*depends)
Interscan interval : (0018,0080) Repetition Time : 2000 (ms) → 2 (s)
Microtime resolution : (0019,100A) Number of Image in Mosaic : 40 (slices)
Microtime onset : 1 → **Reference Slice**

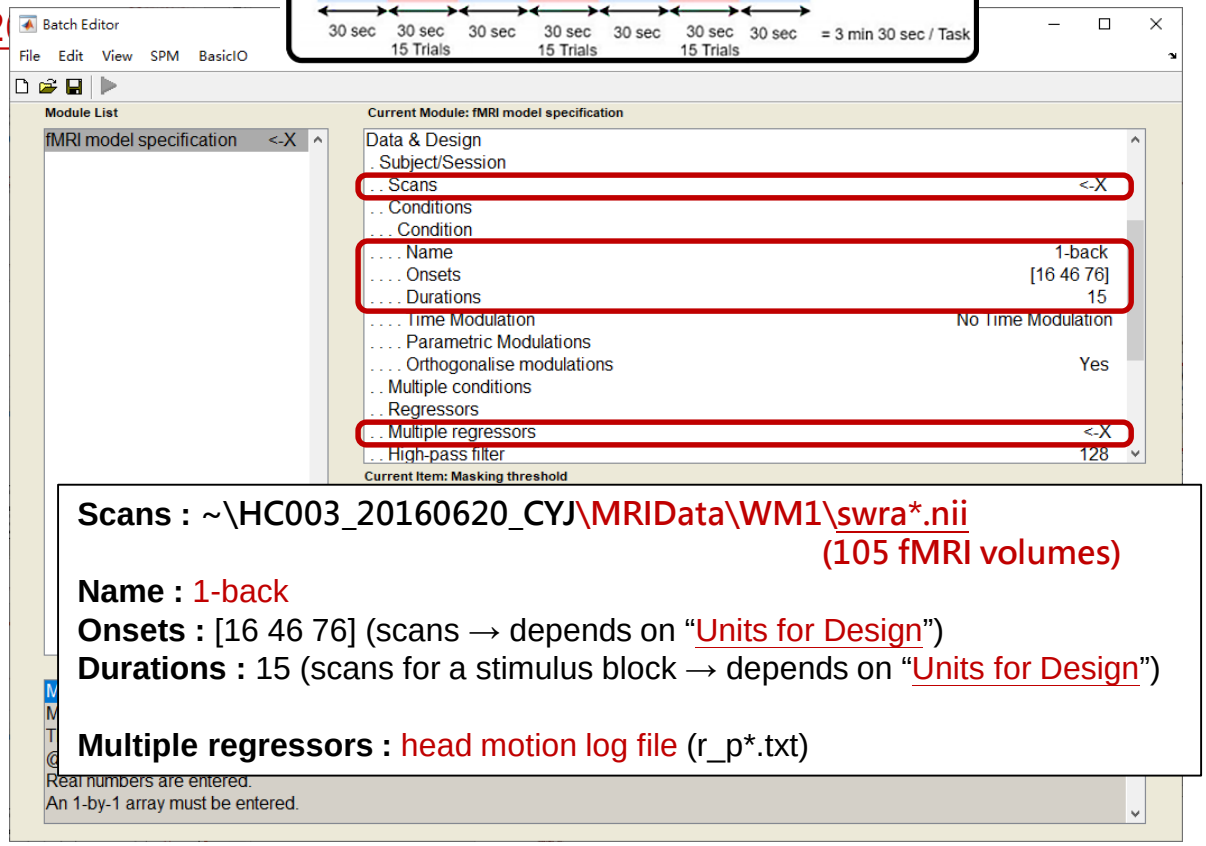
Specify 1st-level Analysis Model

>> spm fmri

> Batch
> fMRI_preprocessing_batch_YTLi2(
> Done







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

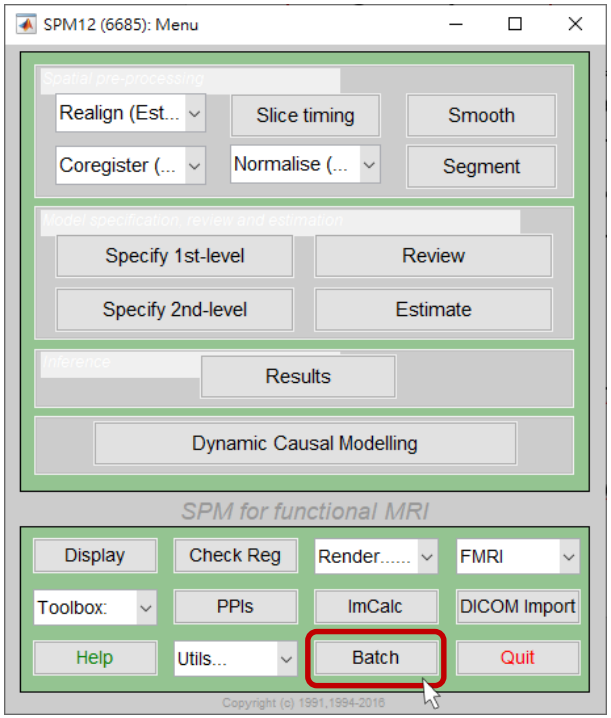
Name : 1-back
Onsets : [16 46 76] (scans → depends on "Units for Design")
Durations : 15 (scans for a stimulus block → depends on "Units for Design")

