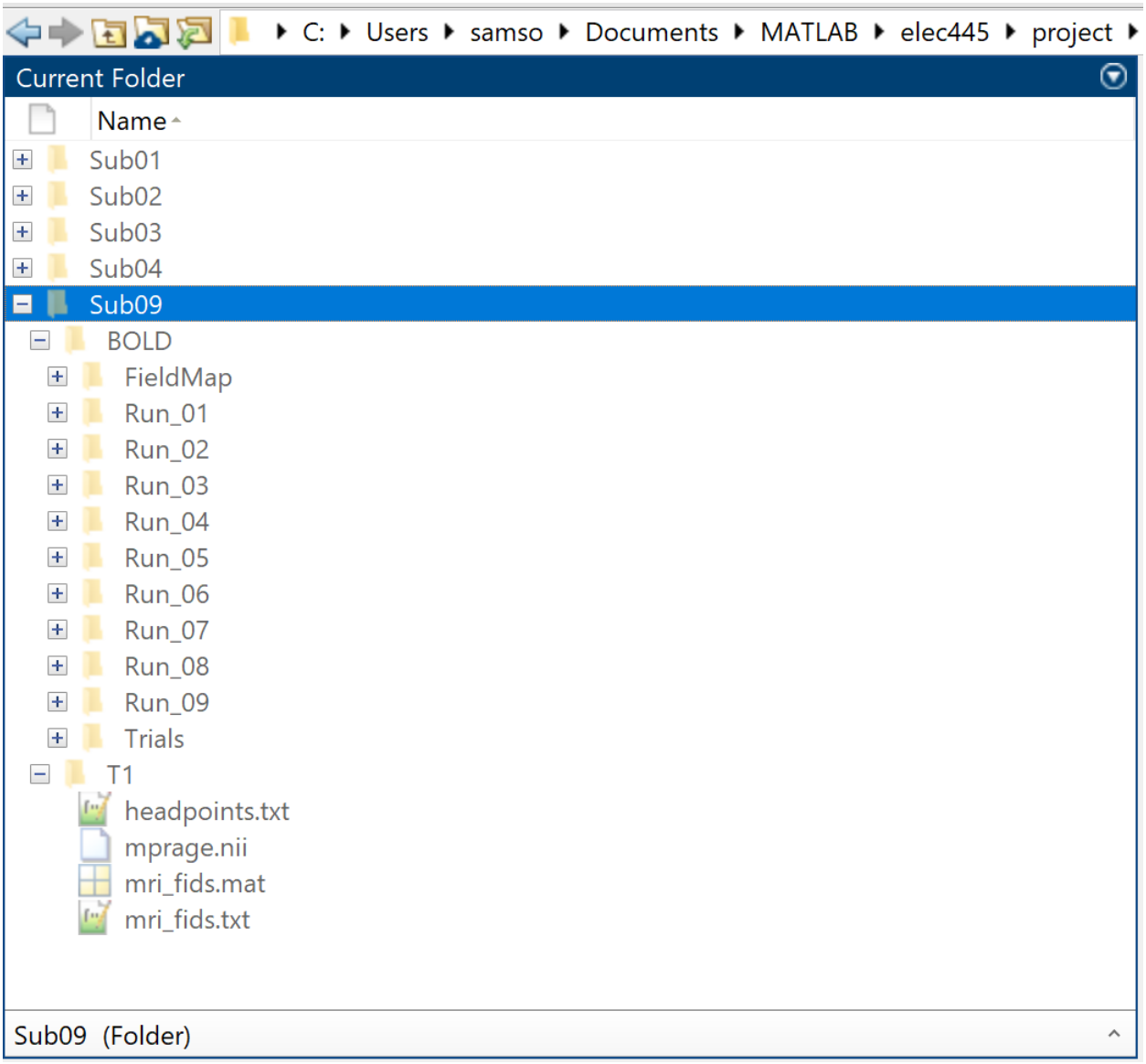
GUIDE TO PROJECT CODE (Pre-Processing)

1.0 Setup

- Create a folder to contain your data:

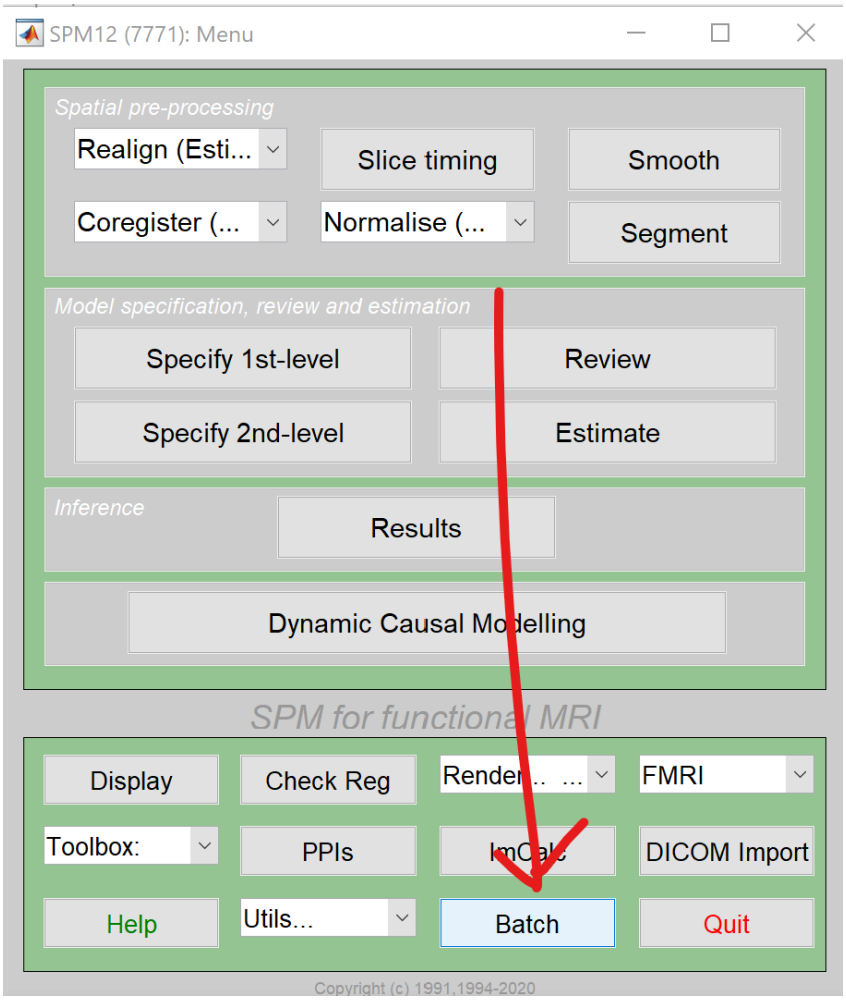


Make sure your subjects have the BOLD and T1 subdirectories with all the data (shown for Sub09).

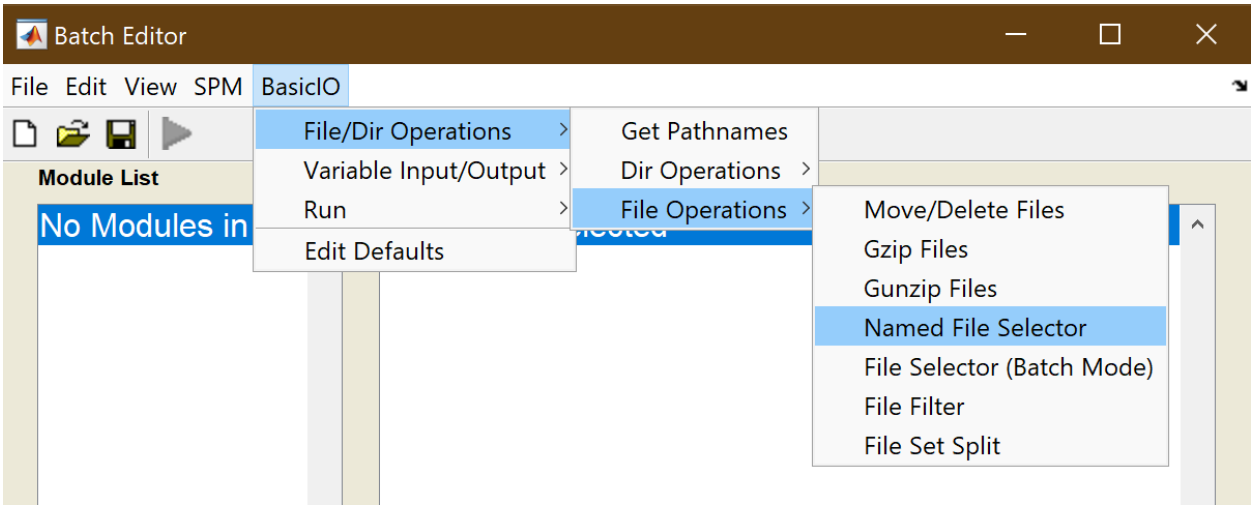
- Start SPM (inside project folder):

2.0 Creating the Pre-Processing Script

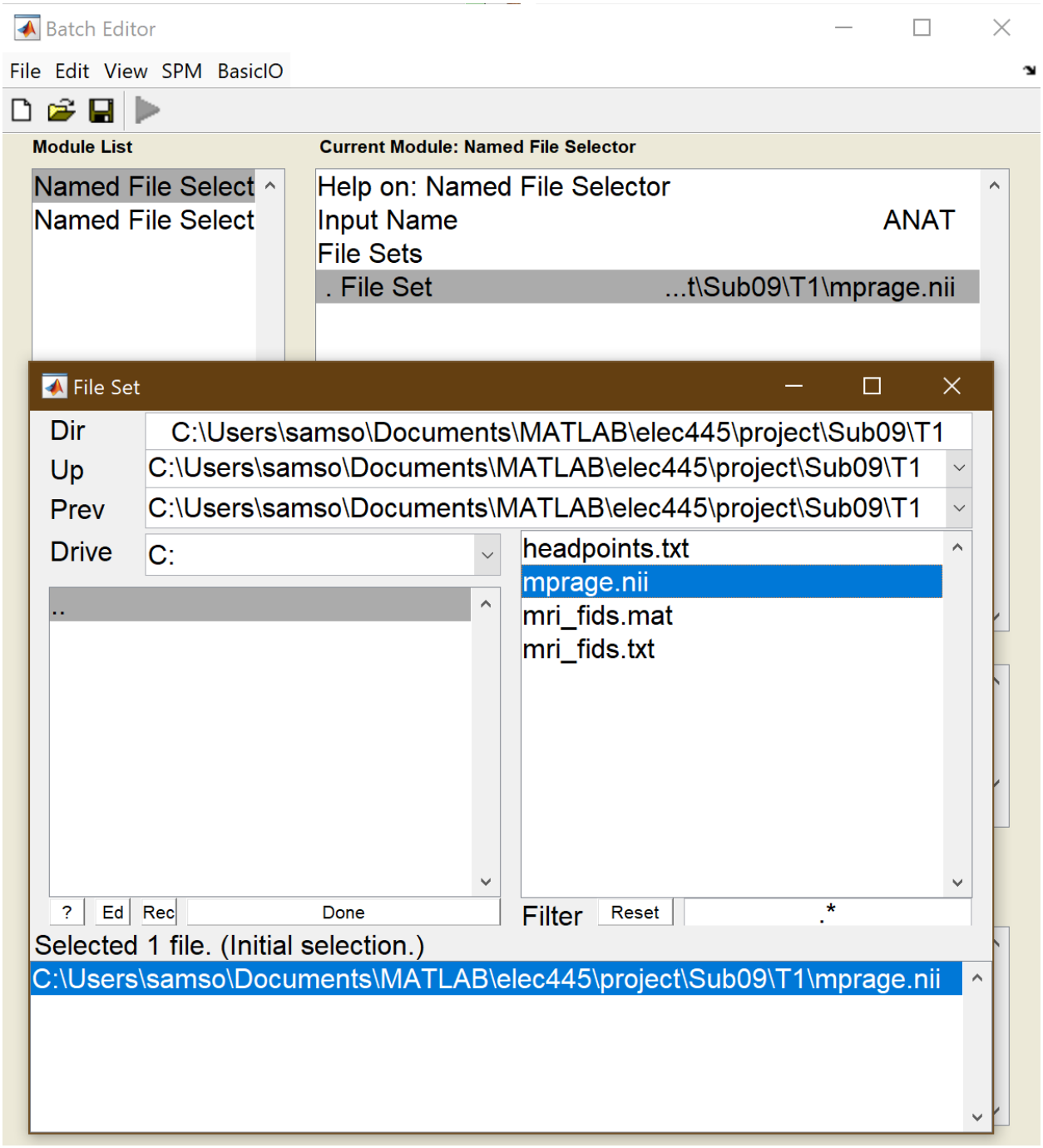
- Click on Batch button



- Add a couple "Named File Selectors" for ANAT, BOLDs



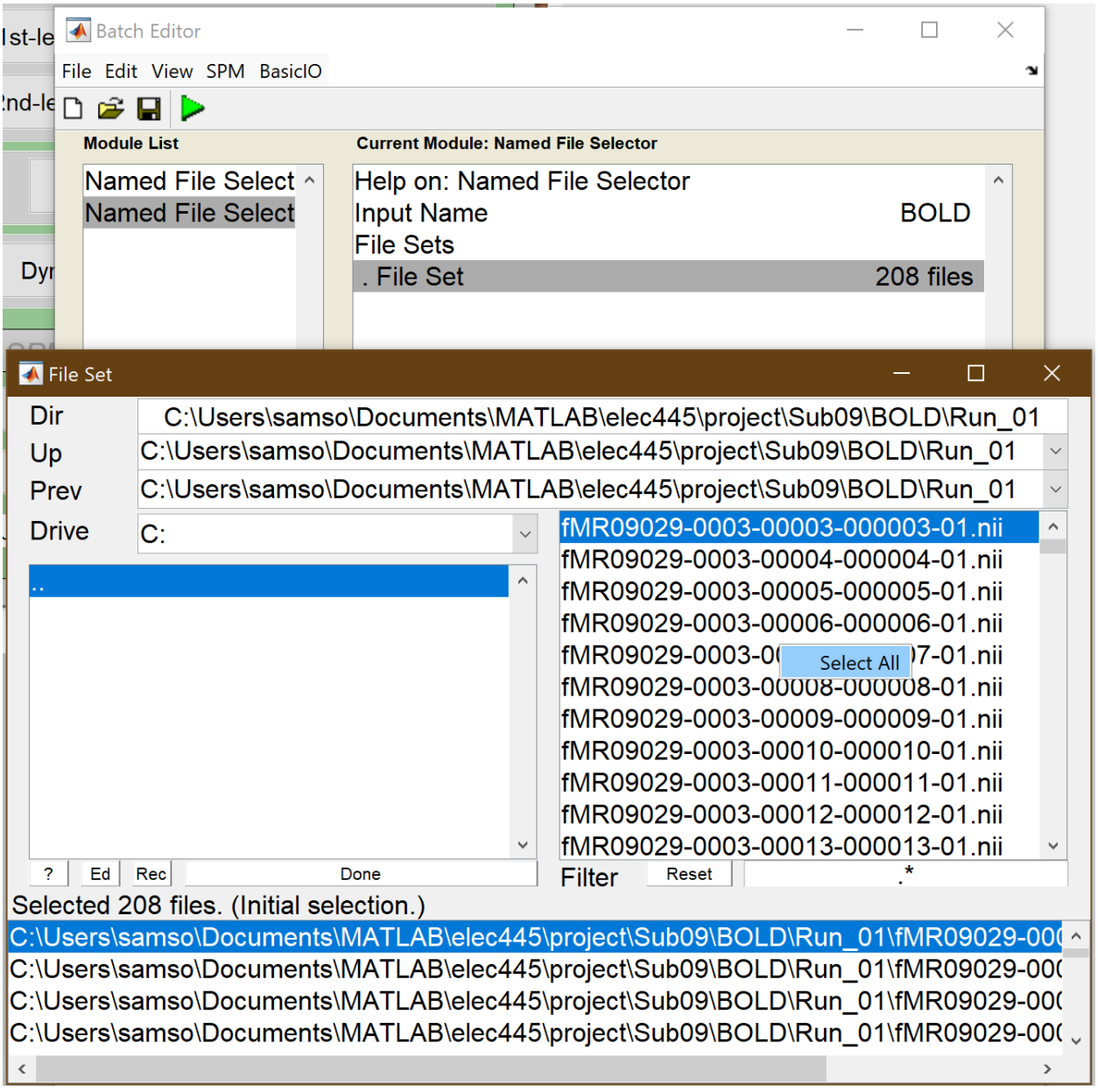
- Setup ANAT



Name it "ANAT"

Choose <Subject>/T1/mprage.nii for "File Set"

