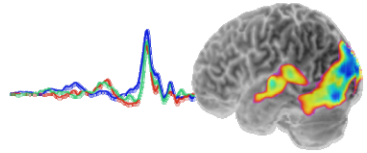
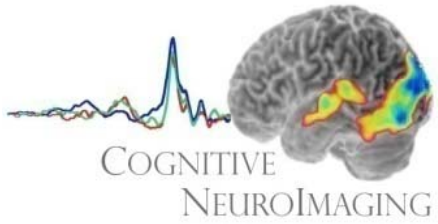


SPM 8

Hwee Ling Lee

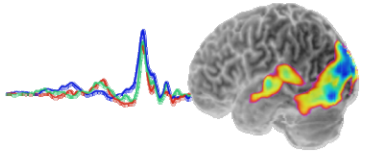
Cognitive Neuroimaging Group,
Max Planck Institute for Biological Cybernetics, Tuebingen, Germany

MAX-PLANCK-GESELLSCHAFT



MPI FOR BIOLOGICAL CYBERNETICS

Data transformations

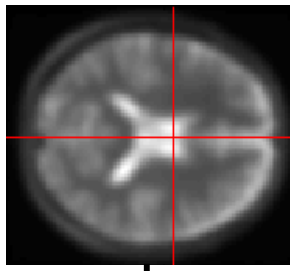


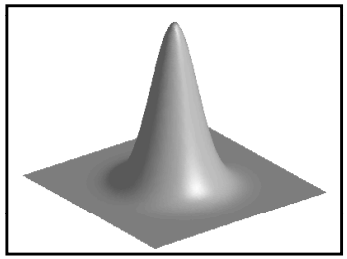
Statistical parametric map (SPM)

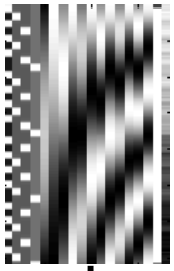
Image time-series

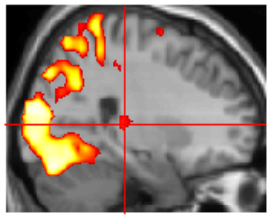
Kernel

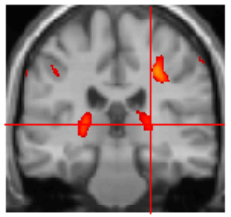
Design matrix

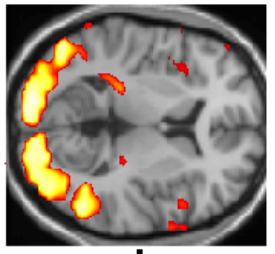












Realignment

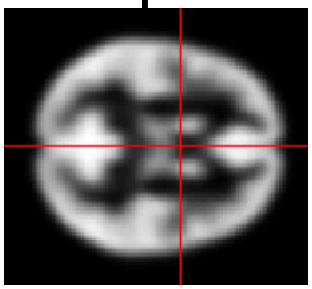
Smoothing

General linear model

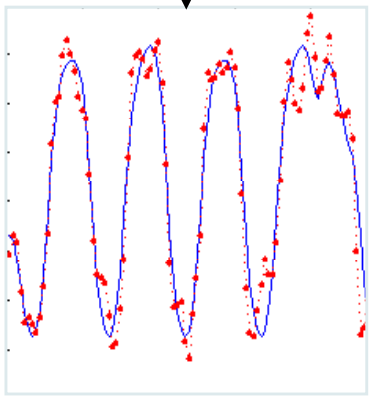
Normalisation

Statistical inference

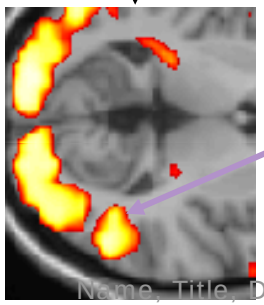
Gaussian field theory



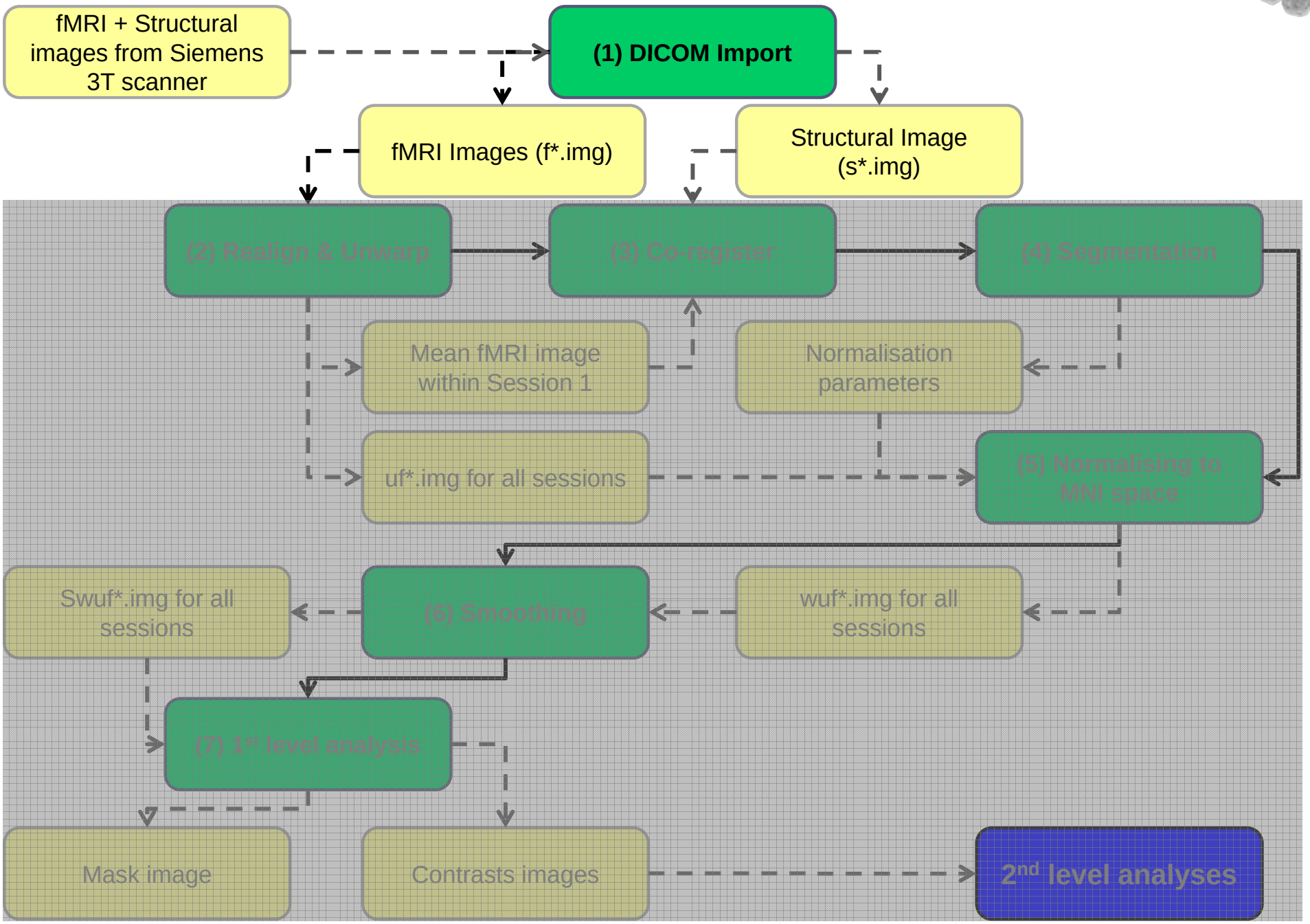
Template



Parameter estimates



p <0.05


fMRI + Structural images from Siemens 3T scanner
(1) DICOM Import
fMRI Images (f*.img)
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(2) Realign & Unwarp
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Mean fMRI image within Session 1
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Mask image
Contrasts images
2nd level analyses

Importing images from scanner to SPM

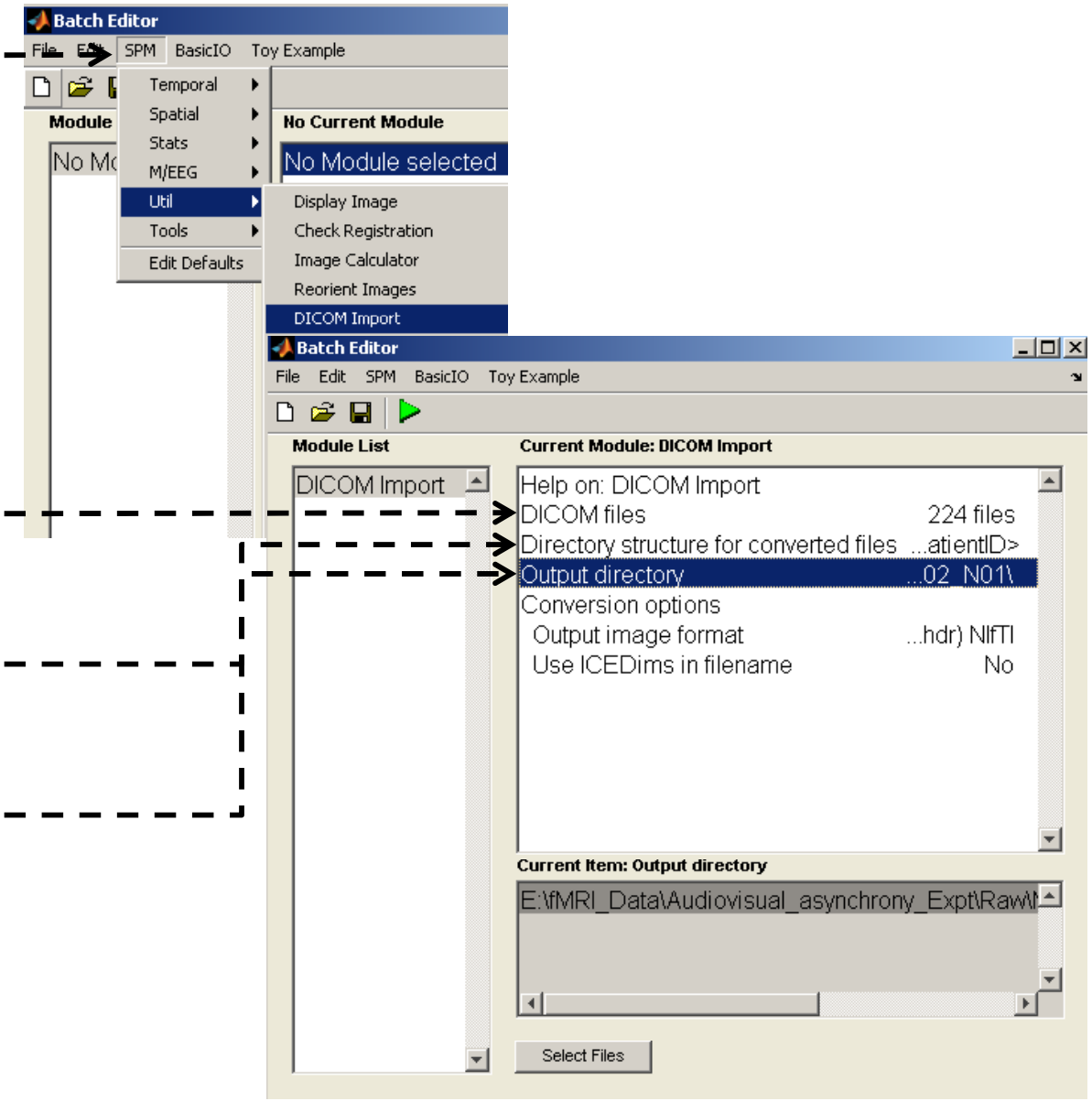
1. Select SPM -> Util -> DICOM Import

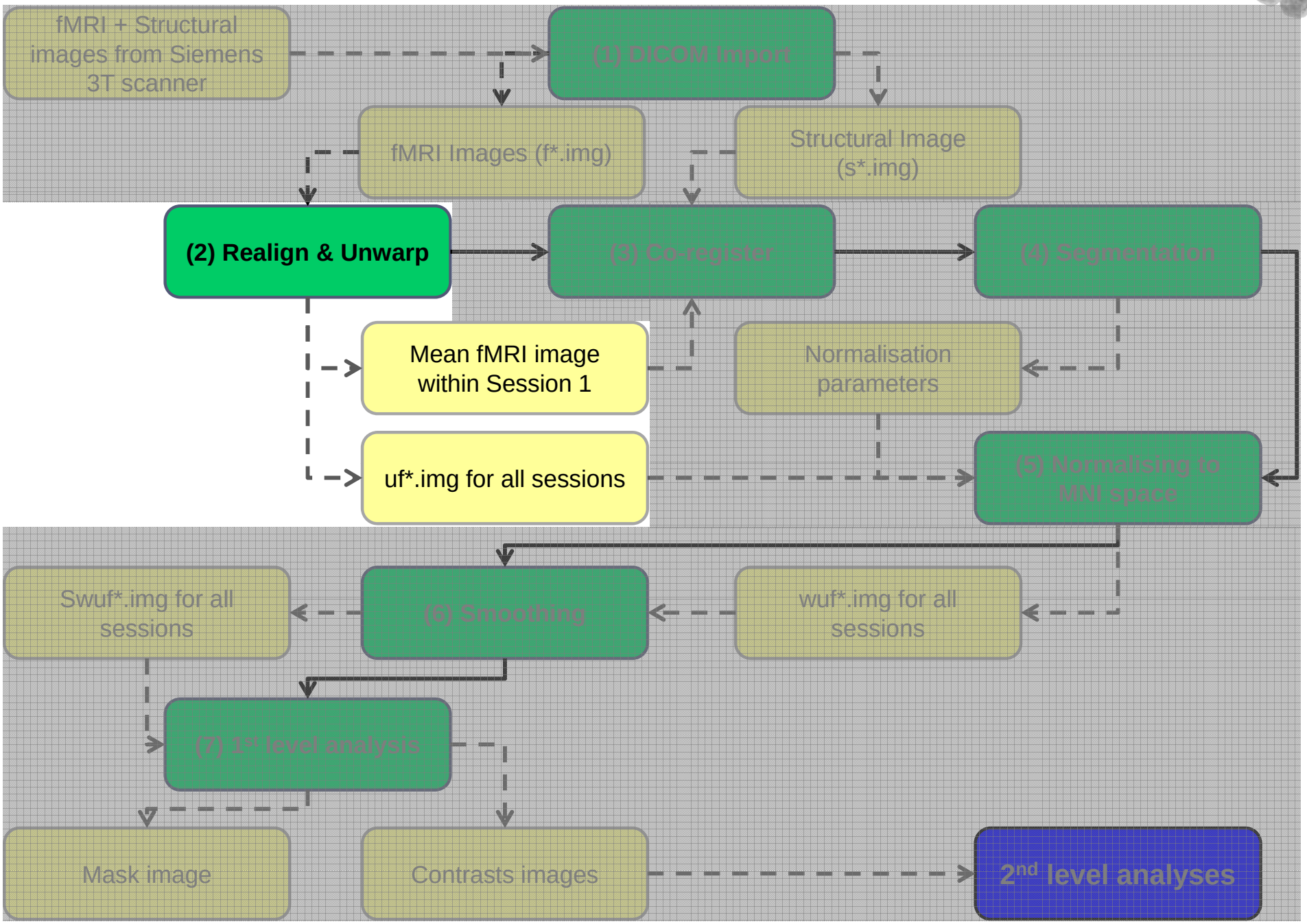
2. Select images from scanner; files usually in DICOM (*.ima) format

