

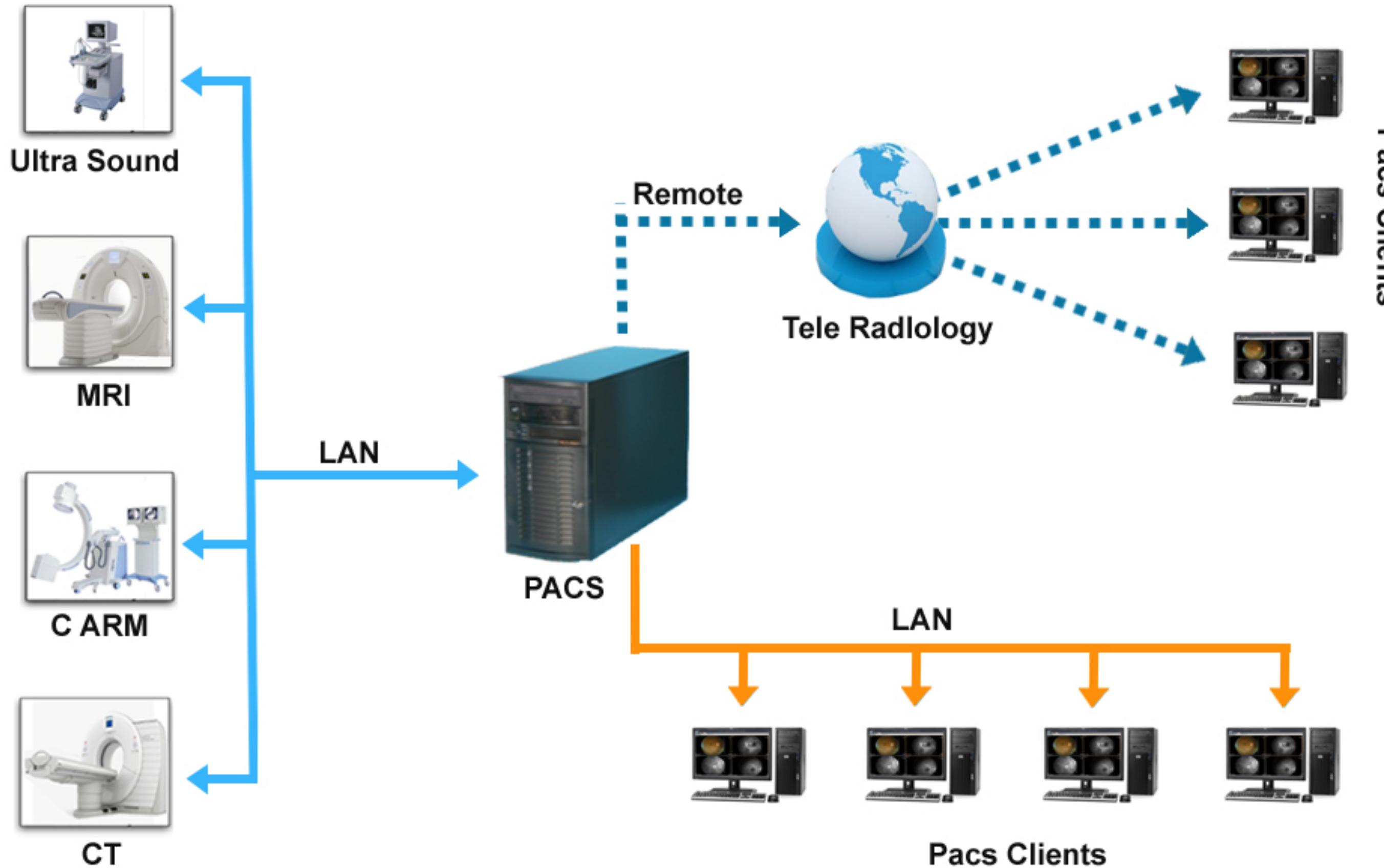
Neuroimaging data analysis preprocessing in SPM12 toolbox

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Severance Biomedical Science Institute,
Yonsei University College of Medicine

의료영상시스템 체계과 형태

PACS란?



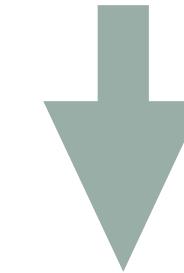
“환자등록번호는 고유한(Unique) 번호로 각 병원의 시스템 내에서는 1명의 환자가 1개의 고유한 ID를 갖는다.”

“의료영상 이외의 환자 정보는 별도의 데이터베이스에서 관리하는 것이 일반적이다.”

“의료영상저장전송시스템(Picture Archiving and Communication System, PACS)은 디지털 의료영상이미지를 DICOM 국제표준규약에 맞게 저장,가공,전송하는 시스템이다.”

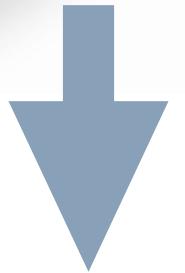
MRI Scanners and its File Formats

Siemens



.ima
(DICOM)

GE



.dcm
(DICOM)

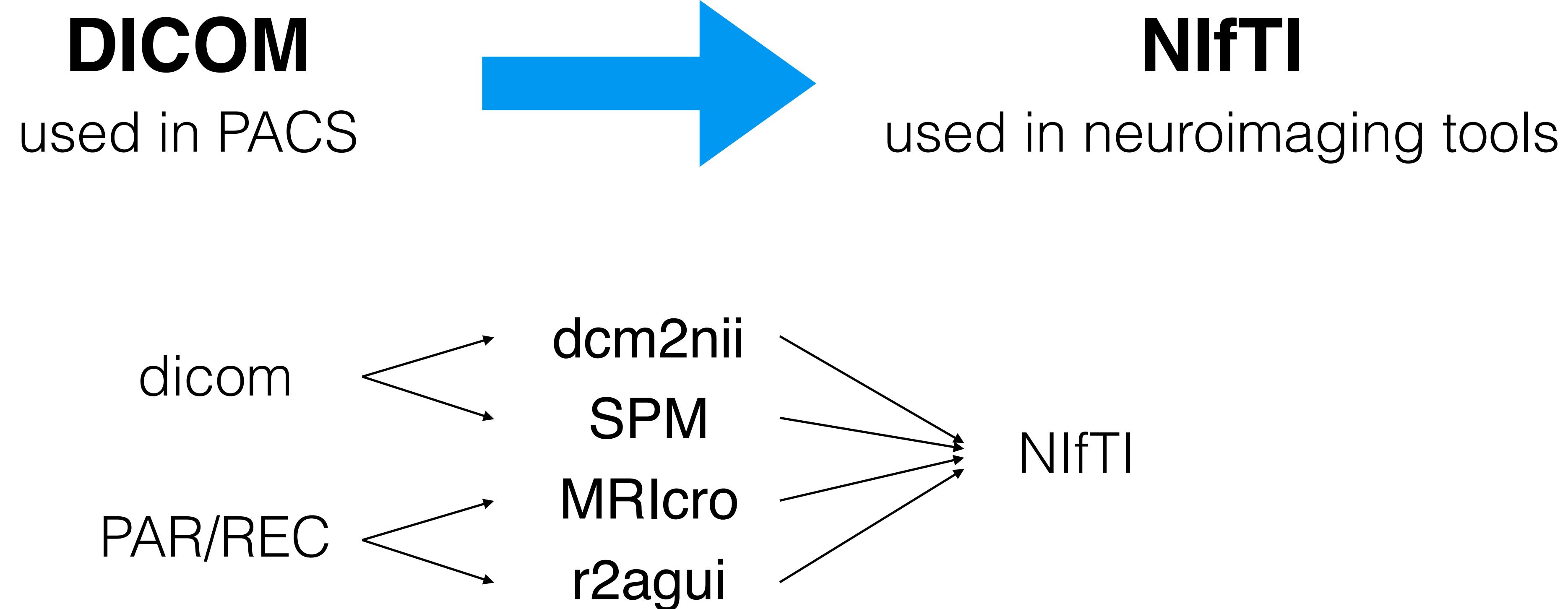
Philips



.PAR(.REC)
(philips format)

“Digital Imaging and Communications in Medicine (DICOM)은 의료용 기기에서 디지털 영상표현과 통신에 사용되는 여러 가지 표준을 총칭하는 말”

File Conversion to NIfTI

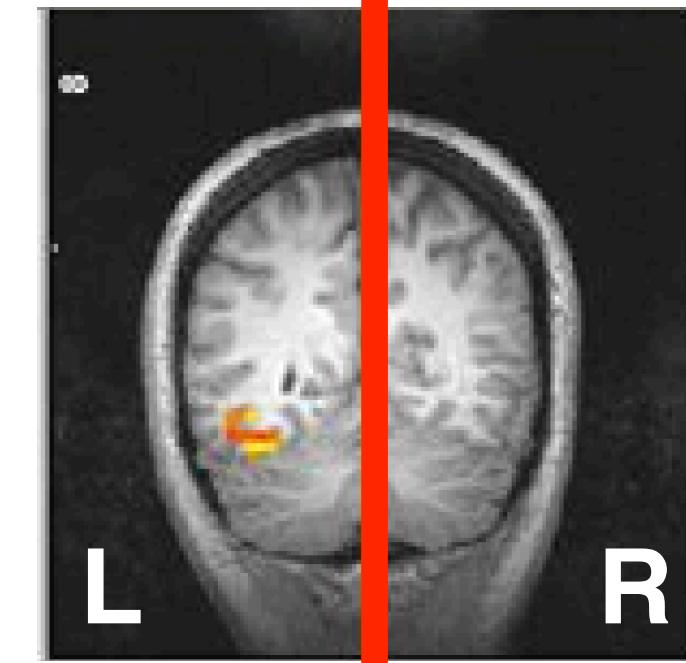


Left is what?

Neurologic convention

“left is left”

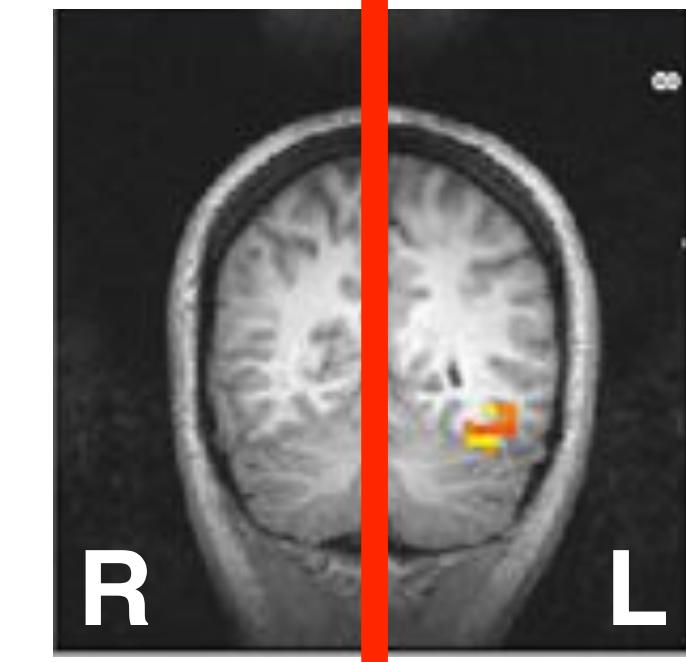
NIfTI files



Radiologic convention

“left is right”

DICOM files



Make sure you know what your magnet and software are doing before publishing left/right info!

DICOM images contain more information than NIfTI files such as direction of image, direction of gradient fields.

in DTI DICOM → images + b-vectors + b-values
in DTI NIfTI → only images

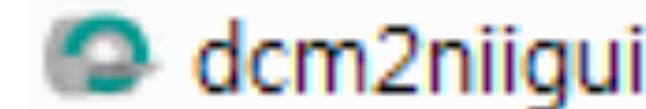
using dcm2nii

available platforms: mac os, windows, linux

Download link: <http://www.nitrc.org/frs/download.php/5630/win.zip>

Unzip win.zip

Execute dcm2niogui



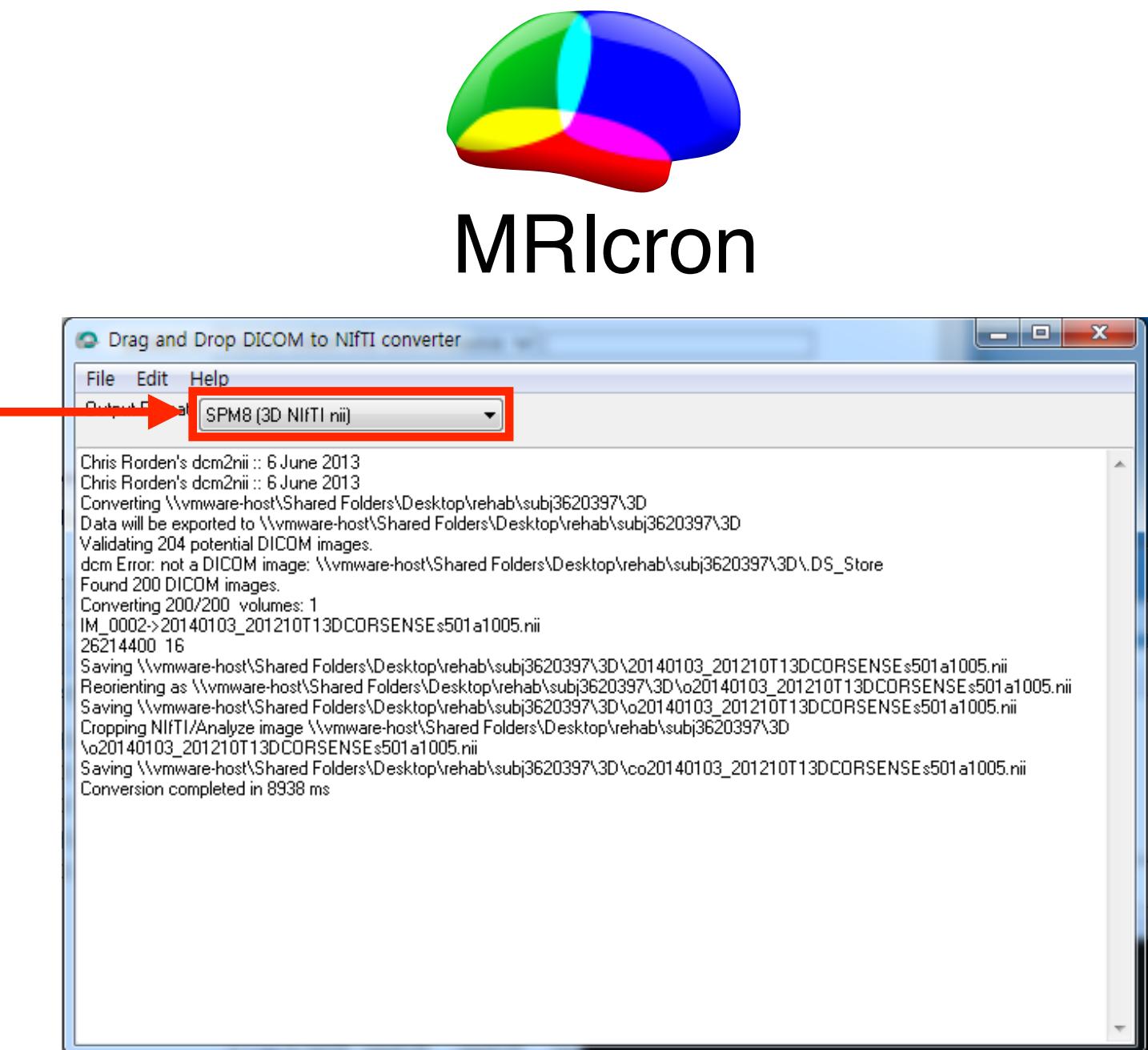
Select FSL/SPM8 (4D NifTI nii) in 'Output Format' menu

Select [DICOM to NifTI] in **File** menu

Select folder which contains T1 DICOM

Finally, you have three .nii files (if you convert T1)

이름	수정한 날짜	유형	크기
DICOM			
20140103_201210T13DCORSENSe501a1005.nii	2014-04-03 오후...	NII 파일	25,601KB
co20140103_201210T13DCORSENSe501a1005.nii	2014-04-03 오후...	NII 파일	11,256KB
o20140103_201210T13DCORSENSe501a1005.nii	2014-04-03 오후...	NII 파일	12,288KB
DICOMDIR	2014-04-03 오후...	파일	185KB

