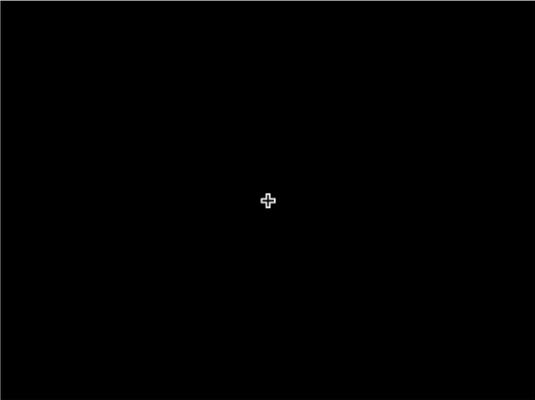
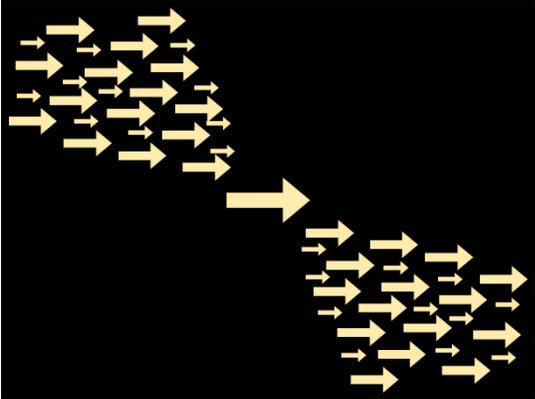


# Tutorial – Preprocessing

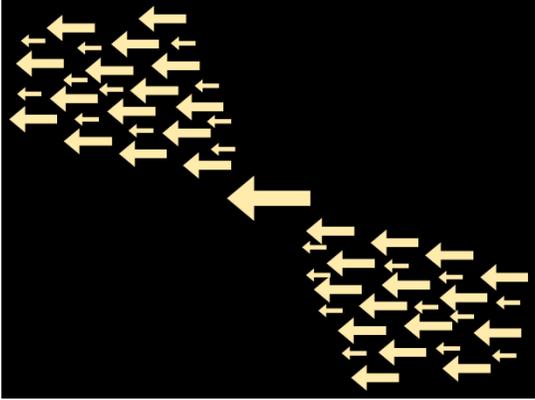
# The experiment



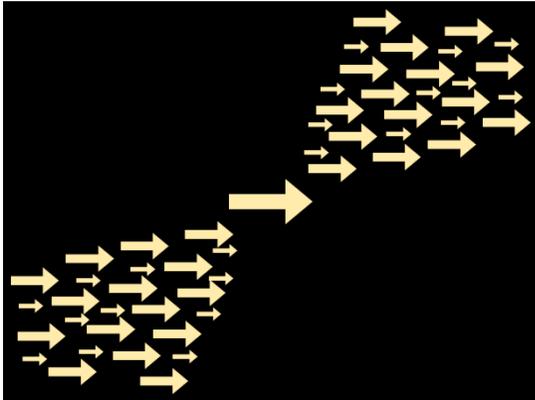
Fixation



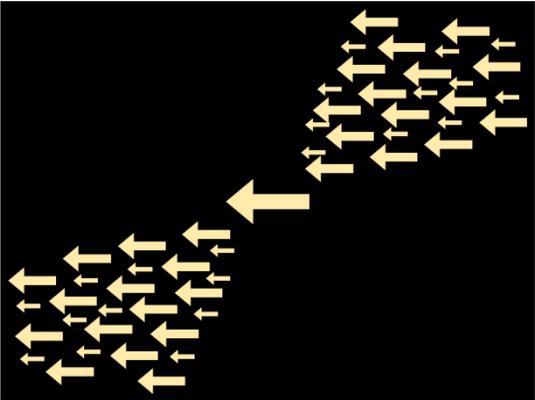
Press right



Top left wedge  
Wedge1



Press left



Top right wedge  
Wedge2

# Design

- First run (fmri01.nii): Block design – same direction of arrow shown in blocks of 15 seconds with null blocks included.
- Second run (fmri02.nii): Event related design – direction of arrow changed every 3 seconds with null trials included.

# Today's tutorial

- First hour: Create your own preprocessing pipeline for one subject.
- Break: Form groups for final presentation MED-Students.
- Second hour: Use a batch and script to process the data.

# Organize data

-  `behav` – Behavioral data
-  `functional` – Functional MRI data for analysis
-  `glm` – First level analysis and results
-  `physlog` – Physiological measurements (not available)
-  `scandata` – Original raw data → **Never touch this during analysis**
-  `structural` – Anatomical/Structural MRI scans for analysis

# Behavioral data (next week)

 BehaviorSummary01	→	Behavior analysis (Errors etc.)
 BehaviorSummary02		
 BehavRun01	→	All behavioral data
 BehavRun02		
 DCMRegs01	→	Regressors for DCM
 IndividualRegs01		
 IndividualRegs02	→	Regressors for all 4 conditions
 LRArrowRegs01		
 LRArrowRegs02	→	<b>Regressors (left arrow vs. right arrow)</b>
 LRPressRegs01		
 LRPressRegs02	→	<b>Regressors (left press vs. right press)</b>
 WedgeModRegs01		
 WedgeModRegs02	→	Wedge regressors with arrow modulation
 WedgeMotorRegs01		
 WedgeMotorRegs02	→	Wedge regressors (event) and motor regressors (events)
 WedgeRegs01		
 WedgeRegs02	→	<b>Regressors (TL-BR wedge vs. TR-BL wedge)</b>