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

Specify 1st-level Analysis Model

>> spm fmri

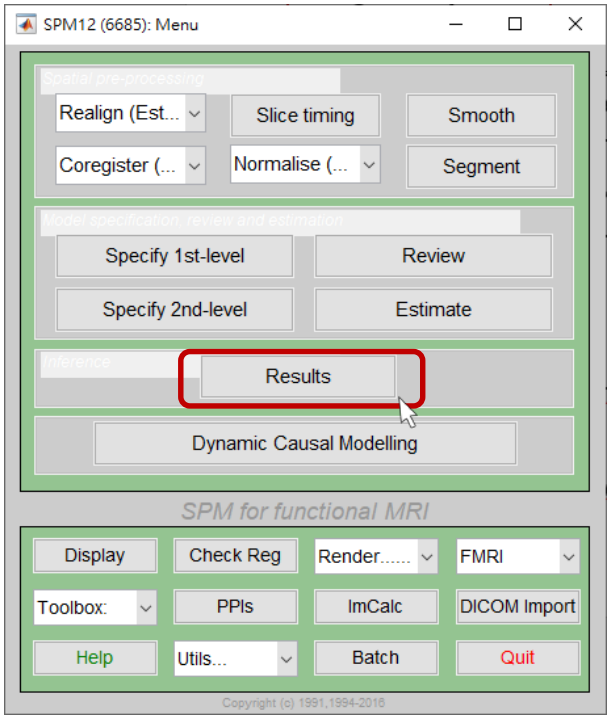
> Batch
> fMRI_preprocessing_batch_YTLi2(
> Done