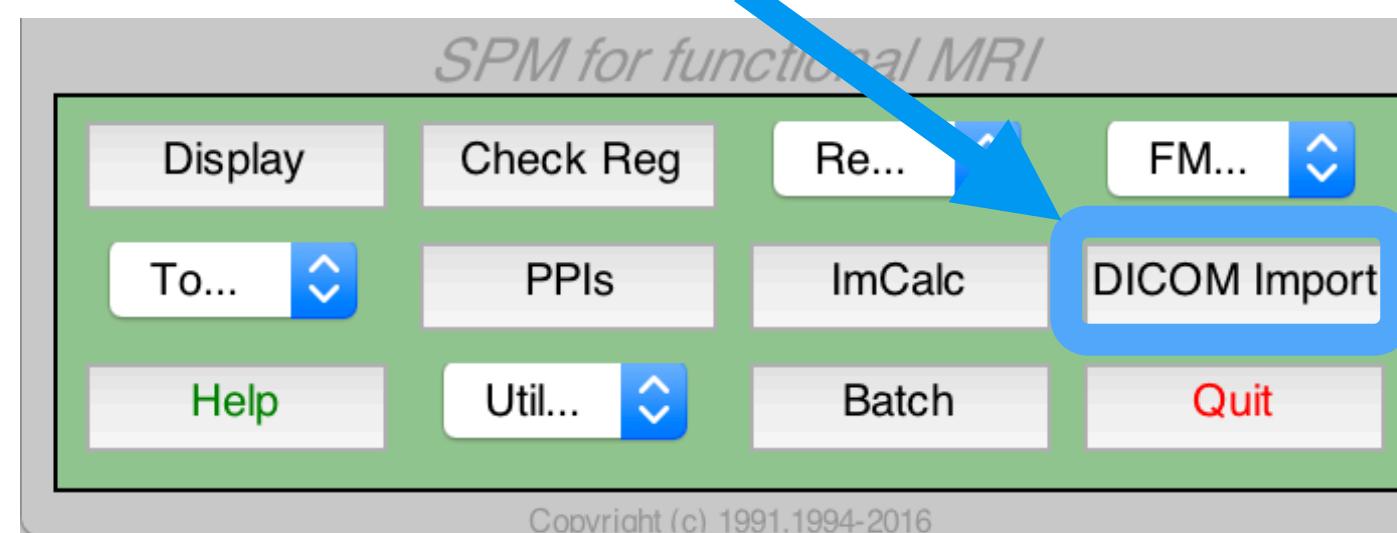


File size가 가장 큰것만 남기고,
나머지는 삭제!

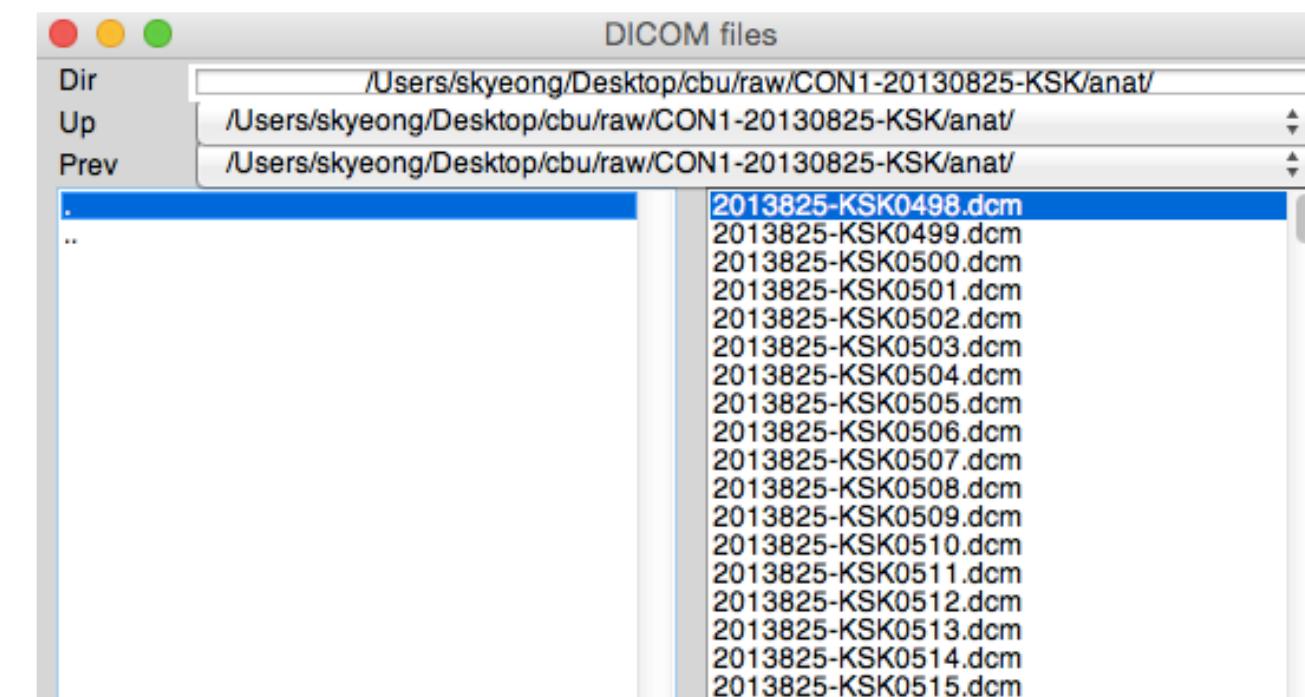
using SPM (DICOM Import)

available platforms: mac os, windows, linux

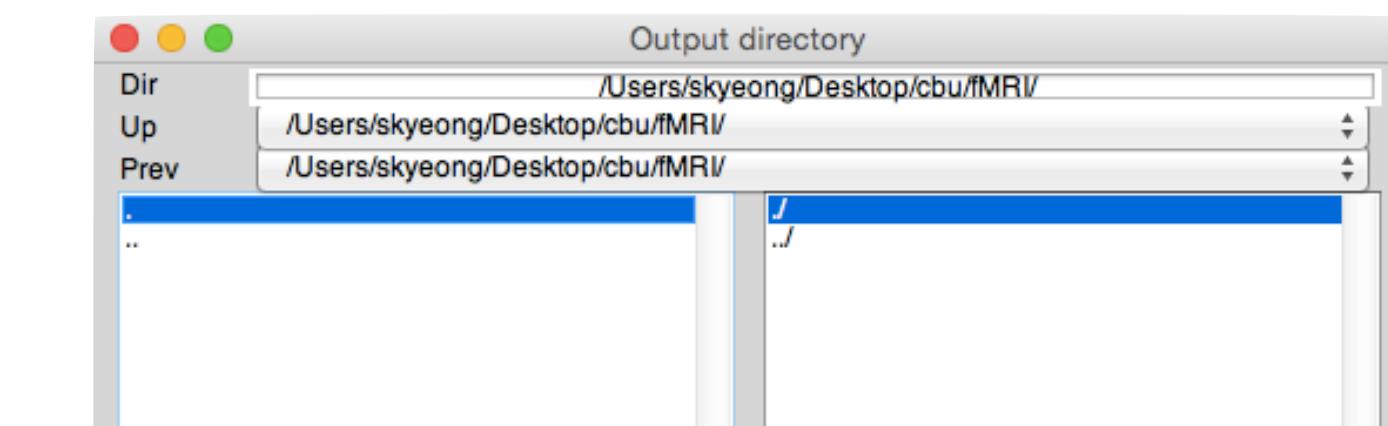
(1) press DICOM import



(2) select DICOM files



(3) select output directory



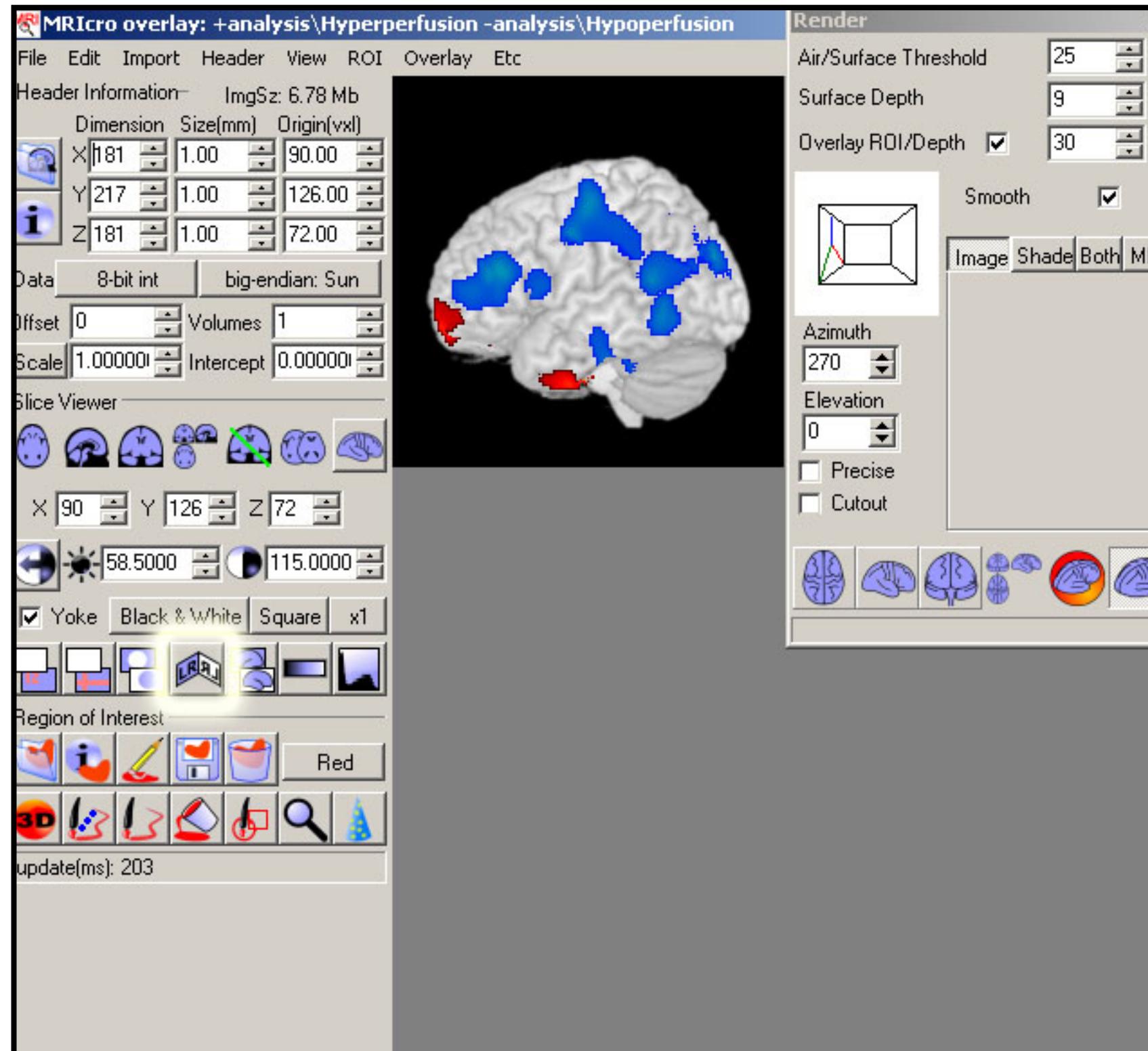
“DICOM Import (in SPM) is very slow compared with other tools.”