3. Select directory structure for converted files to Output directory: /<PatientID>

4. Select output directory. Suggestion: one should create a folder for each subject to store these images.

Output: Typically this will result in two types of images: one type for functional (f*.img) and one type for structural (s*.img)

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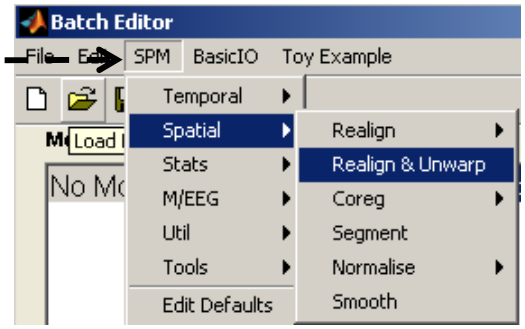
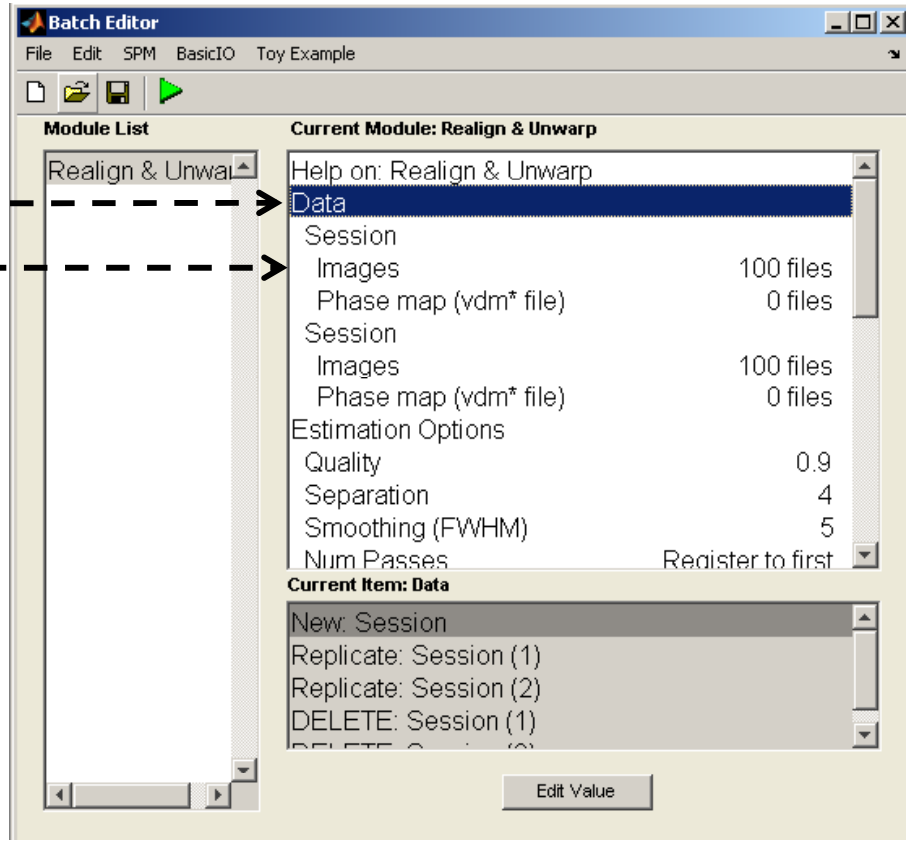
Functional images: Realign & Unwarp

1. Select SPM -> Spatial -> Realign & Unwarp

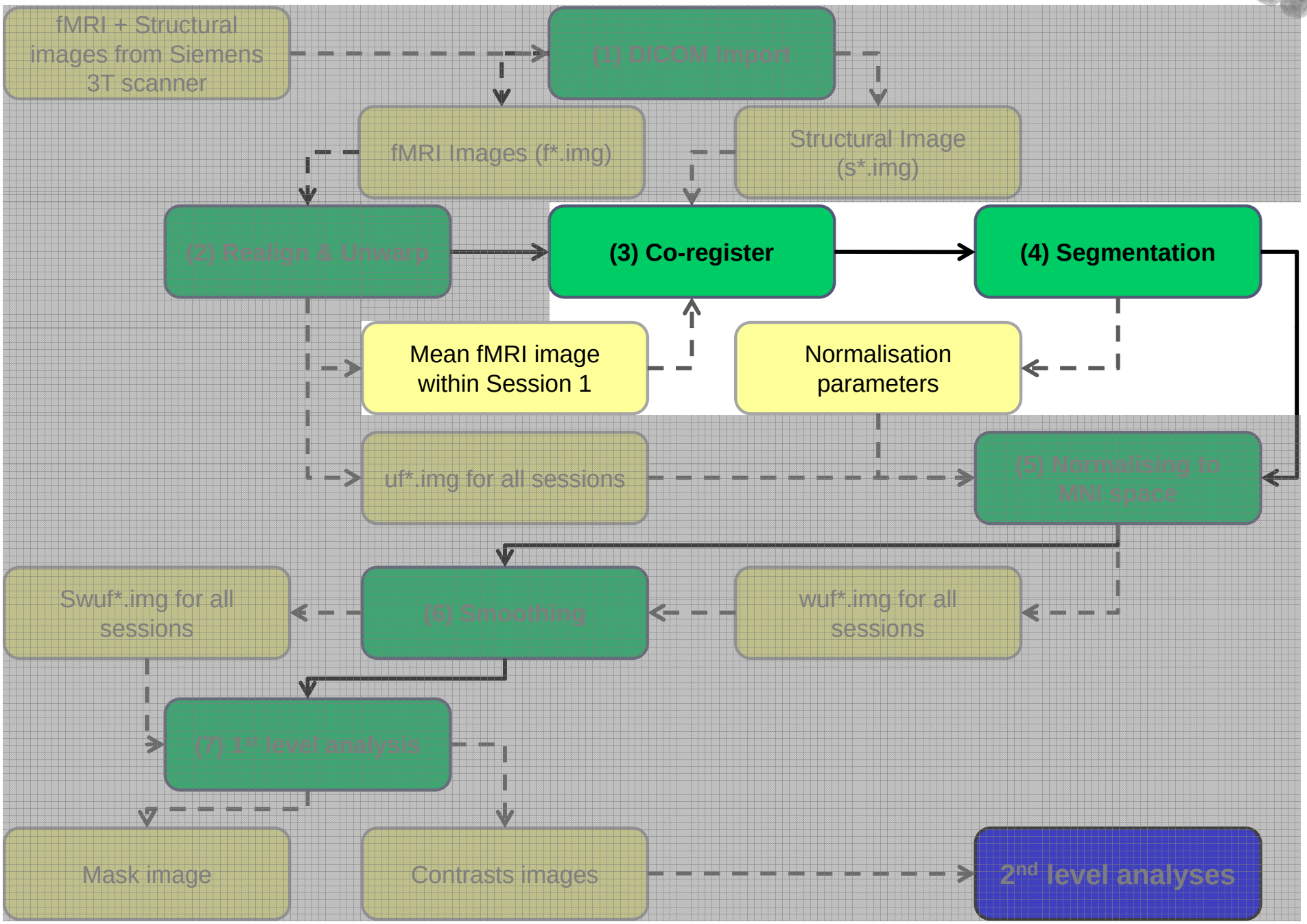


2. Select New: Session.
E.g. In this study, we have two sessions (100 images in each session).

3. For each session, select the f*.img files of each session (after discarding the first few volumes)



Output: uf*.img (for all sessions) + meanuf*.img (for session 1 only) + rp*.txt (for all sessions).
Note: the text files contains the movement parameters to be used at the 1st level analysis.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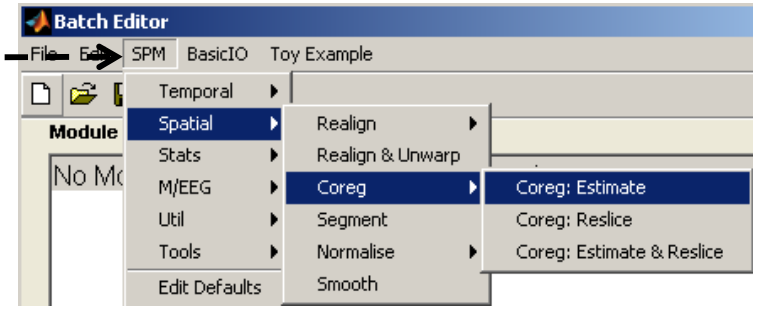
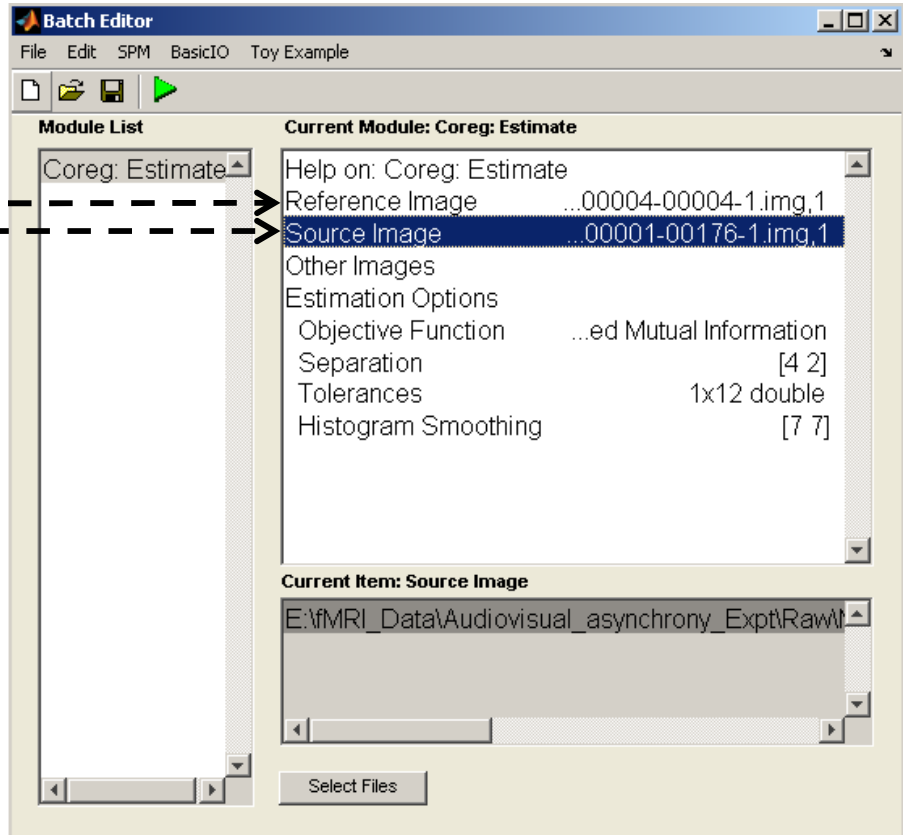
Preparing structural image for Segmentation

1. Select SPM -> Spatial -> Coreg -> Coreg: Estimate



2. Select reference image: meanuf*.img

3. Select source image: s*.img



Output: ***NONE***
When one displays the structural image using SPM, the image will appear to be in same orientation as meanuf*.img

Segmentation

1. Select SPM -> Spatial -> Segment

TIPS

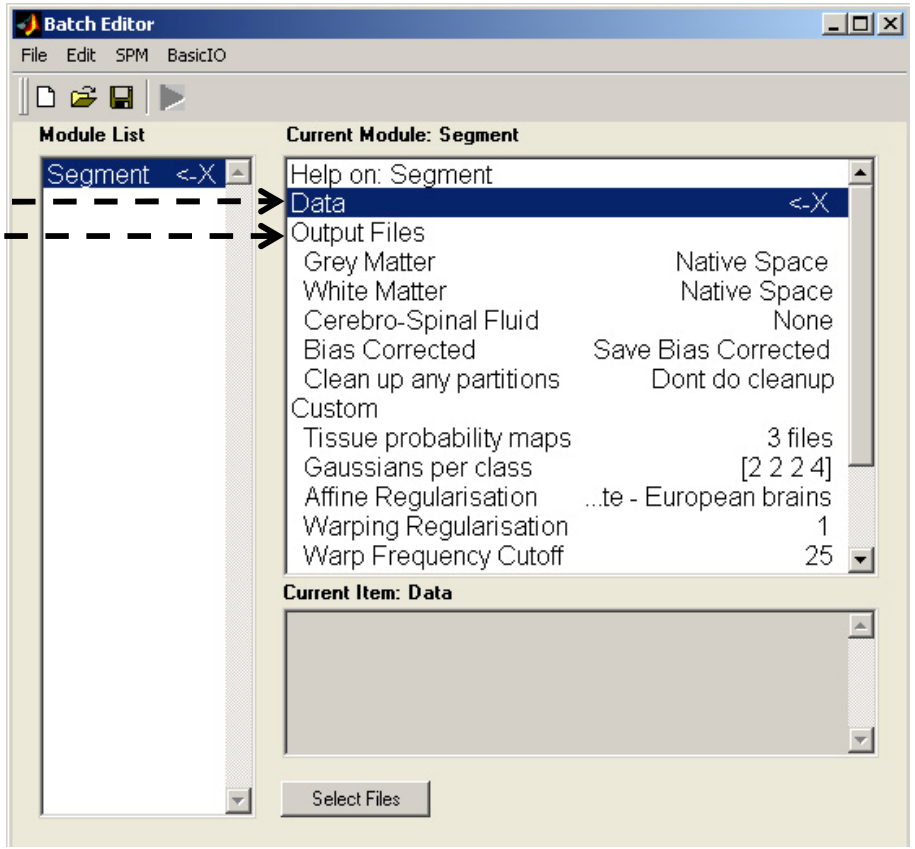
In case where segmentation is unsuccessful, one could try to first align the structural images close to MNI space before segmenting.