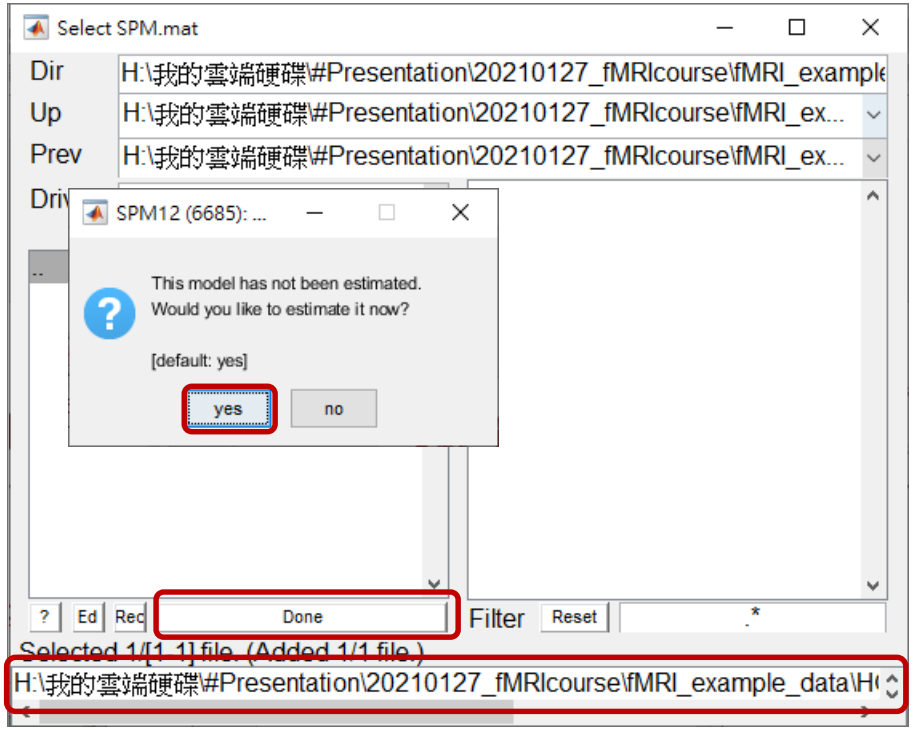


Estimate Model Parameters

>> spm fmri

> Results
> SPM.mat
> Done

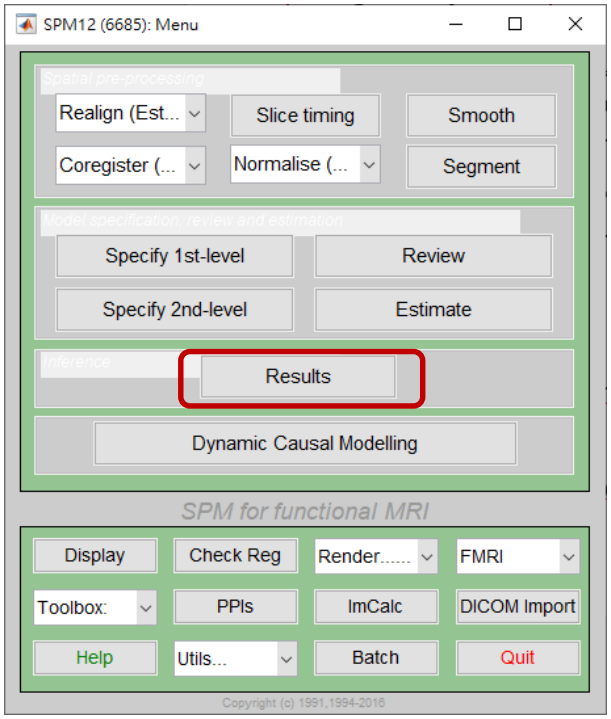


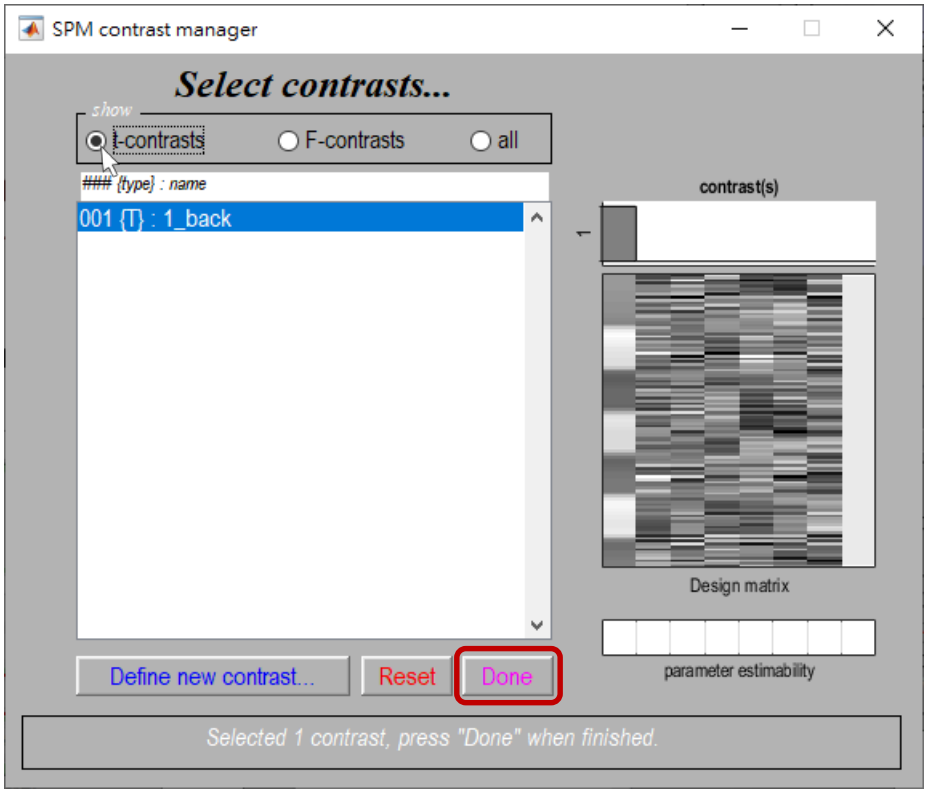


Estimate Model Parameters

>> spm fmri

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