# Copy MRI data from scandata/

b0map\_01\_ec1\_typ0.nii

b0map\_01\_ec1\_typ3.nii

b0map\_01\_ec2\_typ0.nii

b0map\_01\_ec2\_typ3.nii

b0map\_02\_ec1\_typ0.nii

b0map\_02\_ec1\_typ3.nii

b0map\_02\_ec2\_typ0.nii

b0map\_02\_ec2\_typ3.nii

fmri01.nii

fmri02.nii

skstruct.nii

– B0 field maps

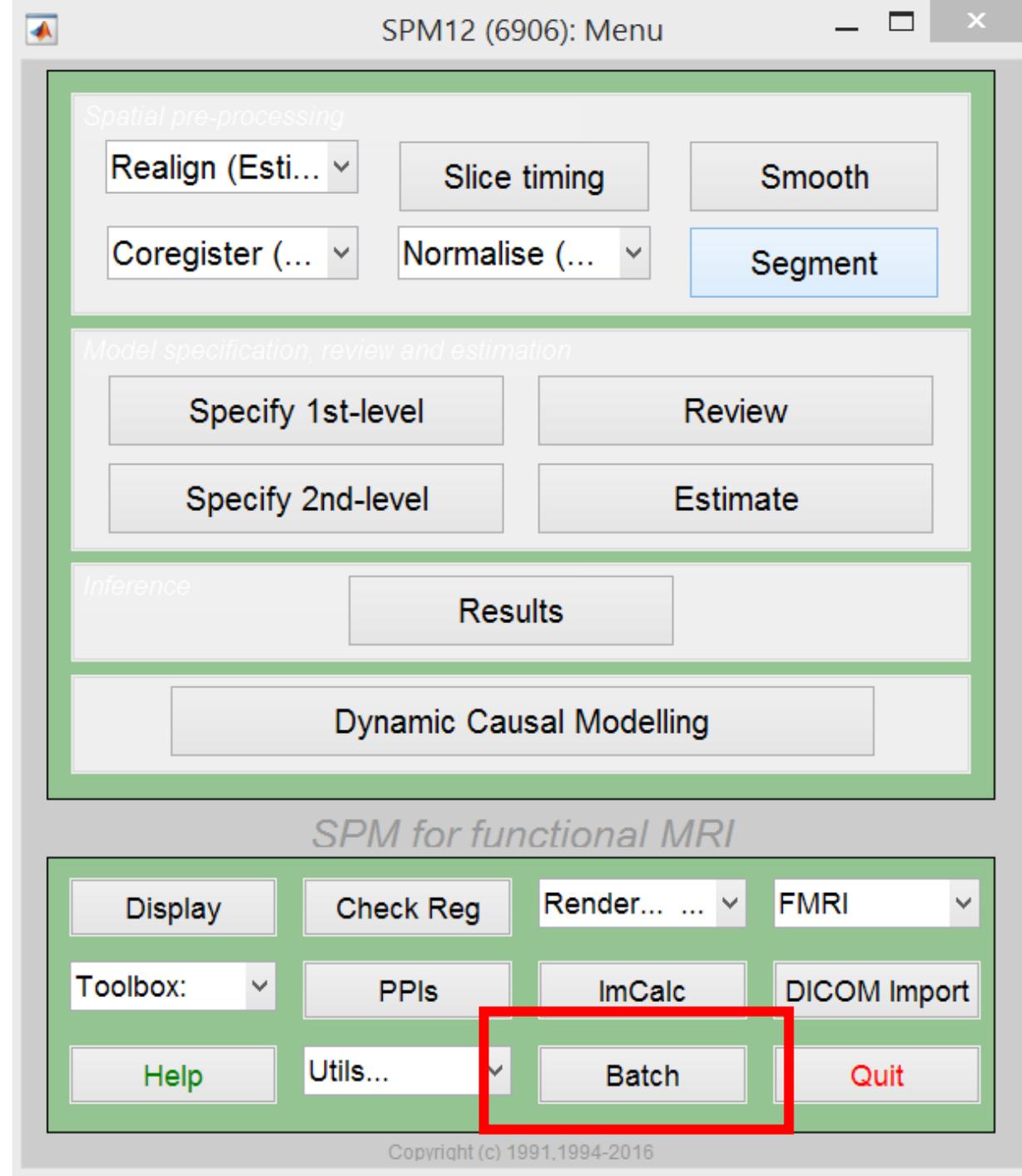
– fMRI data (T2\*) → Copy to folder functional

– Structural data (T1) → Copy to folder structural

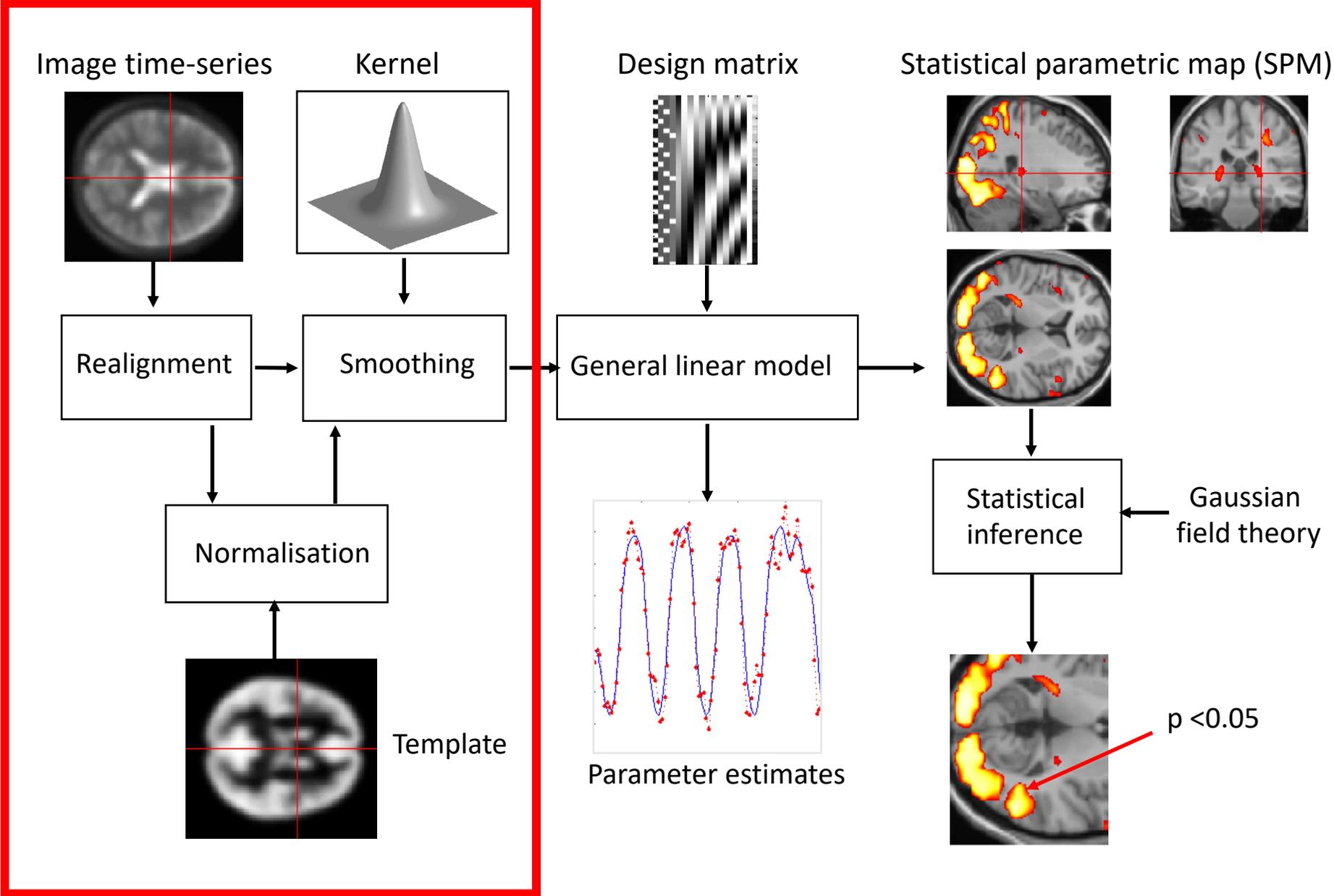
# Try to setup a preprocessing pipeline

- Hint: Try to put a pipeline together that you think is reasonable. It does not have to be exactly the one we used last week.
- Analyse a different subject to your neighbours!
- Feel free to try different parameter settings.