- Display button:
- AC coordinate is within about 3cm from center
- orientation within about 15 degrees of MNI space

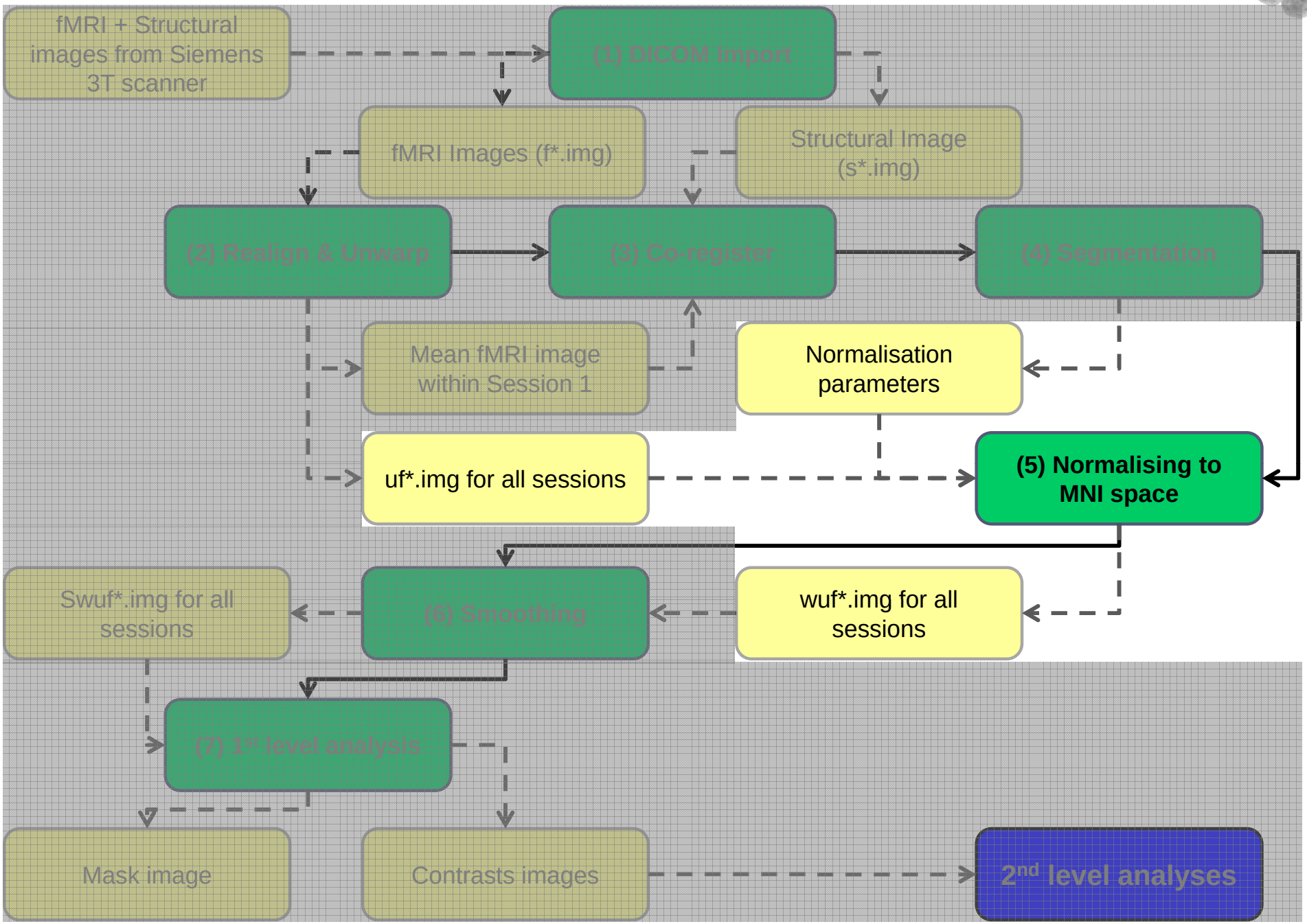
In addition, one could also try to first strip the brain skull before segmenting.

2. Select structural images: s*.img

3. Depending on preference, one could use to have grey/white matter in: *Native Space, Unmodulated Normalised, Modaulated Normalised, Native + Unmodulated Normalised, Native + Modulated Normalised, Native + Modulated + Unmodulated, Modulated + Unmodulated Normalised*



Output: Typically, this will result in two important segmentation parameter files: *_seg_sn.mat and *_seg_inv_sn.mat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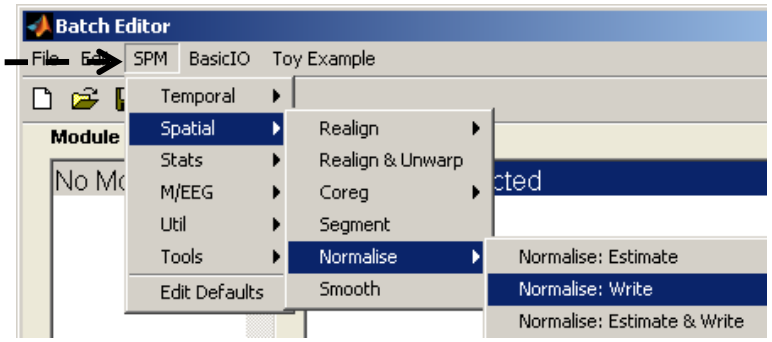
Normalising to MNI space

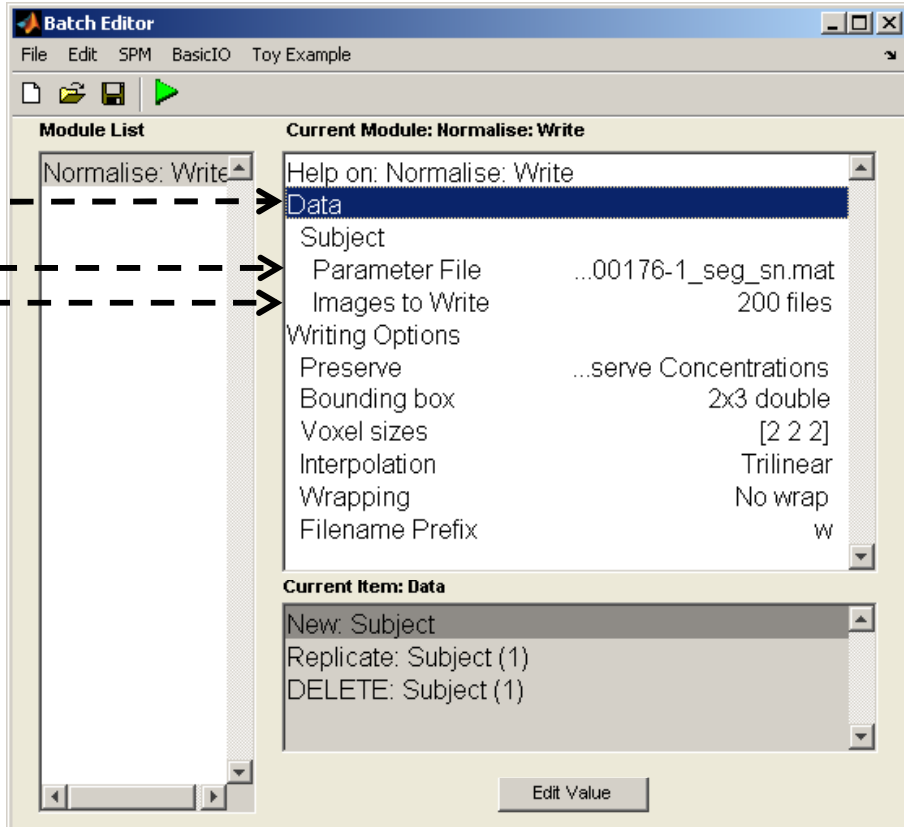
1. Select SPM -> Spatial -> Normalise -> Normalise: Write