- Setup BOLDs

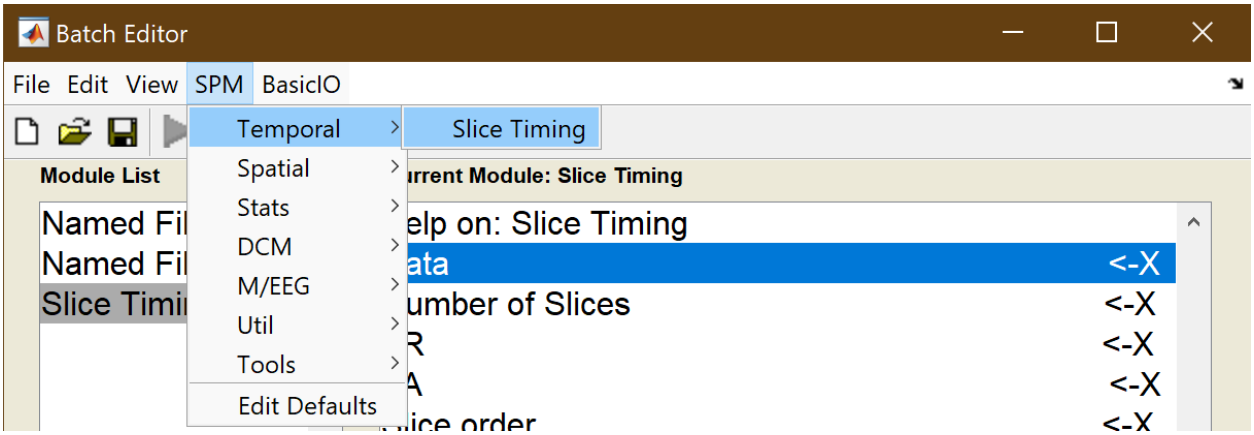


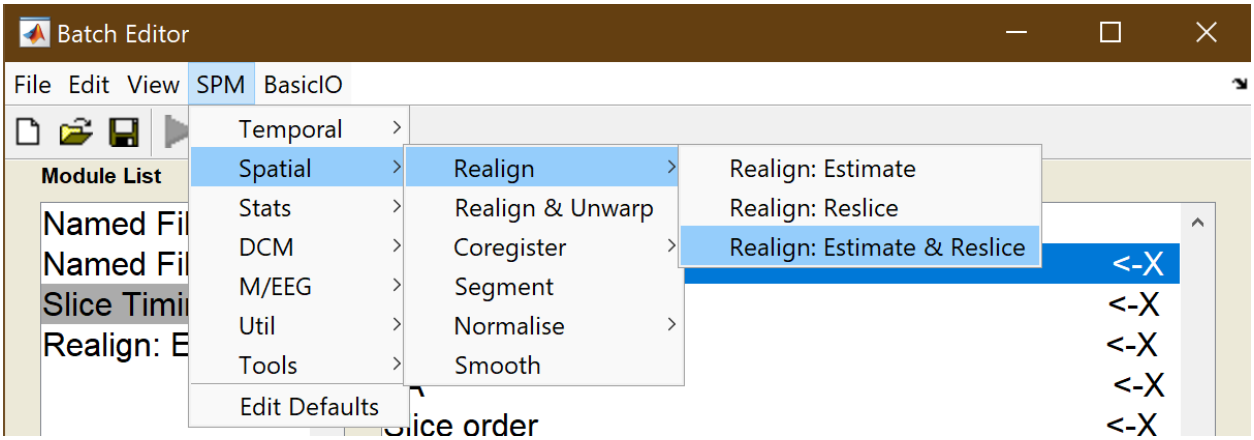
Name it “BOLD”

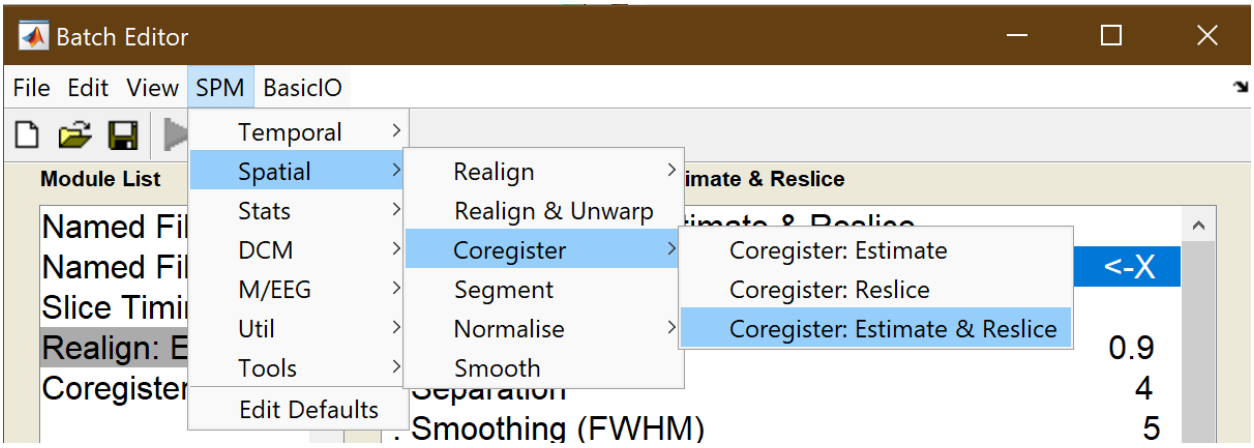
Choose ALL FILES in desired Subject Run <Subject>/BOLD/<Run_#>/<SLECT ALL>

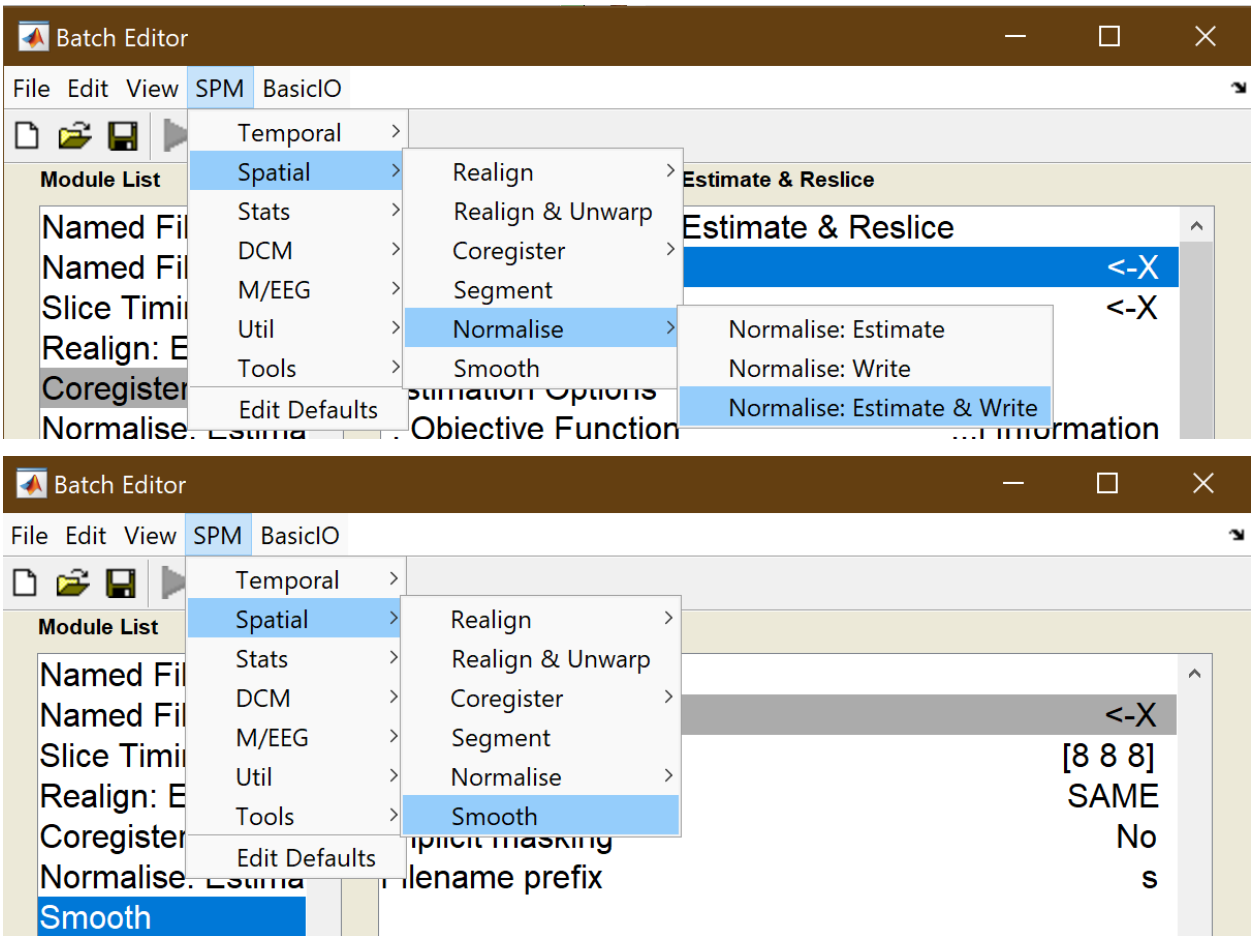
There should be 208 BOLD images

- Add all pre-processing steps








Batch Editor
File Edit View SPM BasicIO
Temporal
Spatial
Stats
DCM
M/EEG
Util
Tools
Edit Defaults
Realign
Realign & Unwarp
Coregister
Segment
Normalise
Smooth
Normalise: Estimate
Normalise: Write
Normalise: Estimate & Write
Module List
Estimate & Reslice
Estimate & Reslice
<-X
<-X
Named Fil
Named Fil
Slice Timi
Realign: E
Coregister
Normalise: Estima
Objective Function
Information
Batch Editor
File Edit View SPM BasicIO
Temporal
Spatial
Stats
DCM
M/EEG
Util
Tools
Edit Defaults
Realign
Realign & Unwarp
Coregister
Segment
Normalise
Smooth
Module List
Named Fil
Named Fil
Slice Timi
Realign: E
Coregister
Normalise: Estima
Smooth
<-X
[8 8 8]
SAME
No
s
Filename prefix

- Figure out Acquisition parameters

Find Data Acquisition Information from article: https://www.nature.com/articles/sdata20151

MRI acquisition

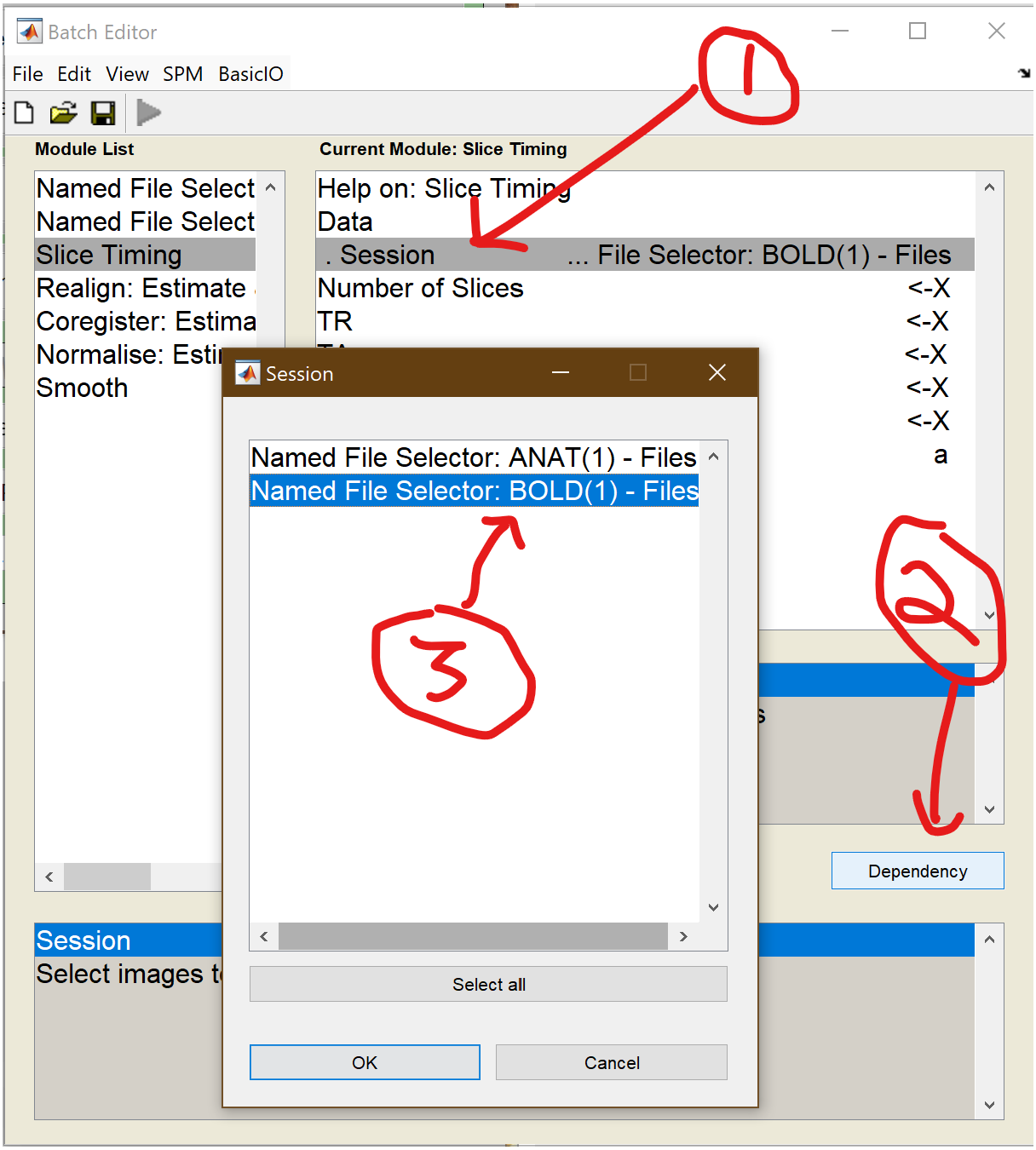
The MRI data were collected from a Siemens 3T TIM TRIO (Siemens, Erlangen, Germany). A standard 1 mm isotropic T1-weighted 'structural' image was acquired using an MPRAGE sequence (TR 2,250 ms, TE 2.98 ms, TI 900 ms, 190 Hz/pixel; flip angle 9°). The face of the participant in the T1 image was subsequently manually removed to help maintain anonymity. The functional data were acquired using an EPI sequence of 33, 3 mm-thick axial slices (TR 2000 ms, TE 30 ms, flip angle 78°). Slices were acquired in an interleaved fashion, with odd then even numbered slices (where slice 1 was the most inferior slice) and a 25% distance spacing (increased where necessary to cover whole of cortex), resulting in a range of voxel sizes of 3×3×3.75 mm to 3×3×4.05 mm across participants. 210 volumes were acquired in each of 9 runs (note that the 3 initial TRs were discarded to allow saturation of T1 effects).