using MRICro

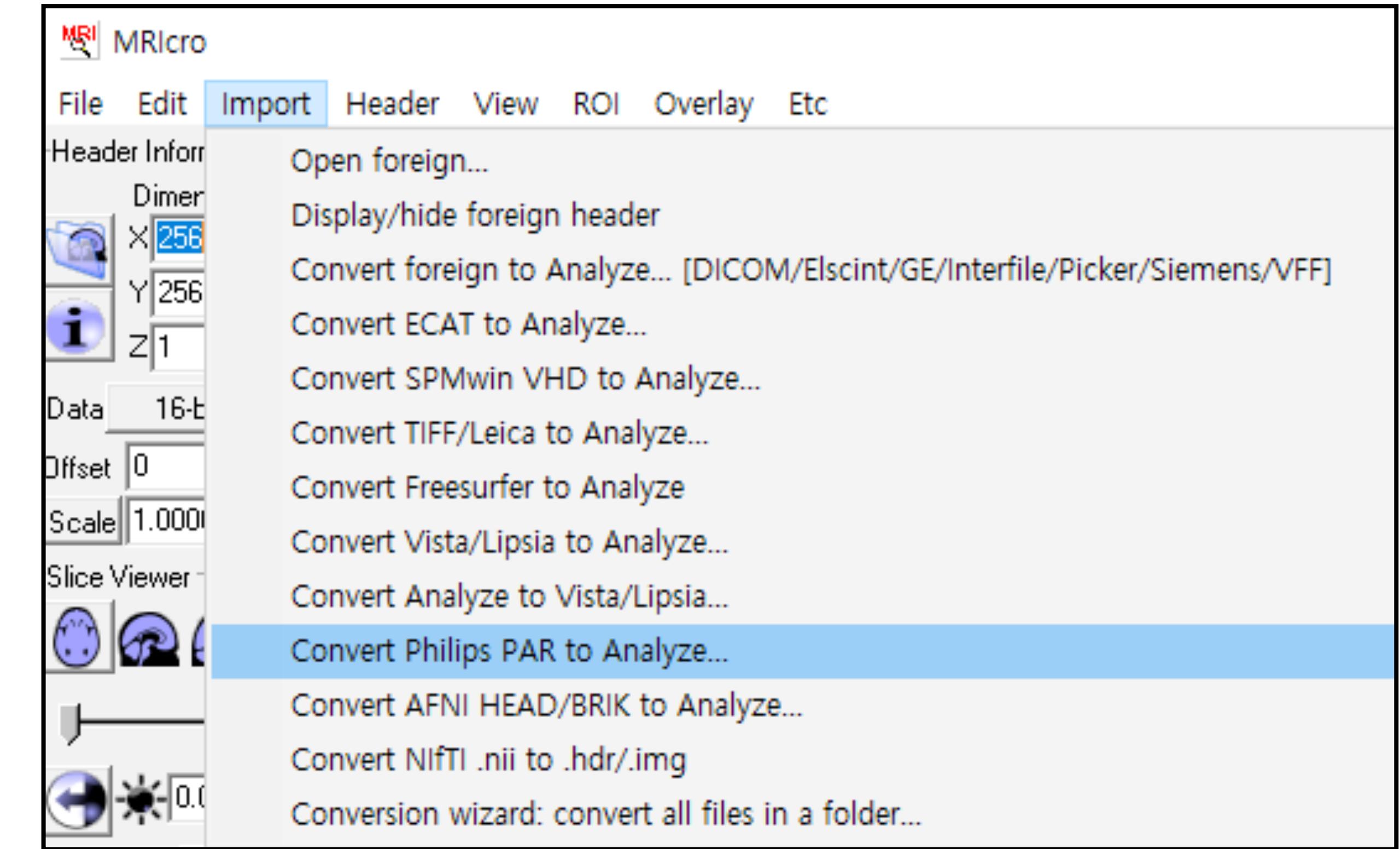


available platforms: windows only

(1) execute MRICro in windows

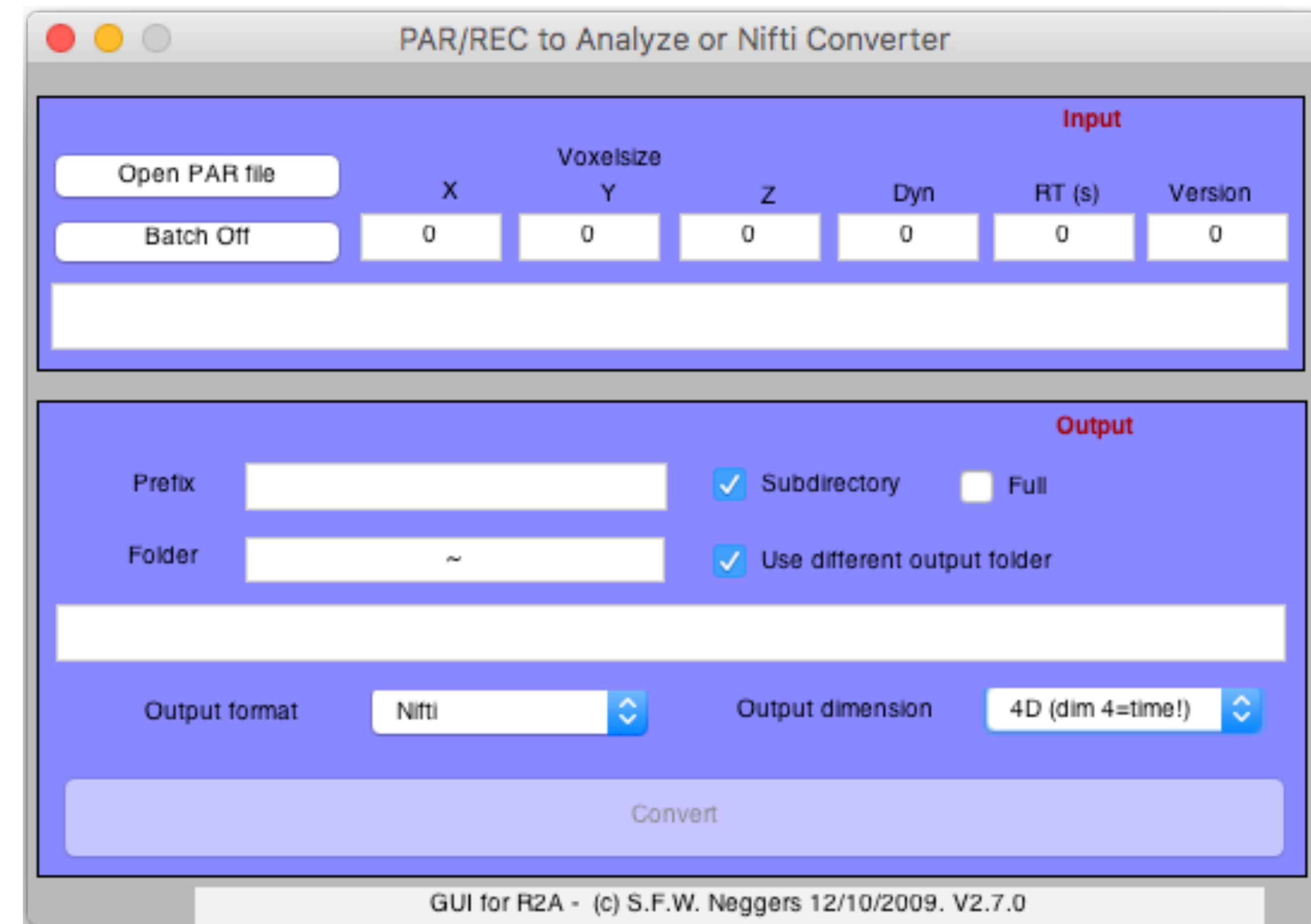


(2) Menu: Import



using r2agui

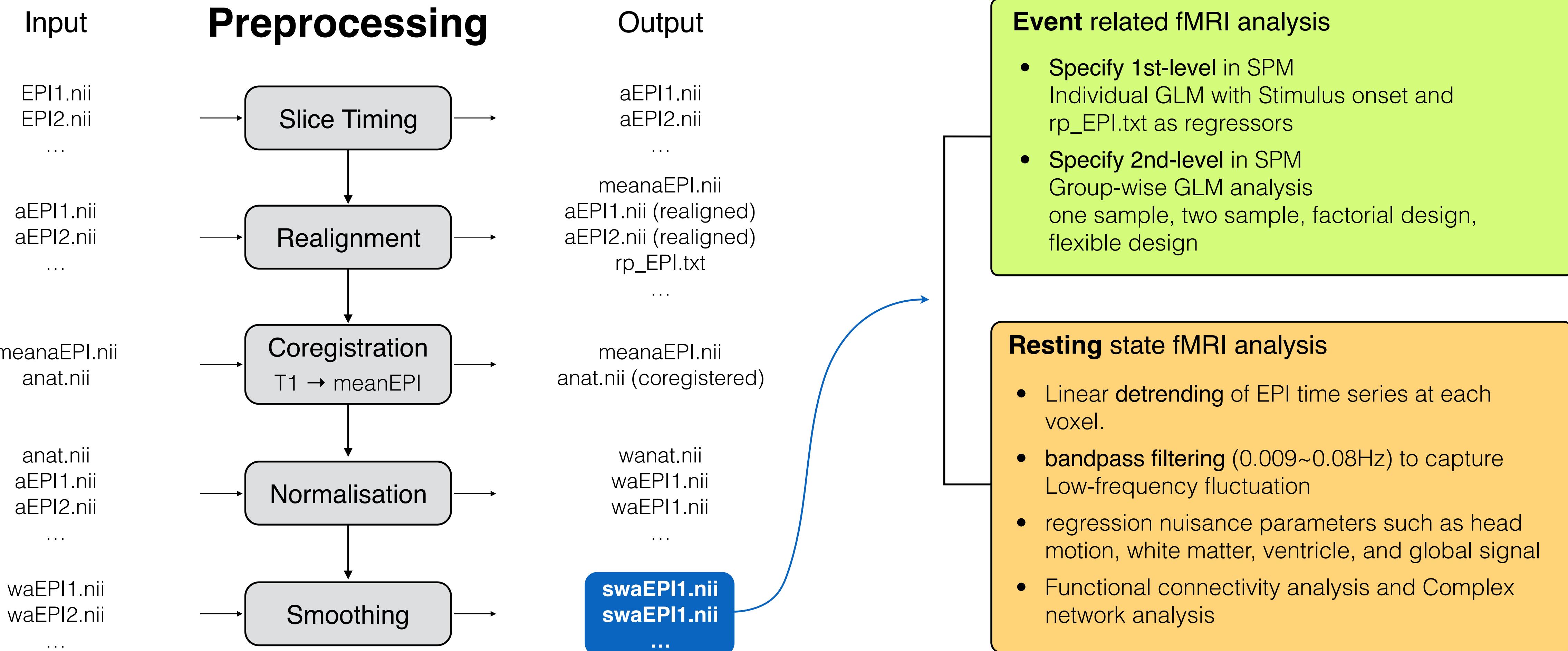
available platforms: Matlab



기능뇌영상 데이터 전처리 실습

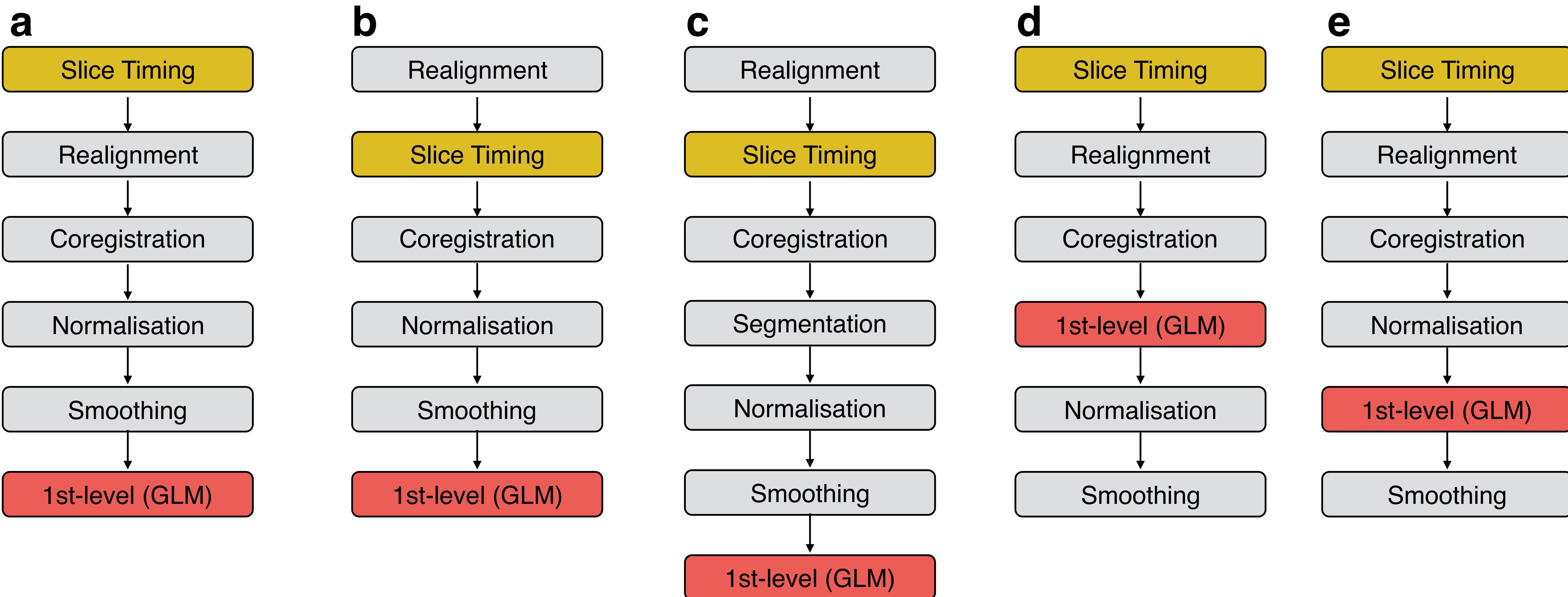
“Steps in the spatial preprocessing of
the task and resting state fMRI data are the same.”

기능뇌영상 전처리 과정



하지만,

실제 연구에서는 다양한 방법이 사용됨



SPMers' prefer to use: **a**, **b** or **c**

FSL/AFNI users prefer to use: **d** or **e**

실습1

방법(b)를 단계별로 따라해보기

Reference) Chapter 31 of SPM12 manual

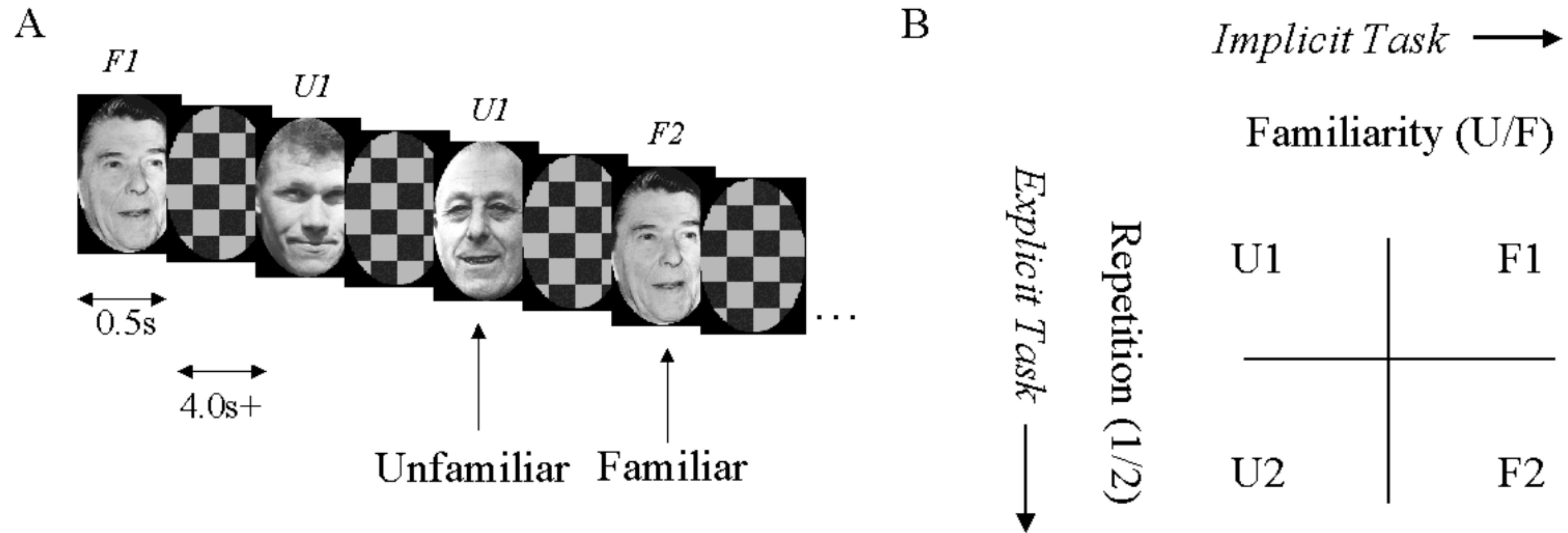
실습 데이터 다운로드

download:

http://www.fil.ion.ucl.ac.uk/spm/download/data/face_rep/face_rep.zip

어떤 데이터 일까?

Face repetition fMRI task



Reference) Henson, R.N.A., Shallice, T., Gorno-Tempini, M.-L. and Dolan, R.J. (2002), Face repetition effects in implicit and explicit memory tests as measured by fMRI. *Cerebral Cortex*, 12, 178-186.

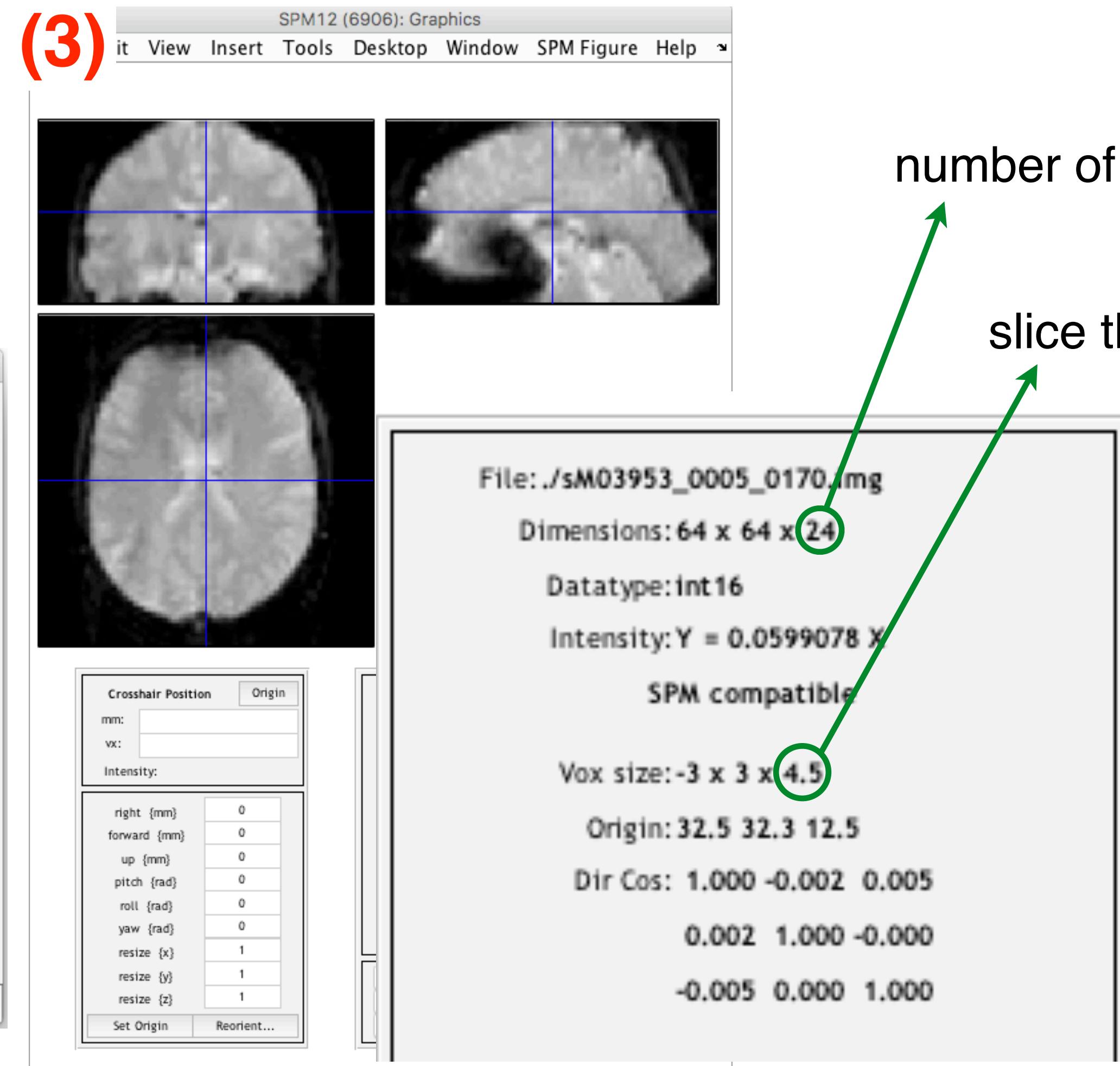
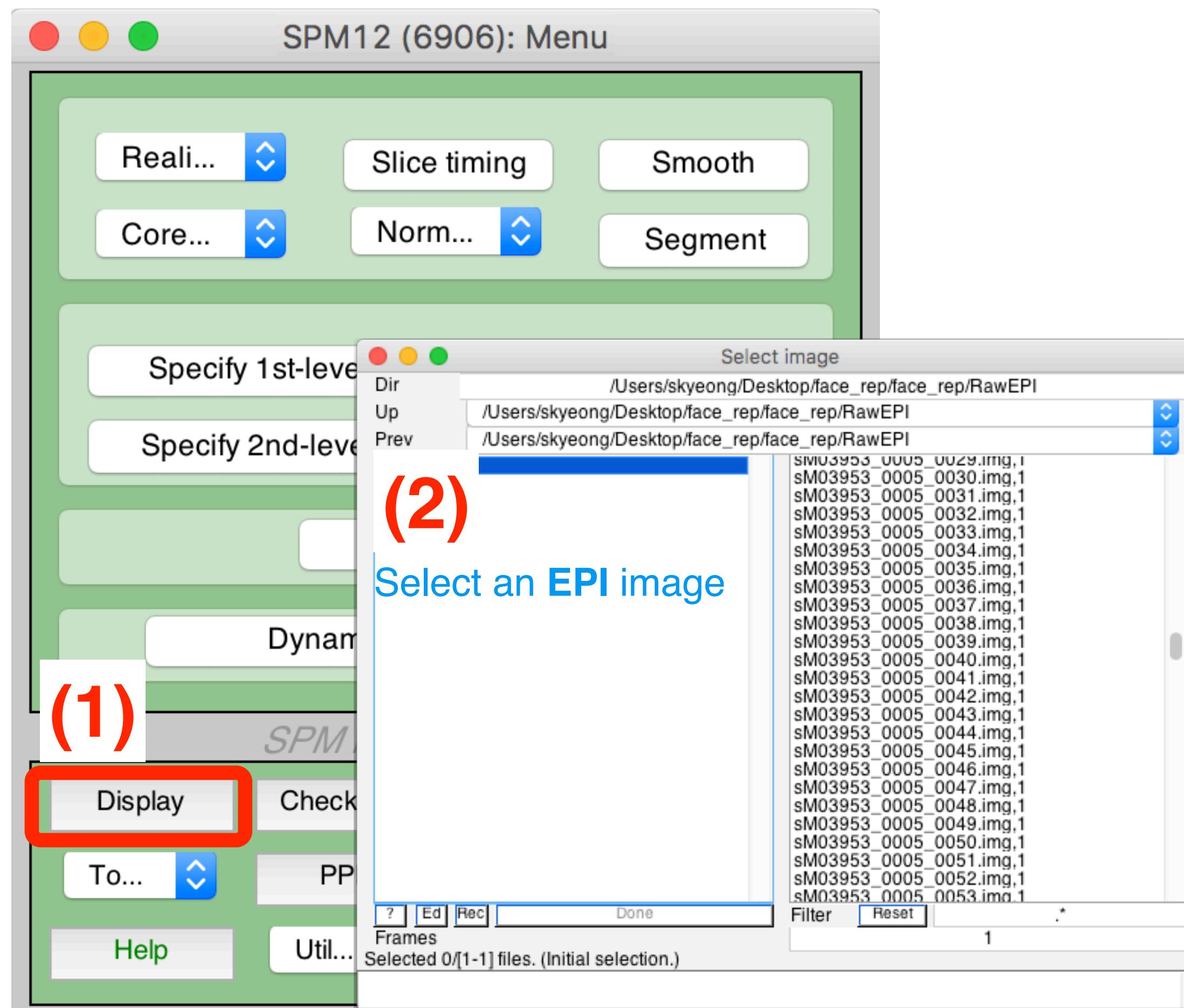
Experiment Information