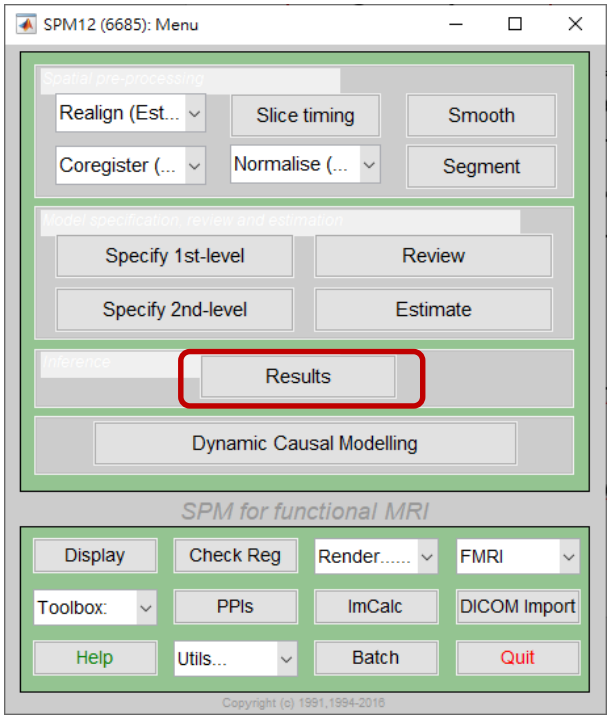


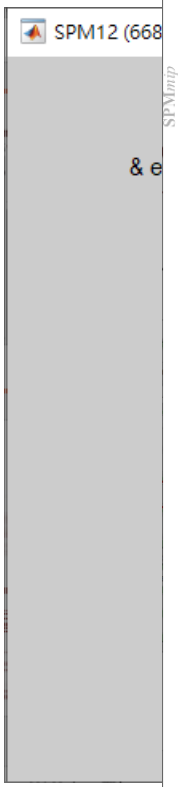


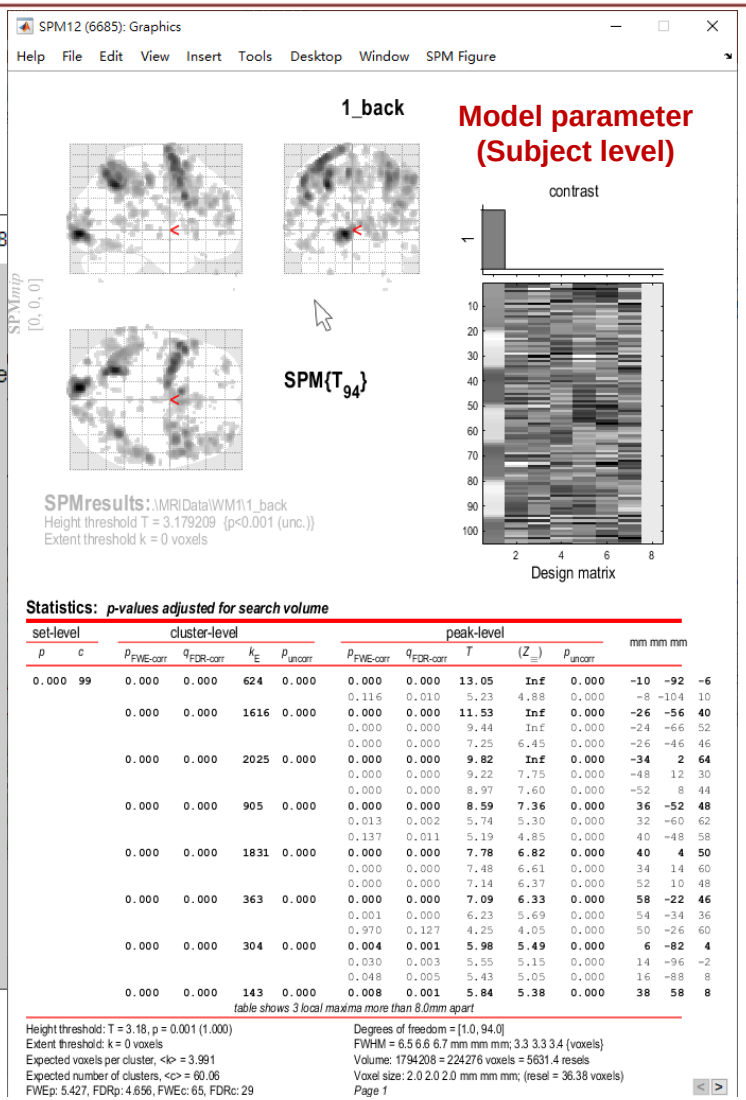
Estimate Model Parameters

>> spm fmri

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







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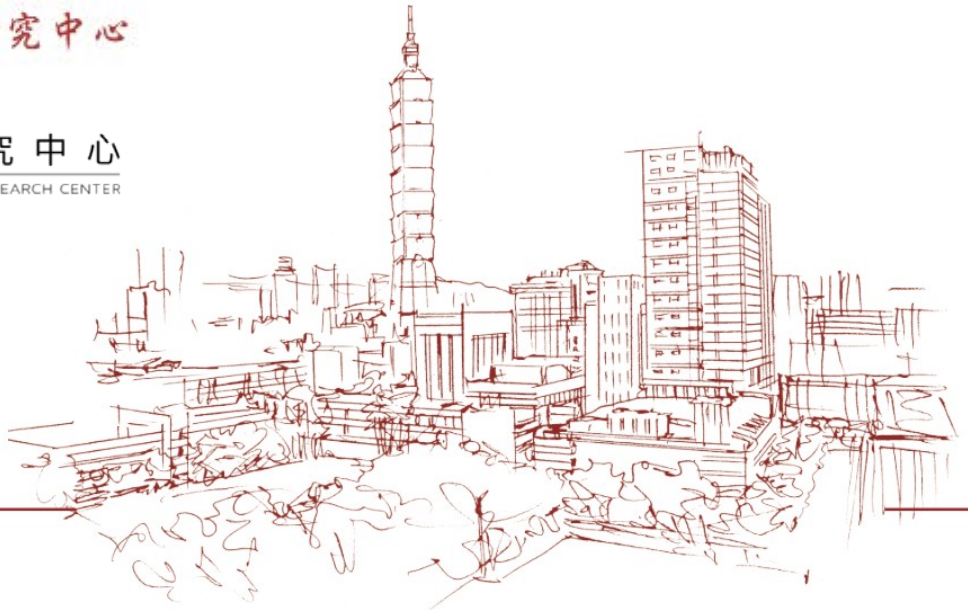