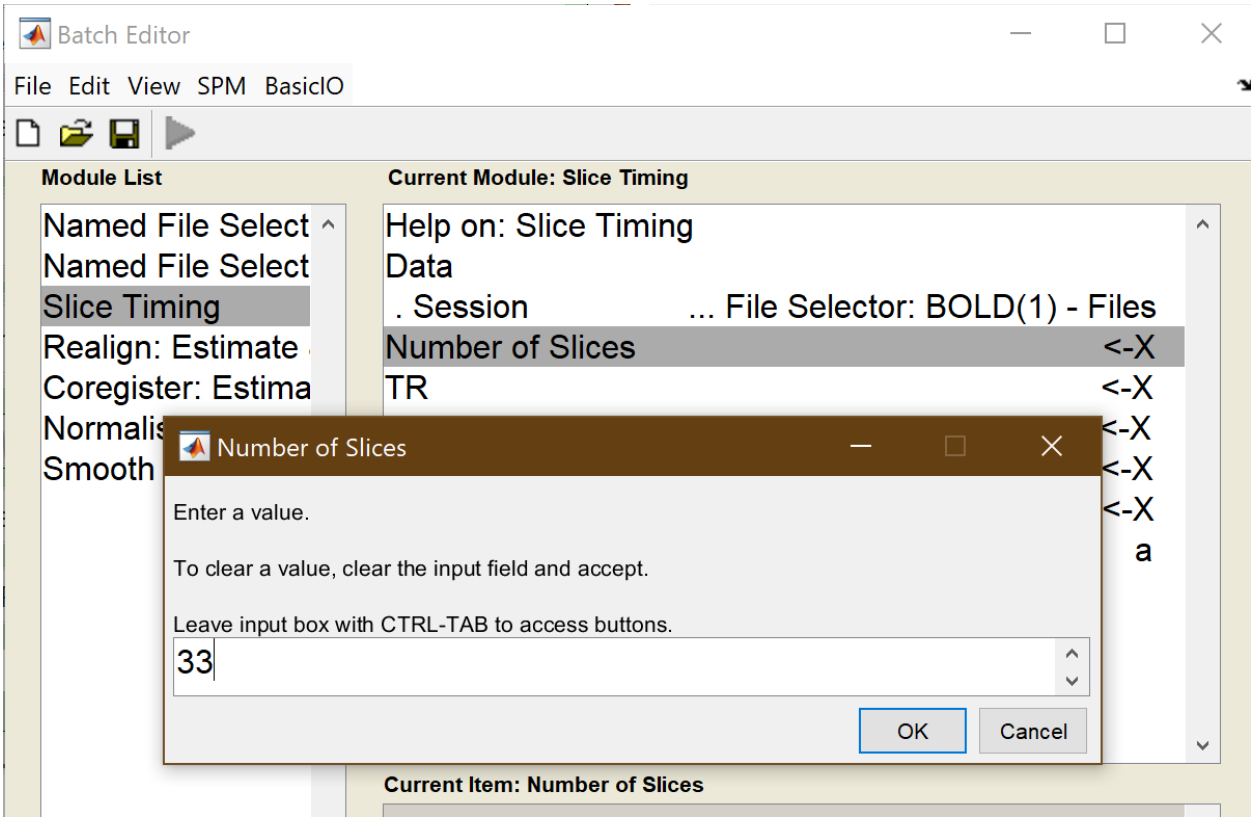
Slices: 33

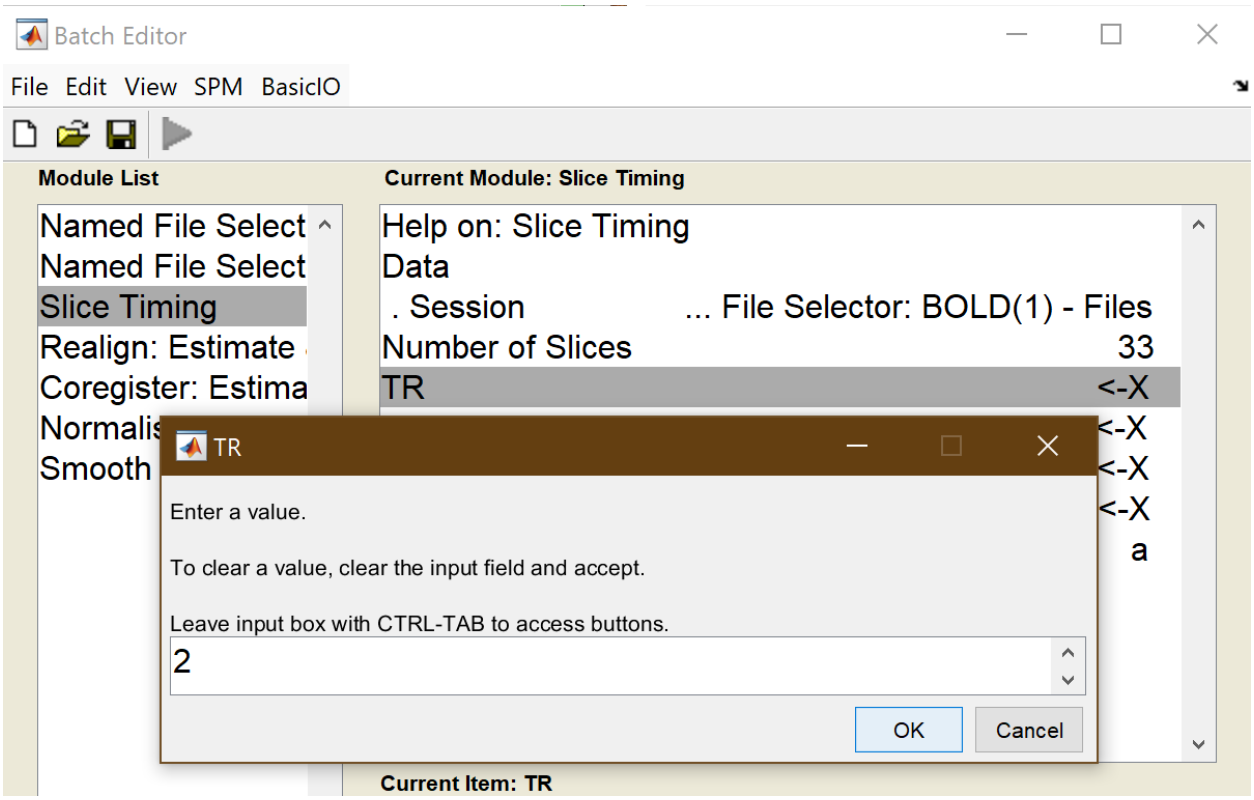
TR: 2

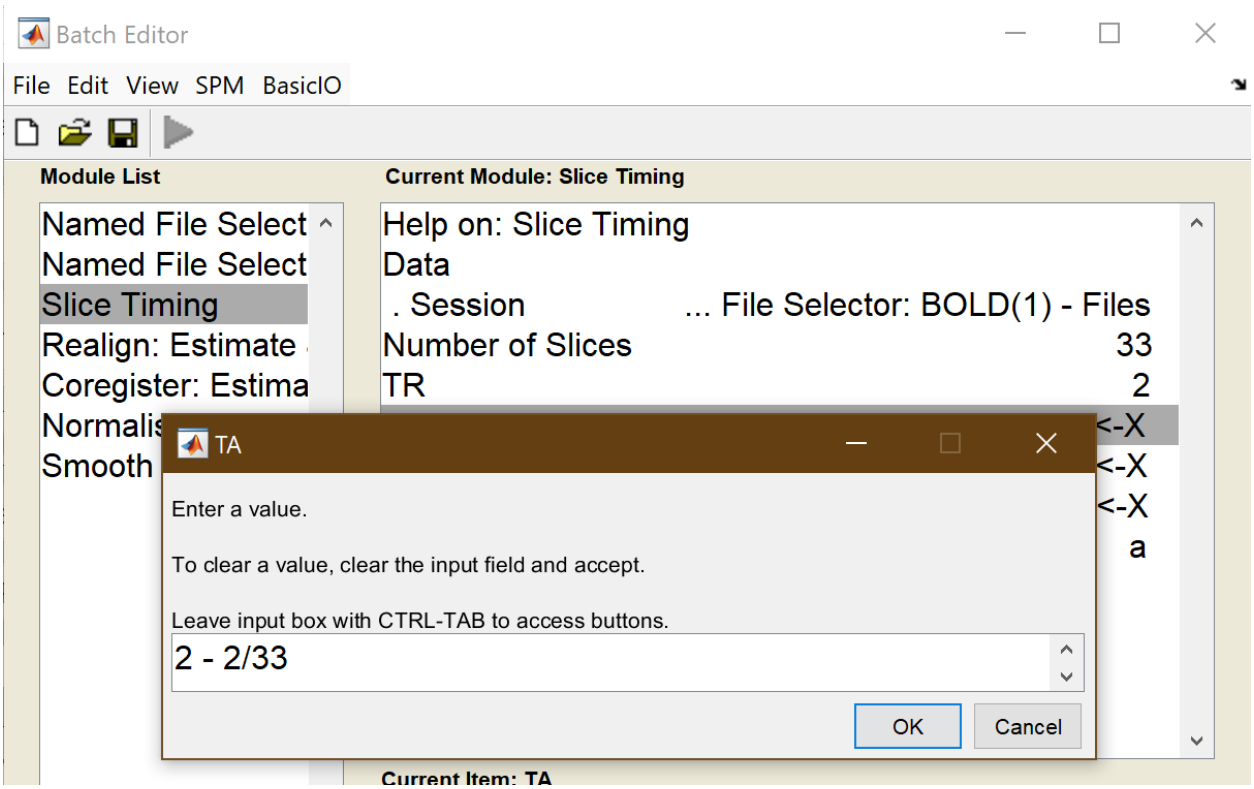
Slice Order: Interleaved Bottom-Up (1 to 33 by 2s, 2 to 32 by 2s)

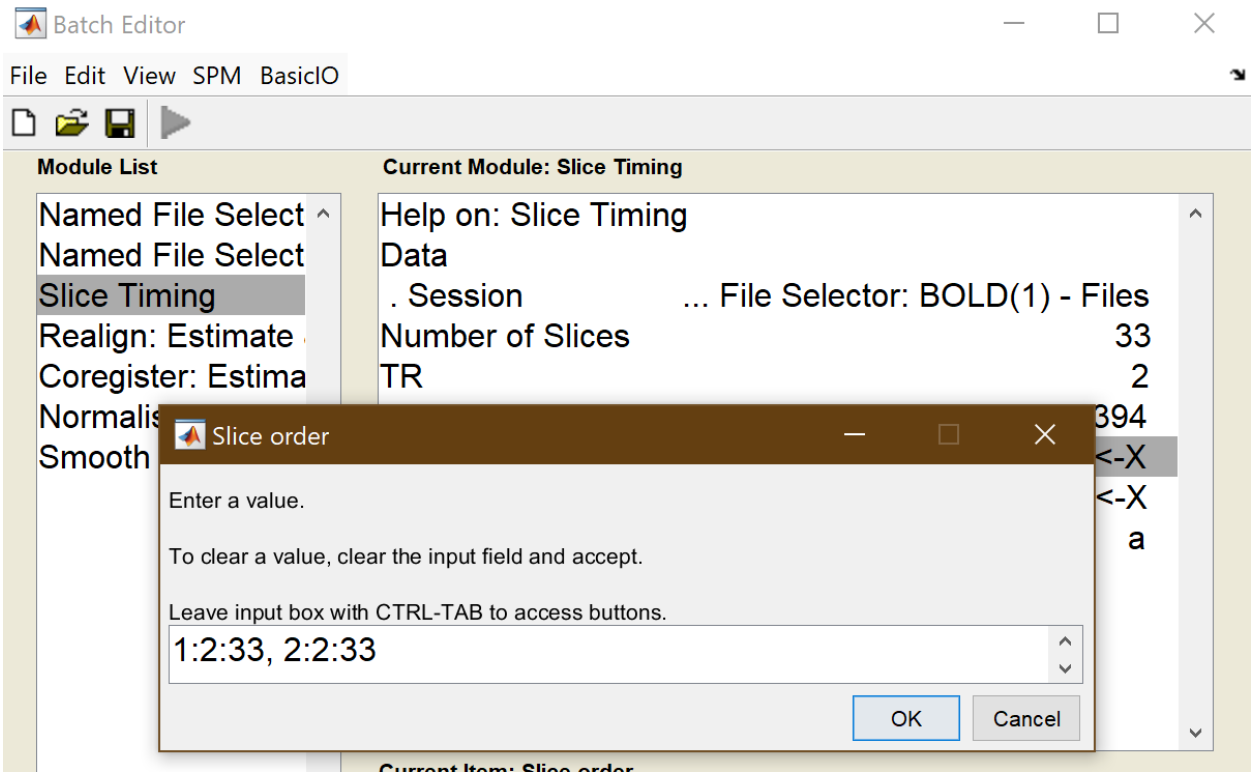
- Setup Slice Timing

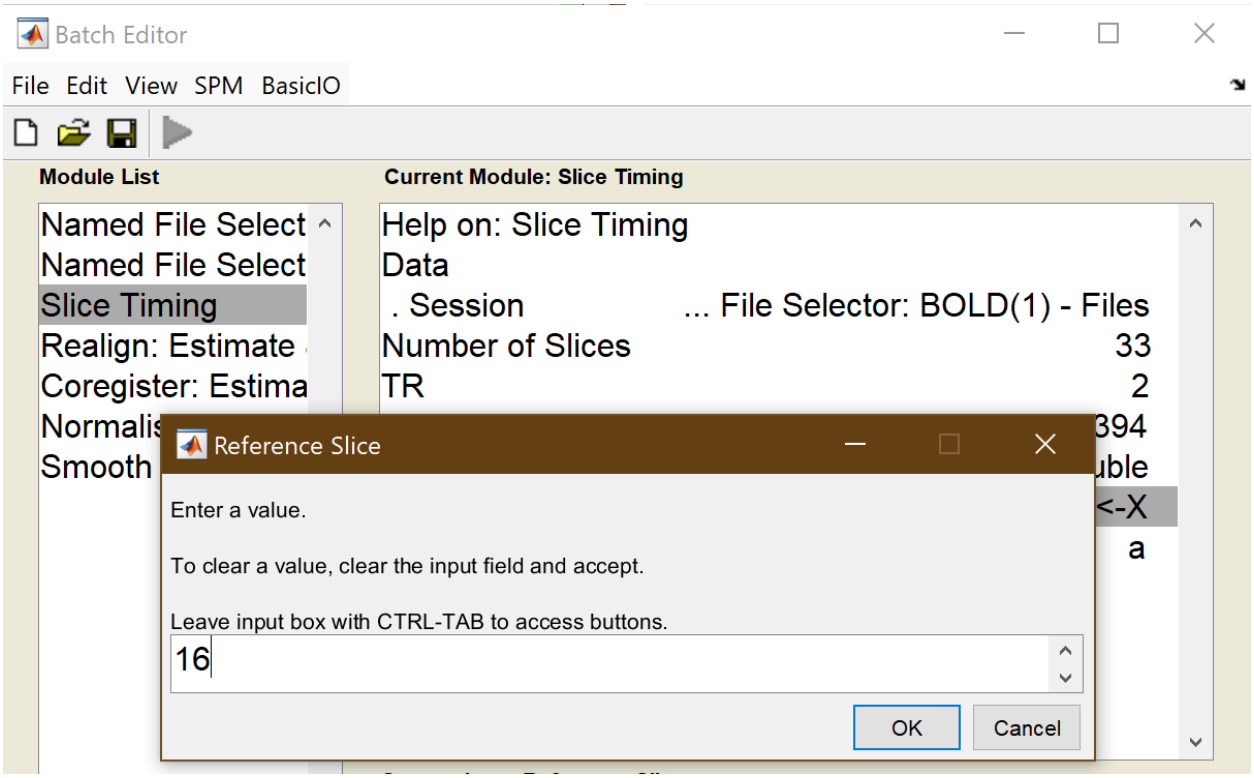



Batch Editor
File Edit View SPM BasicIO
Module List
Current Module: Slice Timing
Named File Select
Named File Select
Slice Timing
Realign: Estimate
Coregister: Estima
Normalis
Smooth
Help on: Slice Timing
Data
. Session
... File Selector: BOLD(1) - Files
Number of Slices
<-X
TR
<-X
<-X
<-X
<-X
a
Number of Slices
Enter a value.
To clear a value, clear the input field and accept.
Leave input box with CTRL-TAB to access buttons.
33
OK
Cancel
Current Item: Number of Slices

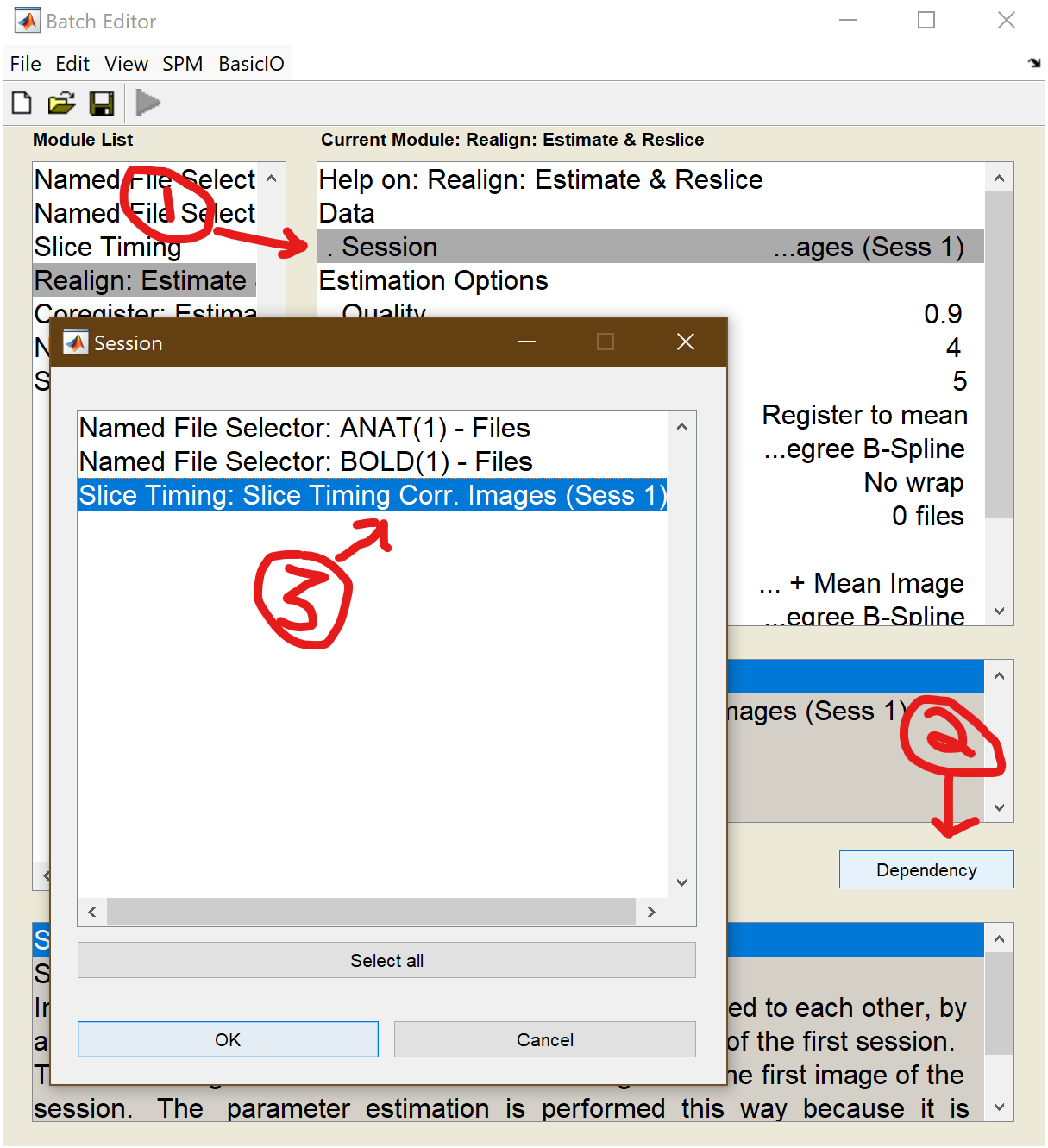

Batch Editor
File Edit View SPM BasicIO
Module List
Current Module: Slice Timing
Named File Select
Named File Select
Slice Timing
Realign: Estimate
Coregister: Estima
Normalis
Smooth
Help on: Slice Timing
Data
. Session
... File Selector: BOLD(1) - Files
Number of Slices
33
TR
<-X
<-X
<-X
<-X
<-X
a
TR
Enter a value.
To clear a value, clear the input field and accept.
Leave input box with CTRL-TAB to access buttons.
2
OK
Cancel
Current Item: TR


Batch Editor
File Edit View SPM BasicIO
Module List
Current Module: Slice Timing
Named File Select
Named File Select
Slice Timing
Realign: Estimate
Coregister: Estima
Normalis
Smooth
Help on: Slice Timing
Data
. Session
... File Selector: BOLD(1) - Files
Number of Slices
33
TR
2
<-X
<-X
<-X
a
TA
Enter a value.
To clear a value, clear the input field and accept.
Leave input box with CTRL-TAB to access buttons.
2 - 2/33
OK
Cancel
Current Item: TA