- 2x2 factorial event-related fMRI
- One session (one subject)
- (Famous vs. Nonfamous) x (1st vs 2nd presentation) of faces against baseline of chequerboard
- 2 presentations of 26 Famous and 26 Nonfamous Greyscale photographs, for 0.5s, randomly intermixed, for fame judgment task (one of two right finger key presses).
- Parameteric factor "lag" = number of faces intervening between repetition of a specific face + 1
- Minimal SOA=4.5s, with probability 2/3 (ie 1/3 null events)
- Continuous EPI (TE=40ms,TR=2s), 24 descending slices (64x64 3x3mm²), 3mm thick, 1.5mm gap

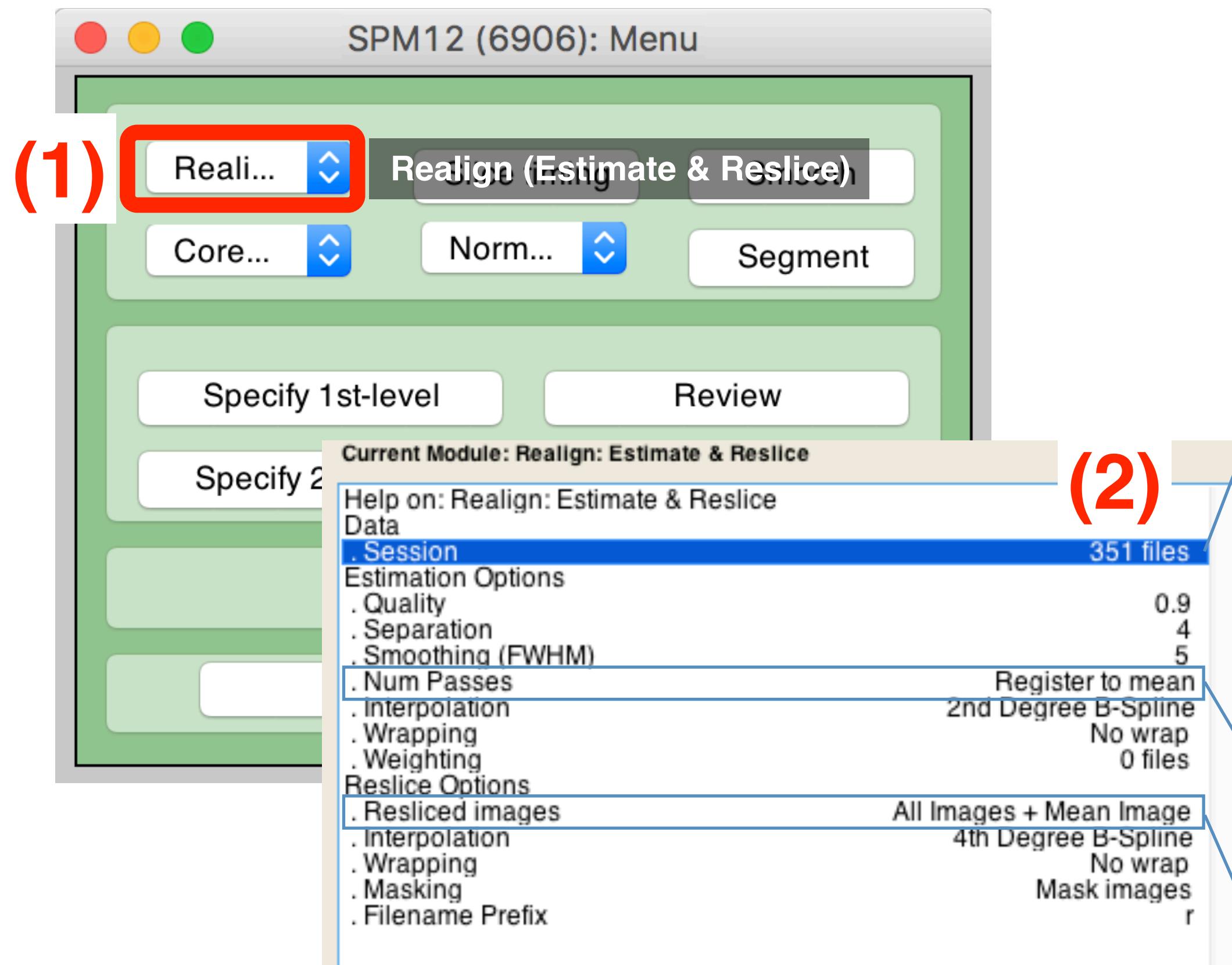
Reference) http://www.fil.ion.ucl.ac.uk/spm/data/face_rep/

Visual inspection

Open images to check quality and parameters

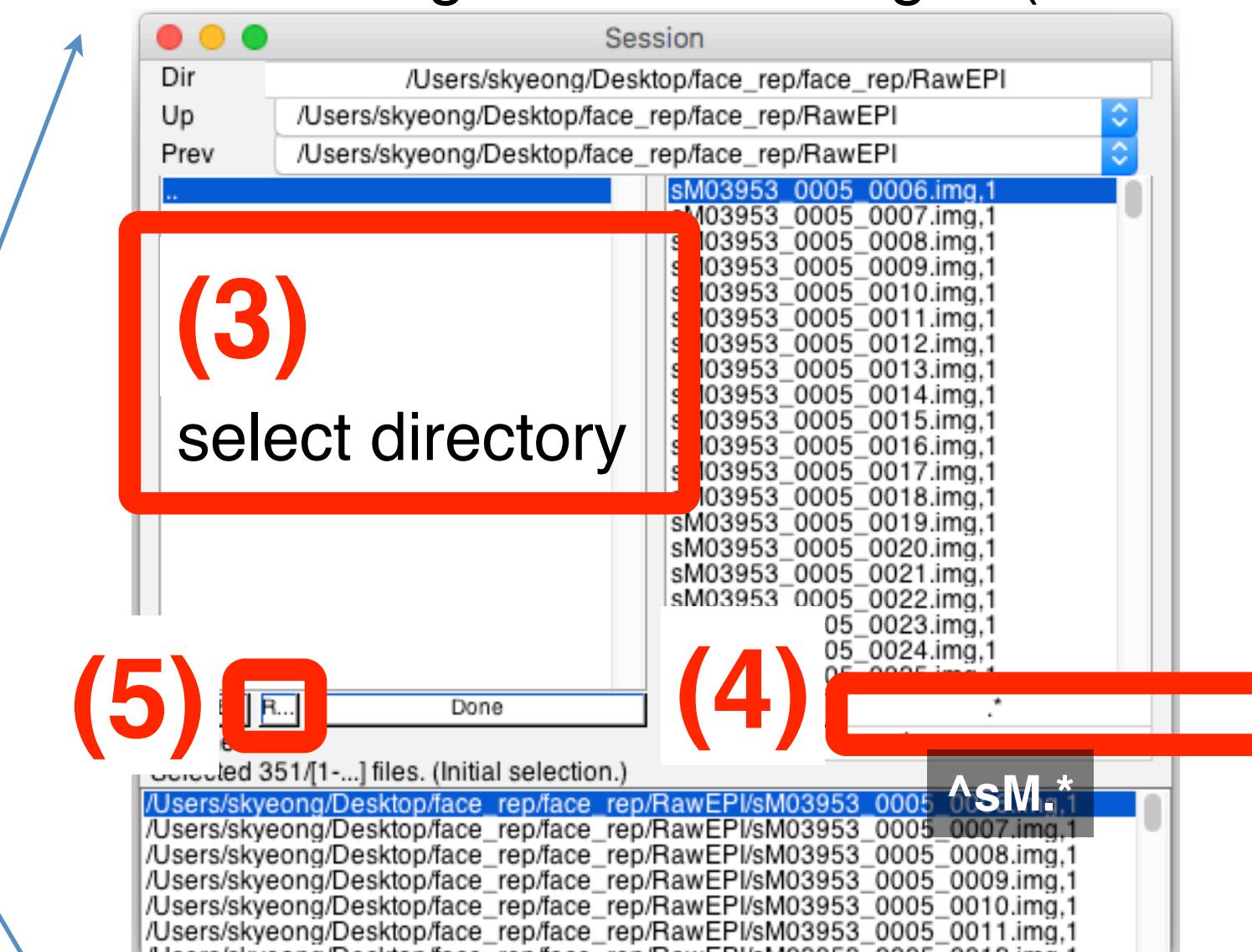


1. Realignment



Data

slice timing corrected images (**sM.*\nii**)



Num Passes

Register to **first**

or Register to **mean**

모든 EPI 영상을 첫번째 EPI에 정합후 meanEPI 생성

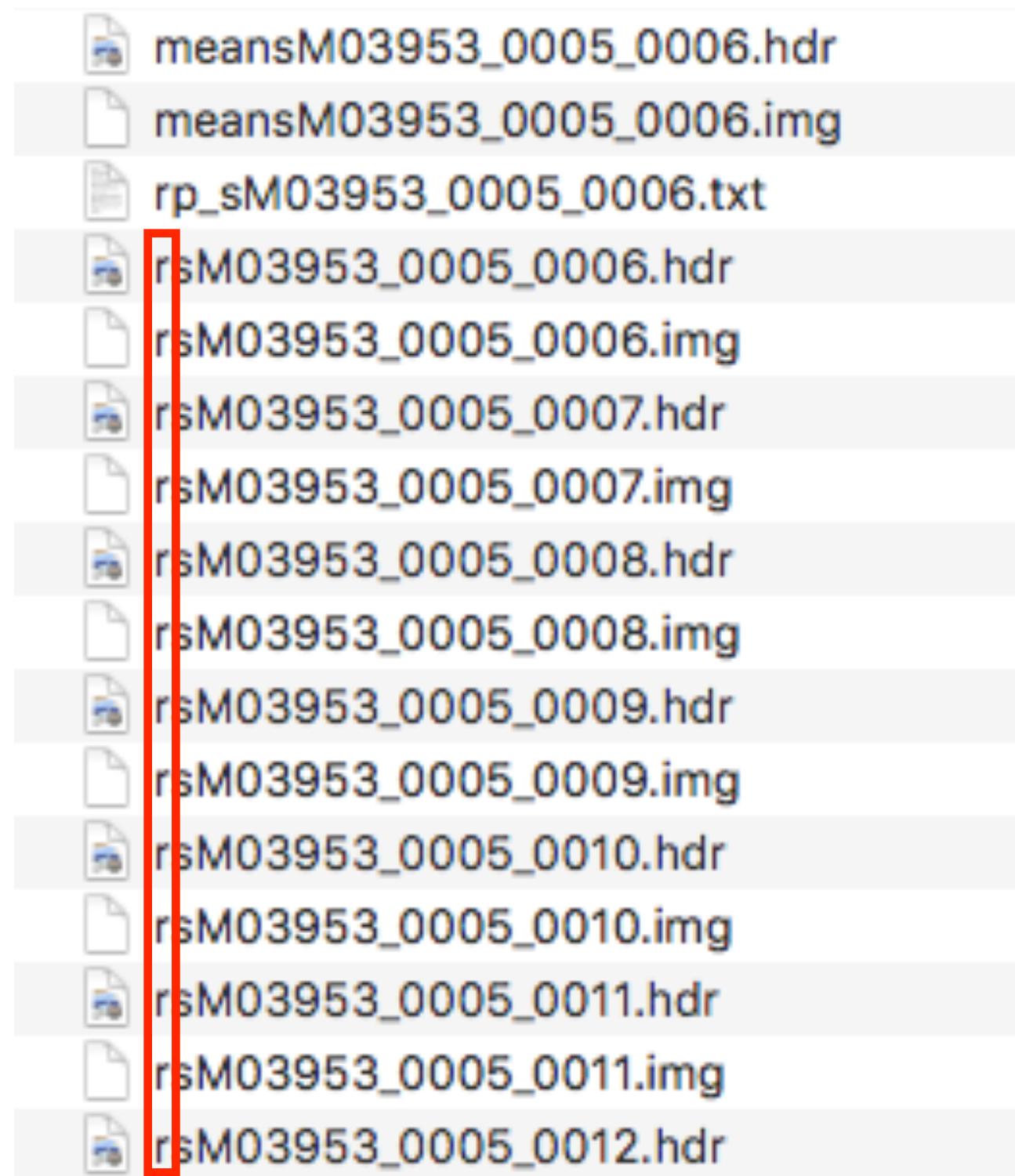
Resliced images

All Images + Mean Image

means**M~~.nii** 가 생성되고,
coregistration에 사용됨.