Analysis of Functional Magnetic Resonance Imaging (fMRI)

Group-Level Statistical Analysis
(2nd level analysis)

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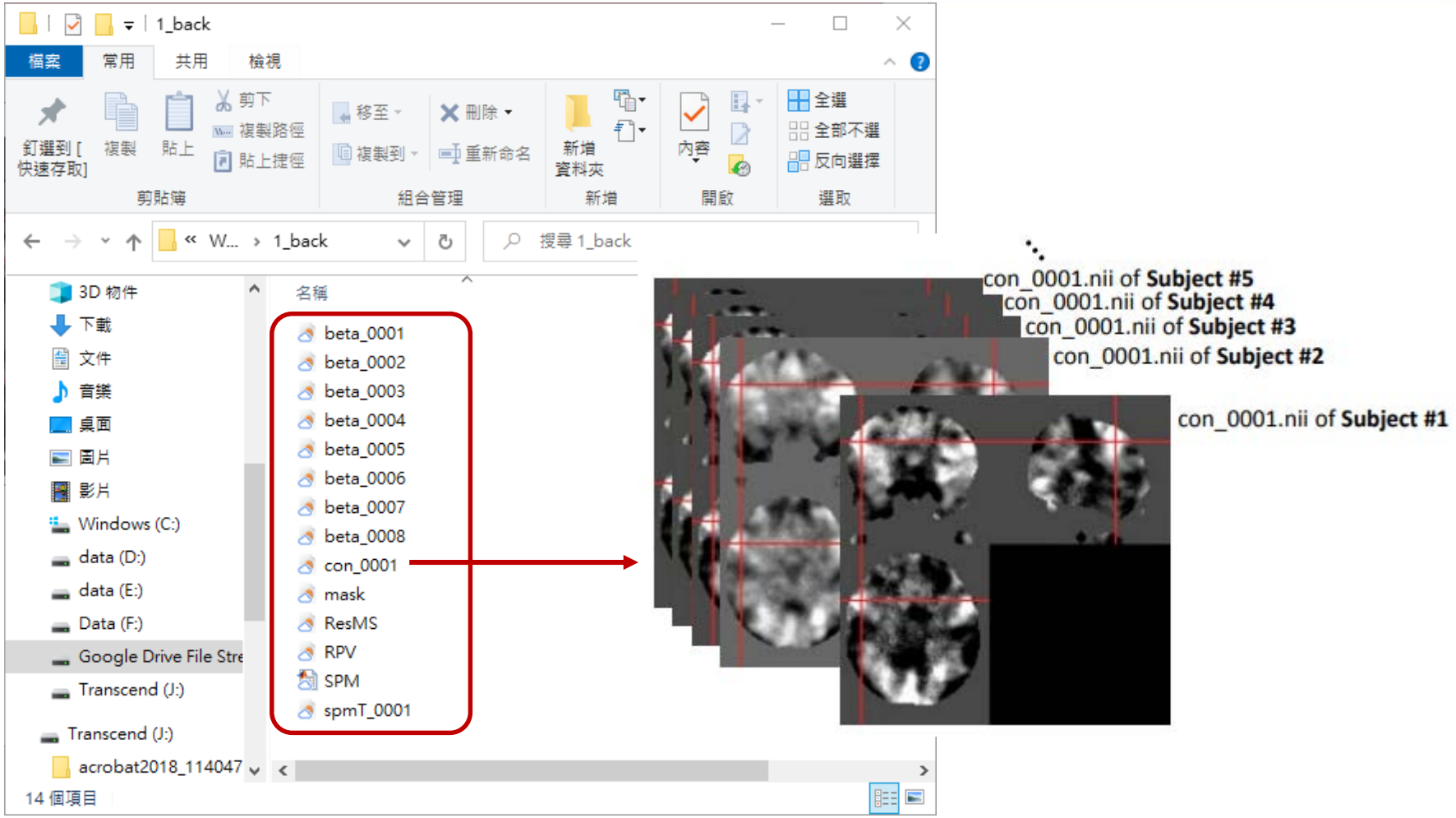
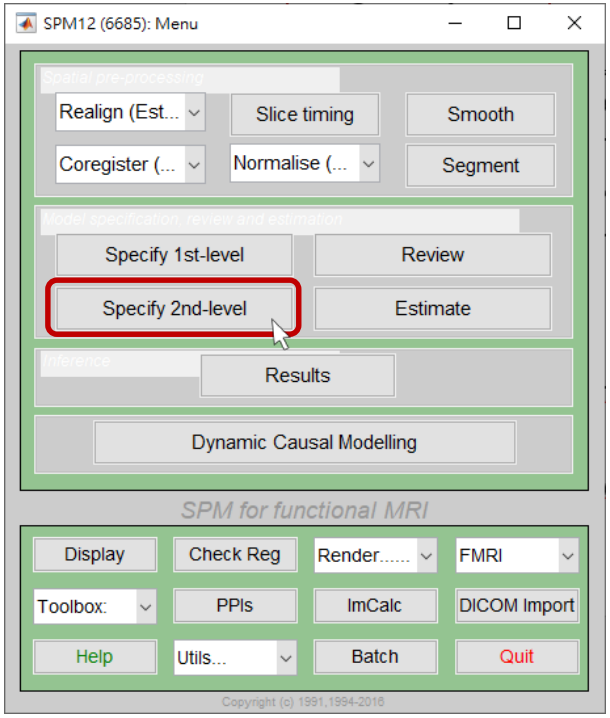
Statistical Inference on Group Data