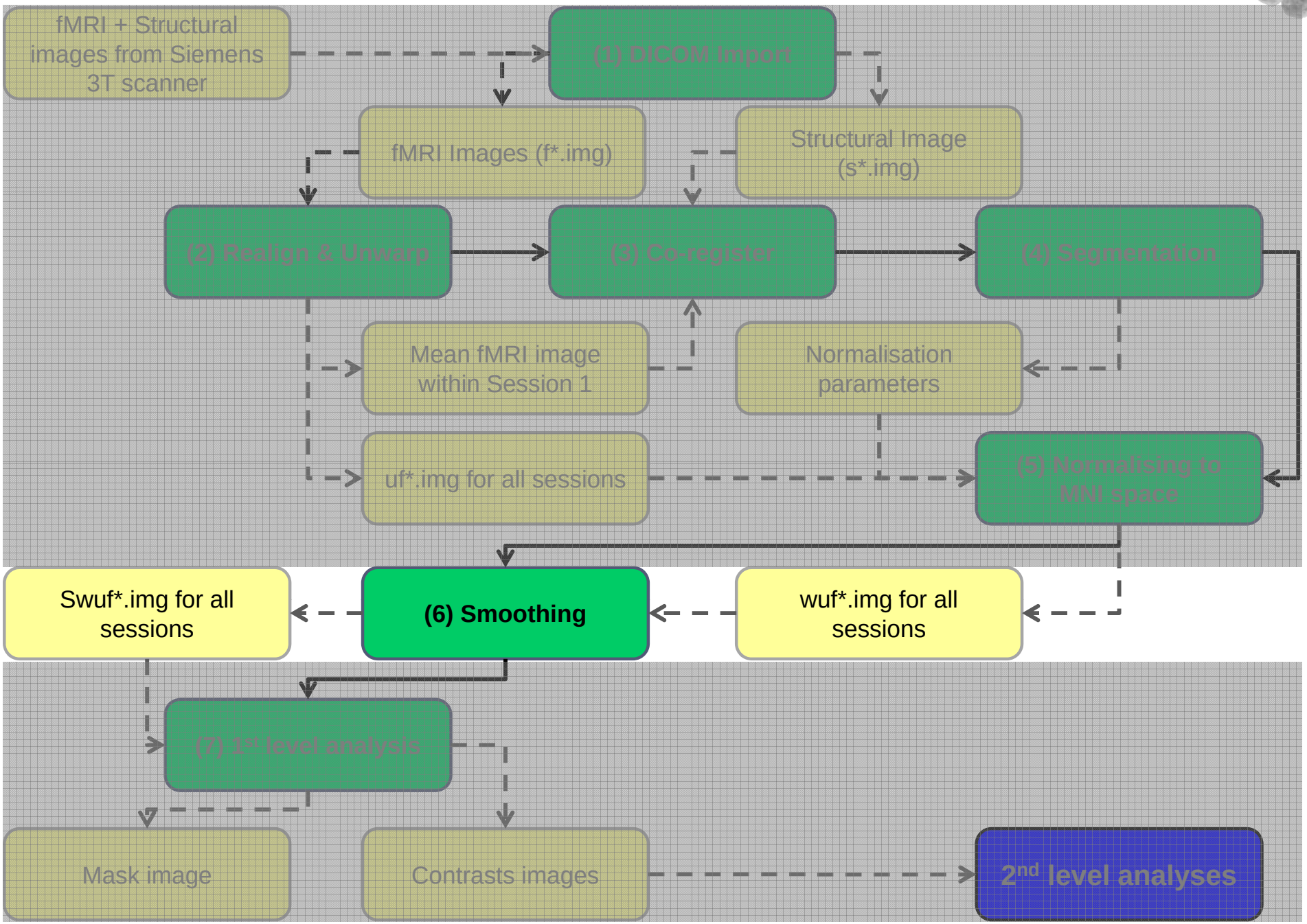
2. Select New: Subject

3. Select parameter file. *_seg_sn.mat

3. Select all uf*.img files from ***ALL*** sessions



Output: wuf*.img files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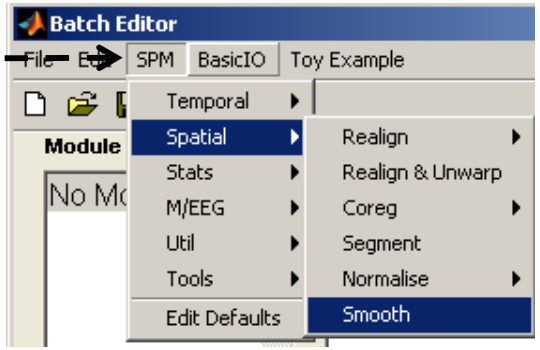
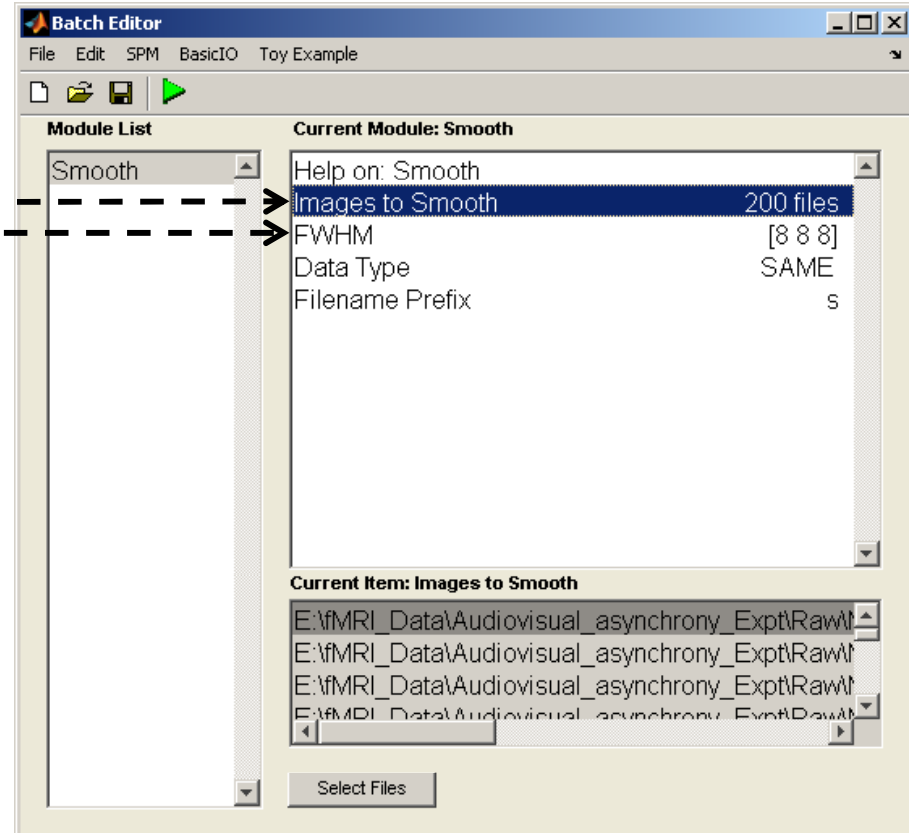
Preparing for 1st level analysis

1. Select SPM -> Spatial -> Smooth

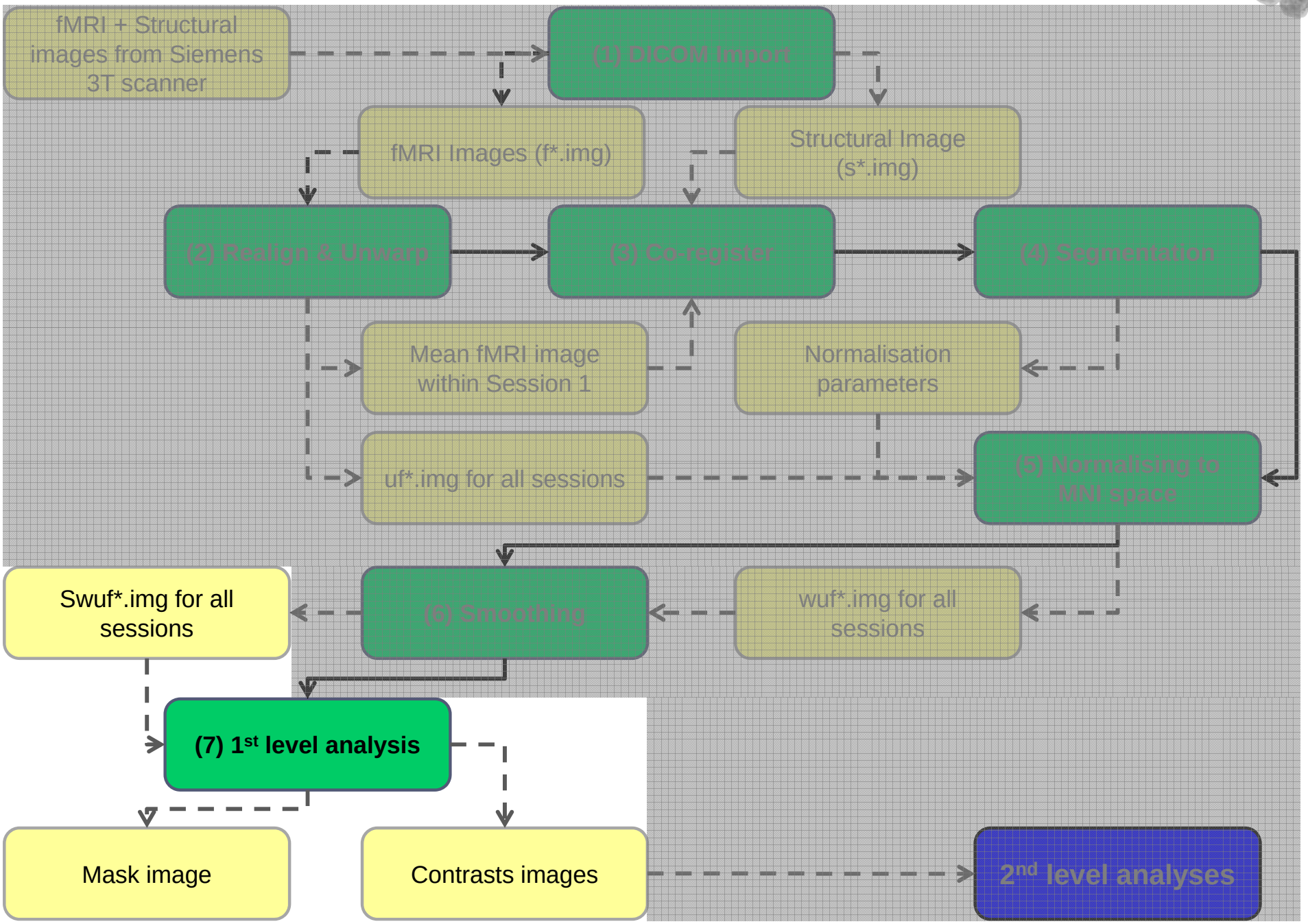


2. Select all wuf*.img from ***ALL*** sessions

2. FWHM: **[6 6 6]** for ***Single subject analyses*** and **[8 8 8]** for ***group level analyses***



Output: swuf*.img files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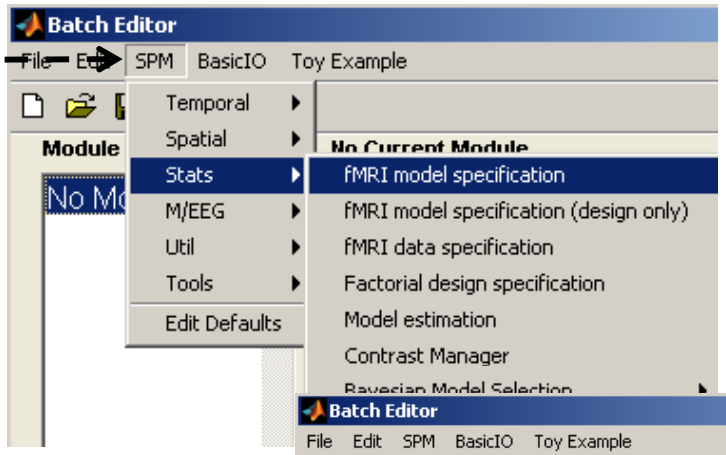
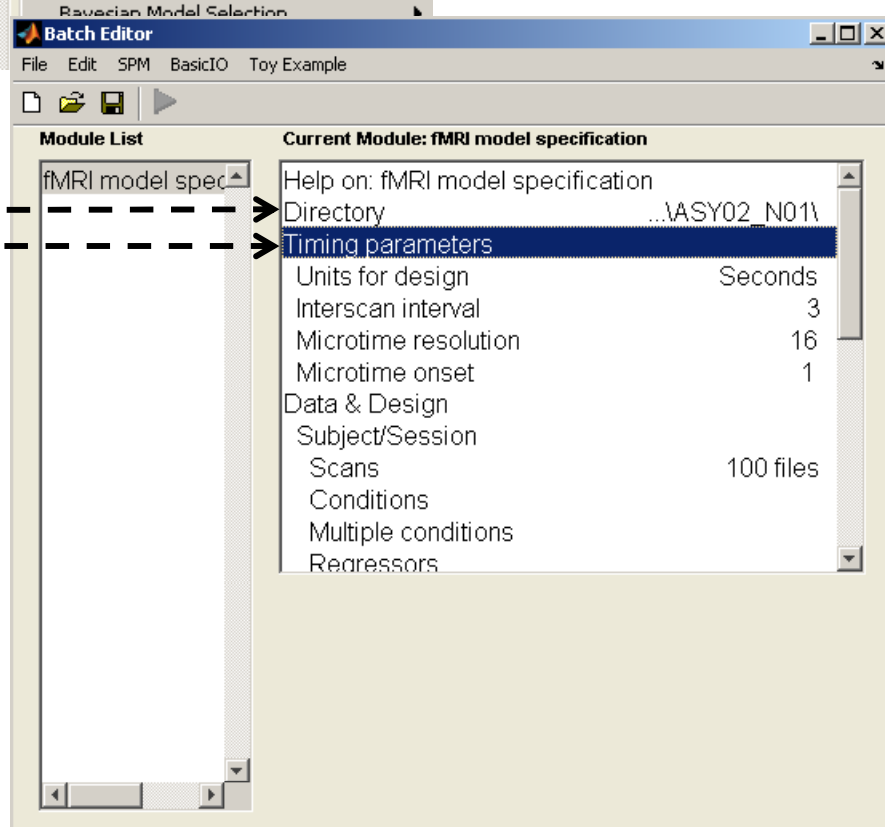
Specifying the 1st level analysis (Part 1)

1. Select SPM -> Stats -> fMRI model specification



2. Select directory for analysis. Suggestion: one should create new folders for the 1st level analysis.

3. Timing parameters:
Units for design: Seconds
Interscan interval: (your EPI TR)
Microtime resolution:16



Specifying the 1st level analysis (Part 2)

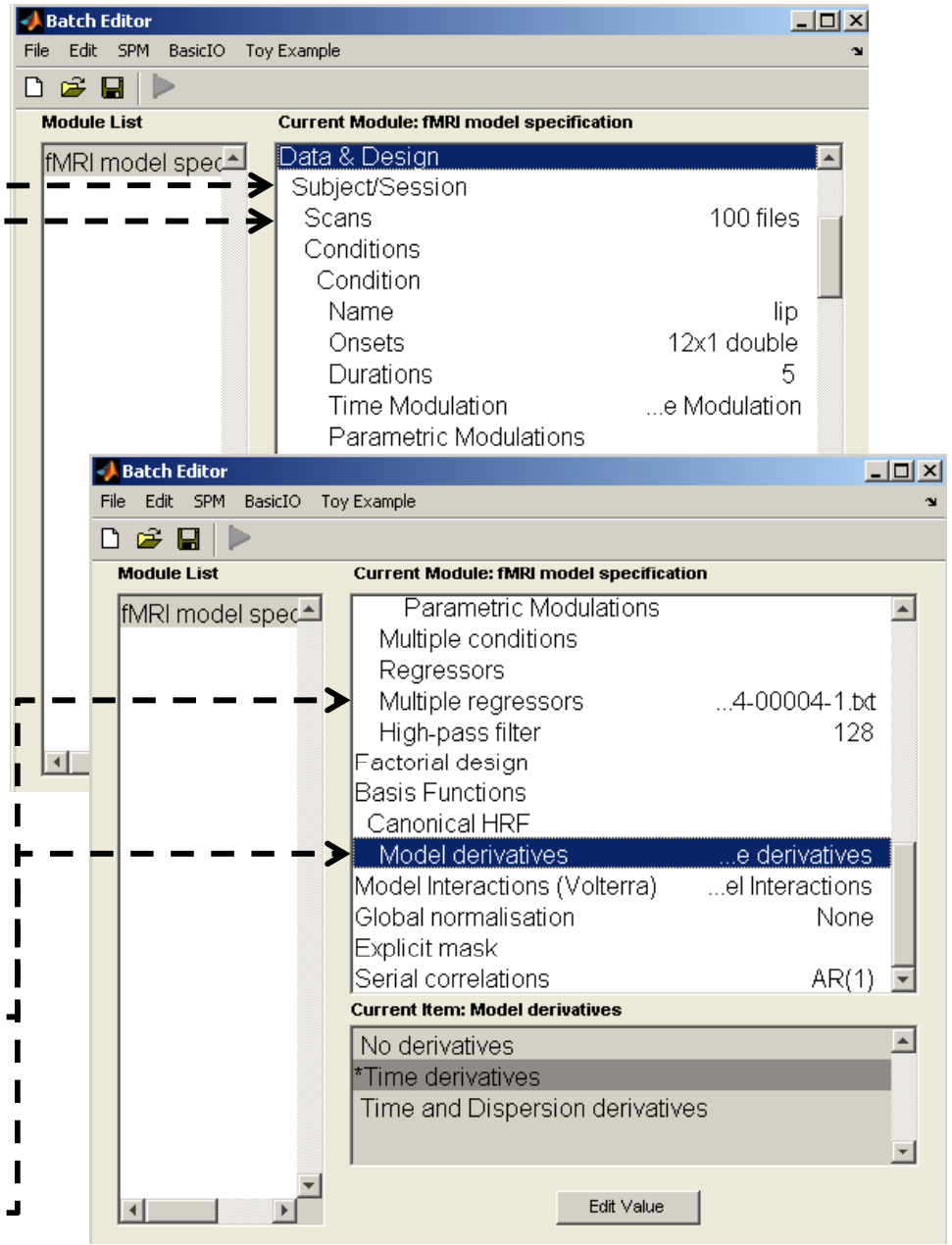
4. Select New: Subject/Session
The number of sessions is dependent on your experiment.