# SPM main menu

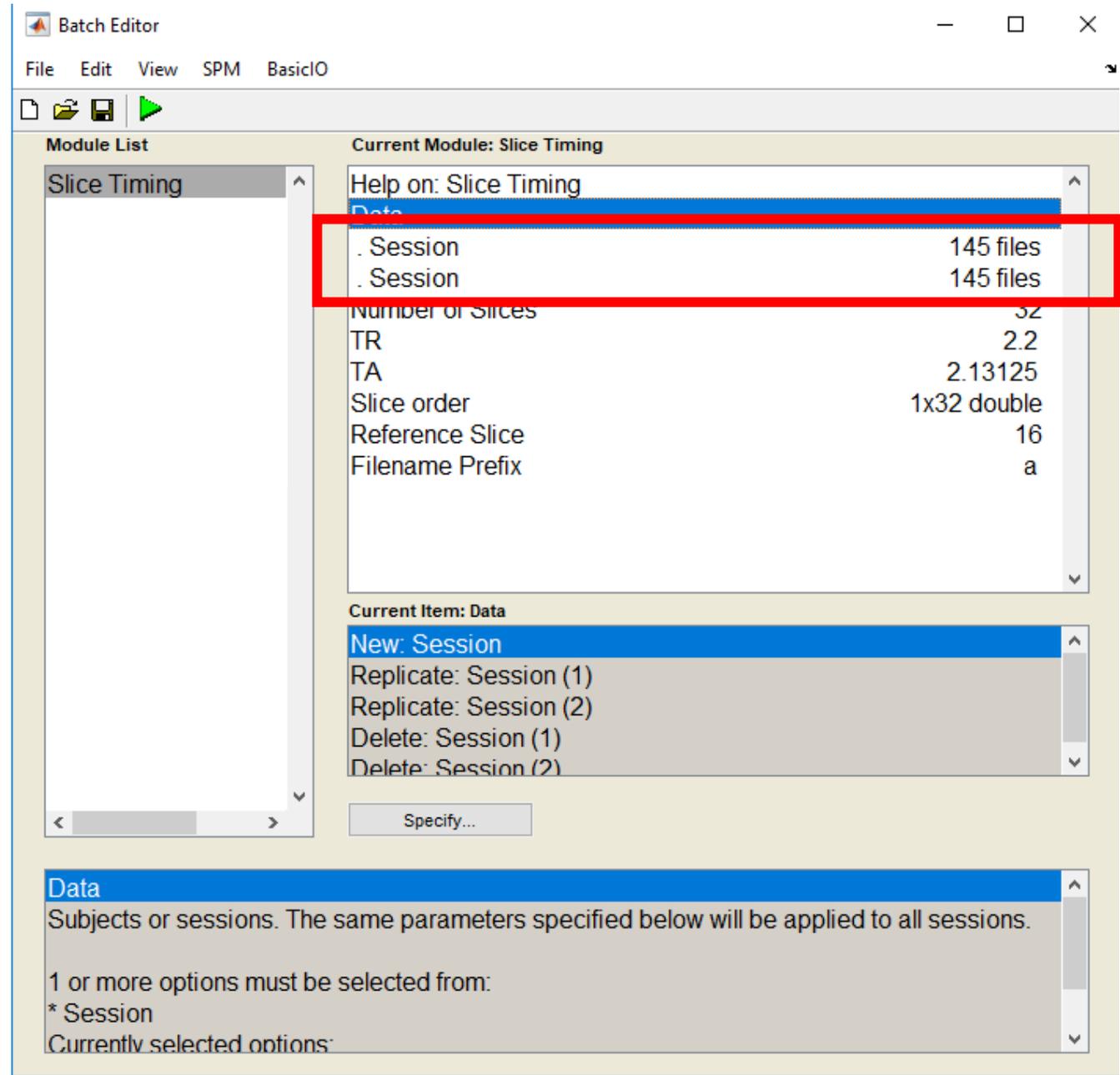


# Preprocessing



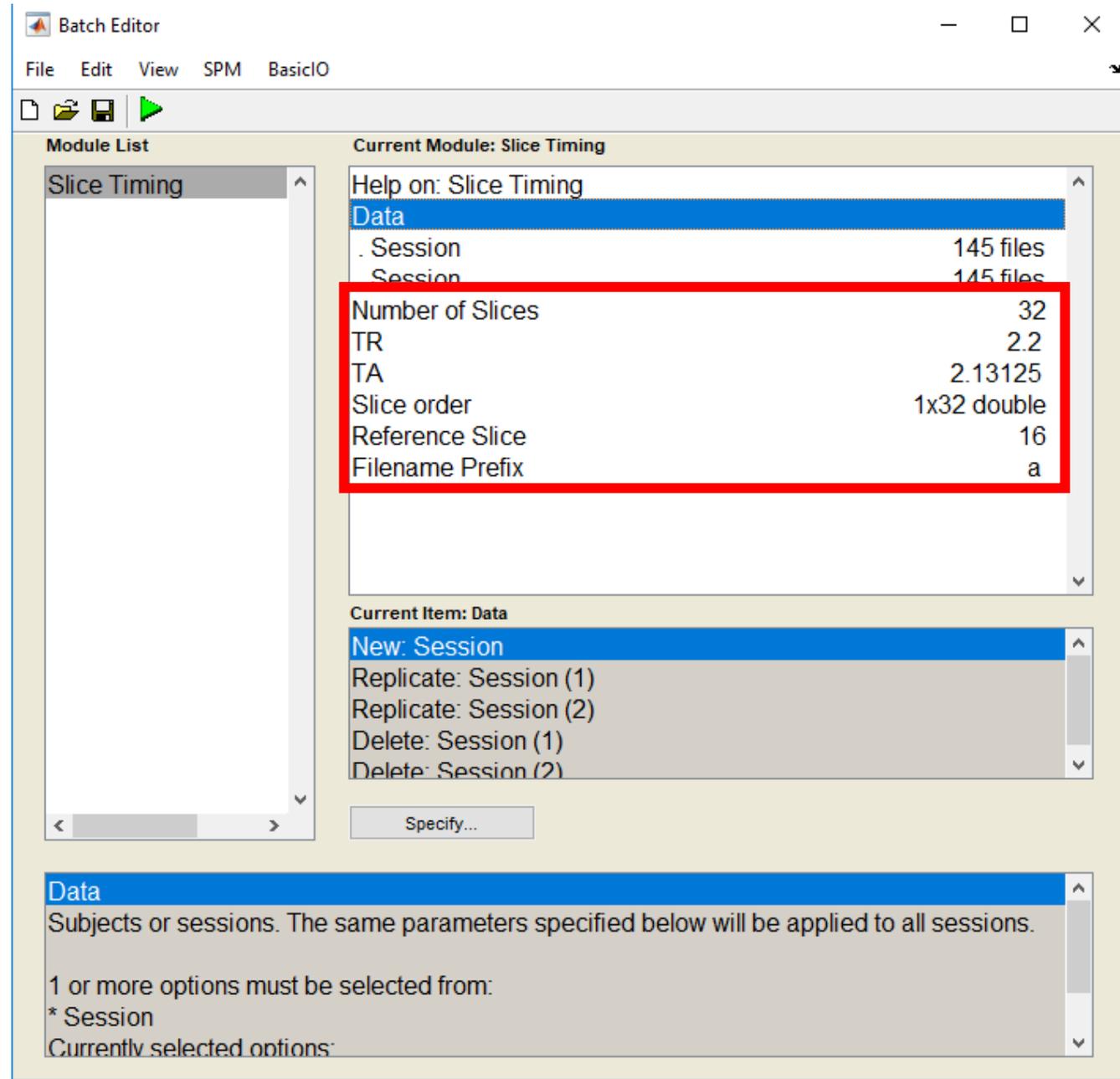
# Add fmri

- Select the run fmri01.nii for the first session, and fmri02.nii for the second session.
- Each contains 145 volumes (i.e. files)