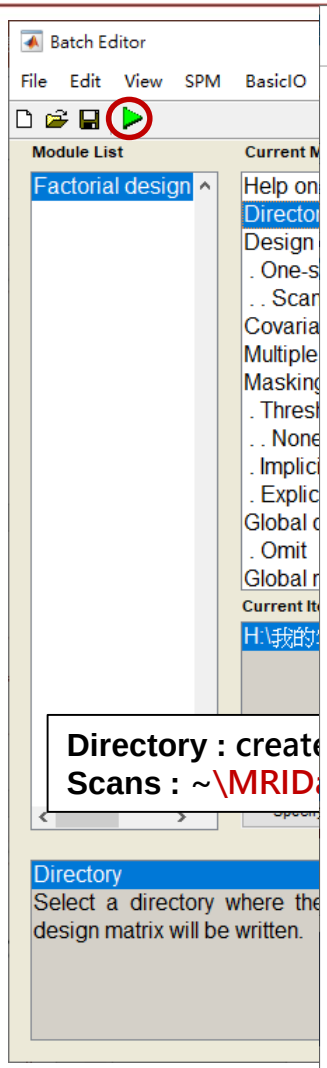


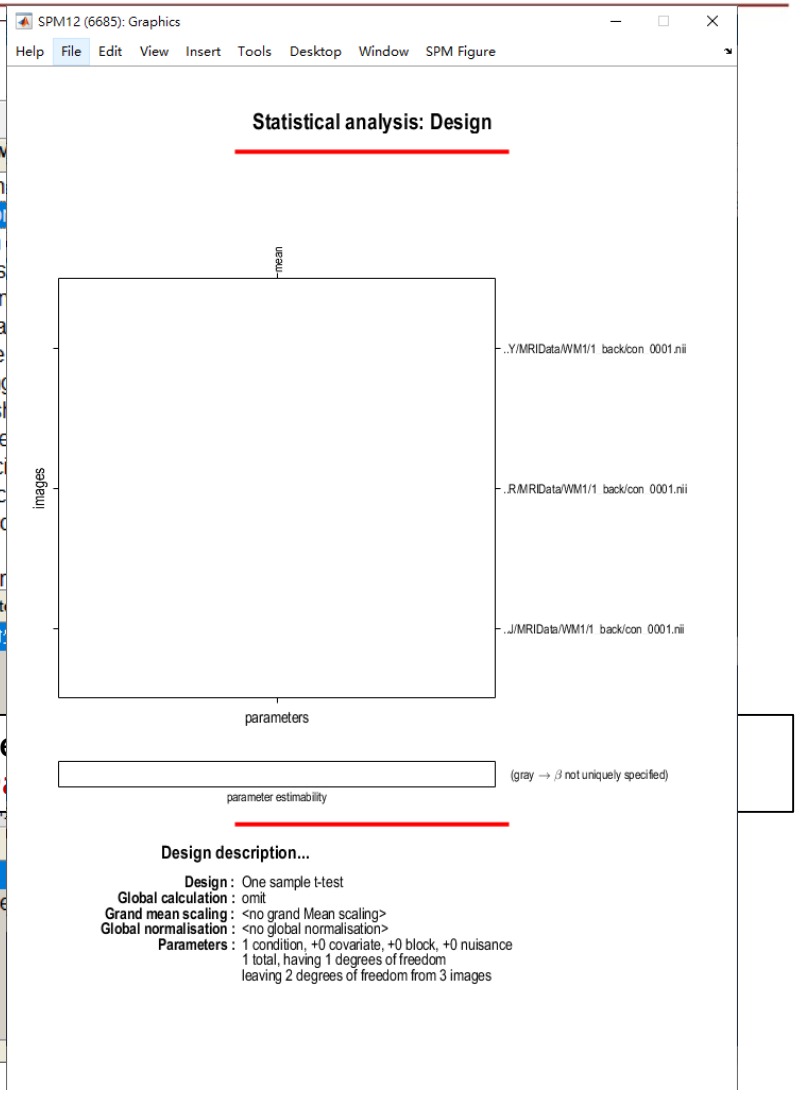
Specify 2nd-level Analysis Model

>> spm fmri

> Specify 2nd-level



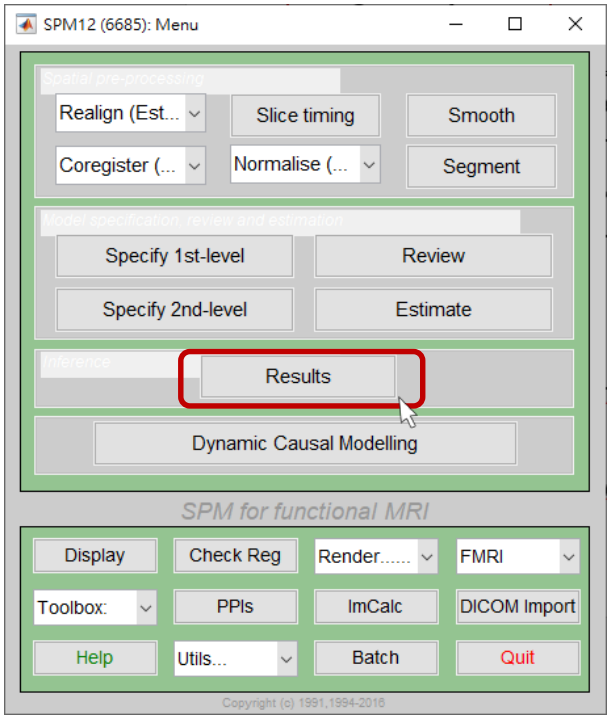


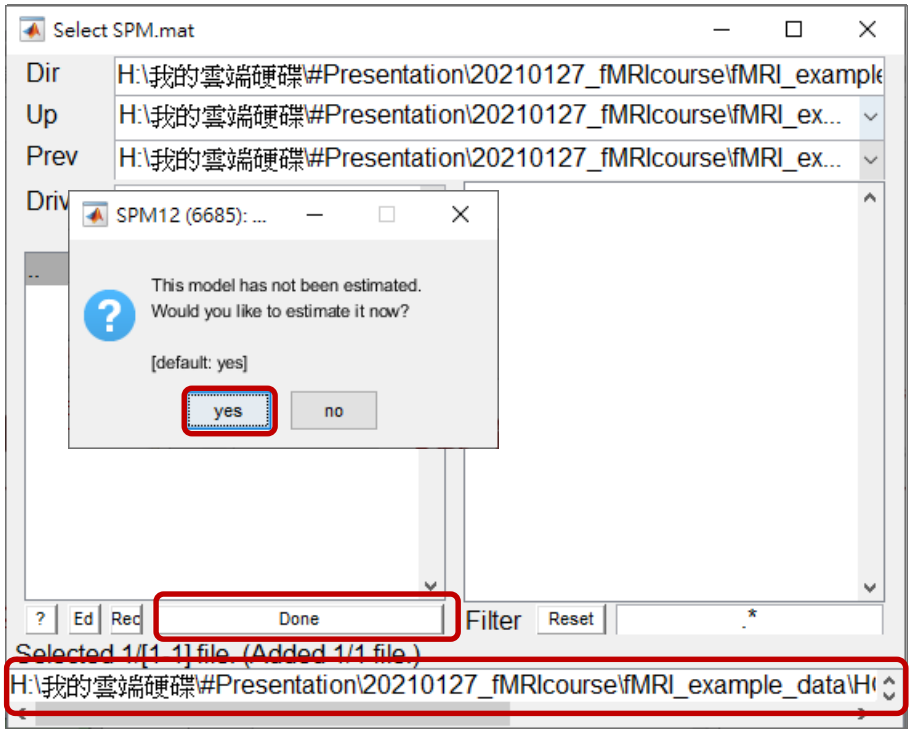


Estimate Model Parameters

>> spm fmri

> Results
> SPM.mat
> Done

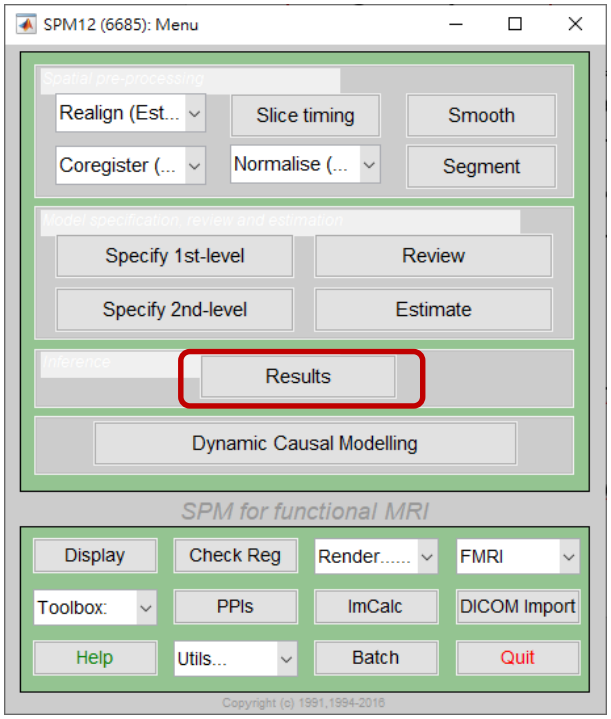


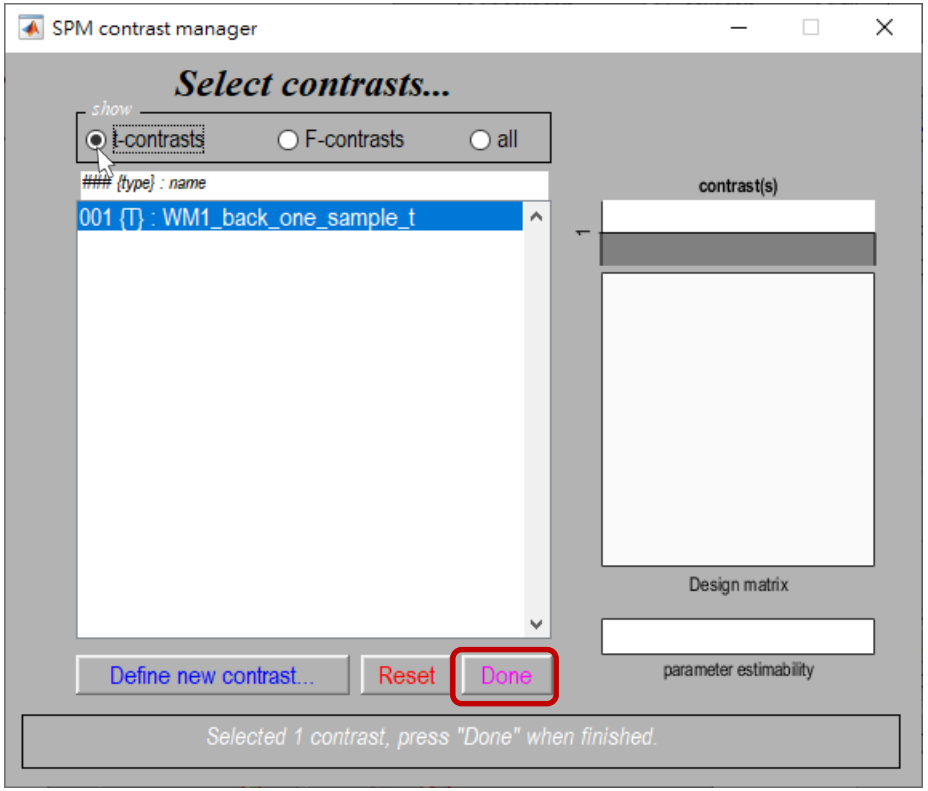