5. Select scans of each session of your experiment. (swuf*.img)

6. Select the conditions. The number of conditions is dependent on your experiment.
Name: (name of each condition)
Onsets: the timing of each stimulus that you collected minus the number of volumes you discard before your preprocessing
Duration: the timing of each stimulus or 0.
Time Modulations: Typically no Time Modulation, but still it depends on your needs
Parametric Modulations: same as above

7. Select multiple regressors. You should concatenate the movements parameters (rp*.txt) of all sessions into one matrix before including in the multiple regressors.

8. Model derivatives: Time derivatives
Everything else remains at default.



1st level analysis (Example)

Displays the names of each condition of each session

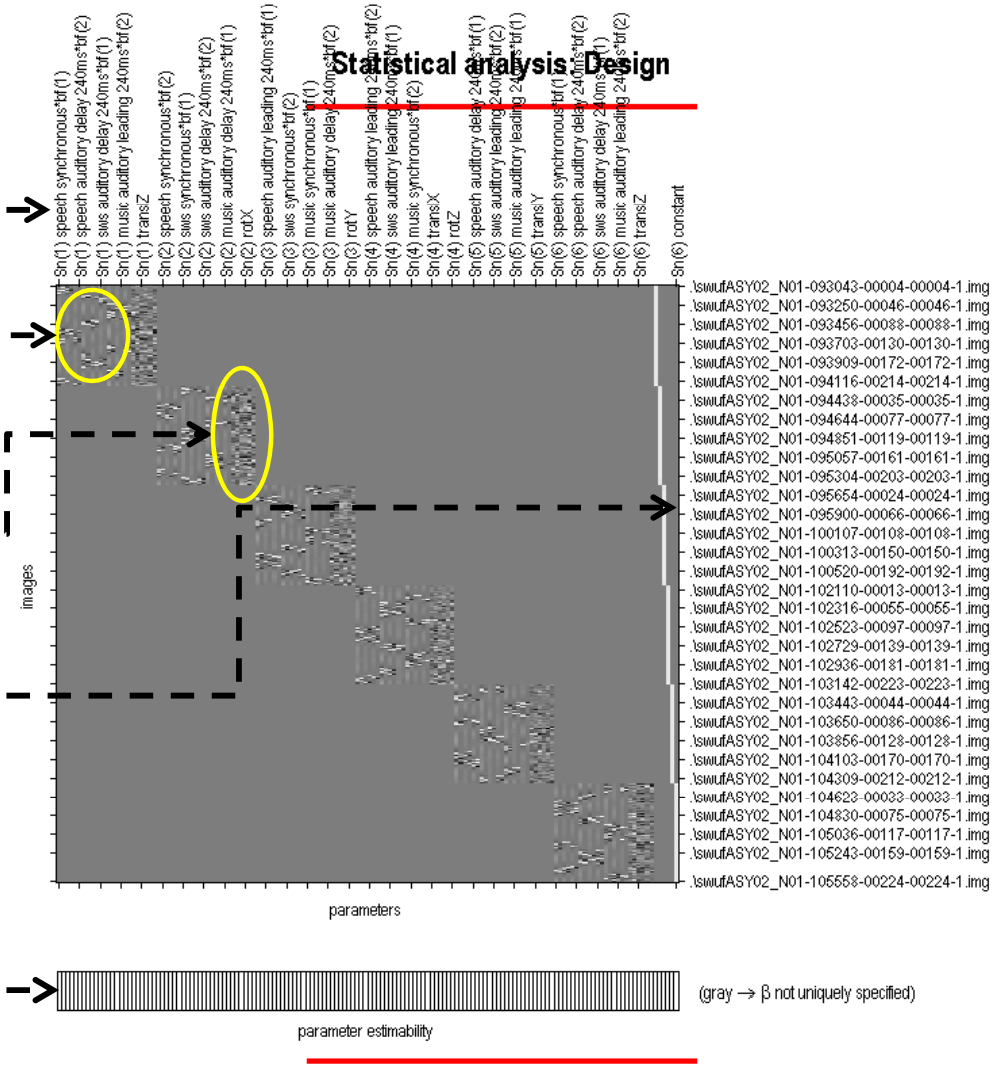
Displays the onsets and durations of the conditions.

Displays the movement parameters

Displays the files for all the sessions

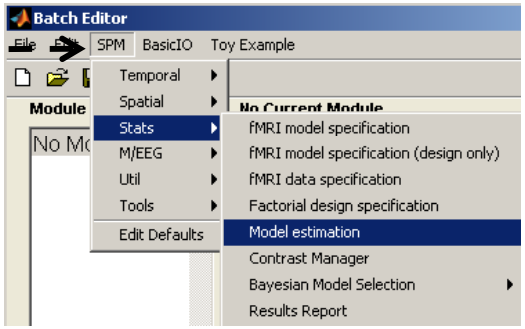
The parameter estimability should be all white. If there are any grey boxes, then it most likely means that onsets of one of the conditions is wrongly specify.

More information regarding your design matrix.



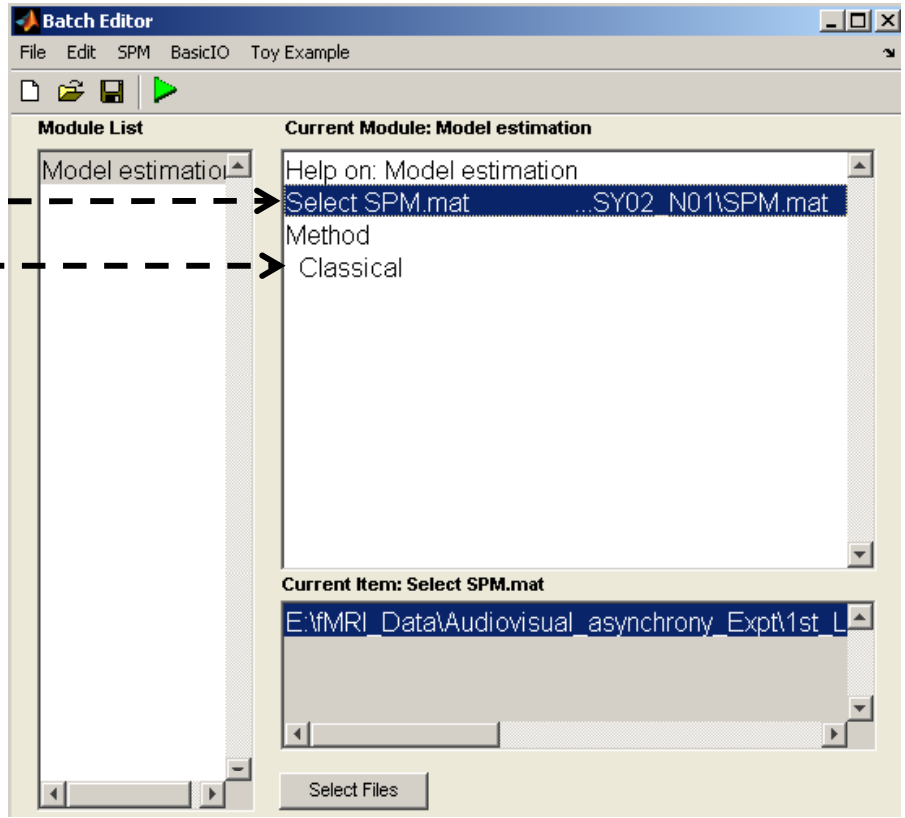
Estimating the 1st level analysis

1. Select SPM -> Stats -> Model estimation



2. Select SPM.mat that you want to estimate.

3. Method: Typically Classical. One also has the option of Bayesian



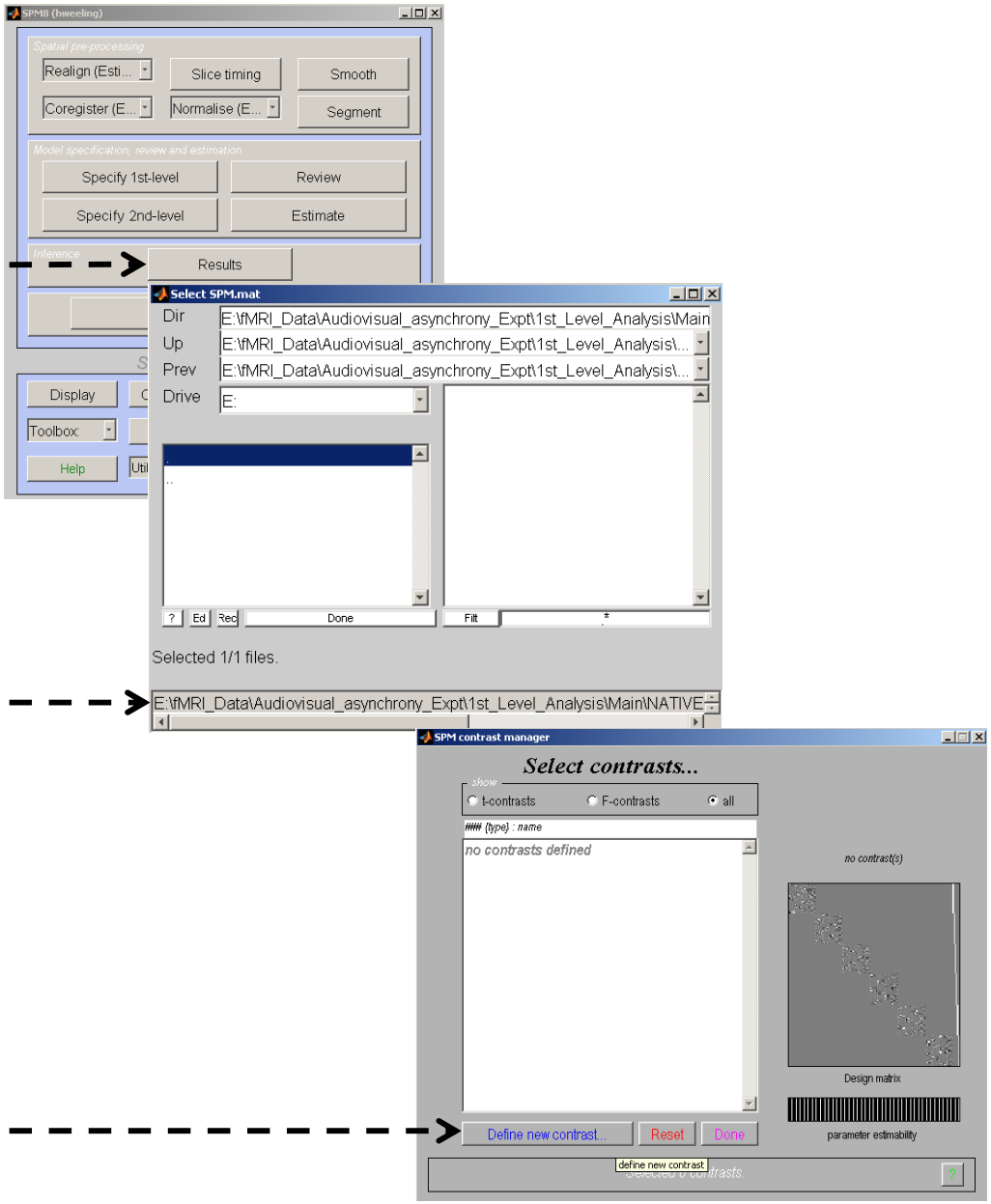
Output: beta images. You can now specify the contrast that you want to view.

Specifying contrasts at 1st level analysis

1. Select Results

2. Select SPM.mat.

3. Select define new contrast

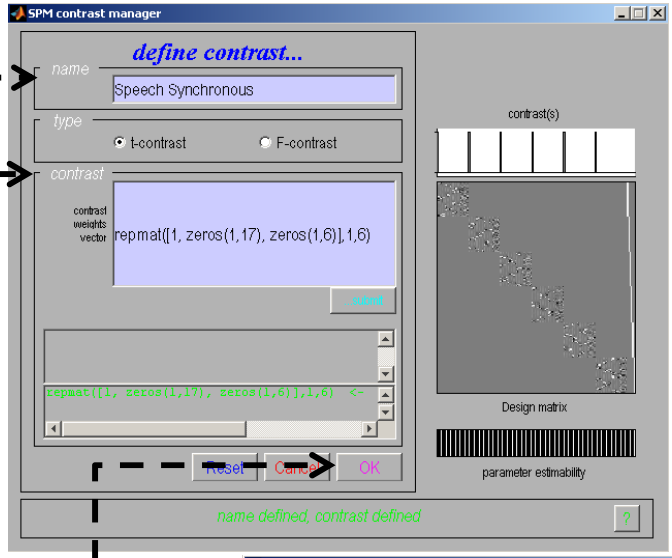


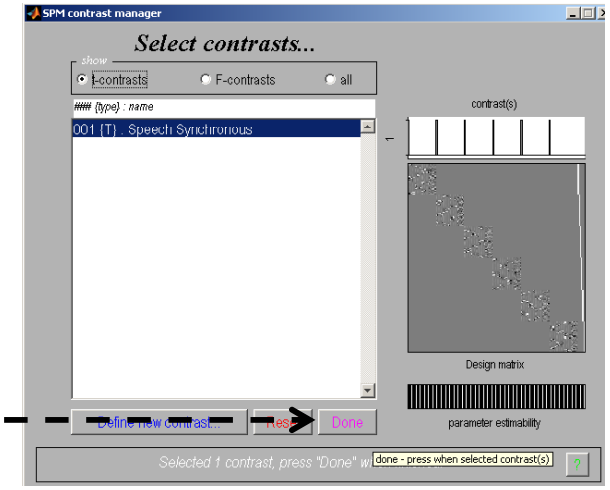
Specifying contrasts at 1st level analysis

1. Specify the name of contrast

2. Specify the matrix for the contrast. The number of columns of the matrix is equivalent to the number of conditions*2 (for time derivatives) + 6 (movement parameters for each session. E.g. In this study, there were 6 sessions with 9 conditions per session.