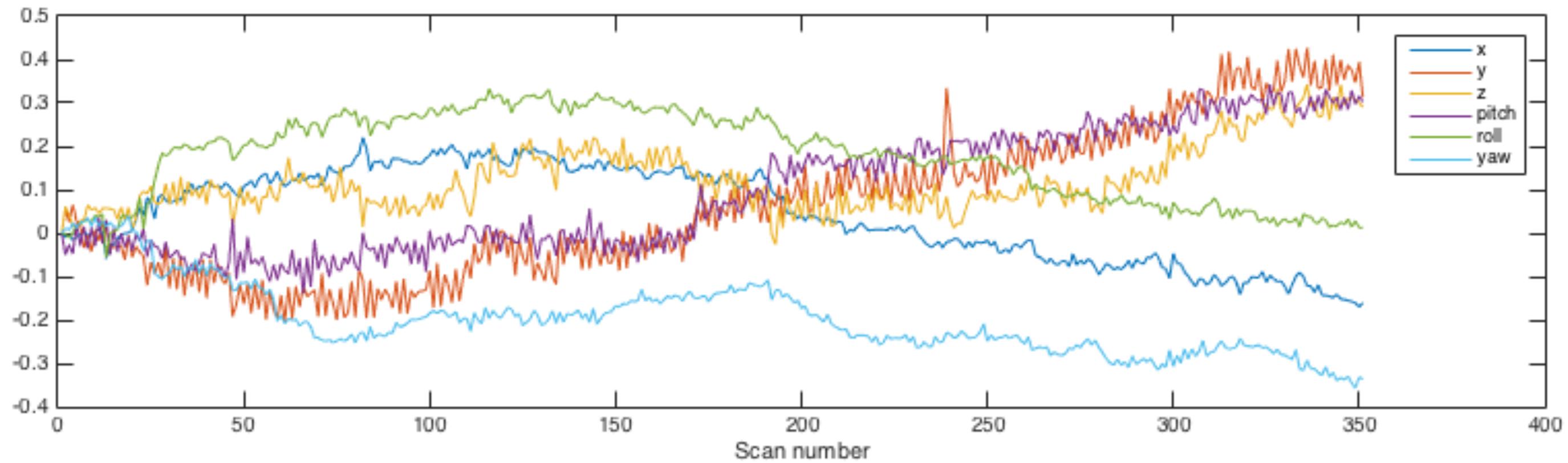
Outputs after Realignment

Output files

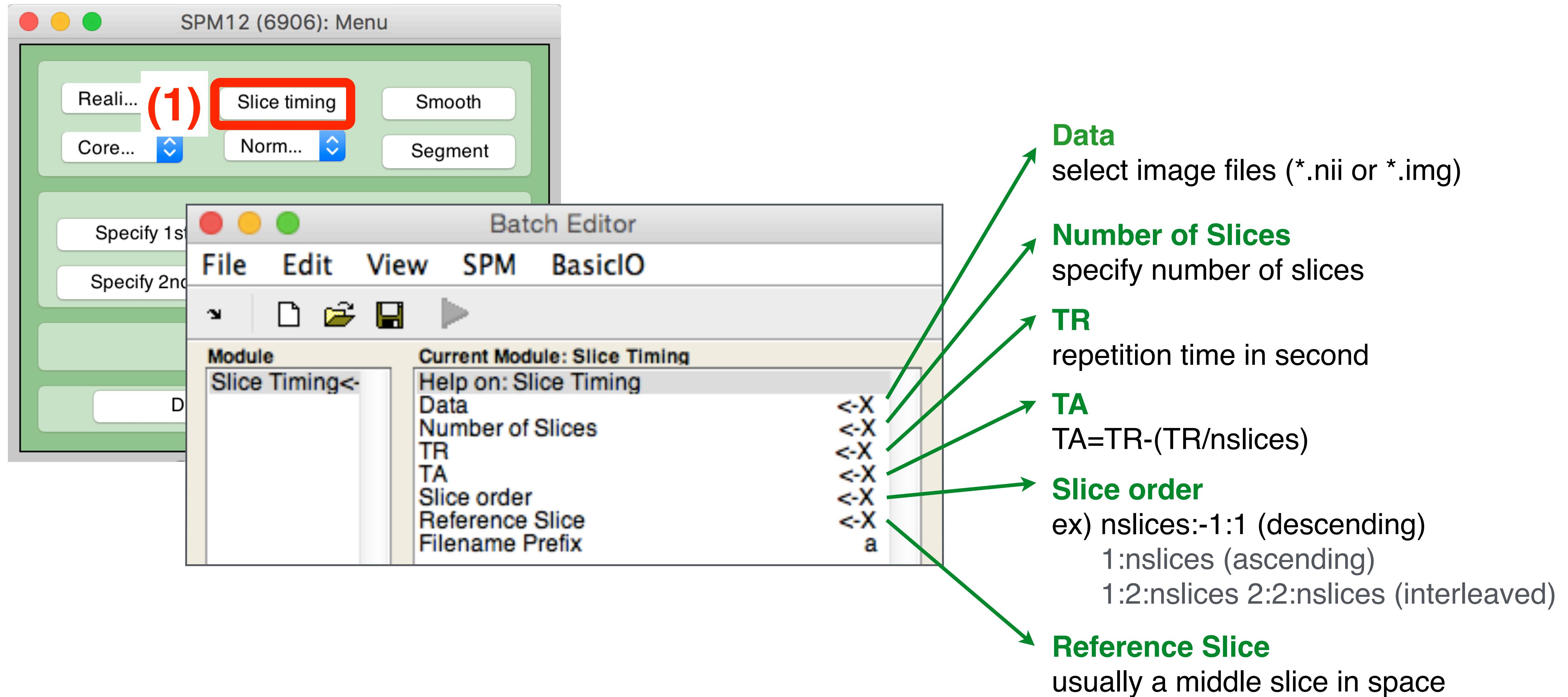


Plot head motion parameters

```
>> DATApath = '/Users/skyeong/Desktop/face_rep';
>>
>> % Load Realignment Parameters
>> fn_motion = fullfile(DATApath, 'RawEPI', 'rp_sM03953_0005_0006.txt');
>> MOTION = dlmread(fn_motion);
>> MOTION(:,4:6) = 50*MOTION(:,4:6);
>>
>> % Plot Head Motion - translation
>> figure; plot(1:length(MOTION), MOTION);
>> xlabel('Scan number');
>> legend('x','y','z','pitch','roll','yaw');
```

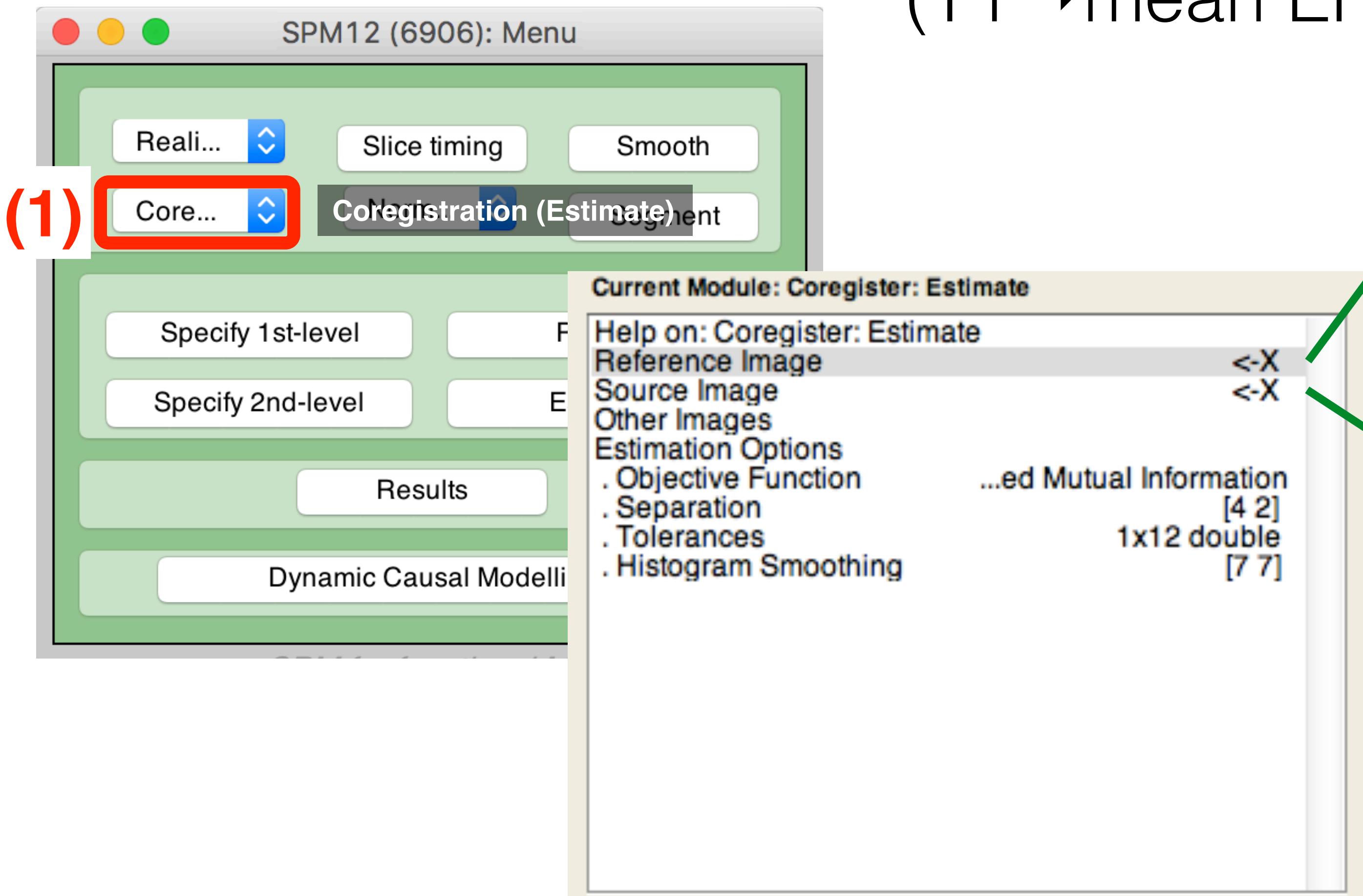


2. Slice timing correction



3. Coregistration

(T1 → mean EPI)



Reference Image

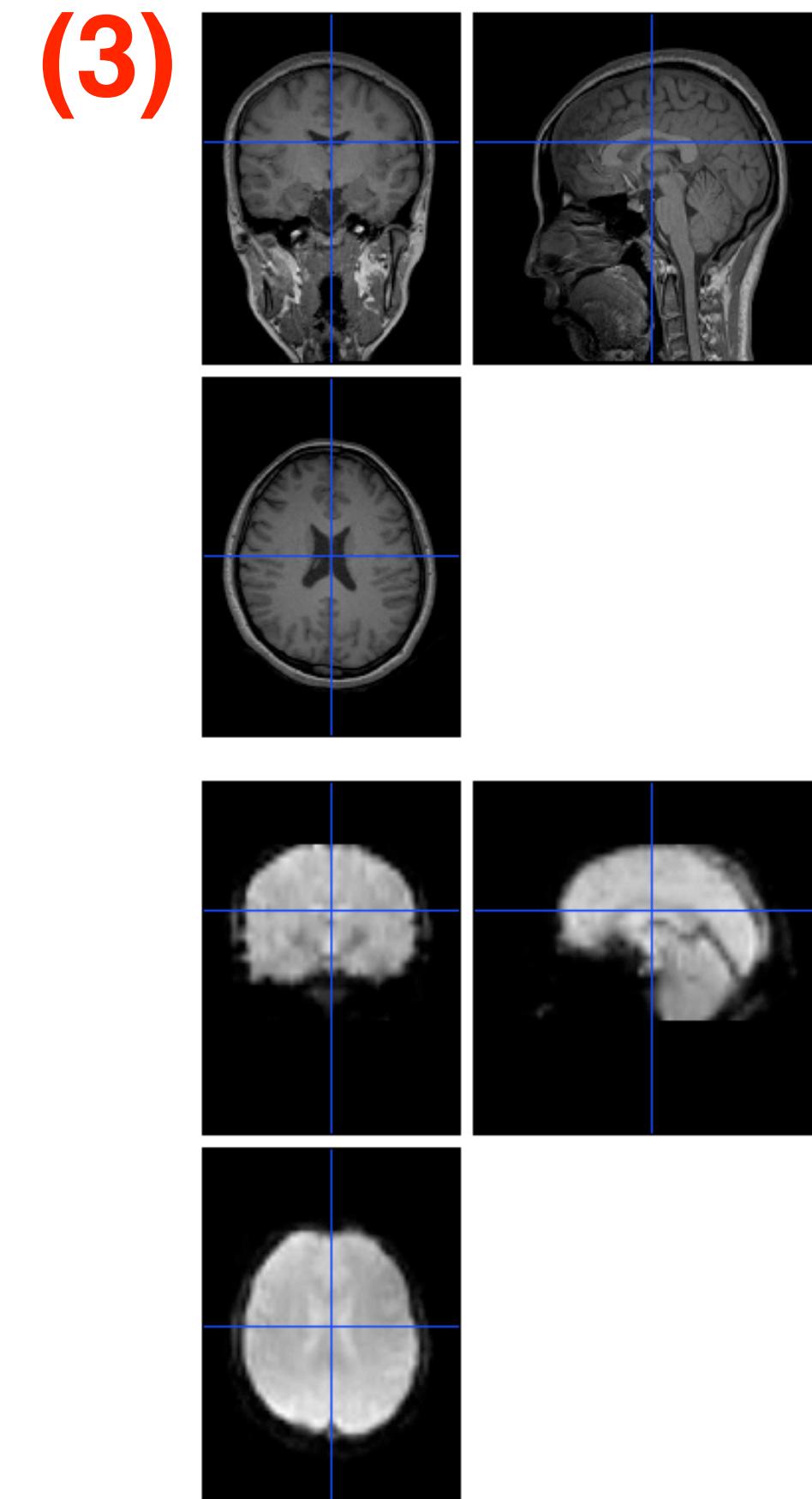
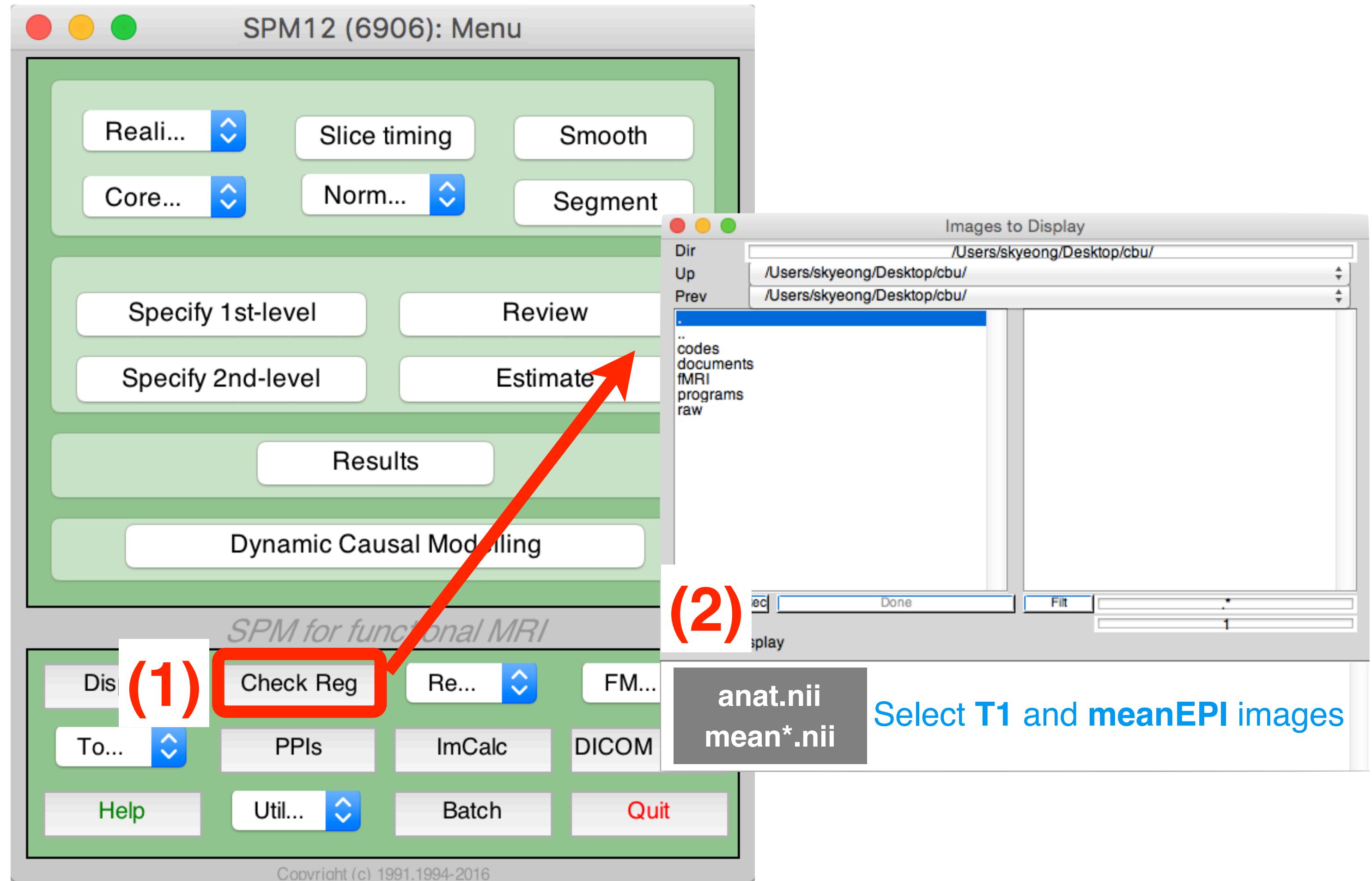
select “mean EPI image” which was created after realignment process

Source Image

select anatomical (T1) image

* fMRI 과제가 여러개인 경우에 T1 영상을 각 fMRI 과에별로 복사해서 사용할 것을 권장함.