# Slice timing

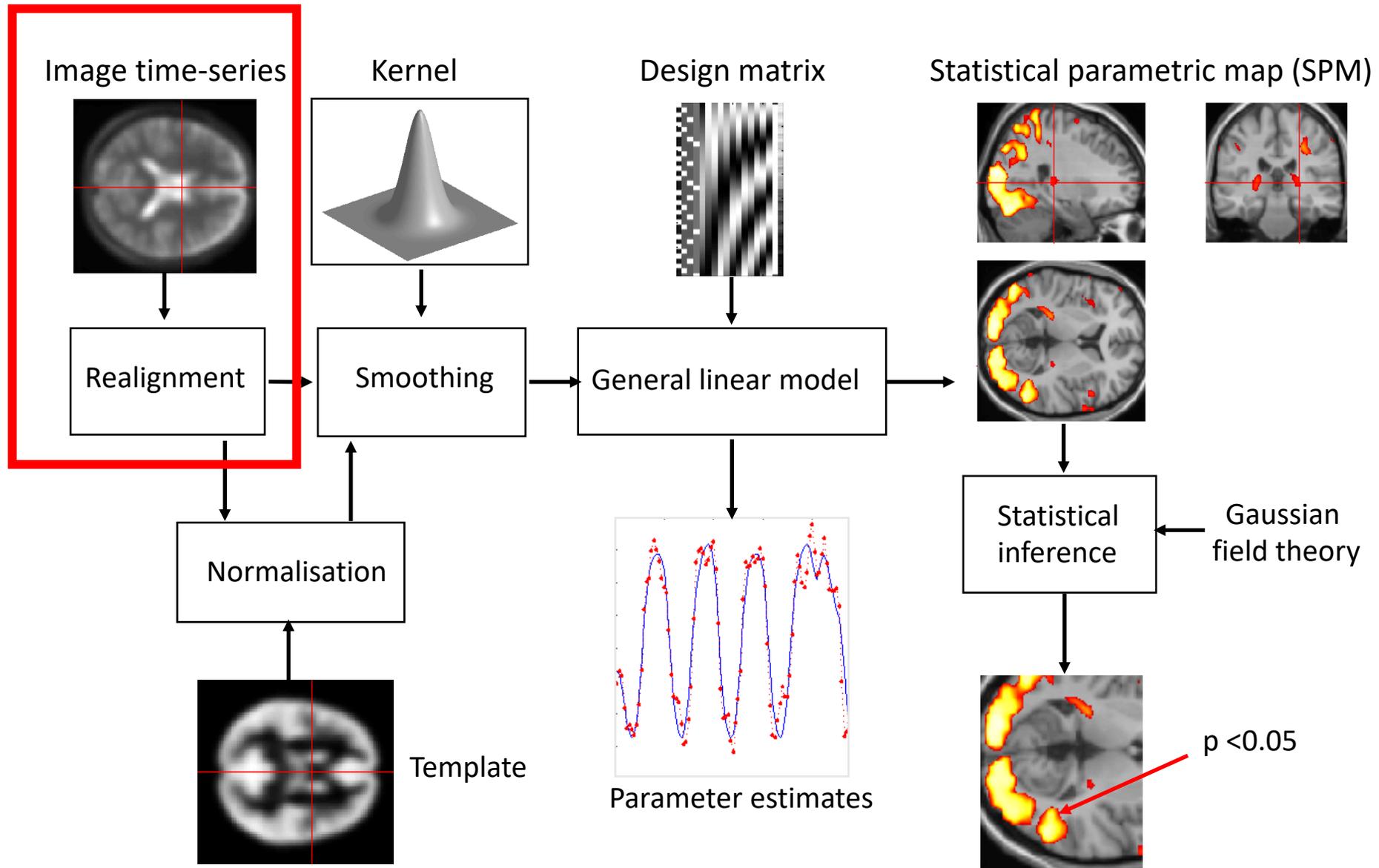
- Parameters (known from scanner setup)
  - #Slices:  $n=32$
  - Repetition time:  $TR = 2.2s$
  - $TA = TR * (n-1) / n$
  - Slice order = [1:32]



The screenshot shows the Batch Editor software interface. The main window is titled "Batch Editor" and has a menu bar with "File", "Edit", "View", "SPM", and "BasicIO". Below the menu bar is a toolbar with icons for file operations and a green play button. The interface is divided into several sections:

- Module List:** A list on the left side showing "Slice Timing" as the selected module.
- Current Module: Slice Timing:** A large panel on the right containing a list of parameters and their values, highlighted with a red border:

Help on: Slice Timing	
Data	
. Session	145 files
. Session	145 files
Number of Slices	32
TR	2.2
TA	2.13125
Slice order	1x32 double
Reference Slice	16
Filename Prefix	a
- Current Item: Data:** A list of actions for the selected item, including "New: Session", "Replicate: Session (1)", "Replicate: Session (2)", "Delete: Session (1)", and "Delete: Session (2)".
- Specify...:** A button located below the "Current Item" list.
- Data:** A section at the bottom of the interface containing text: "Subjects or sessions. The same parameters specified below will be applied to all sessions." and "1 or more options must be selected from:" followed by "\* Session" and "Currently selected options:".



# Realignment

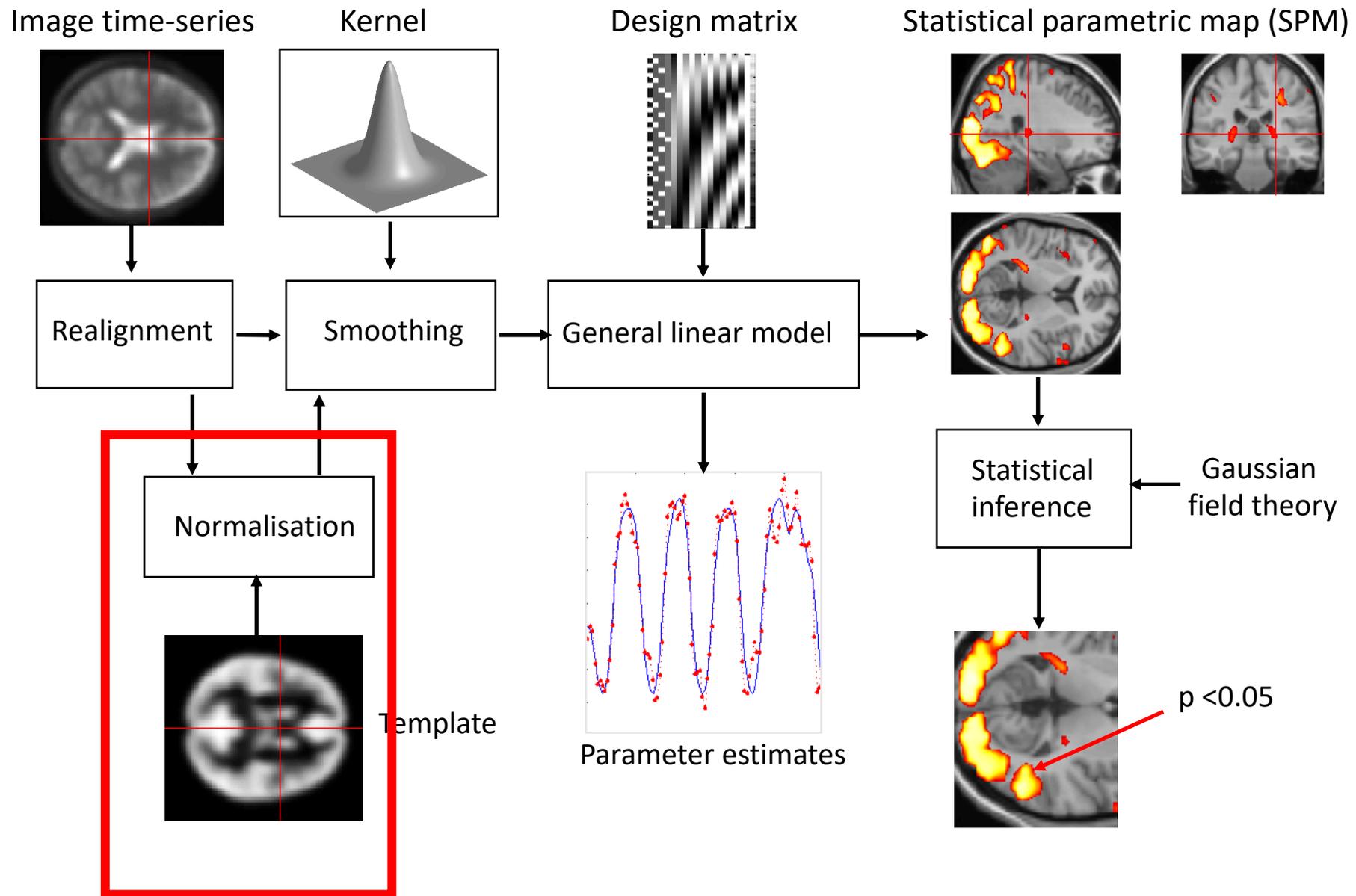
- Use result of «Slice Timing» using Dependencies
- Keep all default parameters.