3. Select OK





3. Select Done

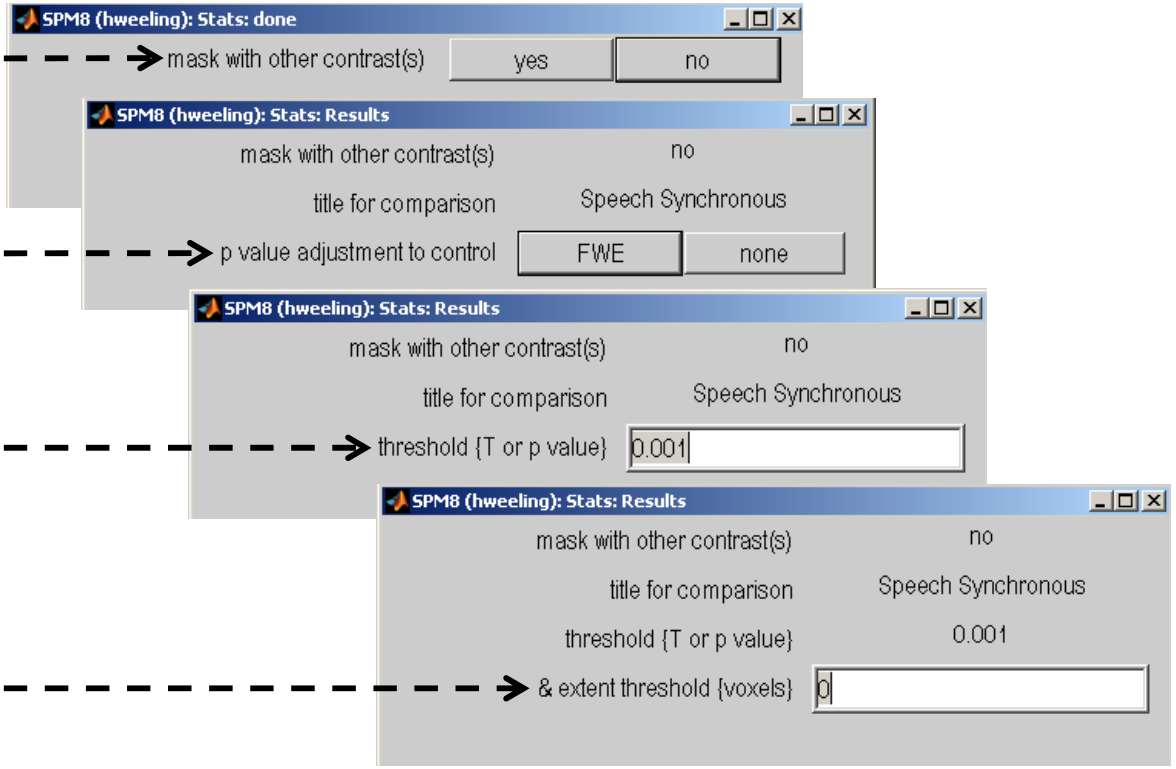
Specifying contrasts at 1st level analysis

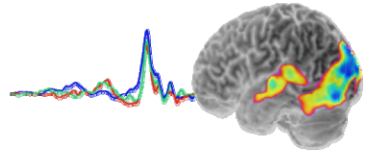
1. mask with other contrast(s): NO

2. Enter for the title for comparison
3. p value adjustment to control: NONE

4. Enter the statistical threshold that you want to test.

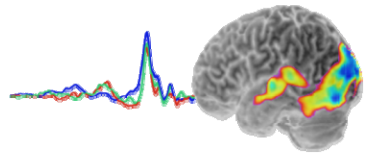
5. Enter the extend threshold (voxels) that you want to include for the test





To achieve better intra-subject alignment, DARTEL is recommended.

Important to take note



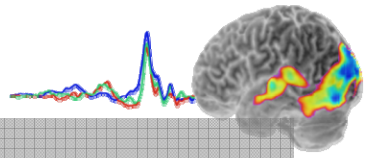
1. Advantages of using DARTEL
   - Improves intra-subject alignment
   - Benefits alignment between modalities (An example of this comes from a recent study).

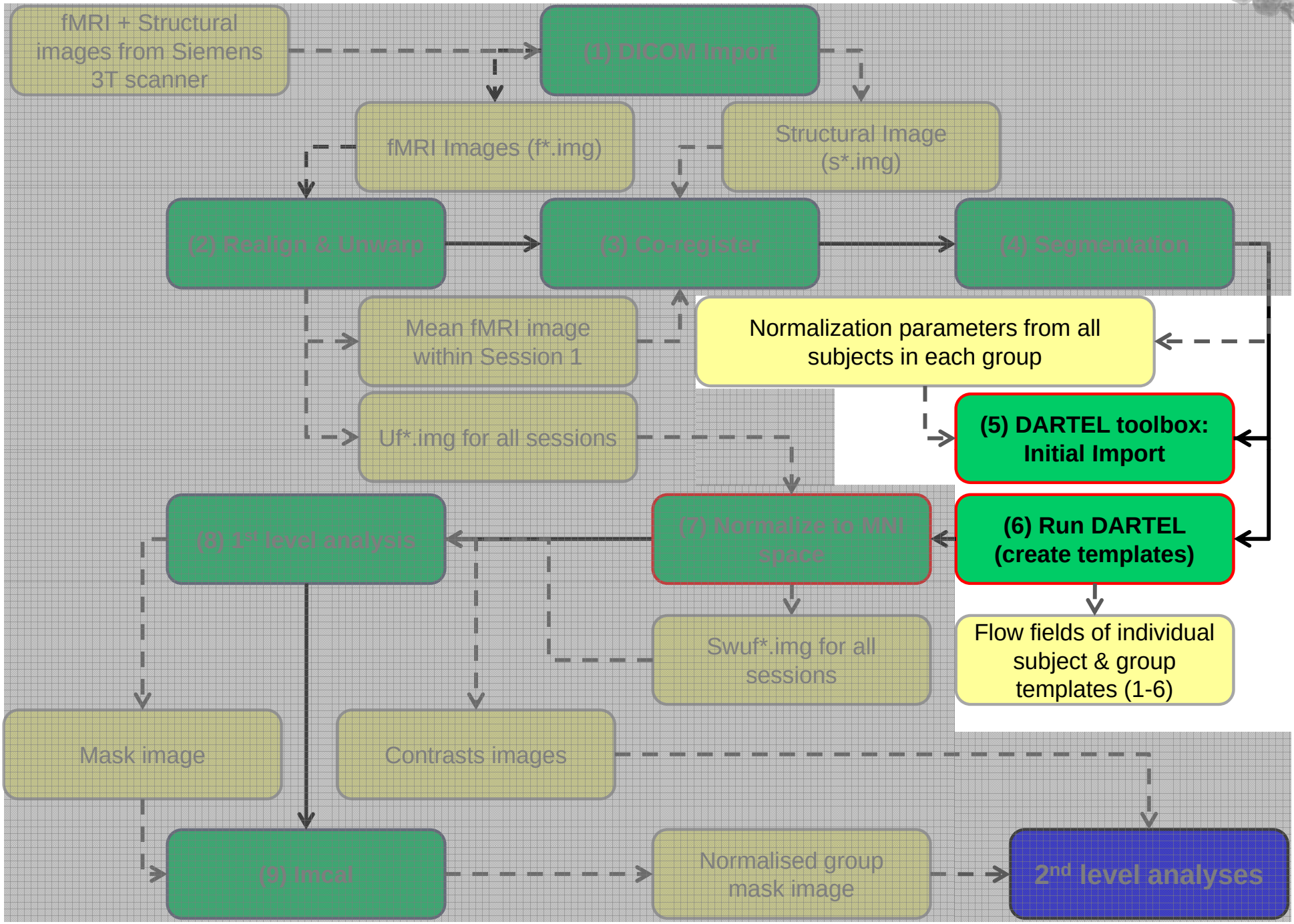
J Alzheimers Dis.. [Epub ahead of print]

Microstructural Diffusion Changes are Independent of Macrostructural Volume Loss in Moderate to Severe Alzheimer's Disease.

Canu E, McLaren DG, Fitzgerald ME, Bendlin BB, Zoccatelli G, Alessandrini F, Pizzini FB, Ricciardi GK, Beltramello A, Johnson SC, Frisoni GB.

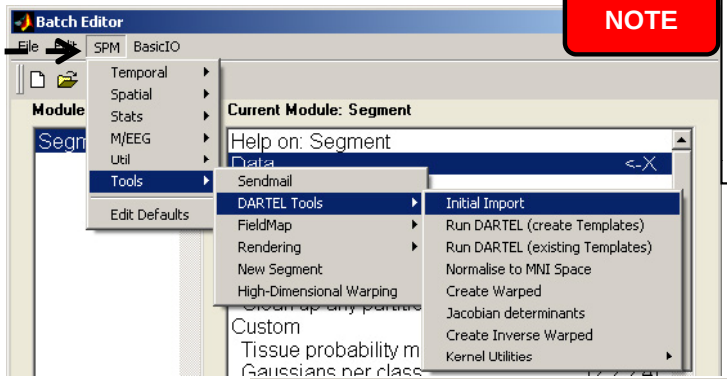
LENITEM - Laboratory of Epidemiology Neuroimaging & Telemedicine, IRCCS Centro San Giovanni di Dio FBF, The National Centre for Research and Care of Alzheimer's and Mental Diseases, Brescia, Italy.




fMRI + Structural images from Siemens 3T scanner
(1) DICOM Import
fMRI Images (f*.img)
Structural Image (s*.img)
(2) Realign & Unwarp
(3) Co-register
(4) Segmentation
Mean fMRI image within Session 1
Normalization parameters from all subjects in each group
Uf*.img for all sessions
(5) DARTEL toolbox: Initial Import
(8) 1st level analysis
(7) Normalize to MNI space
(6) Run DARTEL (create templates)
Swuf*.img for all sessions
Flow fields of individual subject & group templates (1-6)
Mask image
Contrasts images
(9) Imcal
Normalised group mask image
2nd level analyses

DARTEL toolbox: Initial Import

1. Select SPM -> Tools -> DARTEL Tools -> Initial Import



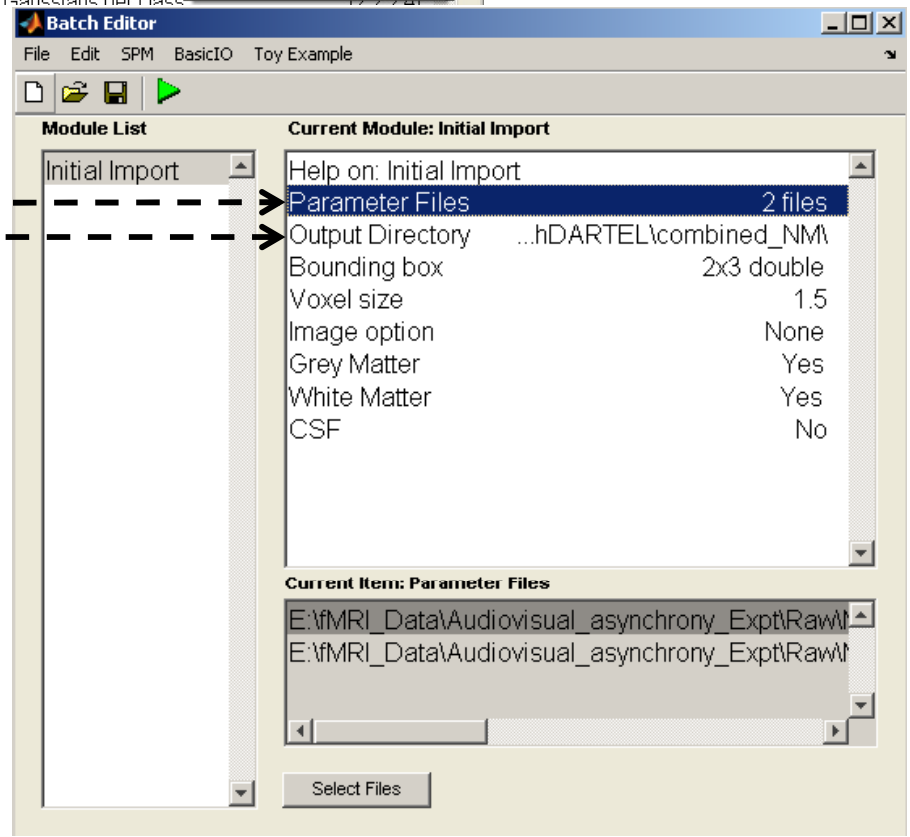
NOTE

Before using the toolbox, it is crucial that ***ALL*** structural images of ***ALL*** subjects in that particular study are collected.

If one has to include more subjects after this step, one has to repeat the whole procedure again.

2. Select parameter files (*_seg_sn.mat) obtained from segmentation in the earlier step.

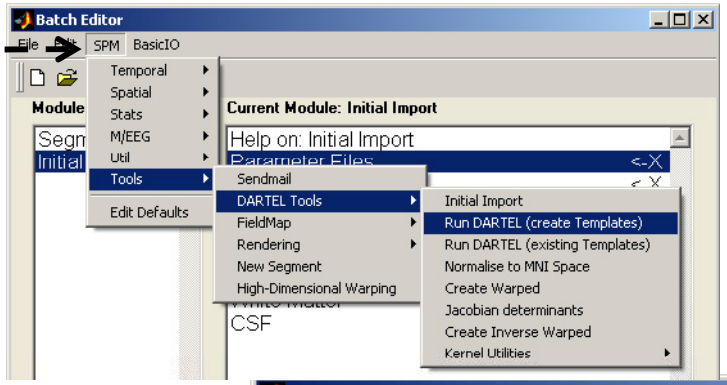
3. Select output directory. Suggestion: one should create a folder to store the flow fields and new averaged templates.