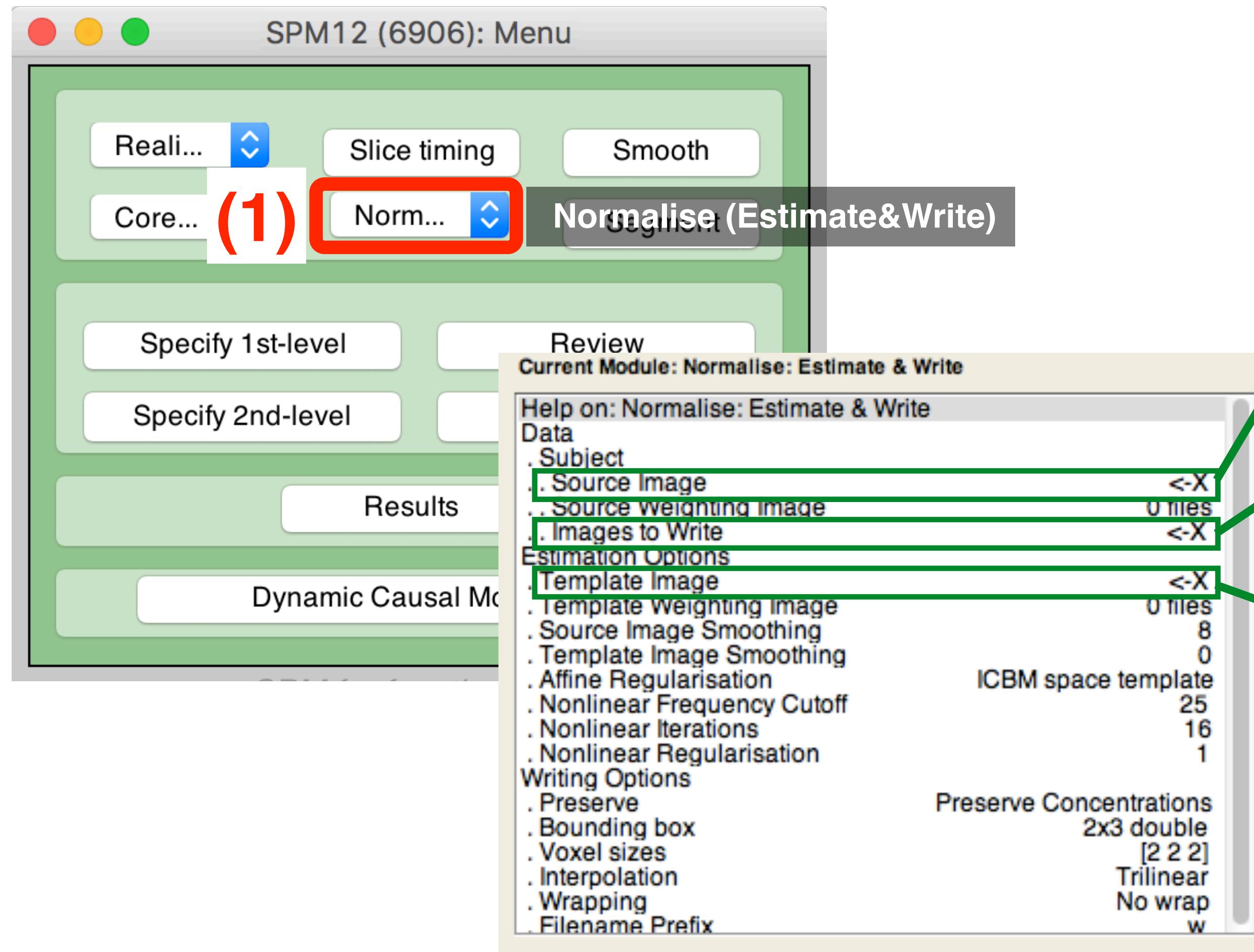
Check Registration



* T1과 meanEPI 영상이 잘 정합 되었는지 반드시 확인!!

4. Normalization

Normalize (Estimate&Write) without segmentation



Source Image

select the coregistered T1 image

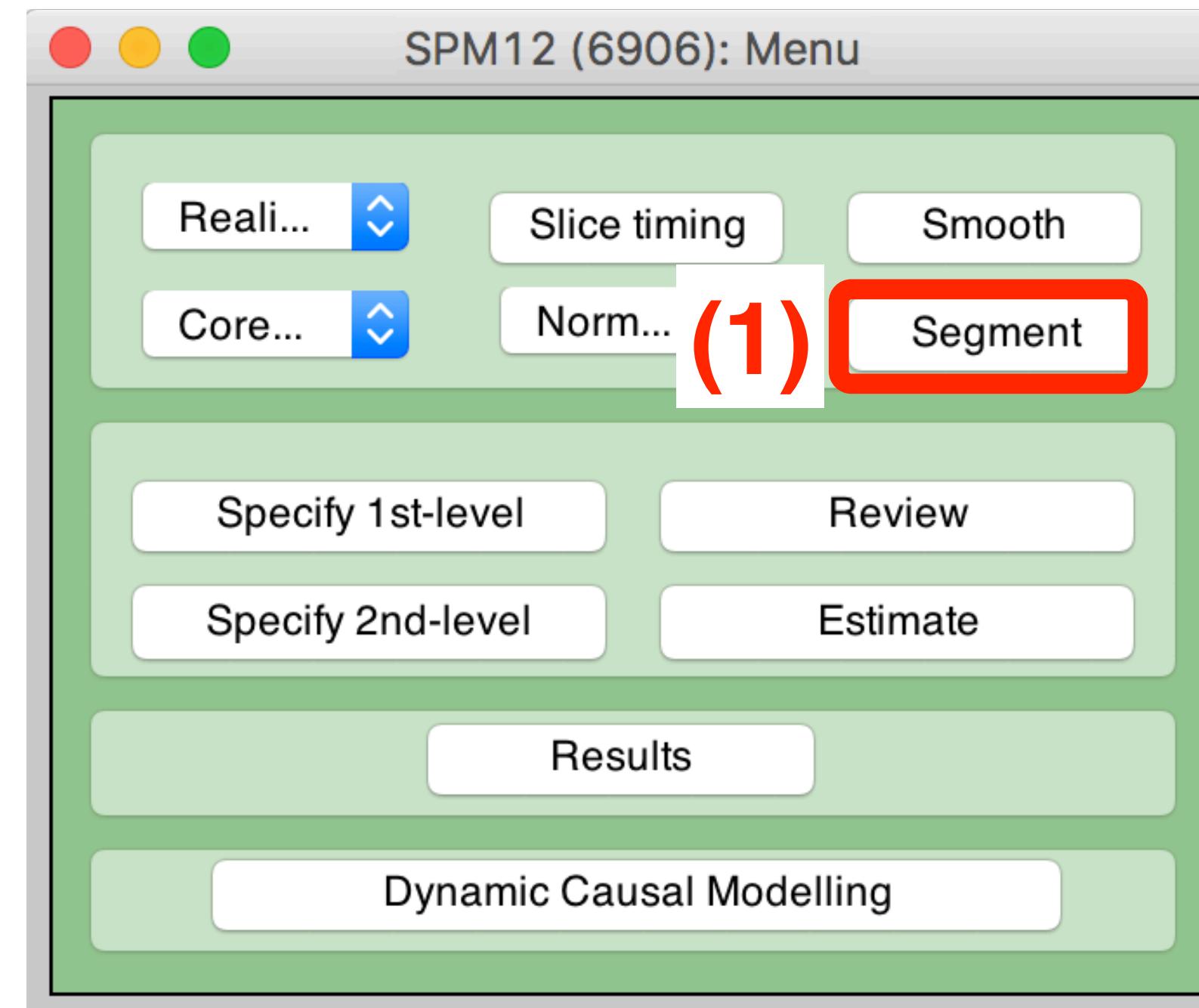
Images to Write

select the coregistered T1 & realigned EPI images

Template Image

select T1 template file (T1.nii)
which is located at SPM8\template

Segmentation



Help on: Segment	
Data	
. Channel	
. . Volumes	...sktop/face rep/face rep/Structural/sM03953_0007.img,1
. . Bias regularisation	light regularisation (0.001)
. . Bias FWHM	60mm cutoff
. . Save Bias Corrected	Save Nothing
Tissues	
. Tissue	
. . Native Tissue	/Users/skyeong/matlabwork/spm12/tpm/TPM.nii,1
. . Warped Tissue	None
. Tissue	
. . Native Tissue	/Users/skyeong/matlabwork/spm12/tpm/TPM.nii,2
. . Warped Tissue	None
. Tissue	
. . Native Tissue	/Users/skyeong/matlabwork/spm12/tpm/TPM.nii,3
. . Warped Tissue	None
. Tissue	
. . Native Tissue	/Users/skyeong/matlabwork/spm12/tpm/TPM.nii,4
. . Warped Tissue	None
. Tissue	
. . Native Tissue	/Users/skyeong/matlabwork/spm12/tpm/TPM.nii,5
. . Warped Tissue	None
. Tissue	
. . Native Tissue	/Users/skyeong/matlabwork/spm12/tpm/TPM.nii,6
. . Warped Tissue	None
Warping & MRF	
. MRF Parameter	
. Clean Up	1
. Warping Regularisation	Light Clean
. Affine Regularisation	1x5 double
. Smoothness	0
. Sampling distance	3
. Deformation Fields	Forward

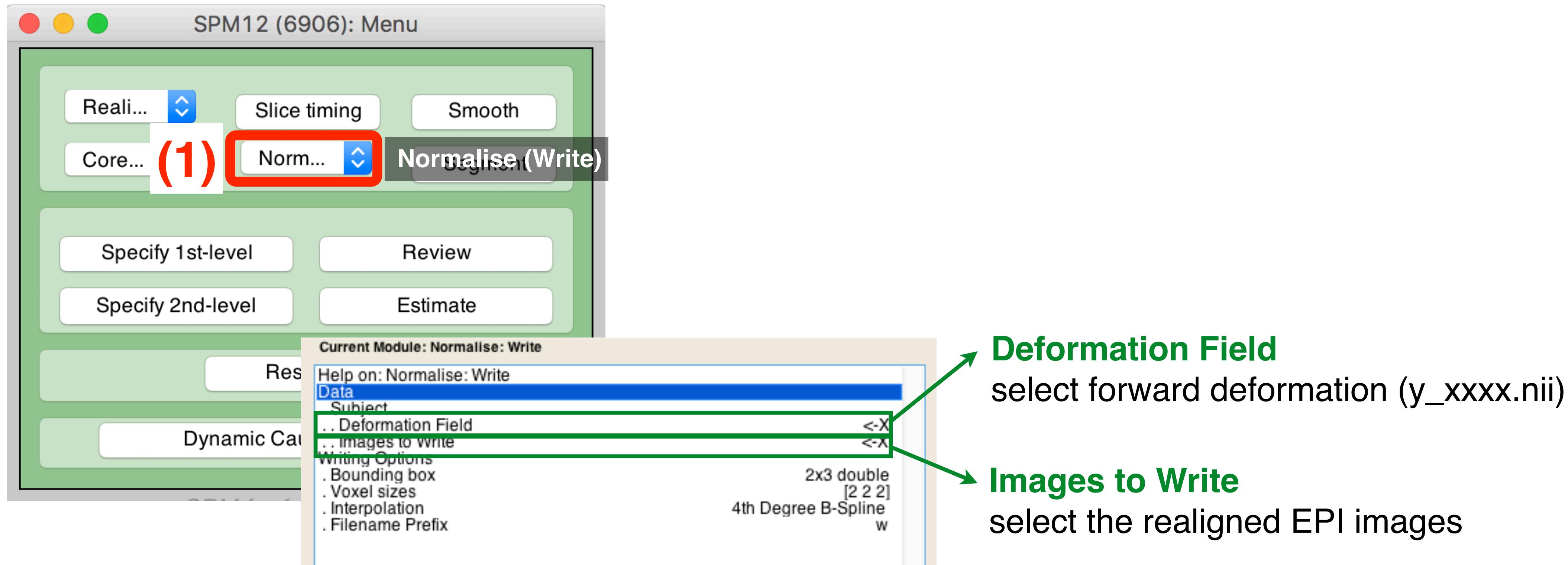
Volumes
select "coregistered T1 image"

Tissues
options to be changed:
Native Tissue: None
Warped Tissue: None

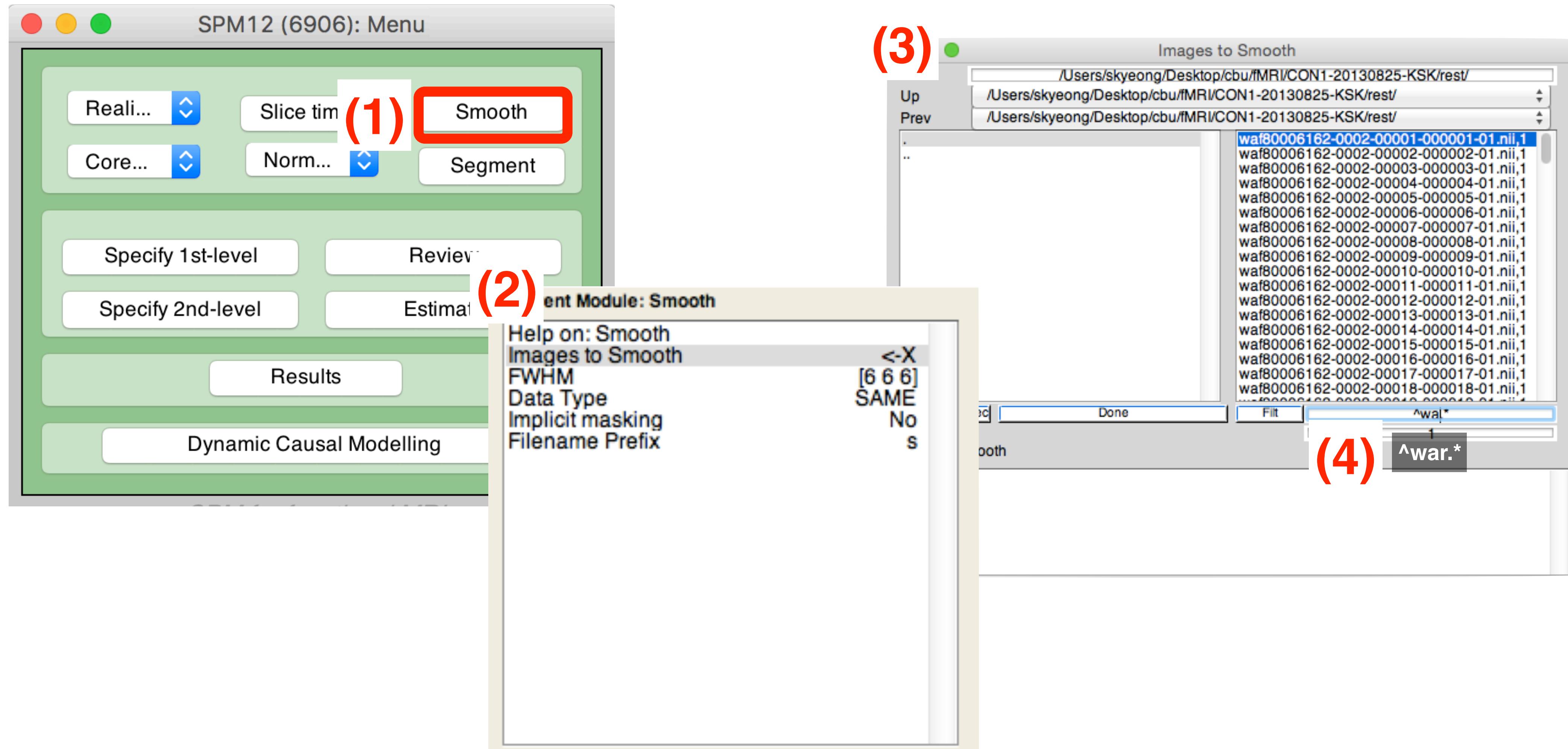
Deformation Fields
option to be changed:
Deformation Fields: Forward