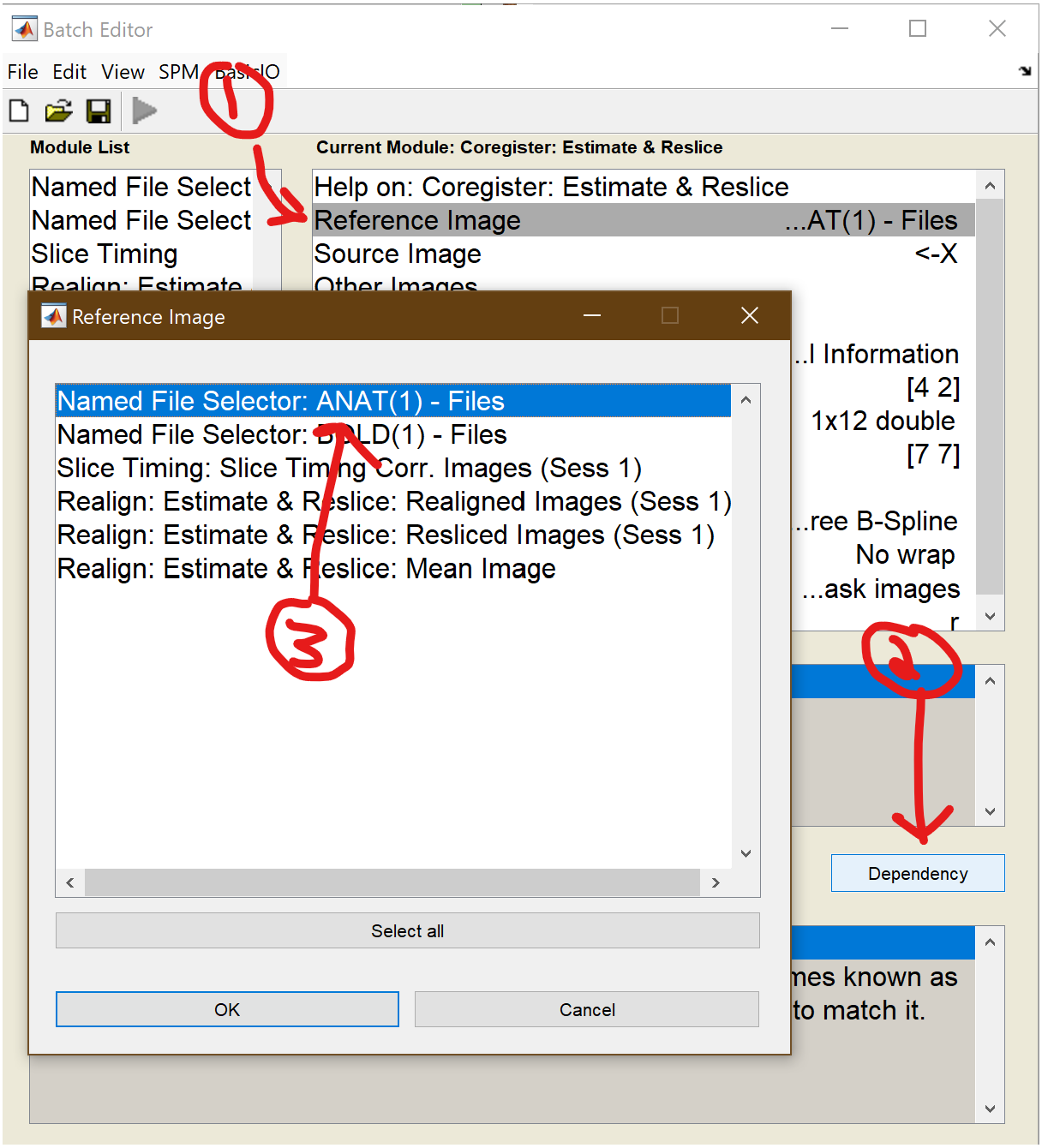

Batch Editor
File Edit View SPM BasicIO
Module List
Current Module: Slice Timing
Named File Select
Named File Select
Slice Timing
Realign: Estimate
Coregister: Estima
Normalis
Smooth
Help on: Slice Timing
Data
. Session
... File Selector: BOLD(1) - Files
Number of Slices
33
TR
2
394
<-X
<-X
a
Slice order
Enter a value.
To clear a value, clear the input field and accept.
Leave input box with CTRL-TAB to access buttons.
1:2:33, 2:2:33
OK
Cancel

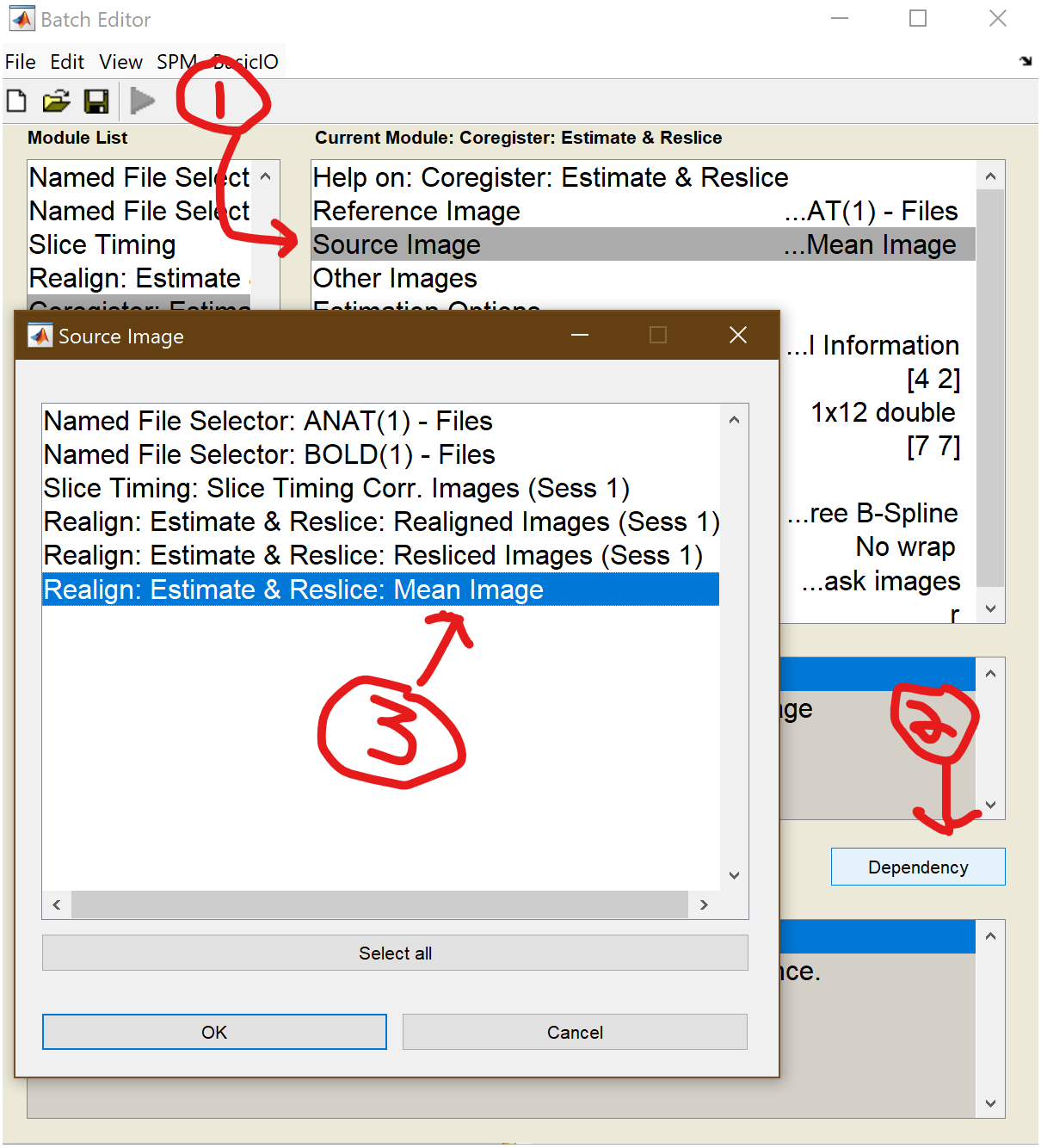

Batch Editor
File Edit View SPM BasicIO
Module List
Current Module: Slice Timing
Named File Select
Named File Select
Slice Timing
Realign: Estimate
Coregister: Estima
Normalis
Smooth
Help on: Slice Timing
Data
. Session
... File Selector: BOLD(1) - Files
Number of Slices
33
TR
2
394
uble
<-X
a
Reference Slice
Enter a value.
To clear a value, clear the input field and accept.
Leave input box with CTRL-TAB to access buttons.
16
OK
Cancel

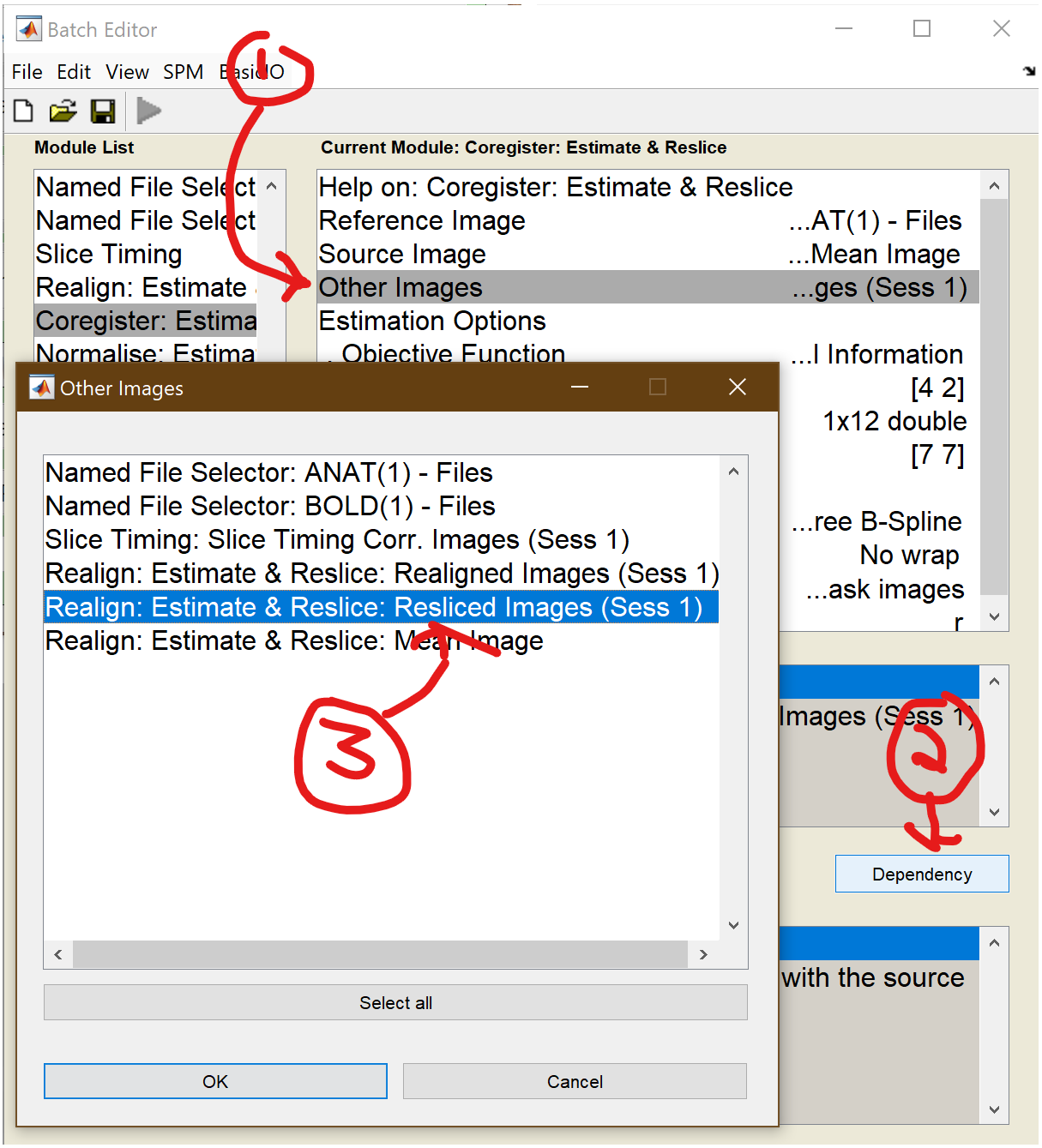
- Setup Realign



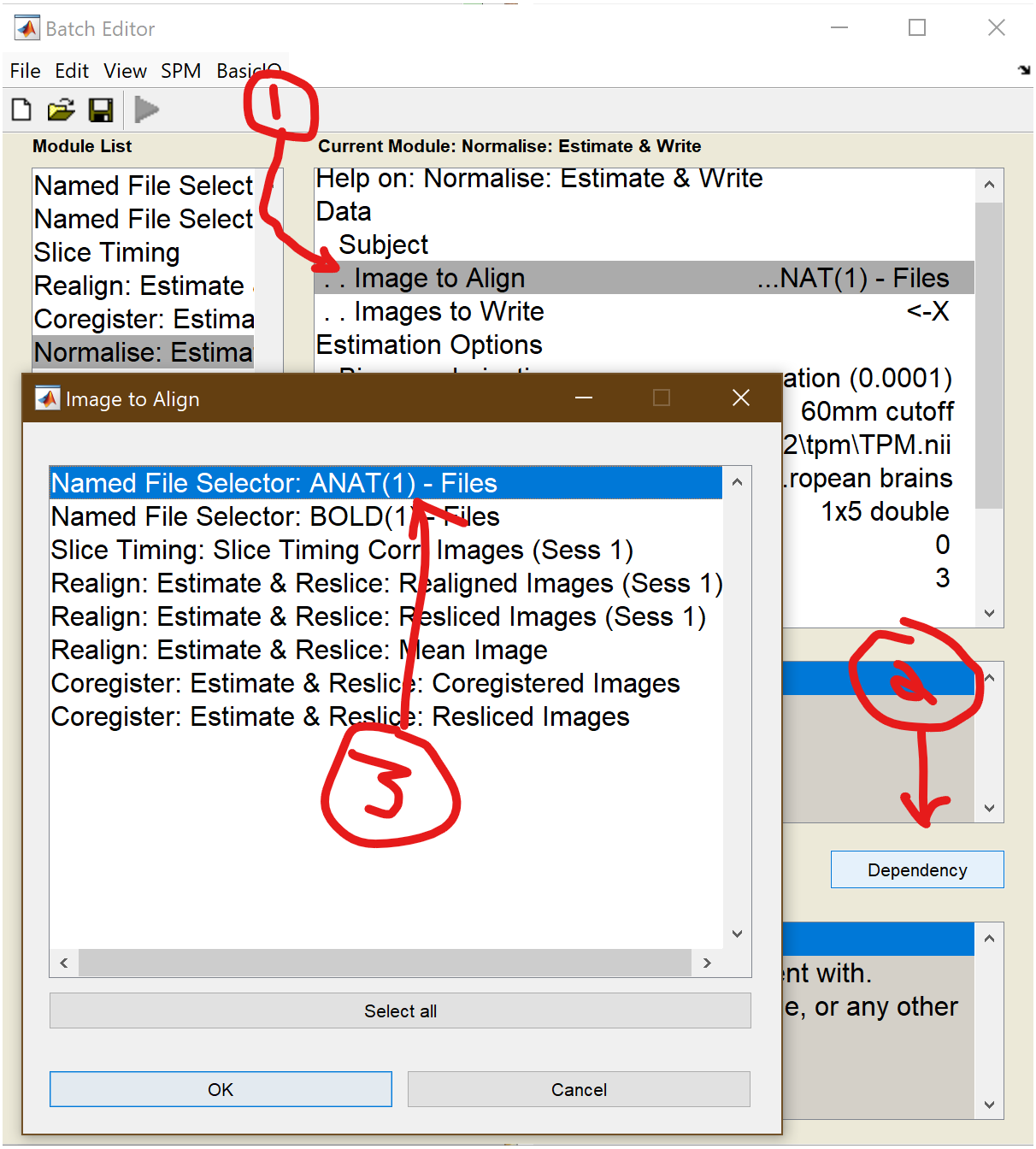
- Setup Coregister

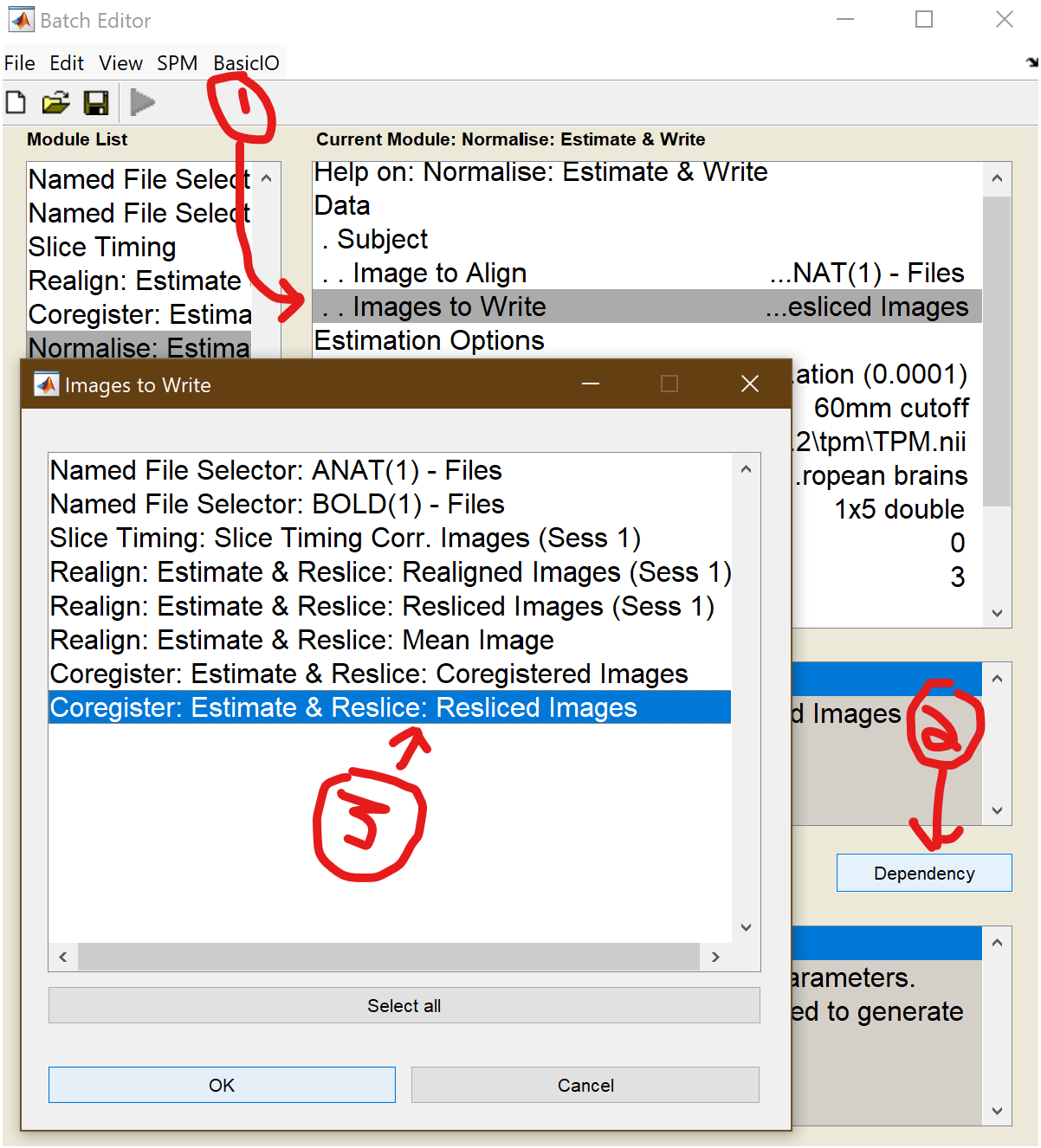



Batch Editor
File Edit View SPM BasicIO
Module List
Current Module: Coregister: Estimate & Reslice
Named File Select
Named File Select
Slice Timing
Realign: Estimate
Help on: Coregister: Estimate & Reslice
Reference Image
...AT(1) - Files
Source Image
...Mean Image
Other Images
...l Information
[4 2]
1x12 double
[7 7]
...ree B-Spline
No wrap
...ask images
r
Dependency
...nce.
Source Image
Named File Selector: ANAT(1) - Files
Named File Selector: BOLD(1) - Files
Slice Timing: Slice Timing Corr. Images (Sess 1)
Realign: Estimate & Reslice: Realigned Images (Sess 1)
Realign: Estimate & Reslice: Resliced Images (Sess 1)
Realign: Estimate & Reslice: Mean Image
Select all
OK
Cancel
1
2
3