Output: Typically this will result in two types of files: rc1*.nii (grey matter) and rc2*.nii (white matter)

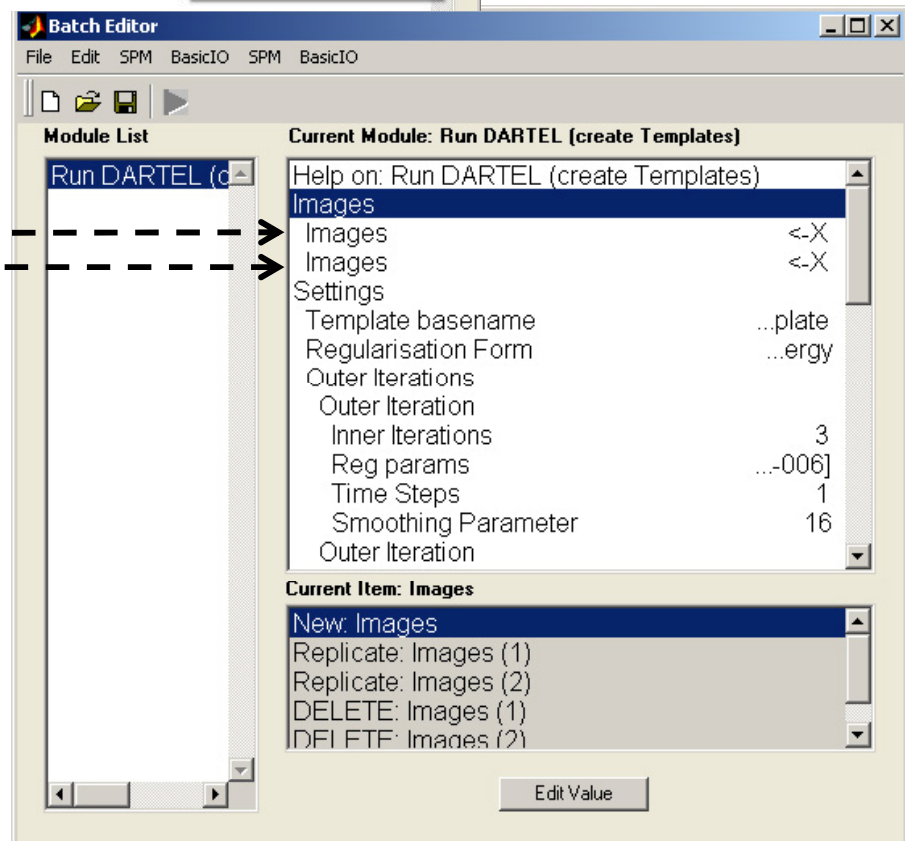
DARTEL toolbox: Run DARTEL

1. Select SPM -> Tools -> DARTEL Tools -> Run DARTEL (create Templates)

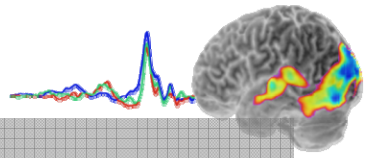


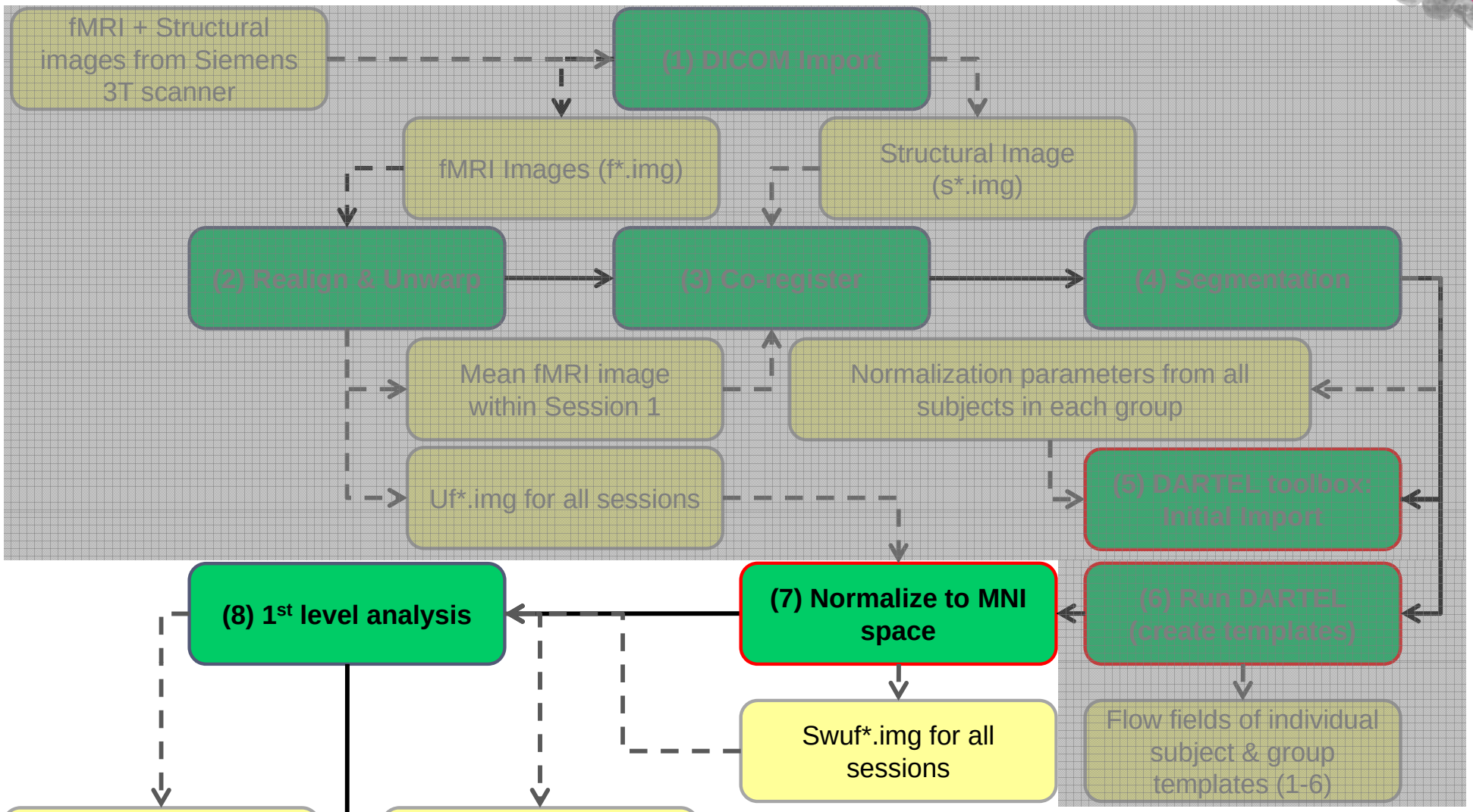
2. Select ***ALL*** rc1*.nii files

3. Select ***ALL*** rc2*.nii files



Output: Typically this will result in 6 templates and individual subject's deformation flow field files (u_rc1*.nii).

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(7) Normalize to MNI space
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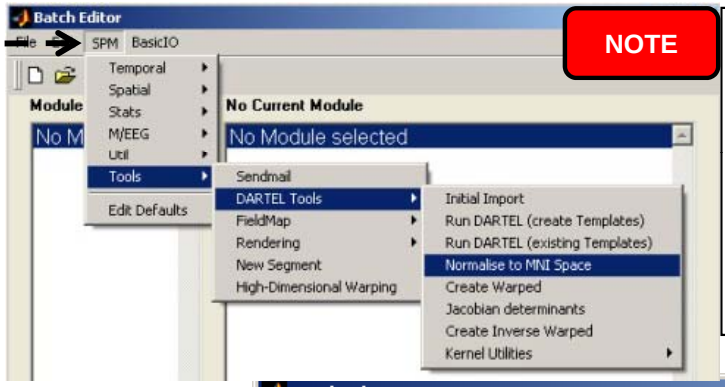
Swuf*.img for all sessions
Flow fields of individual subject & group templates (1-6)
Mask image
Contrasts images
(9) Imcal
Normalised group mask image
2nd level analyses

Normalising fMRI data to MNI space

1. Select SPM -> Tools -> DARTEL Tools -> Run DARTEL (create Templates)



NOTE

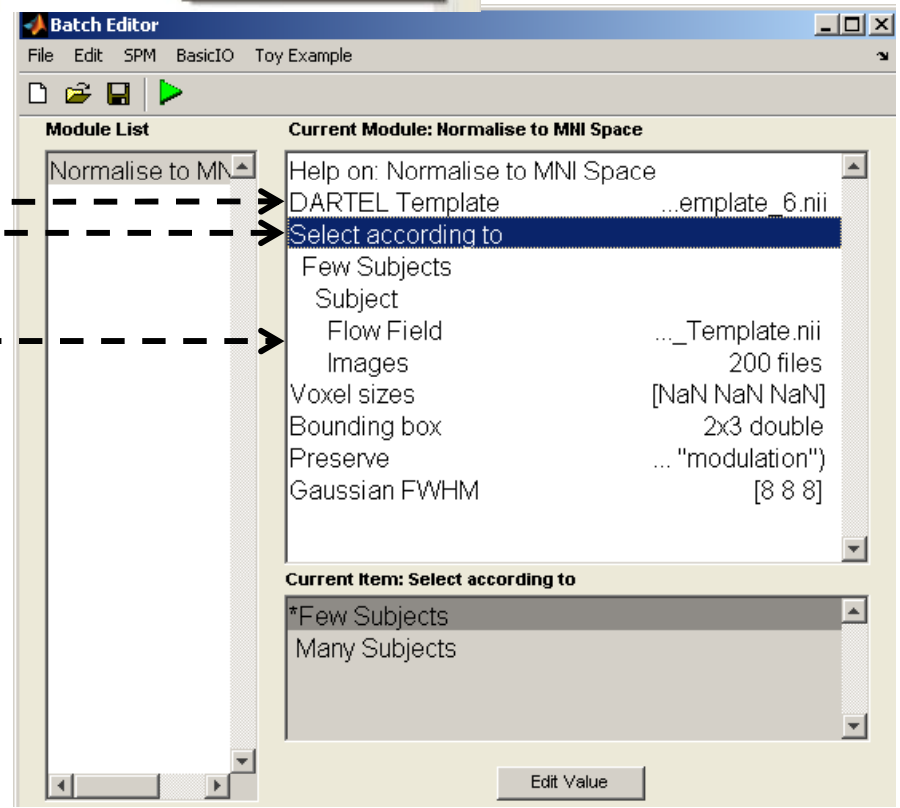
The normalized images will most likely look funny (with streaky bits on top of the brain). This happens because the spatial normalisation procedure tries to fill in all the voxels in the smoothed spatially normalised images. The bits with the streaks are where the fMRI data was cropped off.

It is crucial that one should use this step for normalising functional data as this preserves the original values of the data in the images.

2. Select Template_6.nii

3. Select according to FEW Subjects.

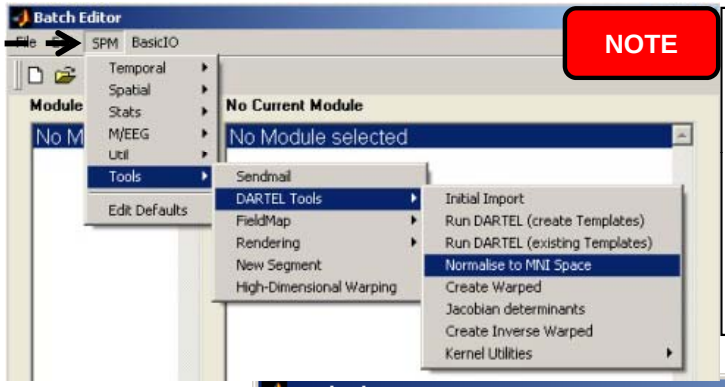
4. Select the flow field (u_rc1*.nii) of one subject and ***ALL uf*.img*** of that subject. You should do this for each subject.



Output: Typically this will result in swuf*.img.
The normalized images have been smoothed by Gaussian FWHM of 8mm

Normalising contrast images to MNI space

1. Select SPM -> Tools -> DARTEL Tools -> Run DARTEL (create Templates)



NOTE

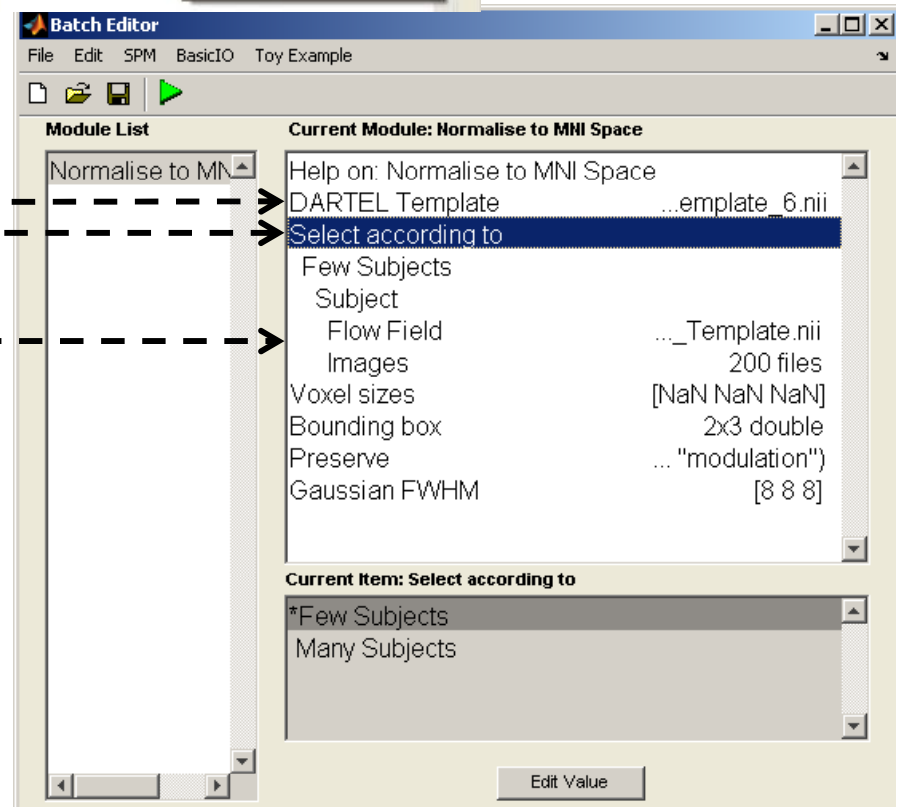
The normalized images will most likely look funny (with streaky bits on top of the brain). This happens because the spatial normalisation procedure tries to fill in all the voxels in the smoothed spatially normalised images. The bits with the streaks are where the fMRI data was cropped off.