Estimate Model Parameters

>> spm fmri

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

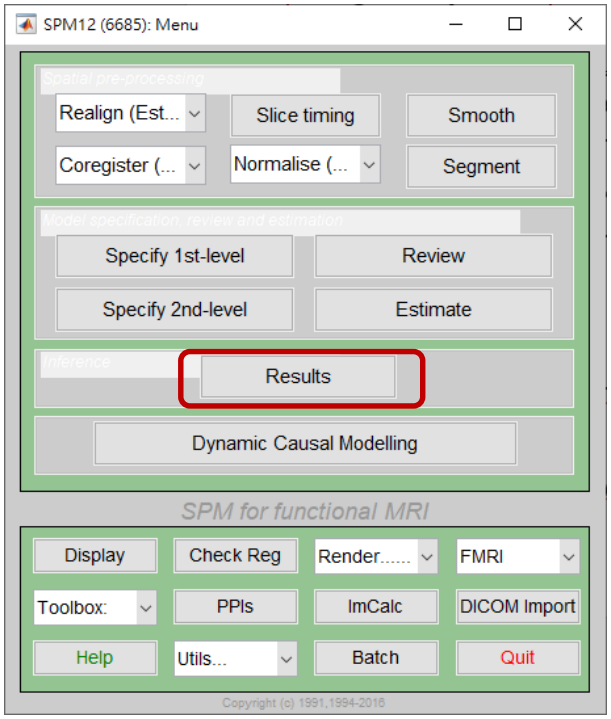


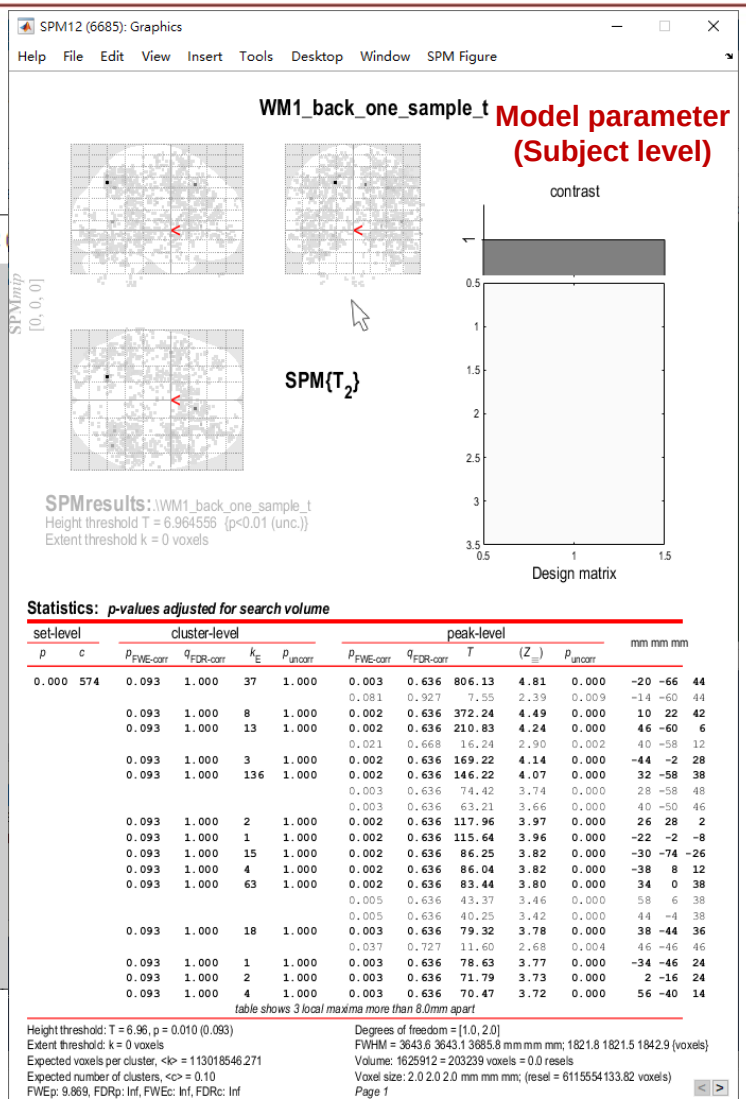


Estimate Model Parameters

>> spm fmri

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





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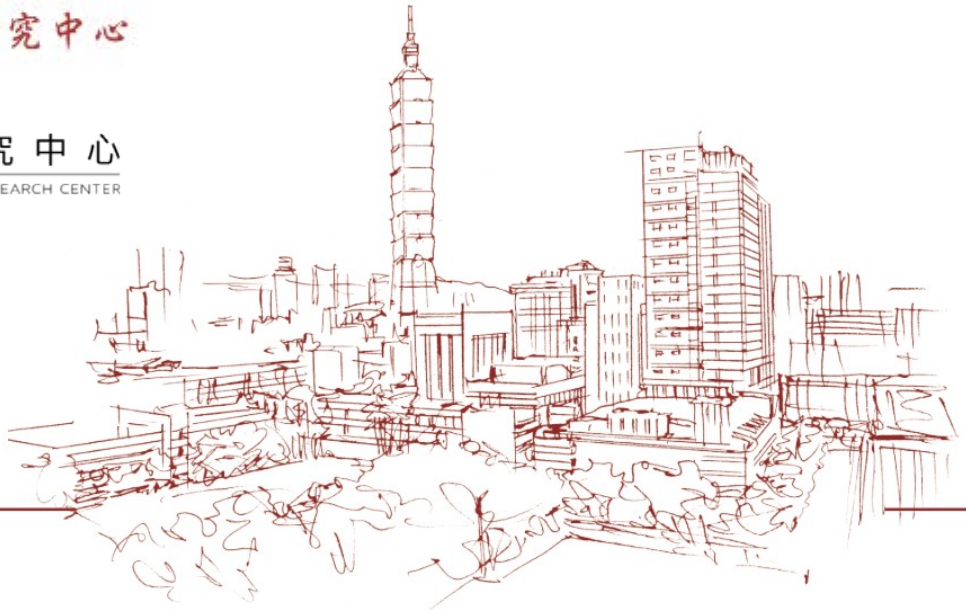

Analysis of Functional Magnetic Resonance Imaging (fMRI)