Normalization after Segmentation

Normalize (Write) using the forward deformation field

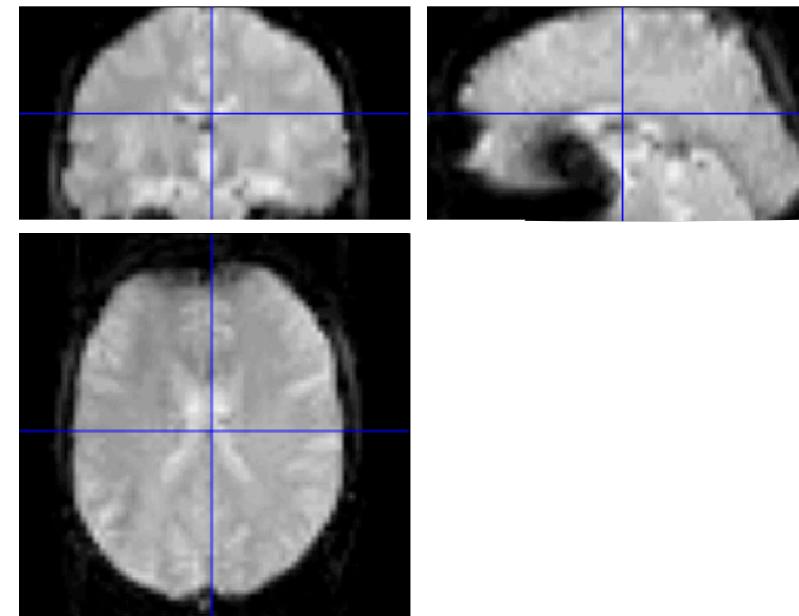


5. Smoothing

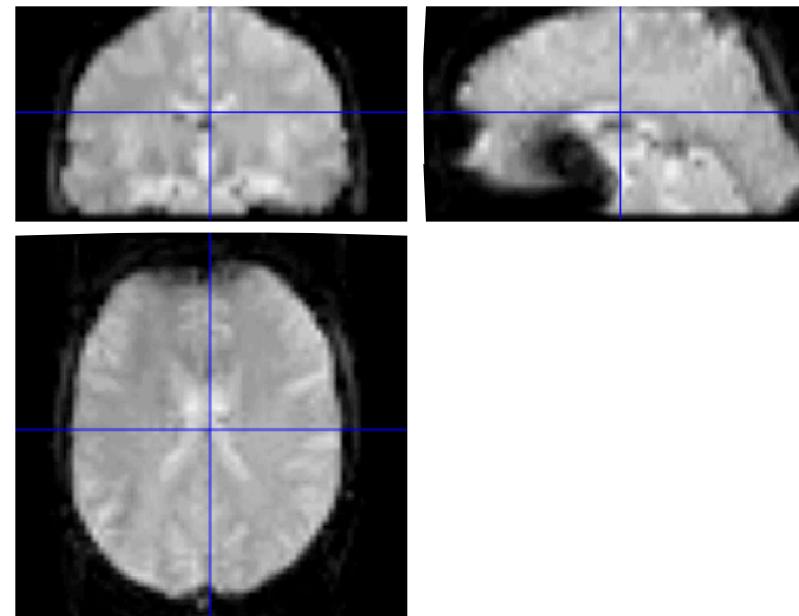


Summary of Preprocessing

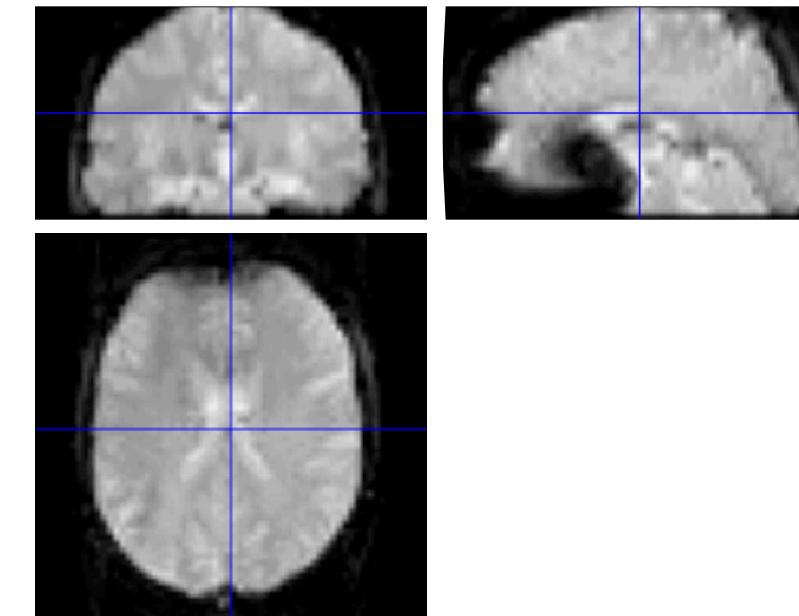
EPI



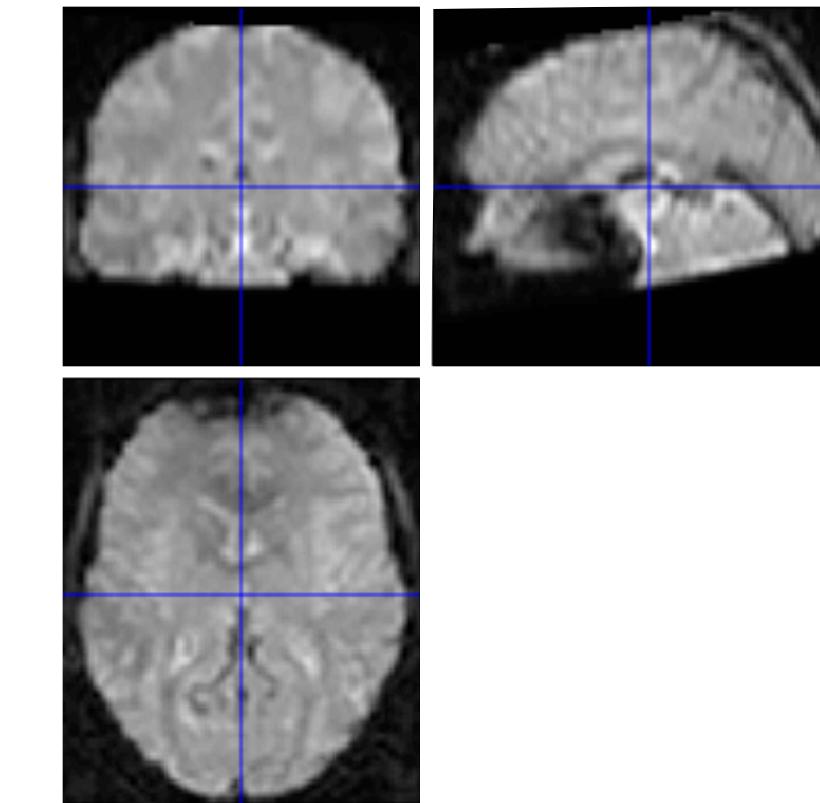
rEPI



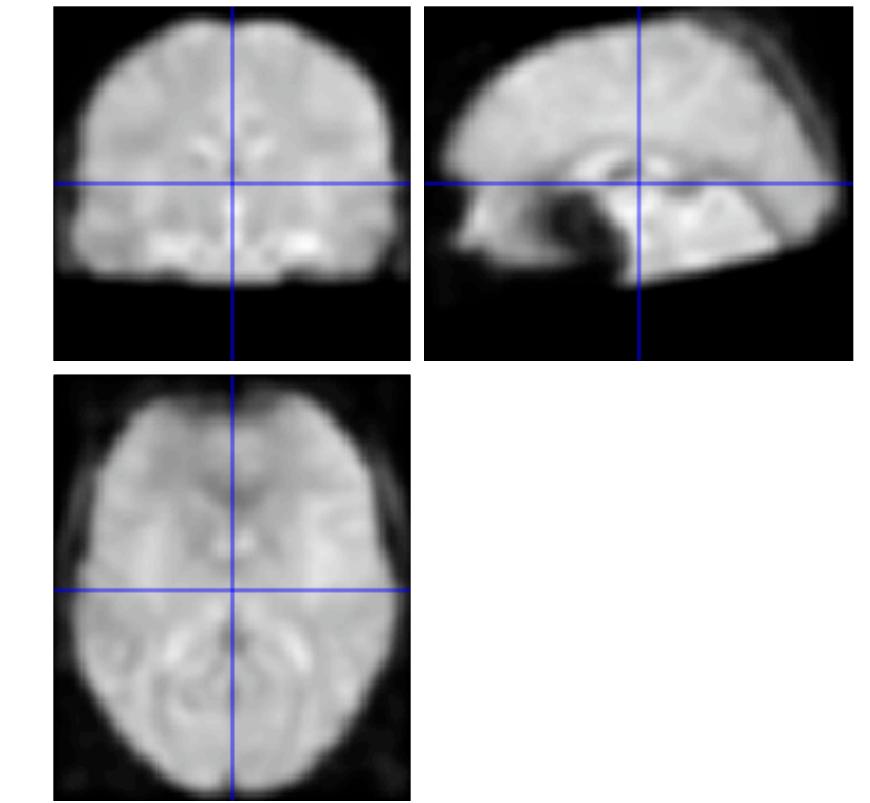
arEPI



warEPI



swarEPI



File: ./sM03953_0005_0100.img

Dimensions: 64 x 64 x 24

Datatype: int16

Intensity: Y = 0.050325 X

SPM compatible

Vox size: -3 x 3 x 4.5

Origin: 32.6 32.3 12.5

Dir Cos: 1.000 -0.003 0.005

0.003 1.000 -0.001

-0.005 0.001 1.000

File: ./rsM03953_0005_0100.img

Dimensions: 64 x 64 x 24

Datatype: int16

Intensity: Y = 0.050325 X

spm - realigned

Vox size: -3 x 3 x 4.5

Origin: 32.5 32.3 12.5

Dir Cos: 1.000 0.000 0.000

0.000 1.000 0.000

0.000 0.000 1.000

File: ./arsM03953_0005_0100.img

Dimensions: 64 x 64 x 24

Datatype: int16

Intensity: Y = 0.050325 X

spm - realigned acq-fix ref-slice 14

Vox size: -3 x 3 x 4.5

Origin: 32.5 32.3 12.5

Dir Cos: 1.000 0.000 0.000

0.000 1.000 0.000

0.000 0.000 1.000

File: ./arsM03953_0005_0100.img

Dimensions: 79 x 95 x 79

Datatype: int16

Intensity: Y = 0.050325 X

Warped

Vox size: -2 x 2 x 2

Origin: 40 57 36

Dir Cos: 1.000 0.000 0.000

0.000 1.000 0.000

0.000 0.000 1.000

File: ./arsM03953_0005_0100.img

Dimensions: 79 x 95 x 79

Datatype: int16

Intensity: Y = 0.050325 X

Warped - conv(6,6,6)

Vox size: -2 x 2 x 2

Origin: 40 57 36

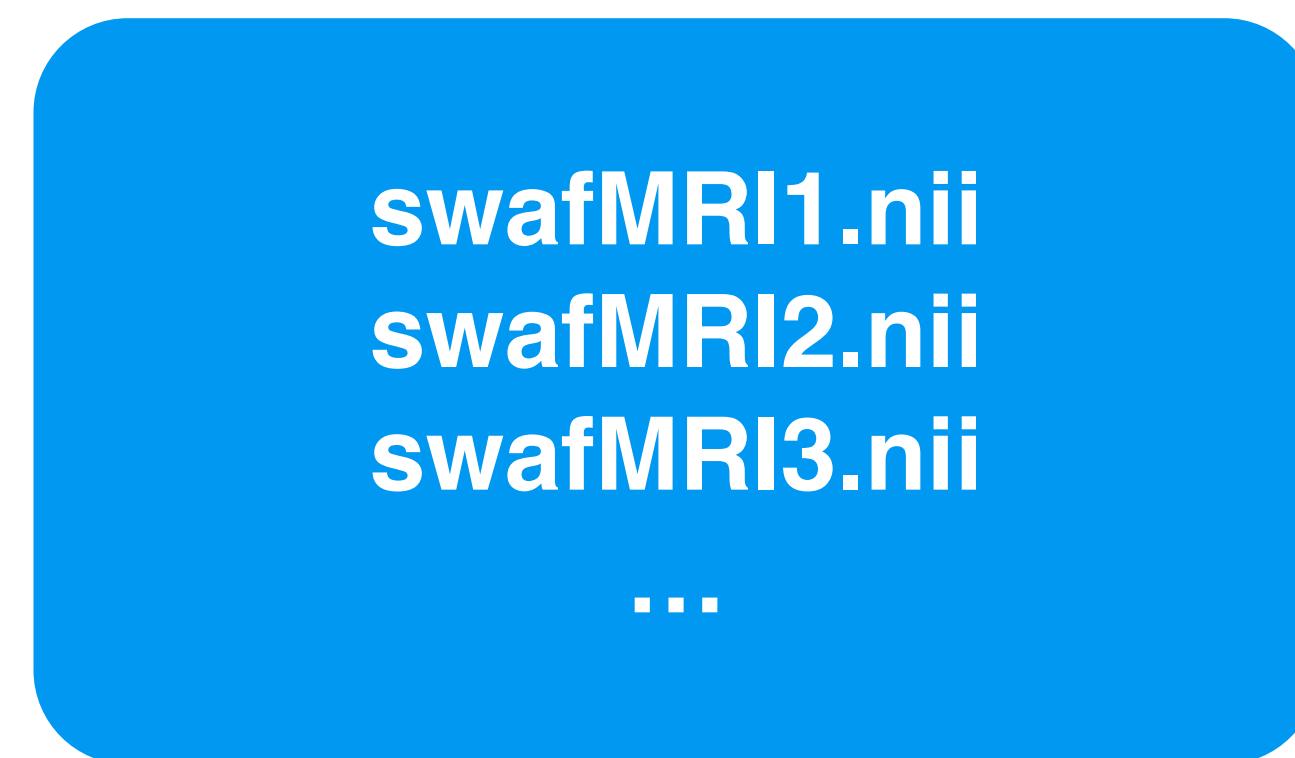
Dir Cos: 1.000 0.000 0.000

0.000 1.000 0.000

0.000 0.000 1.000

Now, we have

Preprocessed fMRI data



Event Related fMRI analysis

- Task-related brain activation
- PPI analysis (connectivity)

Resting State fMRI analysis

- functional connectivity
- graph theoretical analysis

100명 데이터를 전처리 해야 한다면?