The screenshot shows the 'Batch Editor' window with the 'Realign: Estimate & Reslice' module selected. The 'Module List' on the left shows 'Realign: Estimate & Reslice' as the current module. The main configuration area is divided into several sections:

- Help on: Realign: Estimate & Reslice**: A list of options for the current module, including 'Data', 'Session', 'Estimation Options', and 'Reslice Options'. The 'Data' section is highlighted with a red box, showing two sessions: '...ing Corr. Images (Sess 1)' and '...ing Corr. Images (Sess 2)'.
- Estimation Options**: Parameters for image estimation, including Quality (0.9), Separation (4), Smoothing (FWHM) (5), Num Passes (Register to mean), Interpolation (2nd Degree B-Spline), Wrapping (No wrap), and Weighting (0 files).
- Reslice Options**: Parameters for reslicing, including 'Resliced images' (All Images + Mean Image).
- Current Item: Data**: A list of actions for the current item, including 'New: Session', 'Replicate: Session (1)', 'Replicate: Session (2)', 'Delete: Session (1)', and 'Delete: Session (2)'. The 'New: Session' option is highlighted.

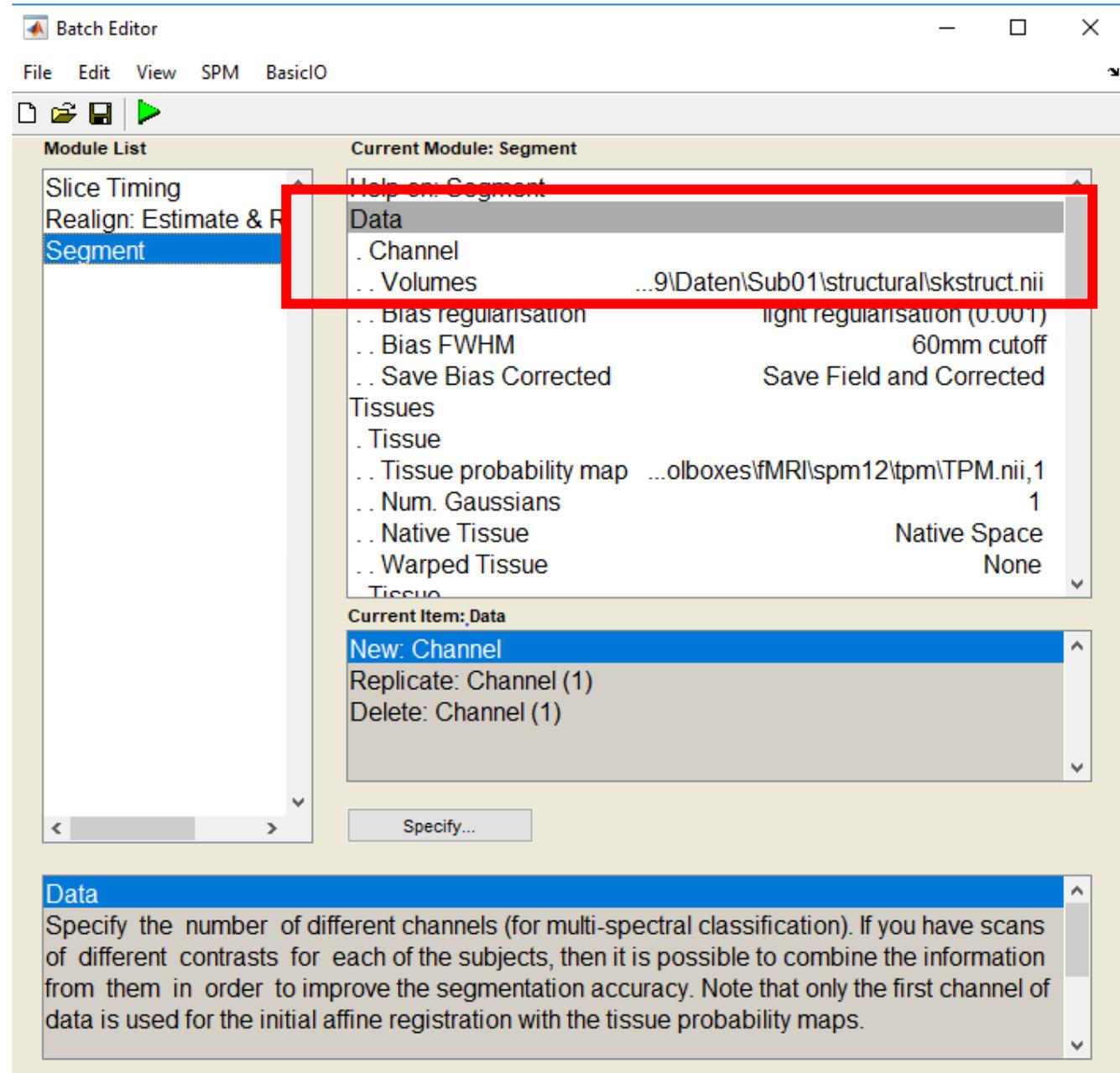
At the bottom of the window, there is a 'Specify...' button and a detailed description of the 'Data' section:

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



# Segment

- Choose skstruct.nii to be segmented.
- This will segment the anatomical and correct it for bias fields (save bias corrected) and compute mapping (deformation) to standard MNI space – «Deformation fields».



Don't forget to change Tissue Probability Maps, TPM.nii

# Coregister

- Coregister the mean functional to the anatomy (bias corrected) both selected via dependencies.
- Apply same transformation to all realigned fmri images (via dependencies).