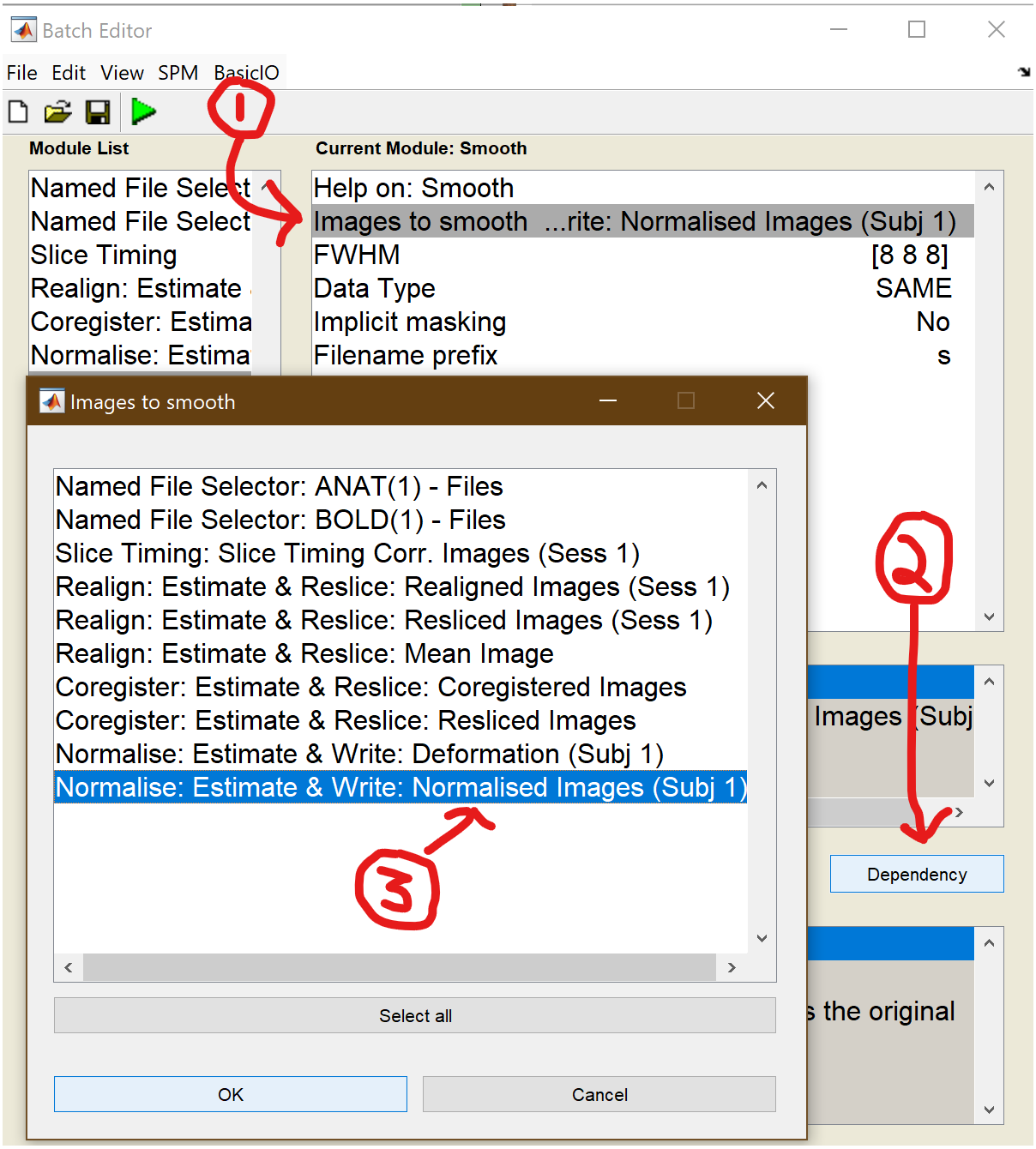

Batch Editor
File Edit View SPM BasicIO
Module List
Current Module: Coregister: Estimate & Reslice
Named File Select
Named File Select
Slice Timing
Realign: Estimate
Coregister: Estima
Normalise: Estima
Help on: Coregister: Estimate & Reslice
Reference Image
Source Image
Other Images
Estimation Options
Objective Function
...AT(1) - Files
...Mean Image
...ges (Sess 1)
...l Information
[4 2]
1x12 double
[7 7]
...ree B-Spline
No wrap
...ask images
r
Images (Sess 1)
Dependency
with the source
Other Images
Named File Selector: ANAT(1) - Files
Named File Selector: BOLD(1) - Files
Slice Timing: Slice Timing Corr. Images (Sess 1)
Realign: Estimate & Reslice: Realigned Images (Sess 1)
Realign: Estimate & Reslice: Resliced Images (Sess 1)
Realign: Estimate & Reslice: Mean Image
Select all
OK
Cancel
1
2
3

- Setup Normalize



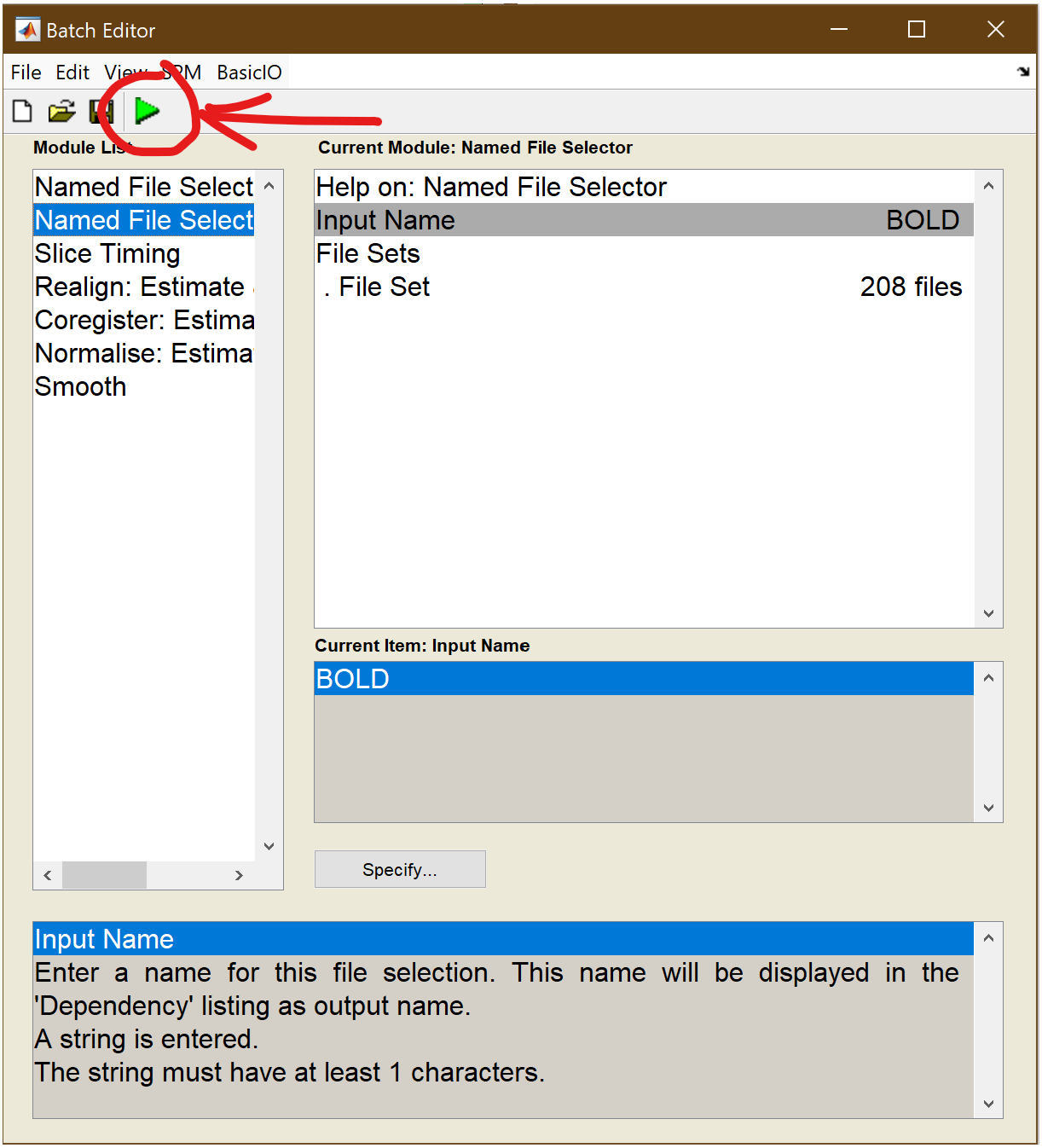

Batch Editor
File Edit View SPM BasicIO
Module List
Current Module: Normalise: Estimate & Write
Named File Select
Named File Select
Slice Timing
Realign: Estimate
Coregister: Estima
Normalise: Estima
Help on: Normalise: Estimate & Write
Data
. Subject
. . Image to Align ...NAT(1) - Files
. . Images to Write ...esliced Images
Estimation Options
ation (0.0001)
60mm cutoff
.2\tpm\TPM.nii
.ropean brains
1x5 double
0
3
d Images
Dependency
arameters.
ed to generate
Images to Write
Named File Selector: ANAT(1) - Files
Named File Selector: BOLD(1) - Files
Slice Timing: Slice Timing Corr. Images (Sess 1)
Realign: Estimate & Reslice: Realigned Images (Sess 1)
Realign: Estimate & Reslice: Resliced Images (Sess 1)
Realign: Estimate & Reslice: Mean Image
Coregister: Estimate & Reslice: Coregistered Images
Coregister: Estimate & Reslice: Resliced Images
Select all
OK
Cancel

- Setup Smoothing

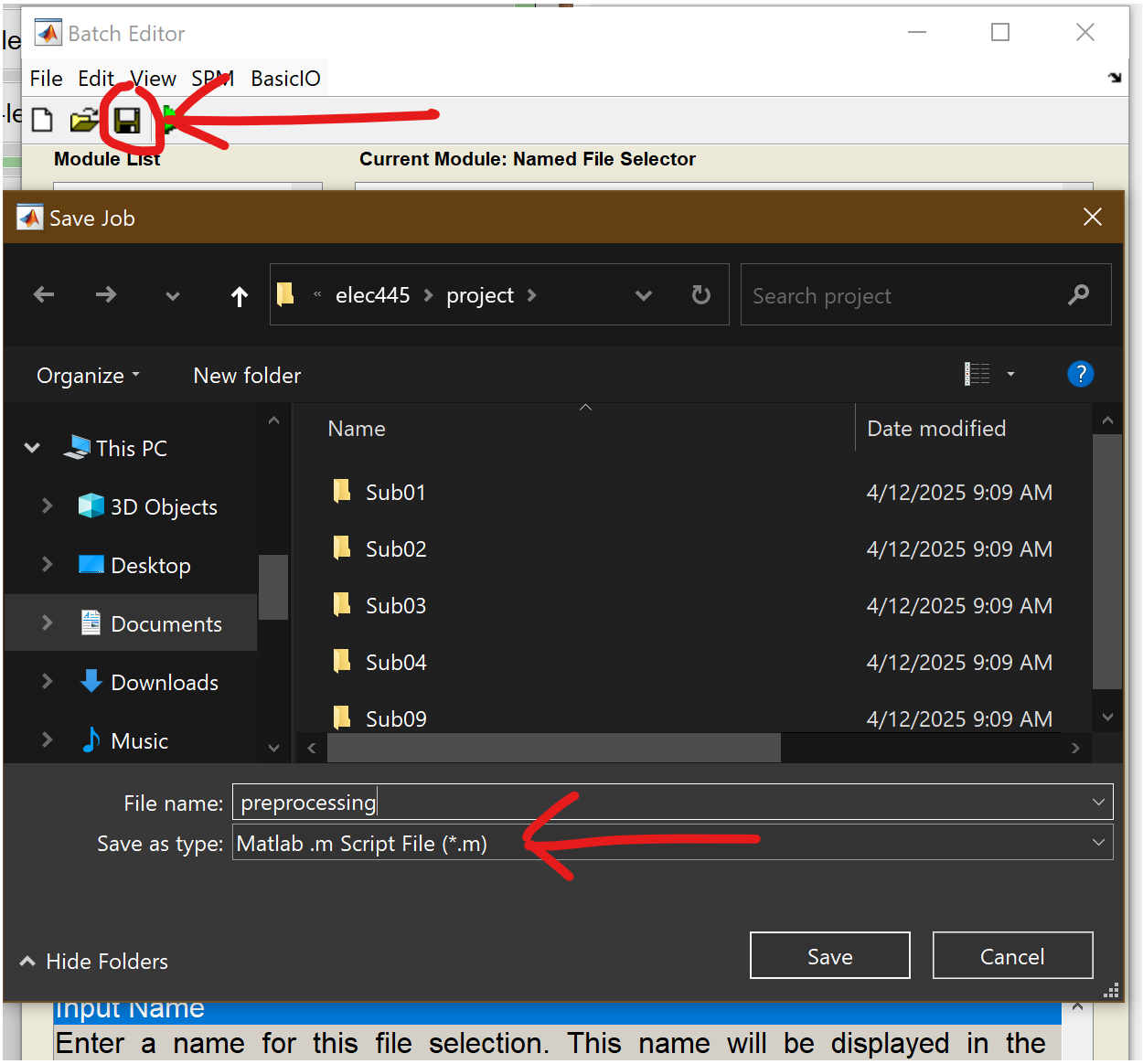


3.0 Running Script

You can run from the Play button for 1 Subject 1 run, but you have to change BOLD named file selector for every Run… and then ANAT and BOLD for every Subject….



OR save the script as Matlab script and make some edits:



Edits to Script – **Add init section to start of Script**:

Yellow – Change for your subject/run

Orange – Sets up the ANAT file for the subject

Red – Sets up the BOLD files for subject/run

The **`if`** statement below BOLD files checks if more files than expected have been imported, and exits script if so. If you want to redo pre-processing, I recommend deleting the Run0# folder and re-copying it from the original data.

