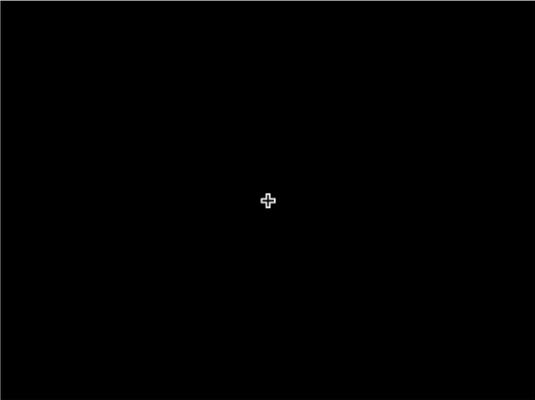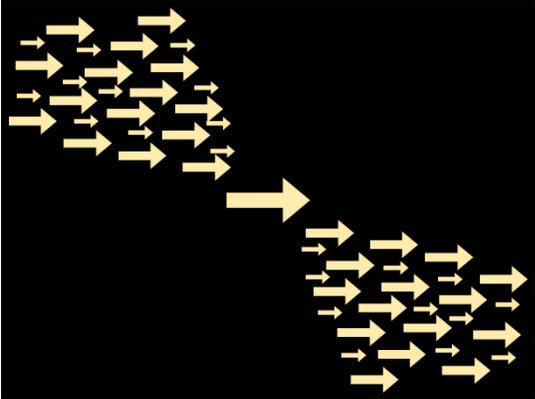# Tutorial – Preprocessing
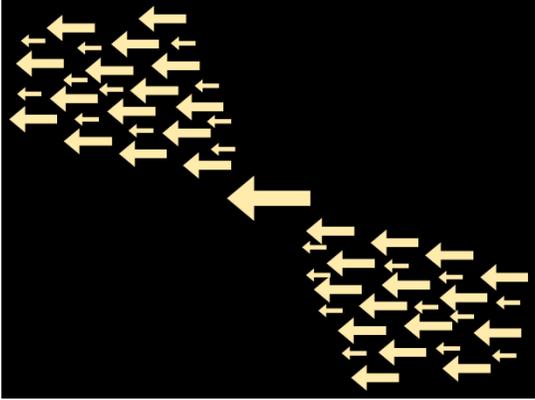
# The experiment
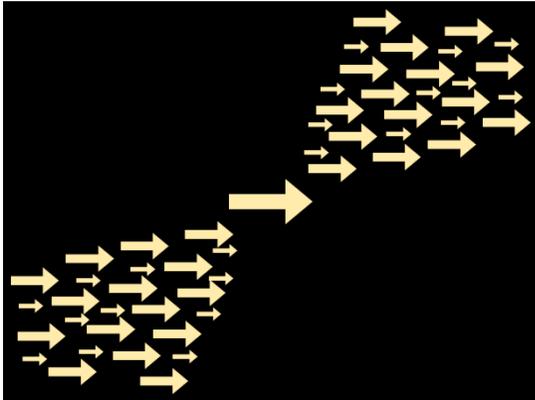


**Fixation**

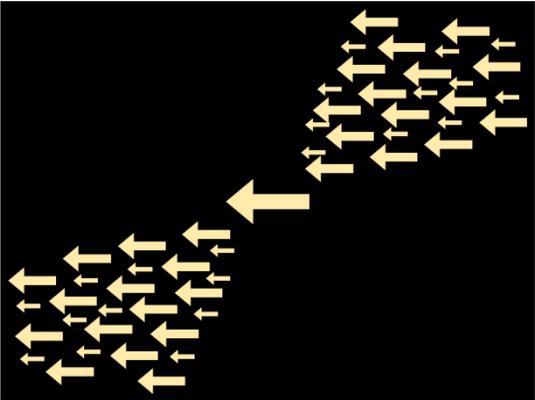Top left wedge
Wedge1

Top right wedge
Wedge2

**Press right**

**Press left**

# 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 → <span style="color:red">Never touch this during analysis</span> |
| 📁 structural | – | Anatomical/Structural MRI scans for analyis |

# Behavioral data (next week)

BehaviorSummary01
BehaviorSummary02 → Behavior analysis (Errors etc.)