The screenshot shows the Batch Editor software interface. The title bar reads "Batch Editor". The menu bar includes "File", "Edit", "View", "SPM", and "BasicIO". The toolbar contains icons for file operations and a green play button. The main window is divided into several sections:

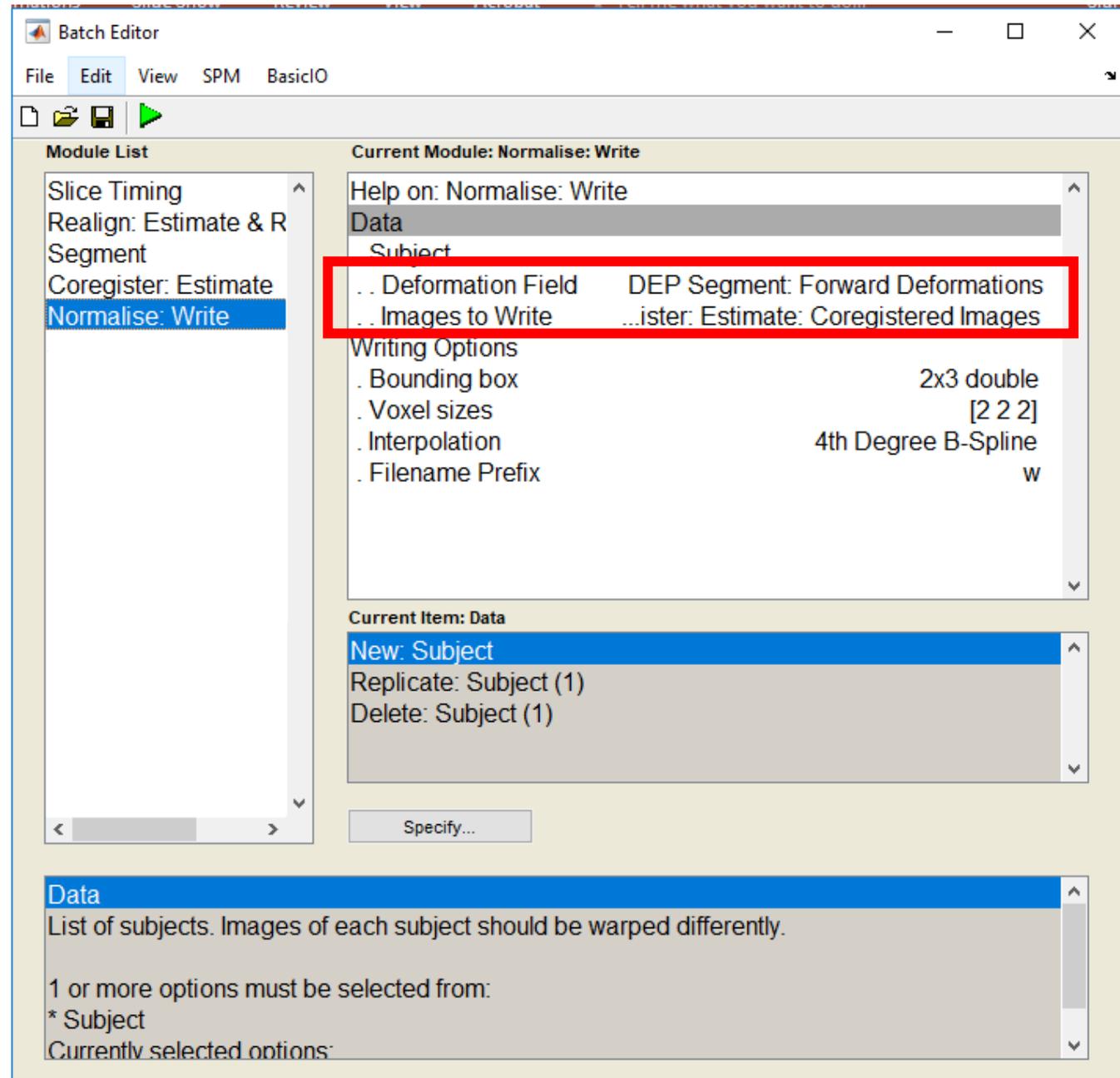
- Module List:** A list of modules on the left, with "Coregister: Estimate" selected and highlighted in blue.
- Current Module: Coregister: Estimate:** A central panel showing the configuration for the selected module. It includes a "Help on: Coregister: Estimate" link and a table of inputs and outputs. A red box highlights the following entries:

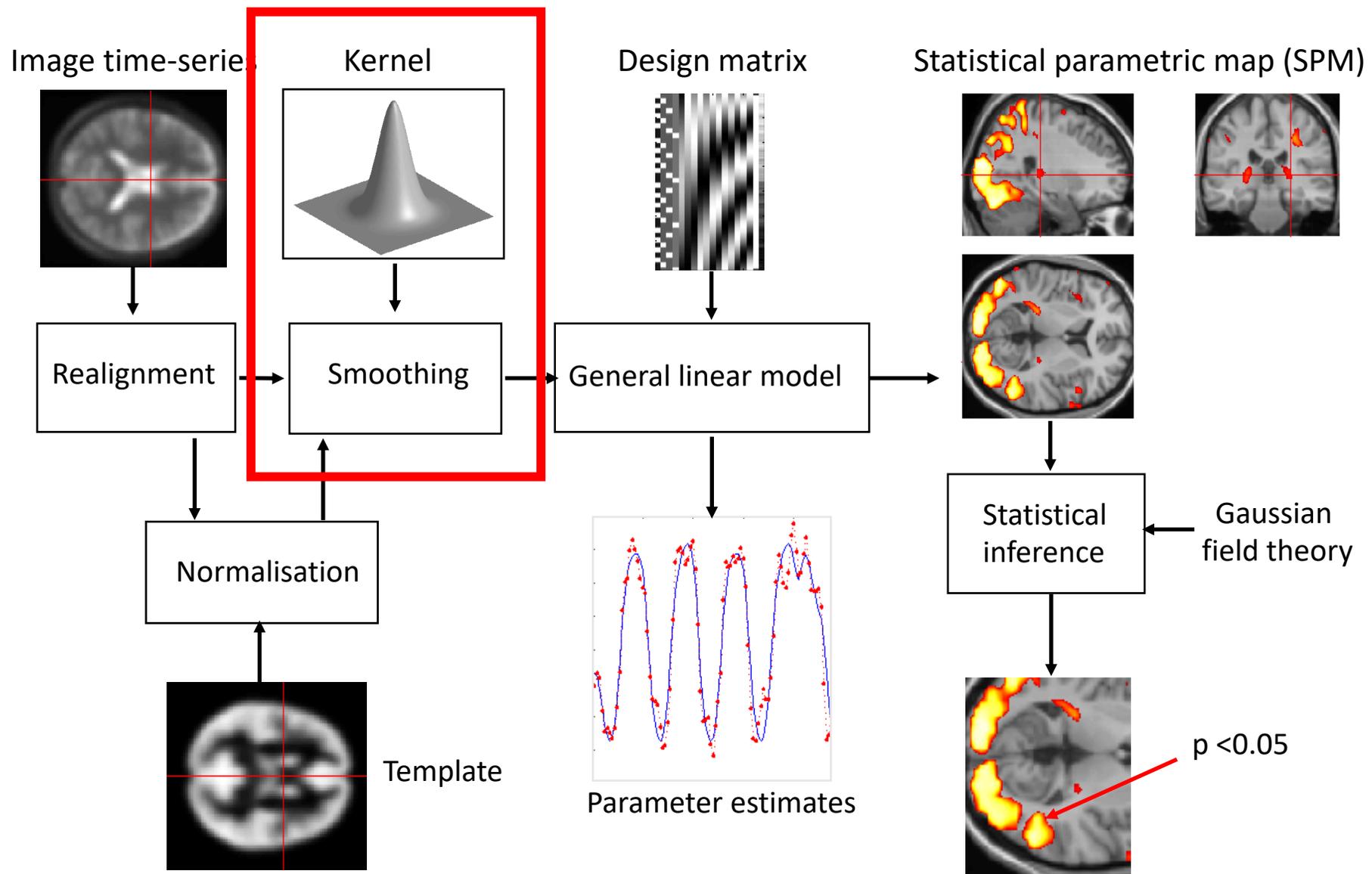
Reference Image	DEP Segment: Bias Corrected (1)
Source Image	...Estimate & Reslice: Mean Image
Other Images	DEP (3 outputs)
- Estimation Options:** A list of options for the estimation process:

. Objective Function	Normalised Mutual Information
. Separation	[4 2]
. Tolerances	1x12 double
. Histogram Smoothing	[7 7]
- Current Item: Reference Image:** A dropdown menu showing "Reference from Segment: Bias Corrected (1)".
- Buttons:** "Specify..." and "Dependency" buttons are located below the configuration panel.
- Reference Image Description:** A text box at the bottom provides a definition: "Reference Image: This is the image that is assumed to remain stationary (sometimes known as the target or template image), while the source image is moved to match it."

# Normalize fmri

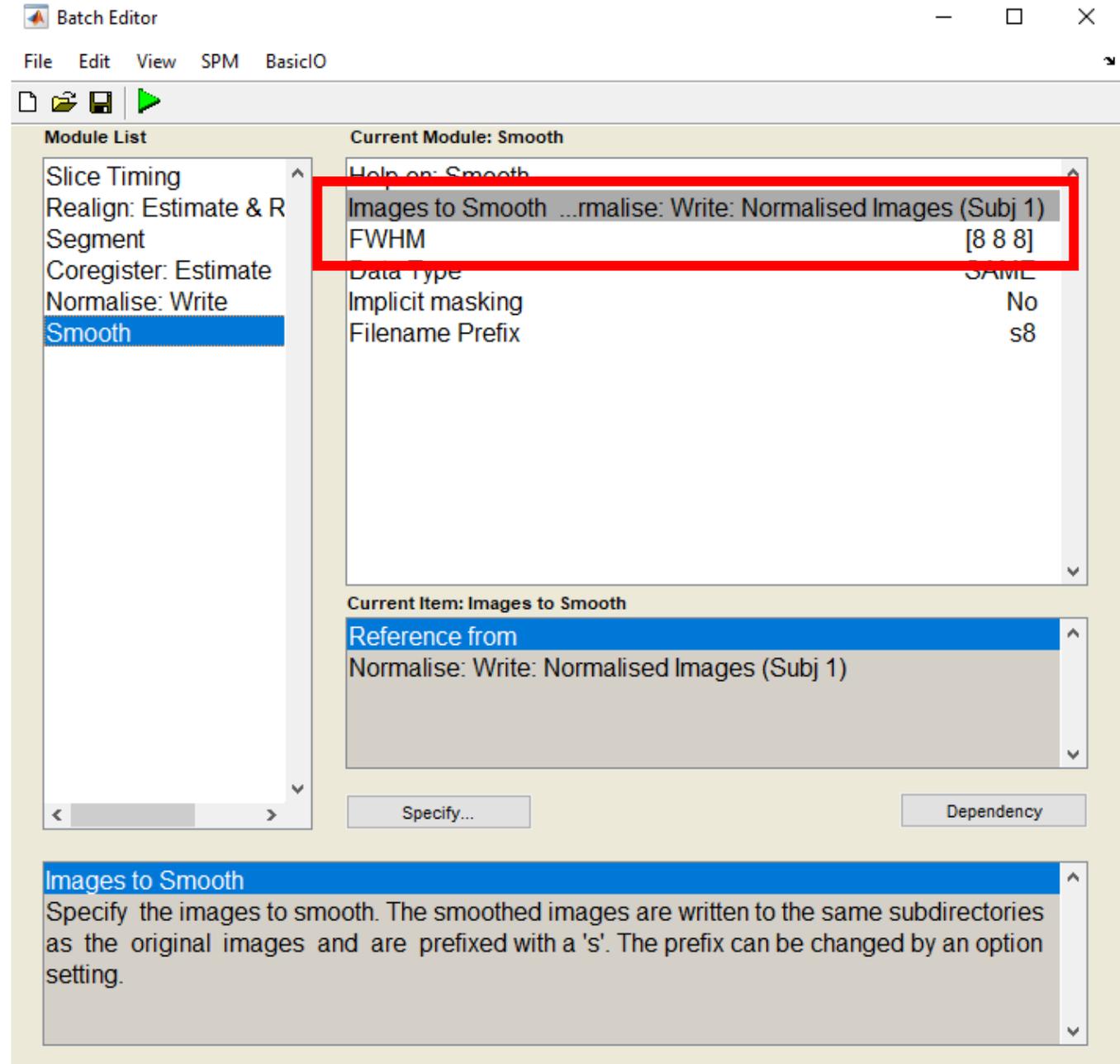
- Deform fMRI images to standard space (use coregistered images and deformation field from anatomy). -> Dependencies