Editor - C:\Users\samso\Documents\MATLAB\elec445\project\preprocessing.m

preprocessing.m

```
%-----------------------------------------------------------------------
% Job saved on 12-Apr-2025 10:30:05 by cfg_util (rev $Rev: 7345 $)
% spm SPM - SPM12 (7771)
% cfg_basicio BasicIO - Unknown
%-----------------------------------------------------------------------

%% INIT
% spm('defaults', 'FMRI'); % uncomment if you want to launch script without opening SPM
spm_jobman('initcfg');
matlabbatch = {};

% modify your dataset folder here:
project_folder = 'C:\Users\samso\Documents\MATLAB\elec445\project\';
% modify your subject here:
subject = 'Sub09'; % 1 to 16, keep 0 padding for 1 digit subjects
% modify the run here:
run = 1; % 1 to 9

subject_folder = append(project_folder, subject);
run_number = append('Run_0', int2str(run));

ANAT_file = append(subject_folder, '\T1\mprage.nii');

BOLDS = dir(fullfile(subject_folder, 'BOLD', run_number, '*.nii'));
BOLD_files = cell(size(BOLDS, 1), 1);
for iFile = 1:size(BOLDS, 1)
    BOLD_files{iFile} = fullfile(BOLDS(iFile).folder, BOLDS(iFile).name);
end

% Check total amount of BOLDs is 208 images
if iFile ~= 208
    disp('There seems to be a problem with the number of BOLD files: ');
    disp(' - Expected BOLD files: 208');
    disp([' - Imported BOLD files: ', int2str(iFile)]);
    disp(['Maybe you already processed this run? ( ', subject, ' : ', run_number, ' )']);
    return;
end

disp(['>> Pre-Processing: ', subject, ' - ', run_number, '...']);

%% SETUP FILES
matlabbatch{1}.cfg_basicio.file_dir.file_ops.cfg_named_file.name = 'ANAT';
matlabbatch{1}.cfg_basicio.file_dir.file_ops.cfg_named_file.files = {{ ANAT_file }};
matlabbatch{2}.cfg_basicio.file_dir.file_ops.cfg_named_file.name = 'BOLD';
matlabbatch{2}.cfg_basicio.file_dir.file_ops.cfg_named_file.files = { BOLD_files }';
```

Added call to spm_jobman at the end to run the job:

```
%% RUN PRE-PROCESSING
spm_jobman('serial', matlabbatch)
disp('>> Preprocessing Done!')
```

Final Pre-Processing Script (save as .m file in project folder alongside all Subjects):

```
%-----------------------------------------------------------------------
% Job saved on 12-Apr-2025 10:30:05 by cfg_util (rev $Rev: 7345 $)
% spm SPM - SPM12 (7771)
% cfg_basicio BasicIO - Unknown
%-----------------------------------------------------------------------

%% INIT
% spm_jobman('serial', matlabbatch) % uncomment if you want to launch script
without opening SPM
spm_jobman('initcfg');
matlabbatch = {};

% modify your dataset folder here:
project_folder = 'C:\Users\samso\Documents\MATLAB\elec445\project\';
% modify your subject here:
subject = 'Sub09'; % 1 to 16, keep 0 padding for 1 digit subjects
% modify the run here:
run = 1; % 1 to 9

subject_folder = append(project_folder, subject);
run_number = append('Run_0', int2str(run));

ANAT_file = append(subject_folder, '\T1\mprage.nii');

BOLDS = dir(fullfile(subject_folder, 'BOLD', run_number, '*.nii'));
BOLD_files = cell(size(BOLDS, 1), 1);
for iFile = 1:size(BOLDS, 1)
    BOLD_files{iFile} = fullfile(BOLDS(iFile).folder, BOLDS(iFile).name);
end

if iFile ~= 208
    disp('There seems to be a problem with the number of BOLD files: ');
    disp(' - Expected BOLD files: 208');
    disp([' - Imported BOLD files: ', int2str(iFile)]);
    disp(['Maybe you already processed this run? ( ', subject, ' : ', run_number, '
)']);
    return;
end

disp(['>> Pre-Processing: ', subject, ' - ', run_number, '...']);

%% SETUP FILES
matlabbatch{1}.cfg_basicio.file_dir.file_ops.cfg_named_file.name = 'ANAT';
matlabbatch{1}.cfg_basicio.file_dir.file_ops.cfg_named_file.files = {{ ANAT_file
}};
matlabbatch{2}.cfg_basicio.file_dir.file_ops.cfg_named_file.name = 'BOLD';
matlabbatch{2}.cfg_basicio.file_dir.file_ops.cfg_named_file.files = { BOLD_files
}';

%% SLICE TIMING
matlabbatch{3}.spm.temporal.st.scans{1}(1) = cfg_dep('Named File Selector: BOLD(1)
- Files', substruct('.','val', '{}',{2}, '.','val', '{}',{1}, '.','val', '{}',{1},
'.','val', '{}',{1}), substruct('.','files', '{}',{1}));
```

```
matlabbatch{3}.spm.temporal.st.nslices = 33;
matlabbatch{3}.spm.temporal.st.tr = 2;
matlabbatch{3}.spm.temporal.st.ta = 1.93939393939394;
matlabbatch{3}.spm.temporal.st.so = [1 3 5 7 9 11 13 15 17 19 21 23 25 27 29 31 33
2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32];
matlabbatch{3}.spm.temporal.st.refslice = 16;
matlabbatch{3}.spm.temporal.st.prefix = 'a';

%% REALIGN
matlabbatch{4}.spm.spatial.realign.estwrite.data{1}(1) = cfg_dep('Slice Timing:
Slice Timing Corr. Images (Sess 1)', substruct('.','val', '{}',{3}, '.','val',
'{}',{1}, '.','val', '{}',{1}), substruct('()',{1}, '.','files'));
matlabbatch{4}.spm.spatial.realign.estwrite.eoptions.quality = 0.9;
matlabbatch{4}.spm.spatial.realign.estwrite.eoptions.sep = 4;
matlabbatch{4}.spm.spatial.realign.estwrite.eoptions.fwhm = 5;
matlabbatch{4}.spm.spatial.realign.estwrite.eoptions.rtm = 1;
matlabbatch{4}.spm.spatial.realign.estwrite.eoptions.interp = 2;
matlabbatch{4}.spm.spatial.realign.estwrite.eoptions.wrap = [0 0 0];
matlabbatch{4}.spm.spatial.realign.estwrite.eoptions.weight = '';
matlabbatch{4}.spm.spatial.realign.estwrite.roptions.which = [2 1];
matlabbatch{4}.spm.spatial.realign.estwrite.roptions.interp = 4;
matlabbatch{4}.spm.spatial.realign.estwrite.roptions.wrap = [0 0 0];
matlabbatch{4}.spm.spatial.realign.estwrite.roptions.mask = 1;
matlabbatch{4}.spm.spatial.realign.estwrite.roptions.prefix = 'r';

%% COREGISTER
matlabbatch{5}.spm.spatial.coreg.estwrite.ref(1) = cfg_dep('Named File Selector:
ANAT(1) - Files', substruct('.','val', '{}',{1}, '.','val', '{}',{1}, '.','val',
'{}',{1}, '.','val', '{}',{1}), substruct('.','files', '{}',{1}));
matlabbatch{5}.spm.spatial.coreg.estwrite.source(1) = cfg_dep('Realign: Estimate &
Reslice: Mean Image', substruct('.','val', '{}',{4}, '.','val', '{}',{1},
'.','val', '{}',{1}, '.','val', '{}',{1}), substruct('.','rmean'));
matlabbatch{5}.spm.spatial.coreg.estwrite.other(1) = cfg_dep('Realign: Estimate &
Reslice: Resliced Images (Sess 1)', substruct('.','val', '{}',{4}, '.','val',
'{}',{1}, '.','val', '{}',{1}, '.','val', '{}',{1}), substruct('.','sess',
'()',{1}, '.','rfiles'));
matlabbatch{5}.spm.spatial.coreg.estwrite.eoptions.cost_fun = 'nmi';
matlabbatch{5}.spm.spatial.coreg.estwrite.eoptions.sep = [4 2];
matlabbatch{5}.spm.spatial.coreg.estwrite.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{5}.spm.spatial.coreg.estwrite.eoptions.fwhm = [7 7];
matlabbatch{5}.spm.spatial.coreg.estwrite.roptions.interp = 4;
matlabbatch{5}.spm.spatial.coreg.estwrite.roptions.wrap = [0 0 0];
matlabbatch{5}.spm.spatial.coreg.estwrite.roptions.mask = 0;
matlabbatch{5}.spm.spatial.coreg.estwrite.roptions.prefix = 'r';

%% NORMALISE
matlabbatch{6}.spm.spatial.normalise.estwrite.subj.vol(1) = cfg_dep('Named File
Selector: ANAT(1) - Files', substruct('.','val', '{}',{1}, '.','val', '{}',{1},
'.','val', '{}',{1}, '.','val', '{}',{1}), substruct('.','files', '{}',{1}));
matlabbatch{6}.spm.spatial.normalise.estwrite.subj.resample(1) =
cfg_dep('Coregister: Estimate & Reslice: Resliced Images', substruct('.','val',
'{}',{5}, '.','val', '{}',{1}, '.','val', '{}',{1}, '.','val', '{}',{1}),
substruct('.','rfiles'));
matlabbatch{6}.spm.spatial.normalise.estwrite.eoptions.biasreg = 0.0001;
```

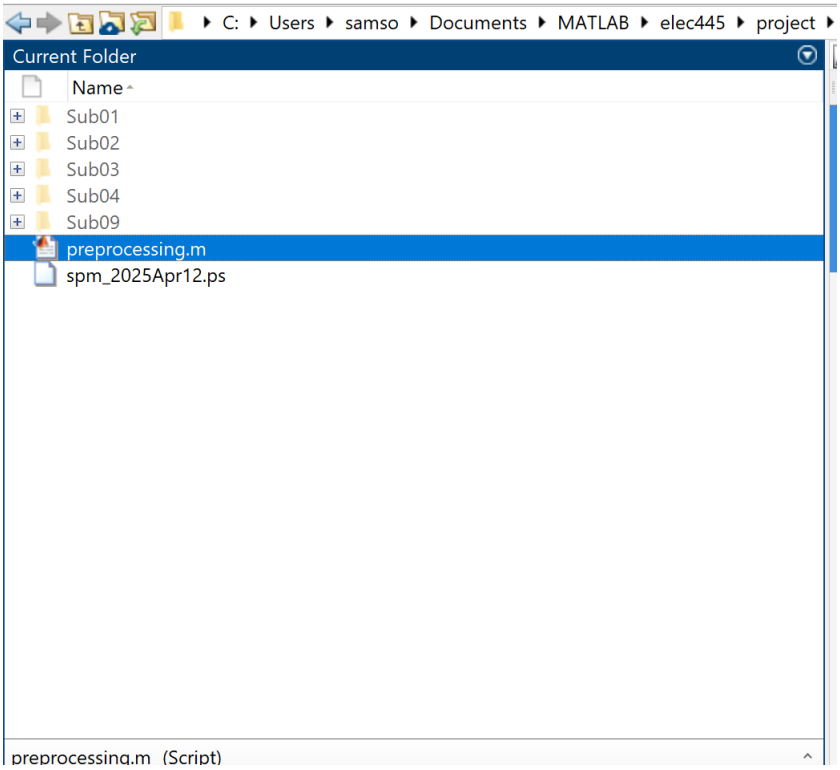
```
matlabbatch{6}.spm.spatial.normalise.estwrite.eoptions.biasfwhm = 60;
matlabbatch{6}.spm.spatial.normalise.estwrite.eoptions.tpm =
{'C:\Users\samso\Documents\MATLAB\spm12\tpm\TPM.nii'};
matlabbatch{6}.spm.spatial.normalise.estwrite.eoptions.affreg = 'mni';
matlabbatch{6}.spm.spatial.normalise.estwrite.eoptions.reg = [0 0.001 0.5 0.05
0.2];
matlabbatch{6}.spm.spatial.normalise.estwrite.eoptions.fwhm = 0;
matlabbatch{6}.spm.spatial.normalise.estwrite.eoptions.samp = 3;
matlabbatch{6}.spm.spatial.normalise.estwrite.woptions.bb = [-78 -112 -70
                                                            78 76 85];
matlabbatch{6}.spm.spatial.normalise.estwrite.woptions.vox = [2 2 2];
matlabbatch{6}.spm.spatial.normalise.estwrite.woptions.interp = 4;
matlabbatch{6}.spm.spatial.normalise.estwrite.woptions.prefix = 'w';

%% SMOOTHING
matlabbatch{7}.spm.spatial.smooth.data(1) = cfg_dep('Normalise: Estimate & Write:
Normalised Images (Subj 1)', substruct('.','val', '{}',{6}, '.','val', '{}',{1},
'.','val', '{}',{1}, '.','val', '{}',{1}), substruct('()',{1}, '.','files'));
matlabbatch{7}.spm.spatial.smooth.fwhm = [8 8 8];
matlabbatch{7}.spm.spatial.smooth.dtype = 0;
matlabbatch{7}.spm.spatial.smooth.im = 0;
matlabbatch{7}.spm.spatial.smooth.prefix = 's';

%% RUN PRE-PROCESSING
spm_jobman('serial', matlabbatch)
disp('>> Preprocessing Done!')
```

Ok, so it takes around ~15 minutes for my CPU to do the pre-processing for 1 Run for a subject.

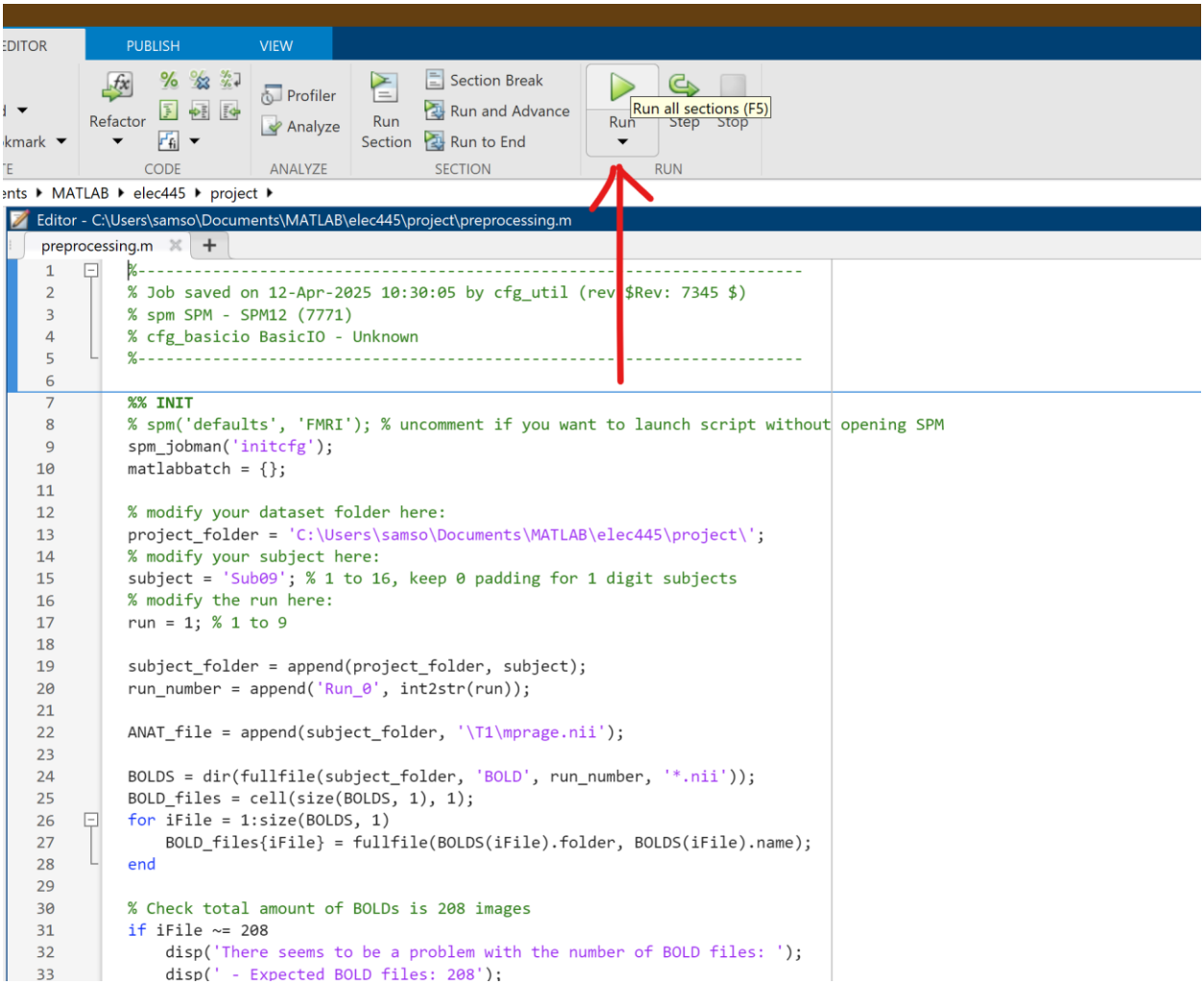
Make sure the above script is saved in project folder beside Sub folders:



Edit these in script for your Subject/Run:

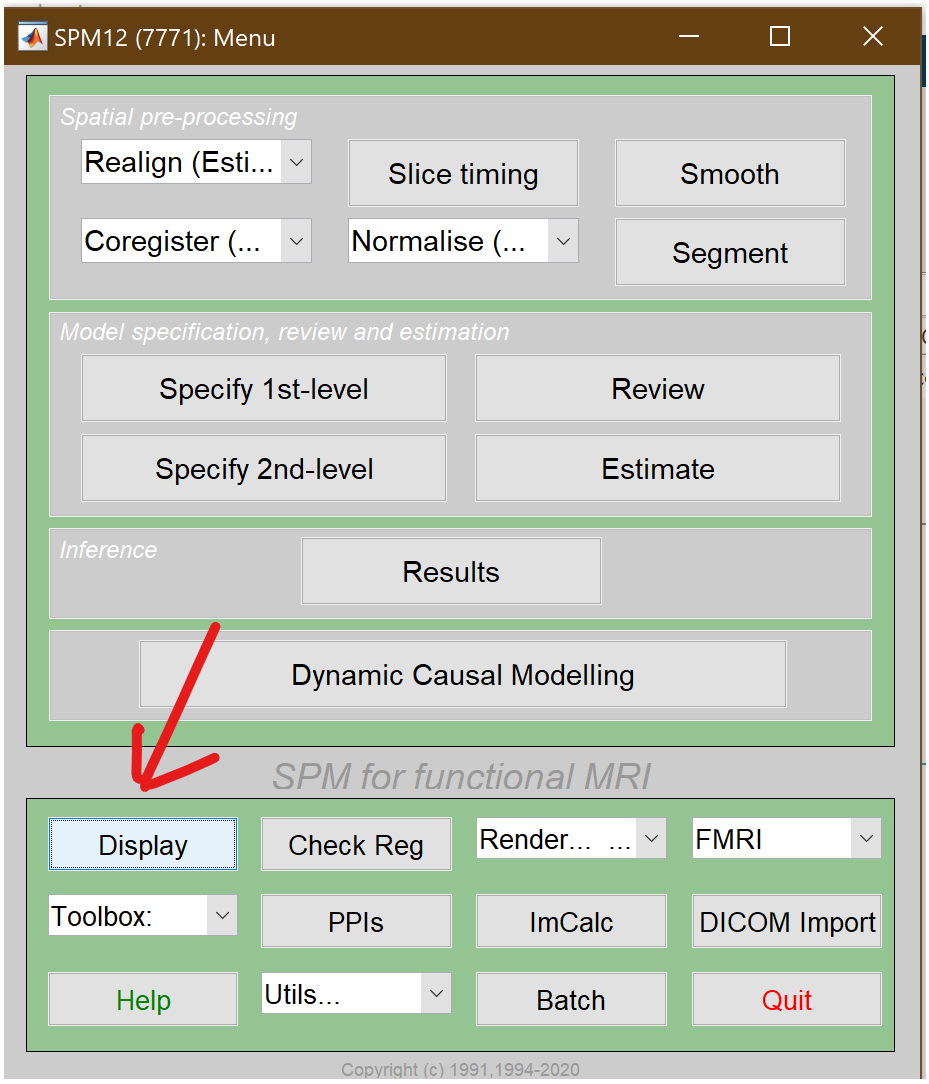
```
11
12  % modify your dataset folder here:
13  project_folder = 'C:\Users\samso\Documents\MATLAB\elec445\project\';
14  % modify your subject here:
15  subject = 'Sub09'; % 1 to 16, keep 0 padding for 1 digit subjects
16  % modify the run here:
17  run = 1; % 1 to 9
18
```