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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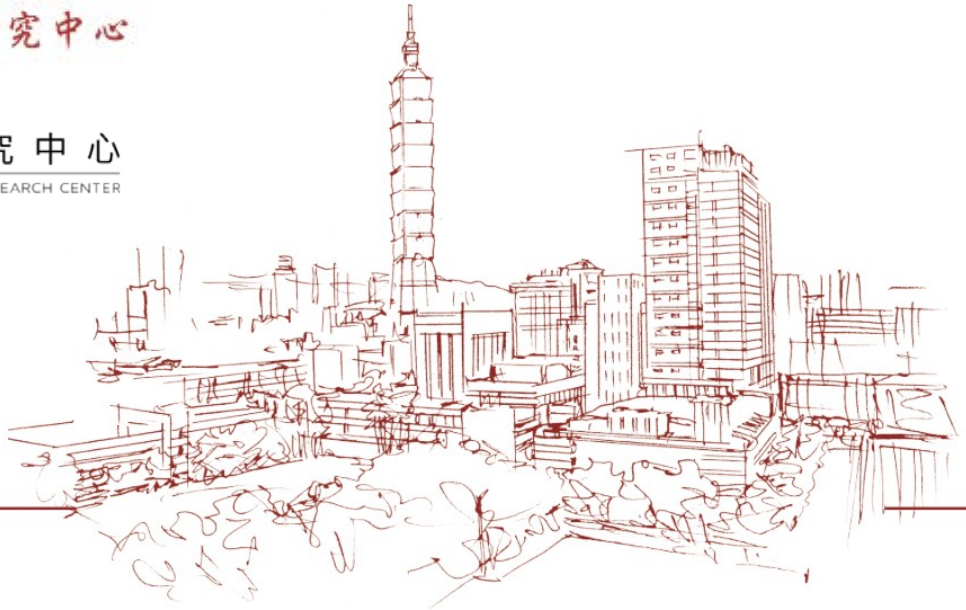

Thanks!

李宜恬 Yi-Tien Li, Ph.D.

TMU Neuroscience Research Center, Taipei Medical University
Translational Imaging Research Center, Taipei Medical University Hospital
angela810727@tmu.edu.tw

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