실습2

나만의 Matlab Scripts 만들기

실습 데이터 다운로드

explore the following link:

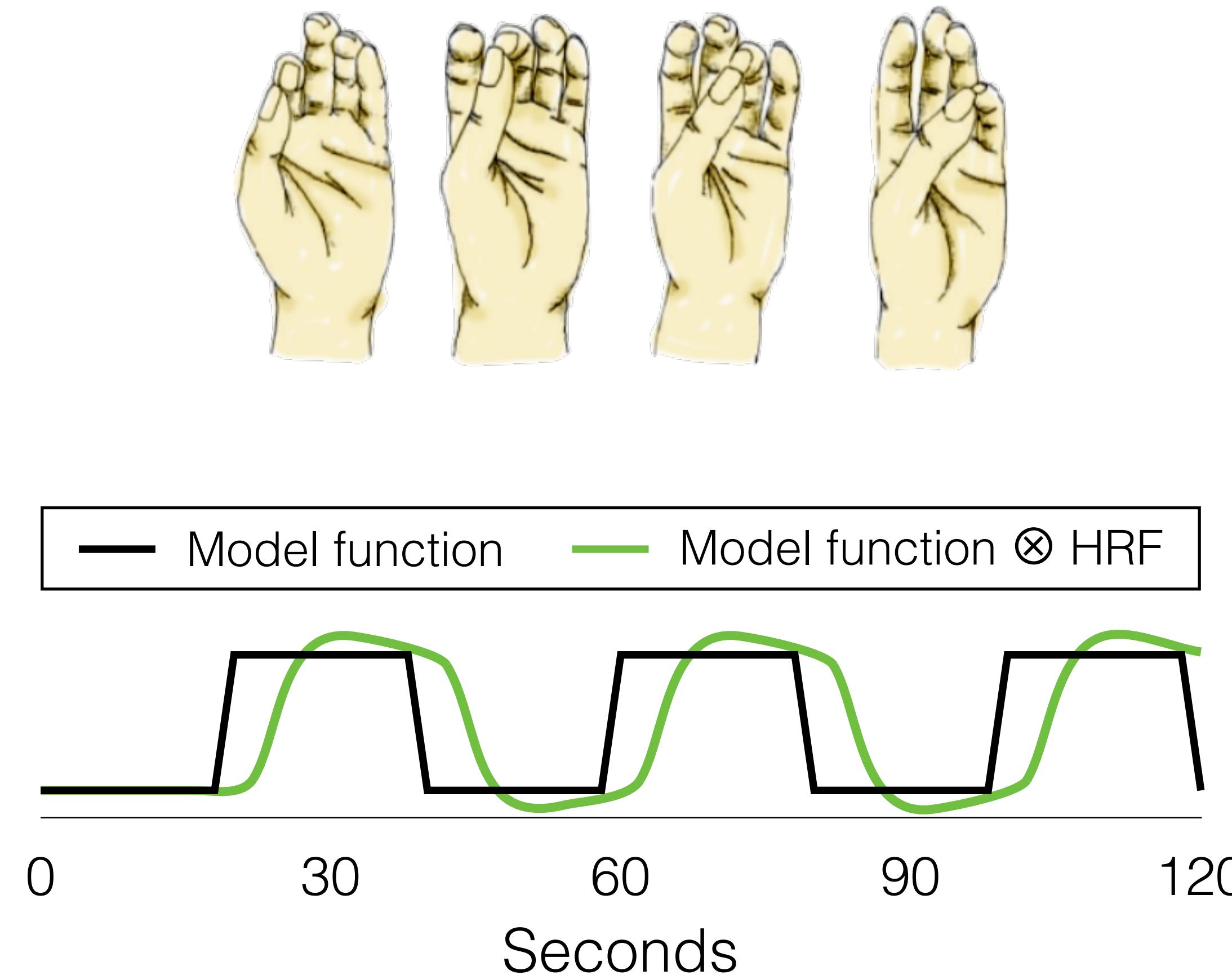
<https://www.facebook.com/groups/1877610655859385/files/>

download files:

subj01.zip, subj02.zip, subj03.zip and subj05.zip

어떤 데이터 일까?

block-design bimanual finger tapping task



TR = 2s
ascending 36 slices
order = interleaved
60 scans

Save Batch Script!

Step1~5를 다시 진행하되,
face_rep 데이터 대신 subj01 데이터를 분석함

1_realignment.m

Matlab script for realignment

```
%-----  
% Job saved on 01-Feb-2017 17:10:03 by cfg_util (rev $Rev: 6460 $)  
% spm SPM - SPM12 (6906)  
% cfg_basicio BasicIO - Unknown  
%-----  
%%  
matlabbatch{1}.spm.spatial.realign.estwrite.data = {  
    {'/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/finger.nii,1'  
     '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/finger.nii,2'  
     '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/finger.nii,3'  
     '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/finger.nii,4'  
     '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/finger.nii,58'  
     '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/finger.nii,59'  
     '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/finger.nii,60'}  
};  
  
matlabbatch{1}.spm.spatial.realign.estwrite.eoptions.quality = 0.9;  
matlabbatch{1}.spm.spatial.realign.estwrite.eoptions.sep = 4;  
matlabbatch{1}.spm.spatial.realign.estwrite.eoptions.fwhm = 5;  
matlabbatch{1}.spm.spatial.realign.estwrite.eoptions.rtm = 1;  
matlabbatch{1}.spm.spatial.realign.estwrite.eoptions.interp = 2;  
matlabbatch{1}.spm.spatial.realign.estwrite.eoptions.wrap = [0 0 0];  
matlabbatch{1}.spm.spatial.realign.estwrite.eoptions.weight = '';  
matlabbatch{1}.spm.spatial.realign.estwrite.roptions.which = [2 1];  
matlabbatch{1}.spm.spatial.realign.estwrite.roptions.interp = 4;  
matlabbatch{1}.spm.spatial.realign.estwrite.roptions.wrap = [0 0 0];  
matlabbatch{1}.spm.spatial.realign.estwrite.roptions.mask = 1;  
matlabbatch{1}.spm.spatial.realign.estwrite.roptions.prefix = 'r';
```

2_slicetiming_correction.m

Matlab script for slice timing correction

```
%-----  
% Job saved on 01-Feb-2017 17:13:23 by cfg_util (rev $Rev: 6460 $)  
% spm SPM - SPM12 (6906)  
% cfg_basicio BasicIO - Unknown  
%-----  
%%  
matlabbatch{1}.spm.temporal.st.scans = {  
    {  
        '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/rfinger.nii,1'  
        '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/rfinger.nii,2'  
        '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/rfinger.nii,3'  
        '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/rfinger.nii,4'  
        '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/rfinger.nii,5'  
        '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/rfinger.nii,56'  
        '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/rfinger.nii,57'  
        '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/rfinger.nii,58'  
        '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/rfinger.nii,59'  
        '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/rfinger.nii,60'  
    }  
};  
matlabbatch{1}.spm.temporal.st.nslices = 36;  
matlabbatch{1}.spm.temporal.st.tr = 2;  
matlabbatch{1}.spm.temporal.st.ta = 1.94444444444444;  
matlabbatch{1}.spm.temporal.st.so = [1 3 5 7 9 11 13 15 17 19 21 23 25 27 29 31 33 35 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36];  
matlabbatch{1}.spm.temporal.st.refslice = 18;  
matlabbatch{1}.spm.temporal.st.prefix = 'a';
```

3_coregistration.m

Matlab script for co-registration

```
%-----  
% Job saved on 01-Feb-2017 17:17:38 by cfg_util (rev $Rev: 6460 $)  
% spm SPM - SPM12 (6906)  
% cfg_basicio BasicIO - Unknown  
%-----  
matlabbatch{1}.spm.spatial.coreg.estimate.ref = {'/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/meanfinger.nii',1};  
matlabbatch{1}.spm.spatial.coreg.estimate.source = {'/Users/skyeong/Desktop/spm_exdata/Finger/subj01/anat/hires.nii',1};  
matlabbatch{1}.spm.spatial.coreg.estimate.other = {};  
matlabbatch{1}.spm.spatial.coreg.estimate.eoptions.cost_fun = 'nmi';  
matlabbatch{1}.spm.spatial.coreg.estimate.eoptions.sep = [4 2];  
matlabbatch{1}.spm.spatial.coreg.estimate.eoptions.tol = [0.02 0.02 0.02 0.001 0.001 0.001 0.01 0.01 0.01 0.001 0.001 0.001];  
matlabbatch{1}.spm.spatial.coreg.estimate.eoptions.fwhm = [7 7];
```

4 normalization.m

Matlab script for normalization

```
%-----  
% Job saved on 01-Feb-2017 17:18:26 by cfg_util (rev $Rev: 6460 $)  
% spm SPM - SPM12 (6906)  
% cfg_basicio BasicIO - Unknown  
%-----  
matlabbatch{1}.spm.spatial.normalise.estwrite.subj.vol = {'/Users/skyeong/Desktop/spm_exdata/Finger/subj01/anat/hires.nii,1'};  
matlabbatch{1}.spm.spatial.normalise.estwrite.subj.resample = {  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/arfinger.nii,1'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/arfinger.nii,2'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/arfinger.nii,3'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/arfinger.nii,4'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/arfinger.nii,59'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/arfinger.nii,60'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/anat/hires.nii,1'  
};  
matlabbatch{1}.spm.spatial.normalise.estwrite.eoptions.biasreg = 0.0001;  
matlabbatch{1}.spm.spatial.normalise.estwrite.eoptions.biasfwhm = 60;  
matlabbatch{1}.spm.spatial.normalise.estwrite.eoptions.tpm = {'/Users/skyeong/matlabwork/spm12/tpm/TPM.nii'};  
matlabbatch{1}.spm.spatial.normalise.estwrite.eoptions.affreg = 'mni';  
matlabbatch{1}.spm.spatial.normalise.estwrite.eoptions.reg = [0 0.001 0.5 0.05 0.2];  
matlabbatch{1}.spm.spatial.normalise.estwrite.eoptions.fwhm = 0;  
matlabbatch{1}.spm.spatial.normalise.estwrite.eoptions.samp = 3;  
matlabbatch{1}.spm.spatial.normalise.estwrite.woptions.bb = [-78 -112 -70  
    78 76 85];  
matlabbatch{1}.spm.spatial.normalise.estwrite.woptions.vox = [2 2 2];  
matlabbatch{1}.spm.spatial.normalise.estwrite.woptions.interp = 4;  
matlabbatch{1}.spm.spatial.normalise.estwrite.woptions.prefix = 'w';
```

5_smoothing.m

Matlab script for smoothing

```
%-----  
% Job saved on 01-Feb-2017 17:23:12 by cfg_util (rev $Rev: 6460 $)  
% spm SPM - SPM12 (6906)  
% cfg_basicio BasicIO - Unknown  
%-----  
%%  
matlabbatch{1}.spm.spatial.smooth.data = {  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/warfinger.nii,1'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/warfinger.nii,2'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/warfinger.nii,3'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/warfinger.nii,4'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/warfinger.nii,5'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/warfinger.nii,6'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/warfinger.nii,58'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/warfinger.nii,59'  
    '/Users/skyeong/Desktop/spm_exdata/Finger/subj01/fmri/warfinger.nii,60'  
};  
%%  
matlabbatch{1}.spm.spatial.smooth.fwhm = [ 6 6 6 ];  
matlabbatch{1}.spm.spatial.smooth.dtype = 0;  
matlabbatch{1}.spm.spatial.smooth.im = 0;  
matlabbatch{1}.spm.spatial.smooth.prefix = 's';
```

Combining all together!

Preprocessing script for single subject

```
% fMRI parameter
%-----
nslices = 36;
TR = 2;
sliceOrd = [1:2:36 2:2:36];
refslice = 18;

% Directory containing Face data
%-----
data_path = '/Users/skyeong/Desktop/spm_exdata/finger';
subjname = 'subj01';

% Initialise SPM
%-----
spm('Defaults','fMRI');
spm_jobman('initcfg');

%%%%%%%%%%%%%
% SPATIAL PREPROCESSING
%%%%%%%%%%%%%
clear matlabbatch

% Select functional and structural scans
%-----
f = spm_select('FPLIST', fullfile(data_path,subjname,'fmri'), '^finger.*\.nii$');
a = spm_select('FPLIST', fullfile(data_path,subjname,'anat'), '^hires.*\.nii$');
f = get_filepath(f);

% Realign
%-----
matlabbatch{1}.spm.spatial.realign.estwrite.data{1} = cellstr(f);

% Slice Timing Correction
%-----
matlabbatch{2}.spm.temporal.st.scans{1} = cellstr(spm_file(f,'prefix','r'));
matlabbatch{2}.spm.temporal.st.nslices = nslices;
matlabbatch{2}.spm.temporal.st.tr = TR;
matlabbatch{2}.spm.temporal.st.ta = TR-TR/nslices;
matlabbatch{2}.spm.temporal.st.so = sliceOrd;
matlabbatch{2}.spm.temporal.st.refslice = refslice;

% Coregister
%-----
matlabbatch{3}.spm.spatial.coreg.estimate.ref = cellstr(spm_file(f(1,:),'prefix','mean'));
matlabbatch{3}.spm.spatial.coreg.estimate.source = cellstr(a);

% Normalise: Estimate and Write
%-----
matlabbatch{4}.spm.spatial.normalise.estwrite.subj.vol = cellstr(a);
matlabbatch{4}.spm.spatial.normalise.estwrite.subj.resample = cellstr([spm_file(f,'prefix','ar');a]);
matlabbatch{4}.spm.spatial.normalise.estwrite.eoptions.tpm = {fullfile(spm('dir'), 'tpm', 'TPM.nii')};
matlabbatch{4}.spm.spatial.normalise.estwrite.woptions.bb = [-78 -112 -70; 78 76 85];
matlabbatch{4}.spm.spatial.normalise.estwrite.woptions.vox = [2 2 2];

% Smooth
%-----
matlabbatch{5}.spm.spatial.smooth.data = cellstr(spm_file(f,'prefix','war'));
matlabbatch{5}.spm.spatial.smooth.fwhm = [6 6 6];

%save('face_batch_preprocessing.mat','matlabbatch');
spm_jobman('run',matlabbatch);
```

Combining all together!

Preprocessing script for multiple subjects

```
% fMRI parameter
%-----
nslices = 36;
TR = 2;
sliceOrd = [1:2:36 2:2:36];
refslice = 18;

% Directory containing Face data
%-----
data_path = '/Users/skyeong/Desktop/spm_exdata/finger';
subjlist = {'subj01','subj02','subj03','subj05'};
nsubj = length(subjlist);

% Initialise SPM
%-----
spm('Defaults','fMRI');
spm_jobman('initcfg');

%%%%%%%%%%%%%
% SPATIAL PREPROCESSING
%%%%%%%%%%%%%
for c=1:nsubj,
    subjname = subjlist{c};
    clear matlabbatch

    % Select functional and structural scans
    %-----
    f = spm_select('FPList', fullfile(data_path,subjname,'fmri'), '^finger.*\.nii$');
    a = spm_select('FPList', fullfile(data_path,subjname,'anat'), '^hires.*\.nii$');
    f = get_filepath(f);

    % Realign
    %-----
    matlabbatch{1}.spm.spatial.realign.estwrite.data{1} = cellstr(f);

    % Slice Timing Correction
    %-----
    matlabbatch{2}.spm.temporal.st.scans{1} = cellstr(spm_file(f,'prefix','r'));
    matlabbatch{2}.spm.temporal.st.nslices = nslices;
    matlabbatch{2}.spm.temporal.st.tr = TR;
    matlabbatch{2}.spm.temporal.st.ta = TR-TR/nslices;
    matlabbatch{2}.spm.temporal.st.so = sliceOrd;
    matlabbatch{2}.spm.temporal.st.refslice = refslice;

    % Coregister
    %-----
    matlabbatch{3}.spm.spatial.coreg.estimate.ref = cellstr(spm_file(f(1,:),'prefix','mean'));
    matlabbatch{3}.spm.spatial.coreg.estimate.source = cellstr(a);

    % Normalise: Estimate and Write
    %-----
    matlabbatch{4}.spm.spatial.normalise.estwrite.subj.vol = cellstr(a);
    matlabbatch{4}.spm.spatial.normalise.estwrite.subj.resample = cellstr([spm_file(f,'prefix','ar');a]);
    matlabbatch{4}.spm.spatial.normalise.estwrite.eoptions.tpm = {fullfile(spm('dir'),'tpm','TPM.nii')};
    matlabbatch{4}.spm.spatial.normalise.estwrite.woptions.bb = [-78 -112 -70; 78 76 85];
    matlabbatch{4}.spm.spatial.normalise.estwrite.woptions.vox = [2 2 2];

    % Smooth
    %-----
    matlabbatch{5}.spm.spatial.smooth.data = cellstr(spm_file(f,'prefix','war'));
    matlabbatch{5}.spm.spatial.smooth.fwhm = [6 6 6];
    %save('face_batch_preprocessing.mat','matlabbatch');
    spm_jobman('run',matlabbatch);
end
```

Coming soon!

General Linear Model (GLM) 리뷰 및 SPM에서 GLM 분석하는 방법!