It is crucial that one should use this step for normalising functional data as this preserves the original values of the data in the images.

2. Select Template_6.nii

3. Select according to FEW Subjects.

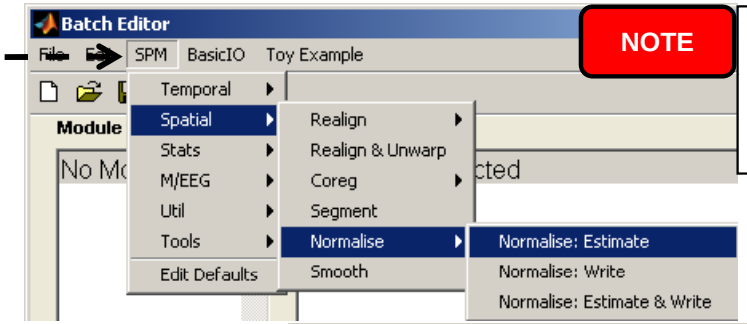
4. Select the flow field (u_rc1*.nii) of one subject and ***contrast images*** created from 1st level analysis of that subject. You should do this for each subject.



Output: Typically this will result in swcon*.img.
The normalized images have been smoothed by Gaussian FWHM of 8mm

Alternative method to normalize to NMI space without smoothing

1. Select SPM -> Spatial -> Normalise -> Normalise: Estimate



NOTE

Create deformation that maps from MNI space to the space of the group average.

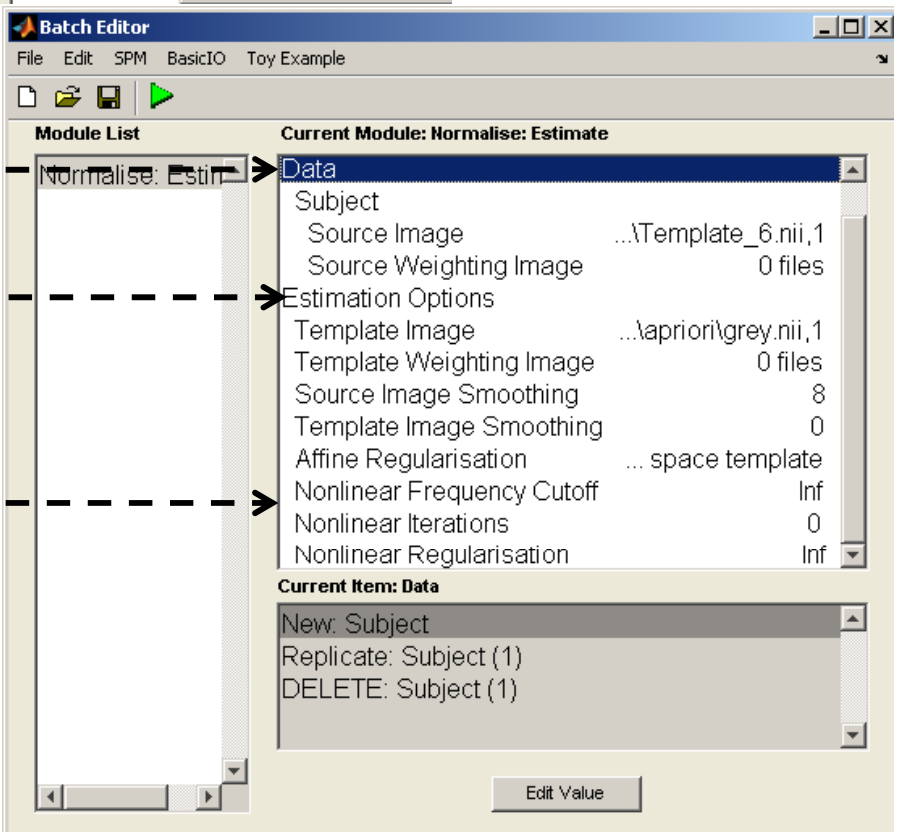
In order to do this, affine spatial normalization is sufficient.

2. Select New: Subject

3. Select source image: Template_6.nii

4. Select template image: spm8/apriori/grey.nii

5. Nonlinear Frequency Cutoff: ***INF***
Nonlinear Iterations: ***0***
Nonlinear Regularisation: ***INF***



Output: Template_6_sn.mat

Alternative method to normalize to NMI space without smoothing

1. Select SPM -> Util -> Deformations

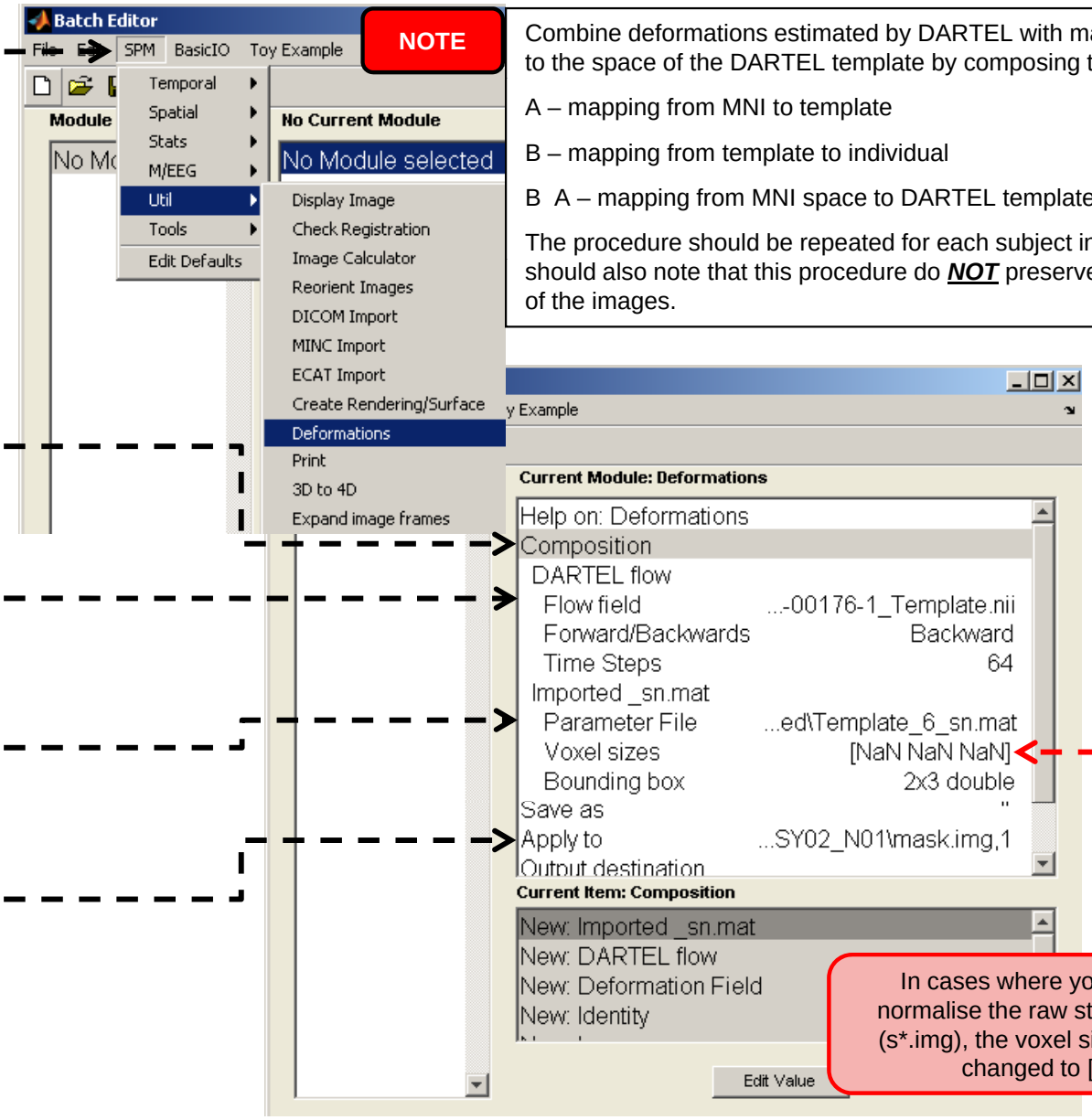
2. Select New: DARTEL flow and New: Imported_sn.mat

3. Select individual subject's flow field (u_rc1*.nii)

4. Select Template_6_sn.mat

5. Select image that you want to apply to.

Output: w*.img



NOTE

Combine deformations estimated by DARTEL with maps from MNI space to the space of the DARTEL template by composing them together:

A – mapping from MNI to template

B – mapping from template to individual

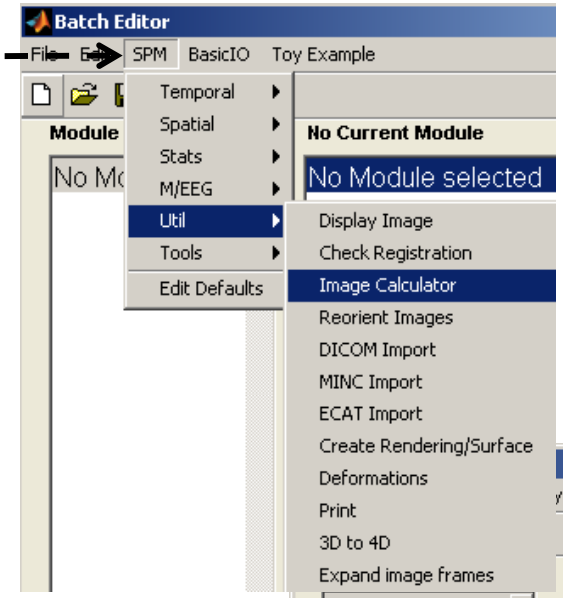
B A – mapping from MNI space to DARTEL template to individual scan

The procedure should be repeated for each subject in the study. One should also note that this procedure do ***NOT*** preserve the original values of the images.

In cases where you attempt to normalise the raw structural image (s*.img), the voxel sizes should be changed to [1 1 1].

Calculating a combined mask image

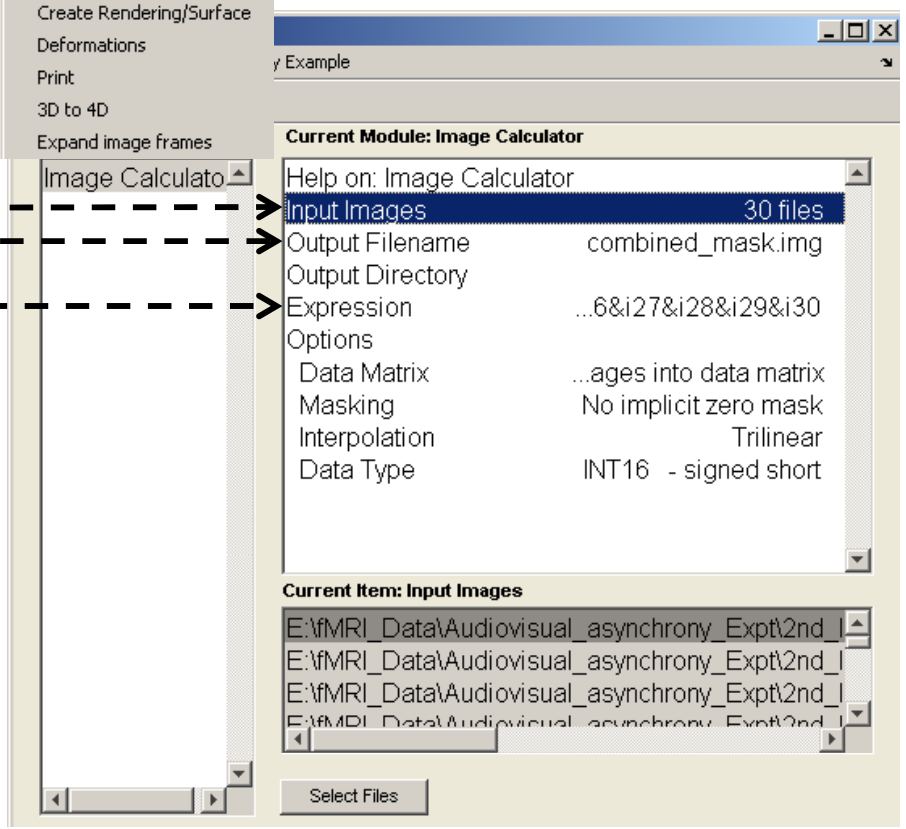
1. Select SPM -> Util -> Deformations



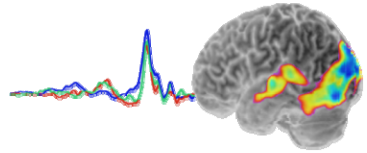
2. Select the mask images of ***ALL*** subjects

3. Enter an output filename

4. Expression: logical AND for combination.
E.g. i1&i2&i3&i4&i5



Output: output filename.img



End