Now run using Play button (or type script name in command window):

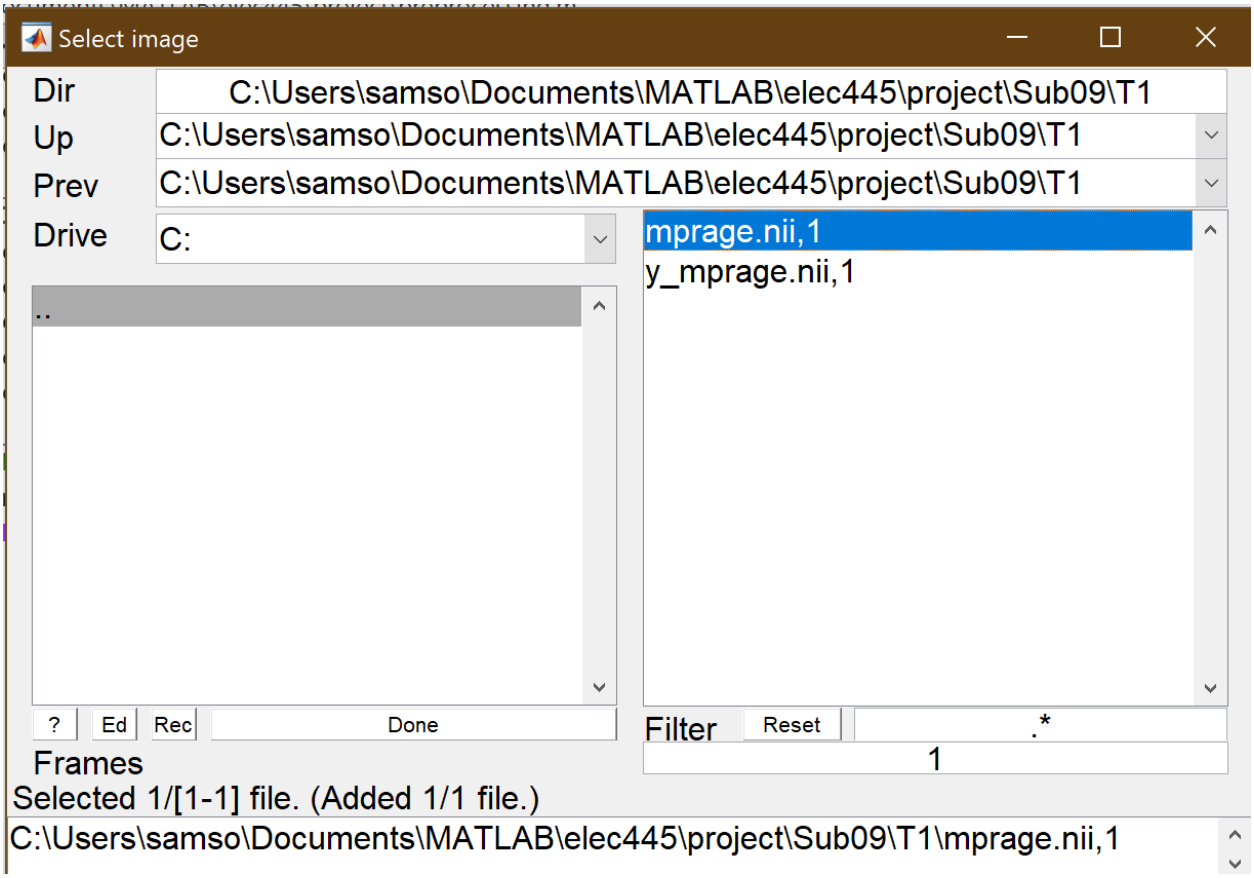


4.0 Visualizing the Pre-Processing Results

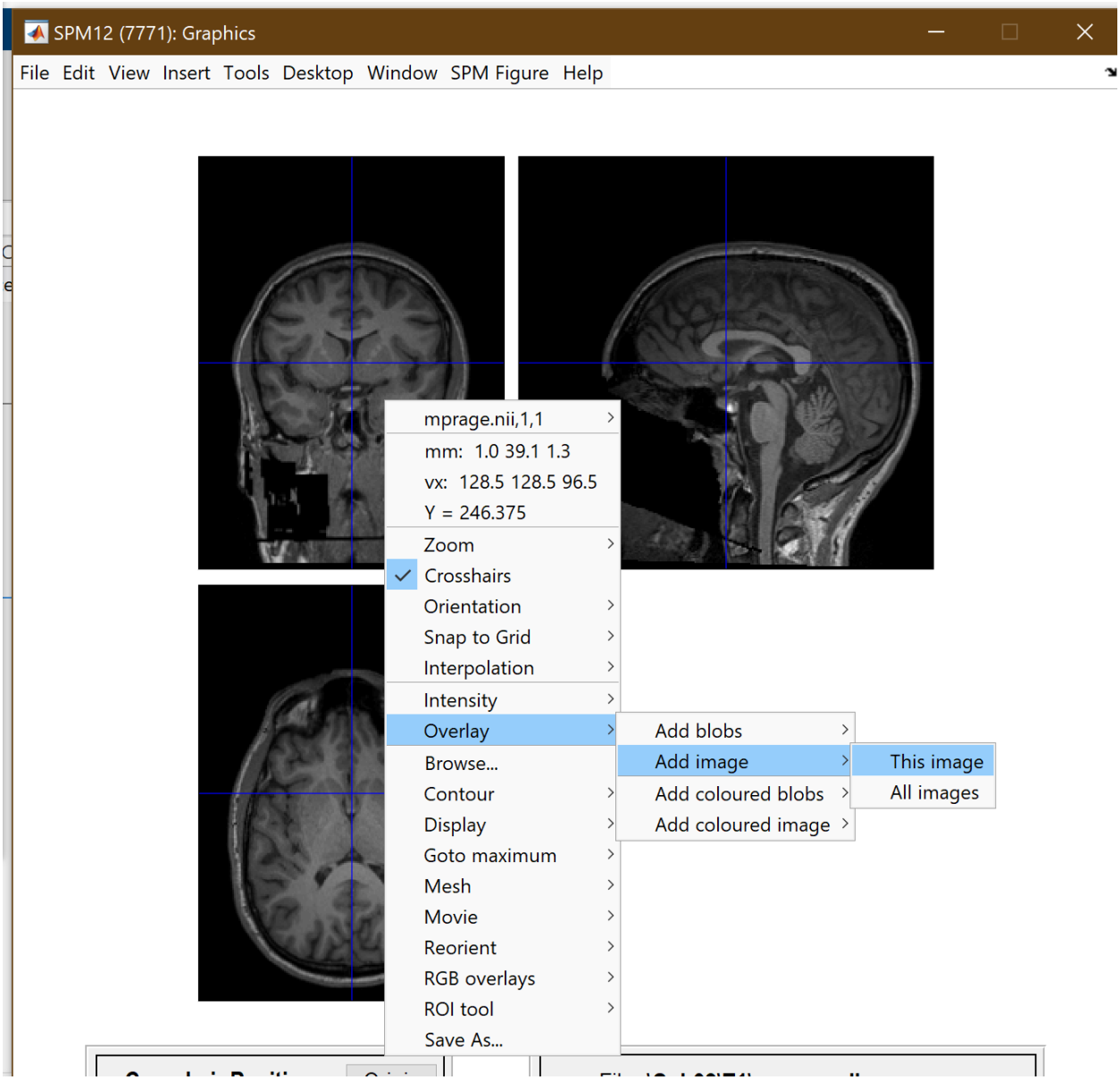
Use the display button to check Slice Timing/Realign/Coregister with T1:



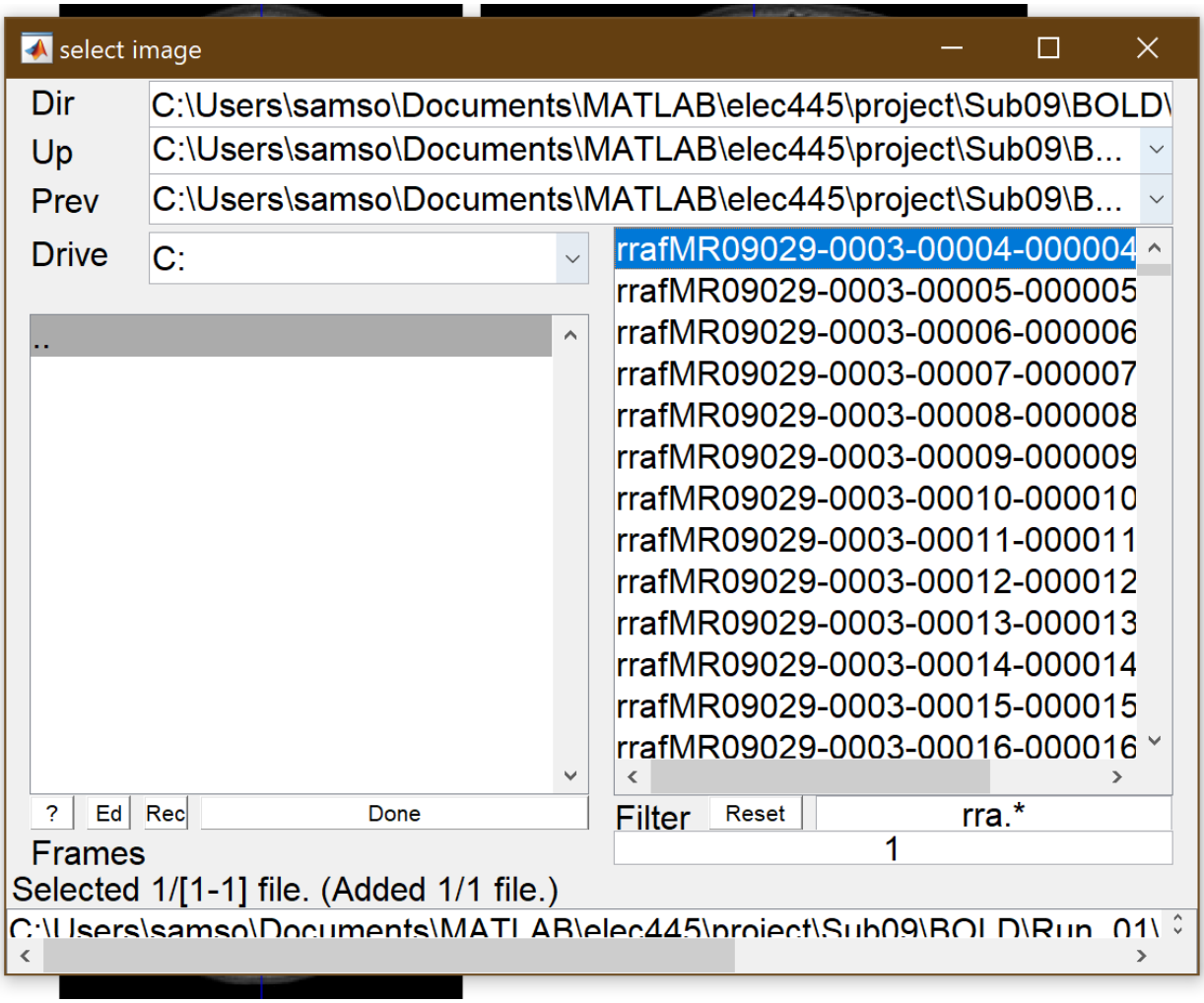
Select the T1 anat as image:



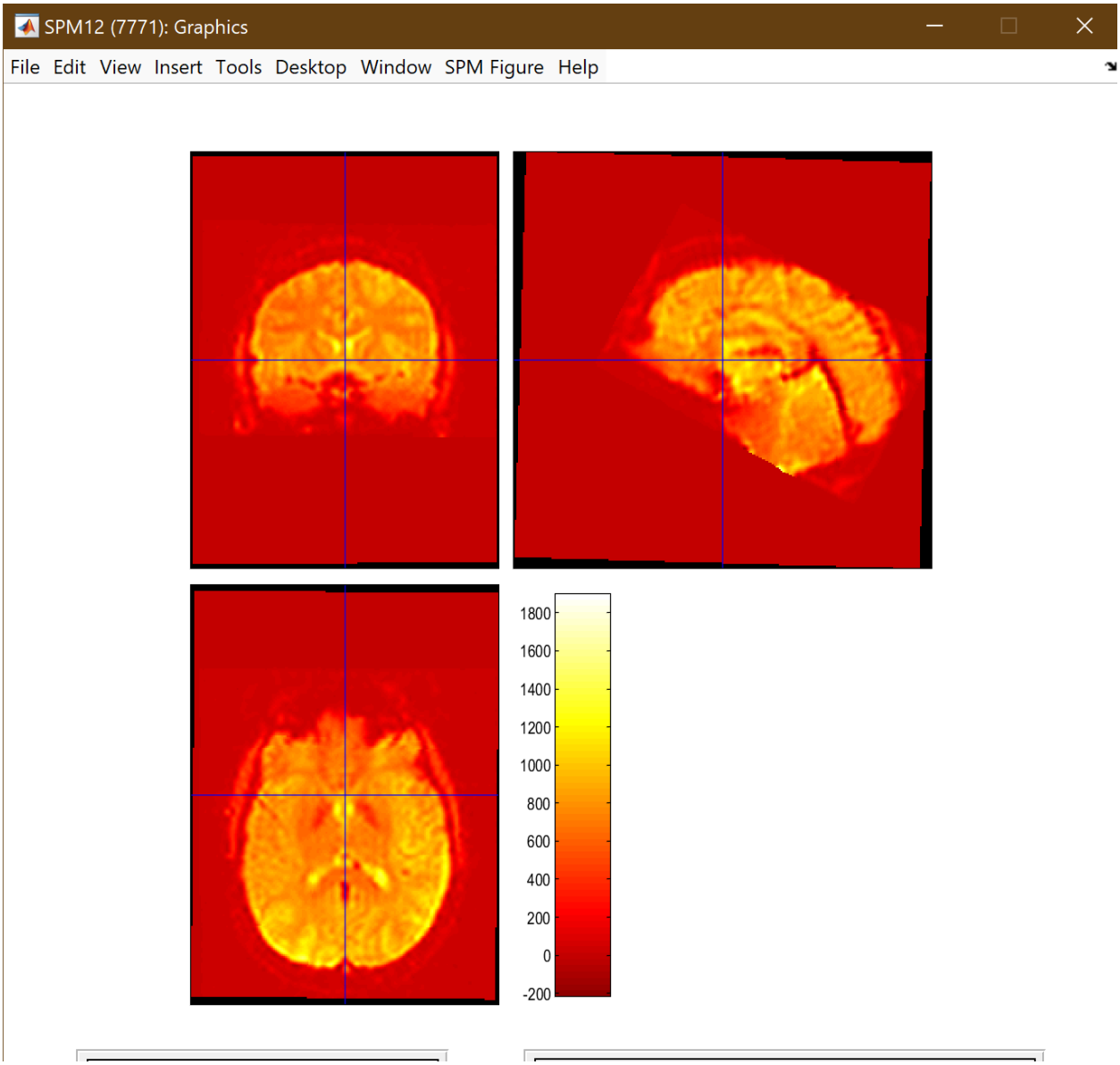
Add an overlay to the T1:



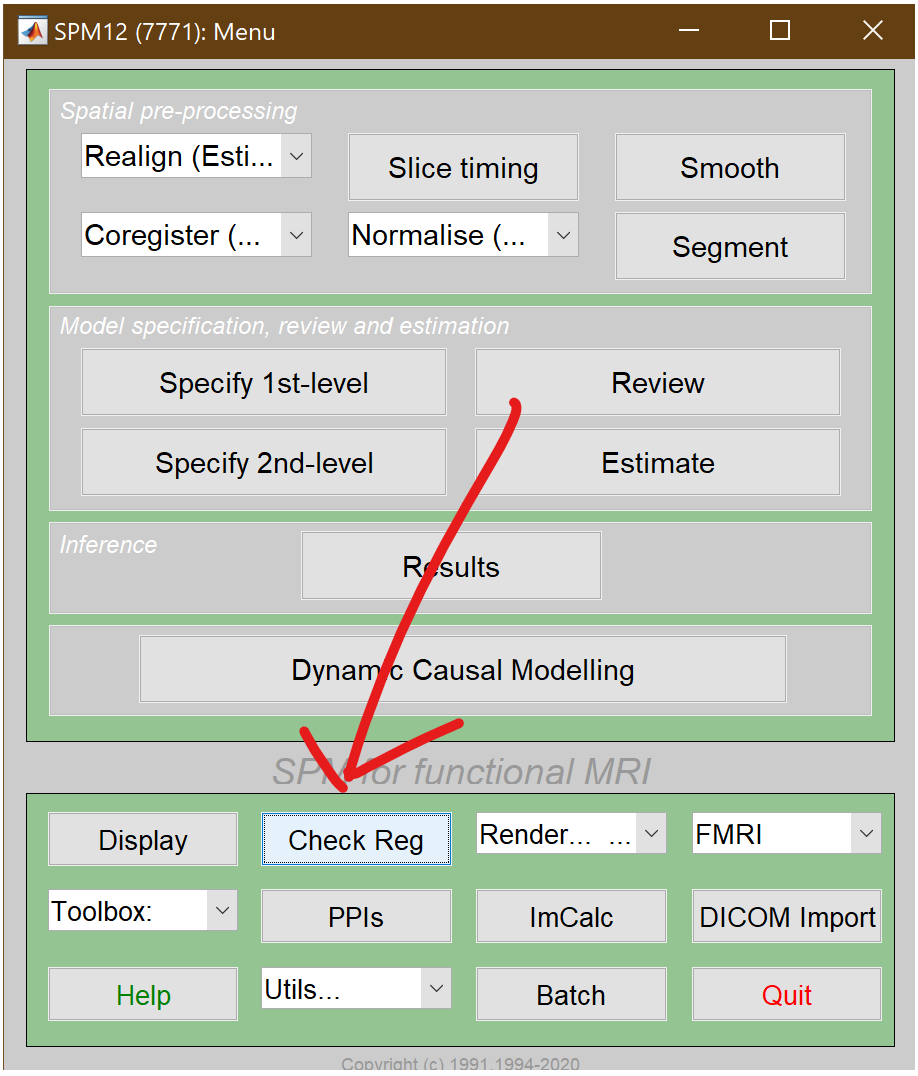
Type ‘rra’ in filter and select first Coregistered image:



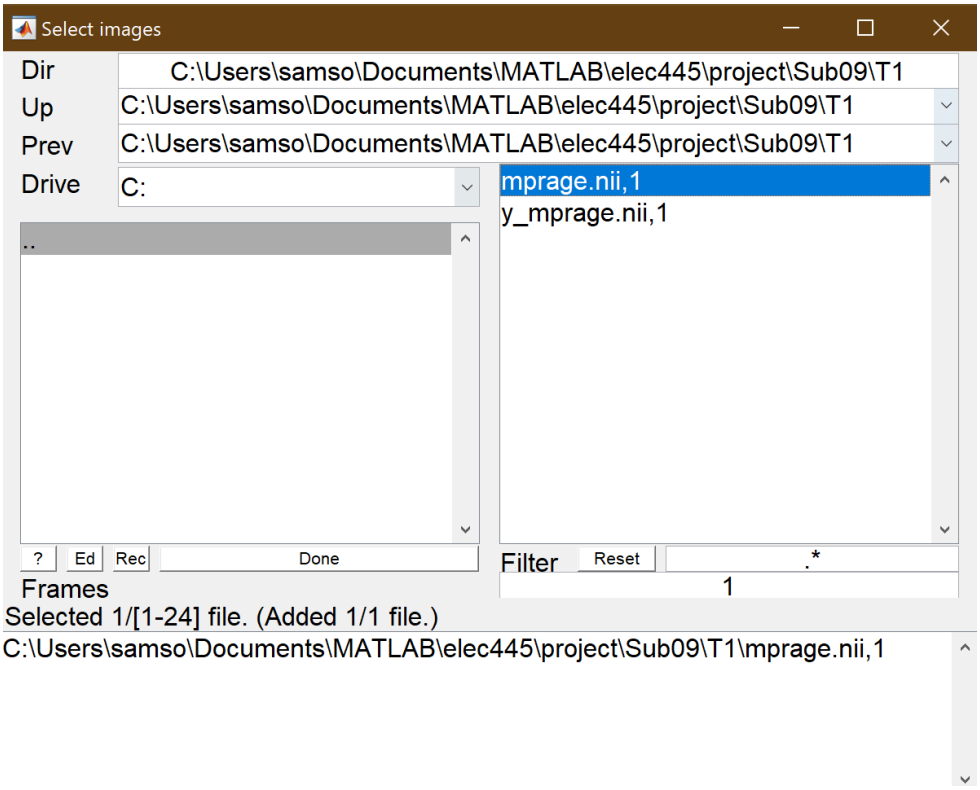
Now make sure it ‘overlaps’ well:



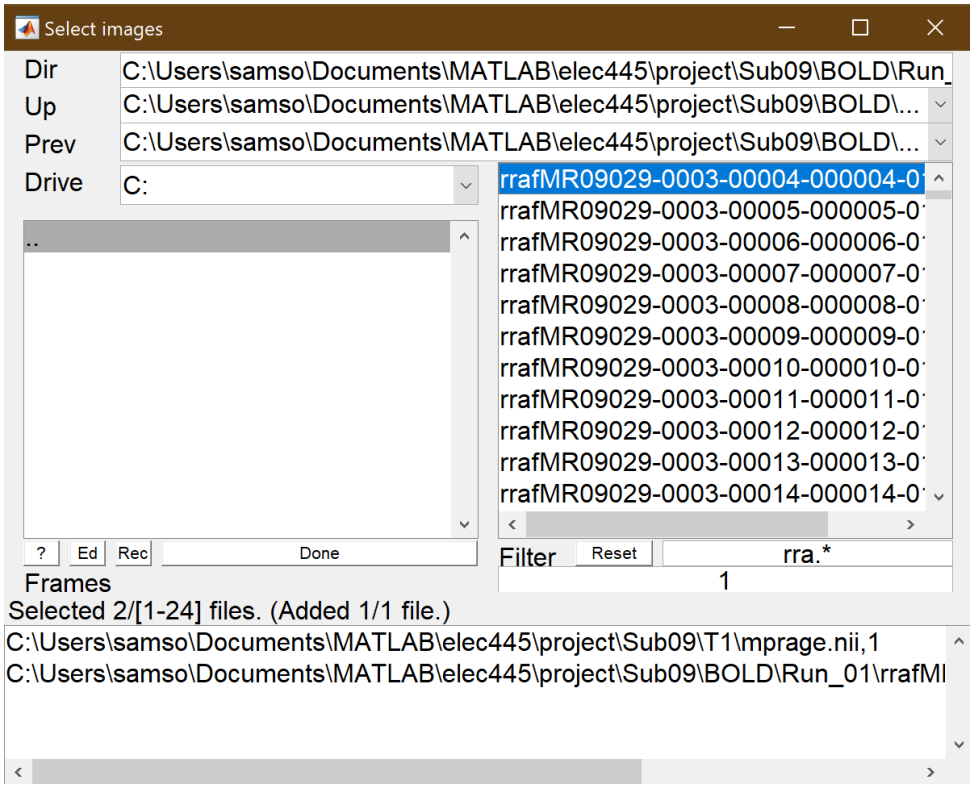
You can also use the “Check Reg” button (maybe is clearer):



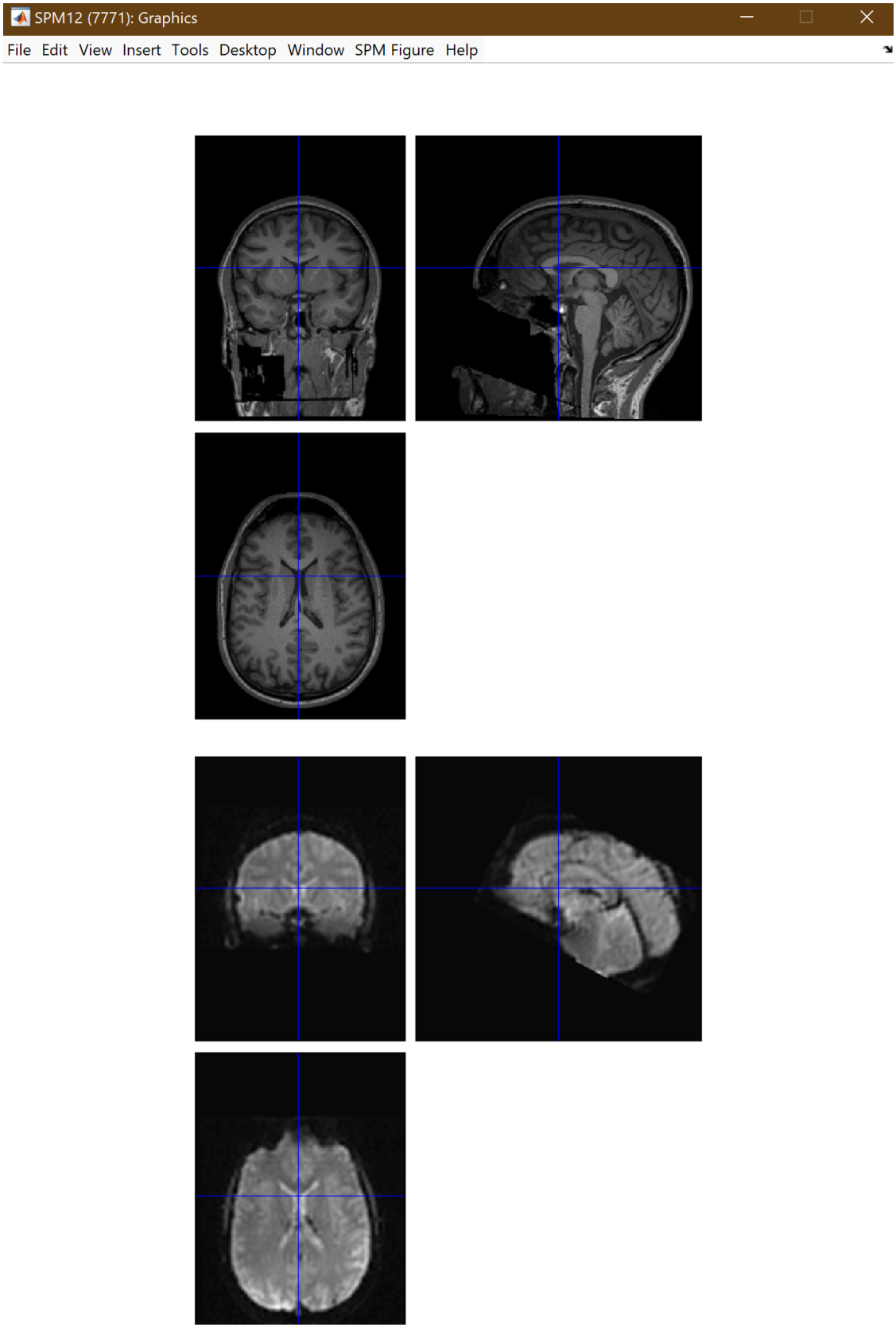
First select the ANAT (**BUT DON'T CLICK DONE YET**):



Now select a file to compare (like first Coregisterer image with 'rra' filter):

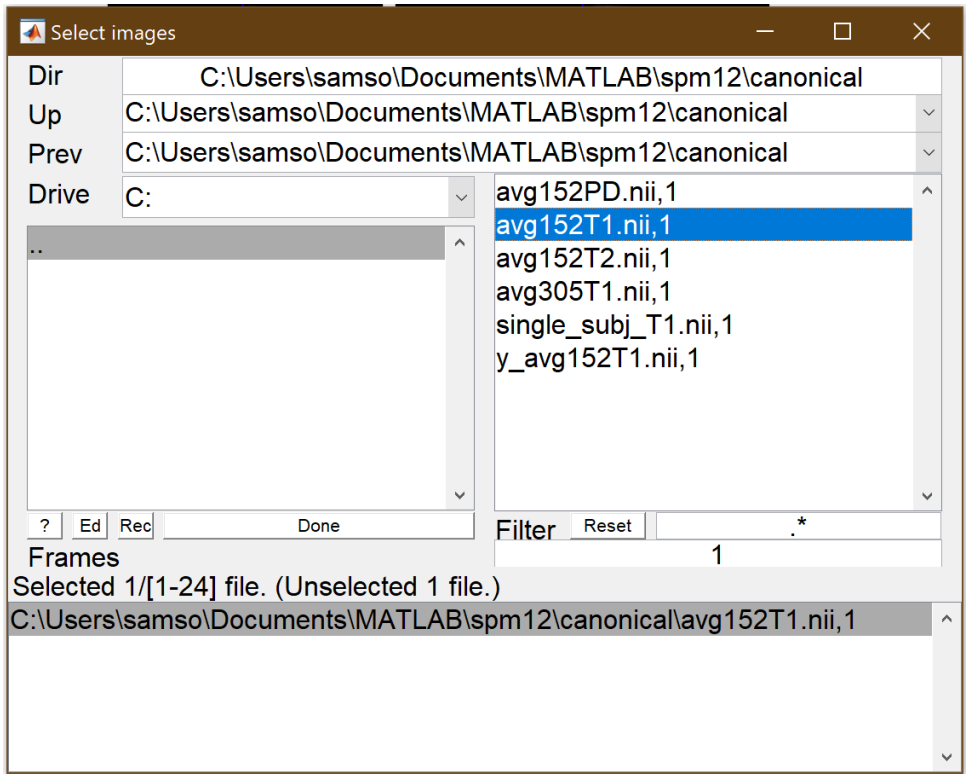


Click Done and make sure they match (cursor position on both images):

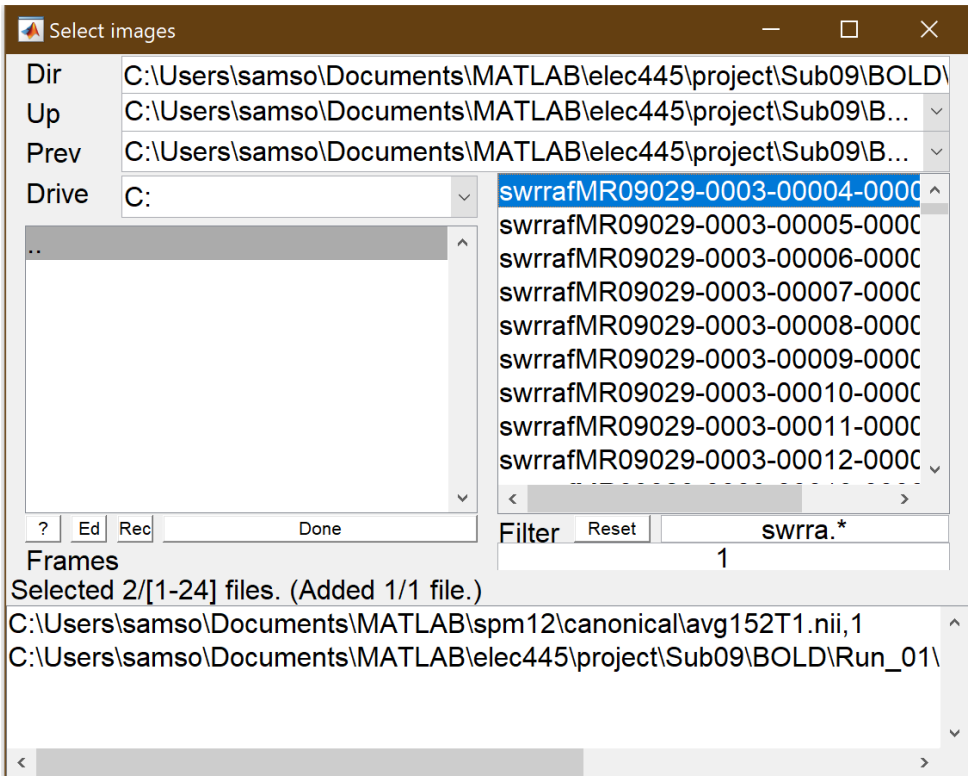


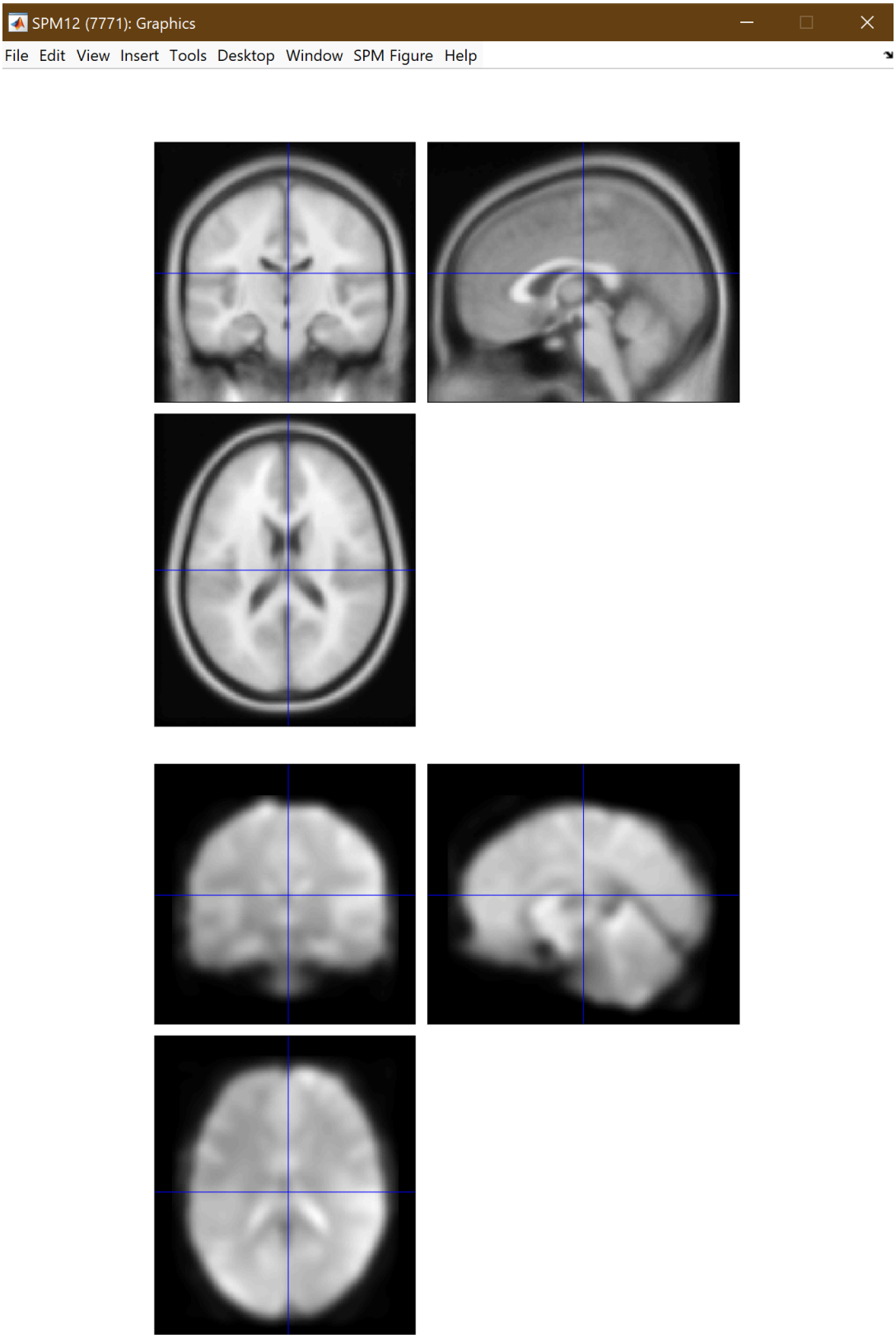
ALSO MAKE SURE TO CHECK NORMALIZE/SMOOTHED IMAGES

Find Template T1 in your SPM installation folders:



Select a Normalize/Smoothed image (filter 'swrra' in BOLD run for Smoothed):





Use Check Reg or Display, whatever you prefer.