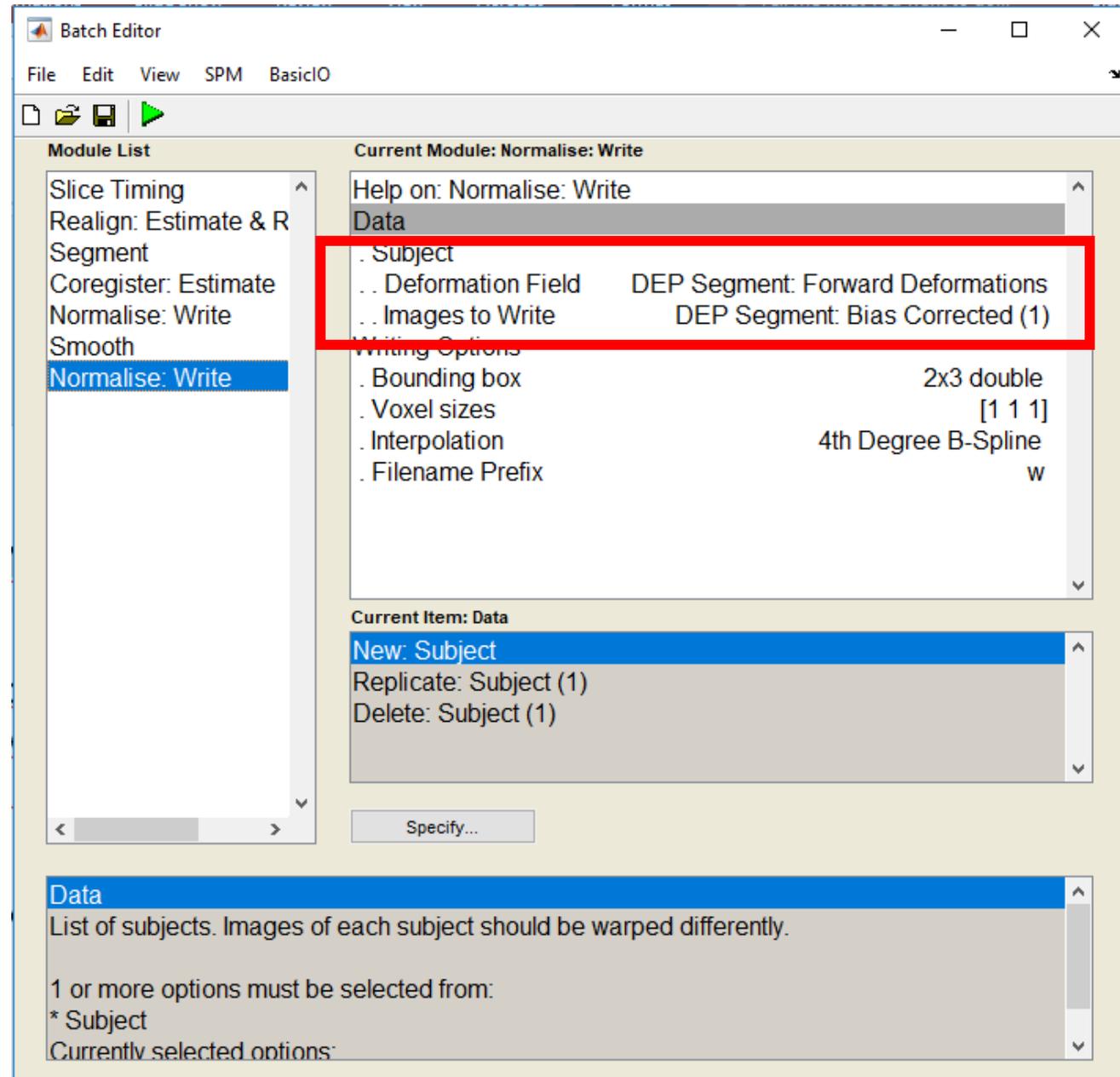
# Smoothing

- Apply smoothing to normalized fMRI data (via dependencies)
- Set FWHM to [8 8 8]

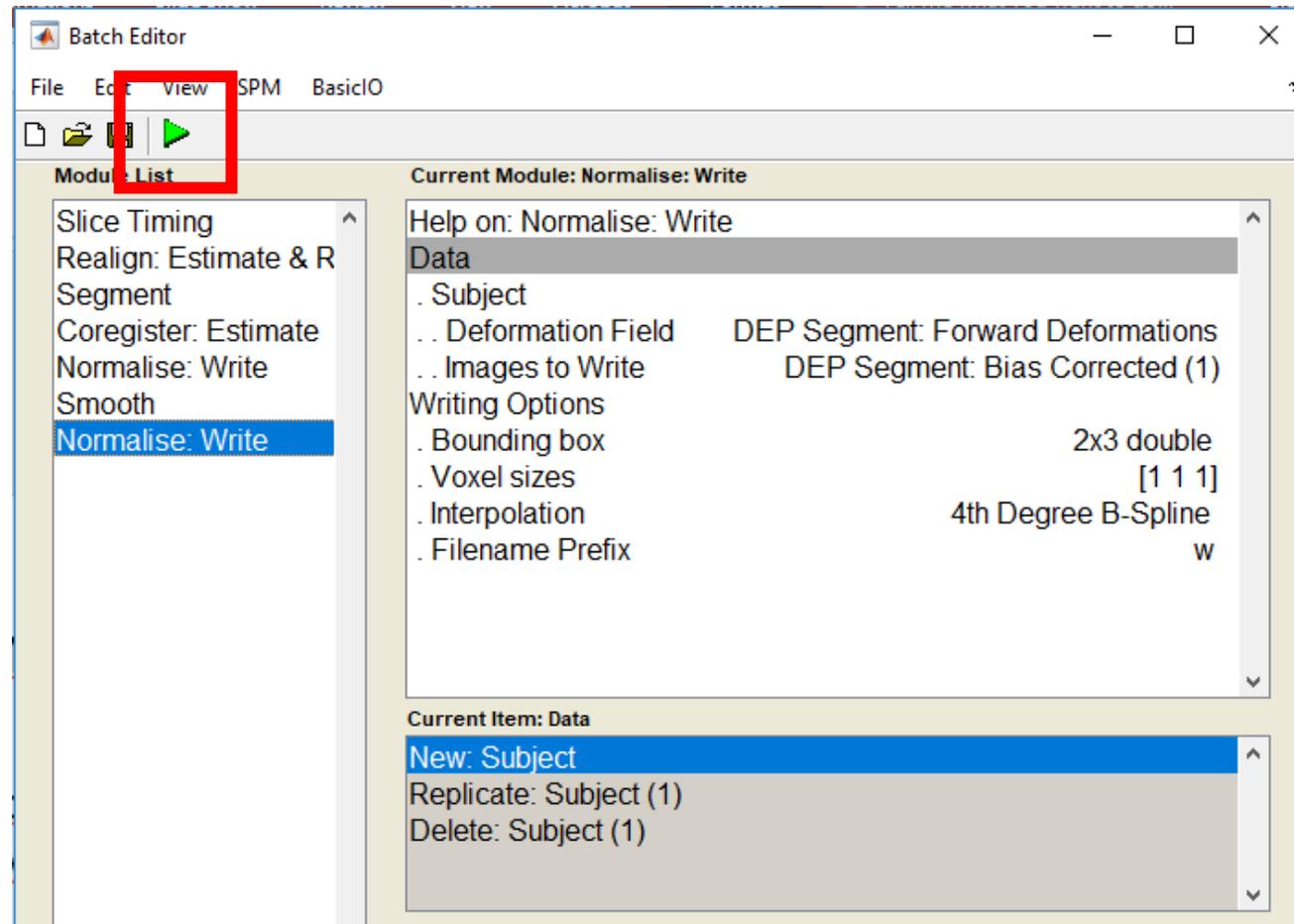


# Normalize anatomy

- Deform skstruct.nii image to standard space (use coregistered image and deformation field from anatomy). -> Dependencies
- Set voxel size to [1 1 1]
- Mainly used for display purposes later on.



# Run the preprocessing batch



# MED students presentations

- Form 4-5 groups of 2-3 people each.
- Each group will give one presentation about their analysis.
- Within your analysis you should present a specific question ( you can come up with your question):
  - E.g. how do results differ between regressors (e.g. LRArrow vs. LRPress)
  - How do results differ across participants?
  - Compare different pipelines, e.g. for preprocessing (with and without slice time correction, ...)
  - How do the results change, when motion regressors are included or not, or with and without derivatives of the HRF.

# MED students presentations

- On Nov. 5 you will present your analysis. Every person needs to present a short part of the presentation (1-2 slides per person).
- We will then discuss your results together.

Break

# Run a batch function directly from matlab.

- In MATLAB go to the code folder where you should have placed the function `teach_prepro_subject.m`.
- Run this function by typing  
`teach_prepro_subject('path/to/Sub01', 2);`  
Where you will need to change the path to match your data storage!
- This should open the batch editor with an entire preprocessing page prespecified.
- Check whether this batch is what you expect and run it.
- Go through the function and try to understand what it is doing.
- Where are the parameters etc. specified?