BehavRun01
BehavRun02 → All behavioral data

DCMRegs01 → Regressors for DCM

IndividualRegs01
IndividualRegs02 → Regressors for all 4 conditions

LRArrowRegs01
LRArrowRegs02 → **Regressors (left arrow vs. right arrow)**

LRPressRegs01
LRPressRegs02 → **Regressors (left press vs. right press)**

WedgeModRegs01
WedgeModRegs02 → Wedge regressors with arrow modulation

WedgeMotorRegs01
WedgeMotorRegs02 → Wedge regressors (event) and motor regressors (events)

WedgeRegs01
WedgeRegs02 → **Regressors (TL-BR wedge vs. TR-BL wedge)**

# 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
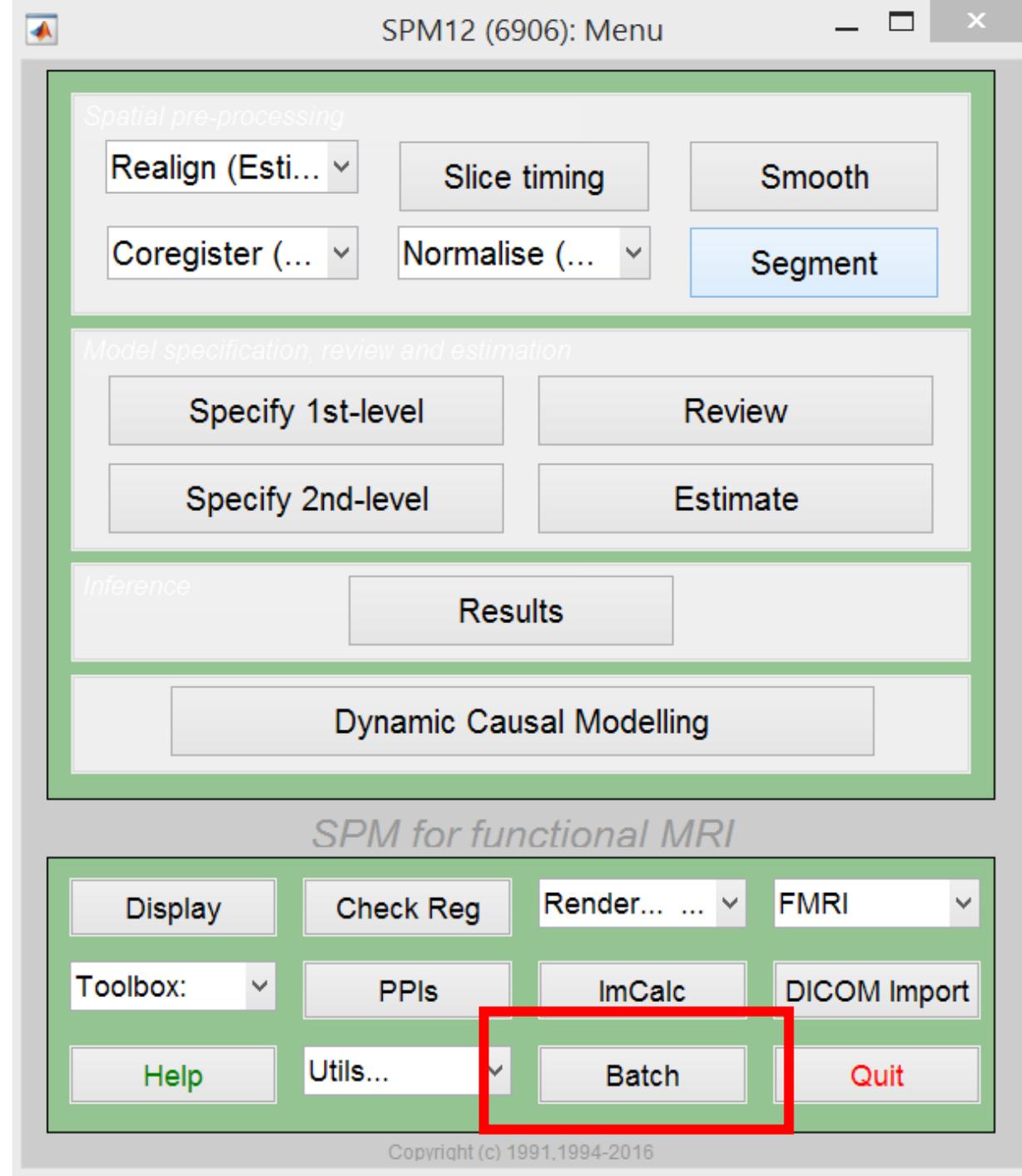
– B0 field maps

fmri01.nii
fmri02.nii

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

skstruct.nii

– 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.
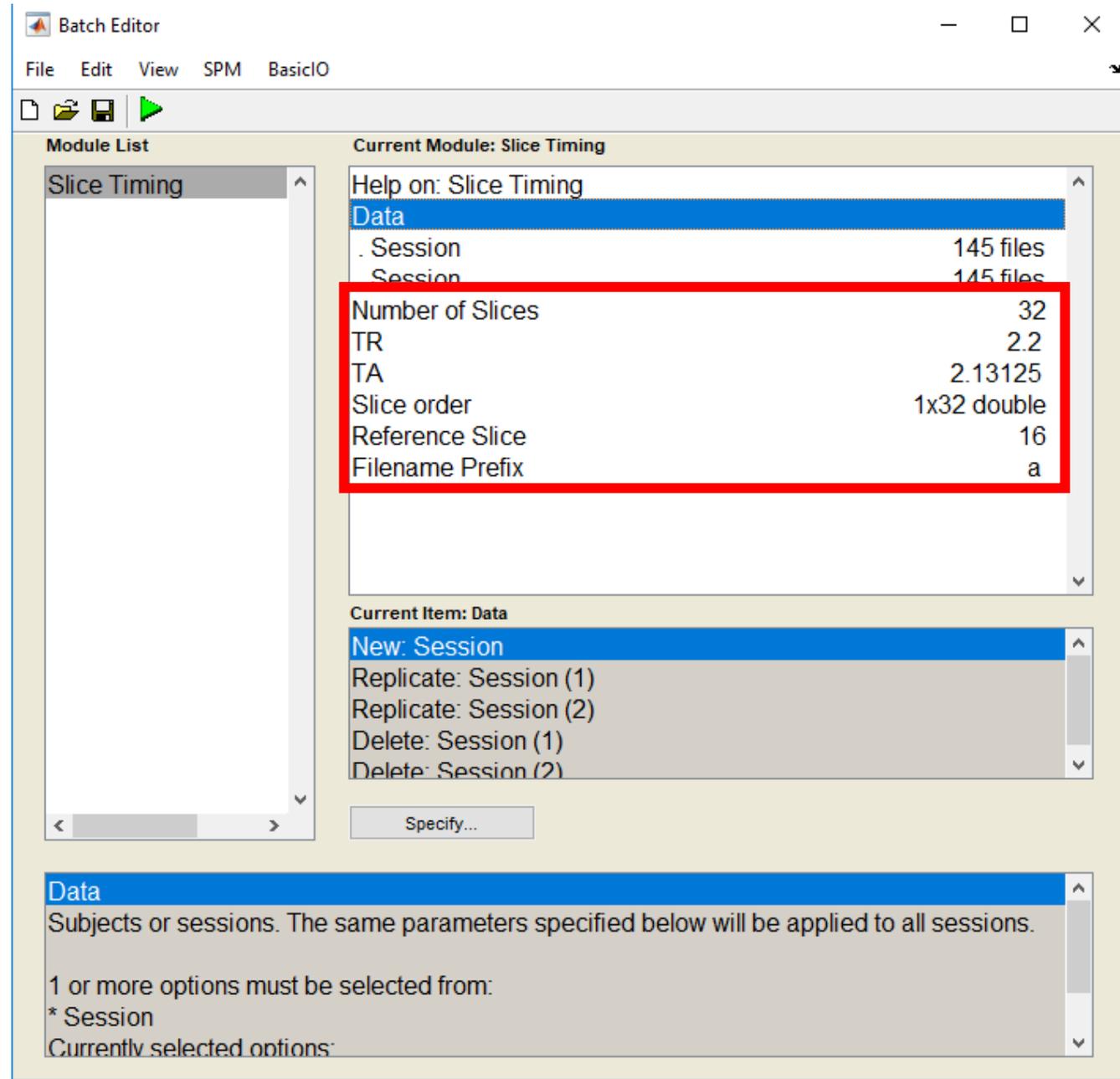
# SPM main menu

# Preprocessing

Image time-series

Kernel

Design matrix

Statistical parametric map (SPM)



Realignment

Smoothing

General linear model

Normalisation

Template

Parameter estimates

Statistical inference

Gaussian field theory

p <0.05
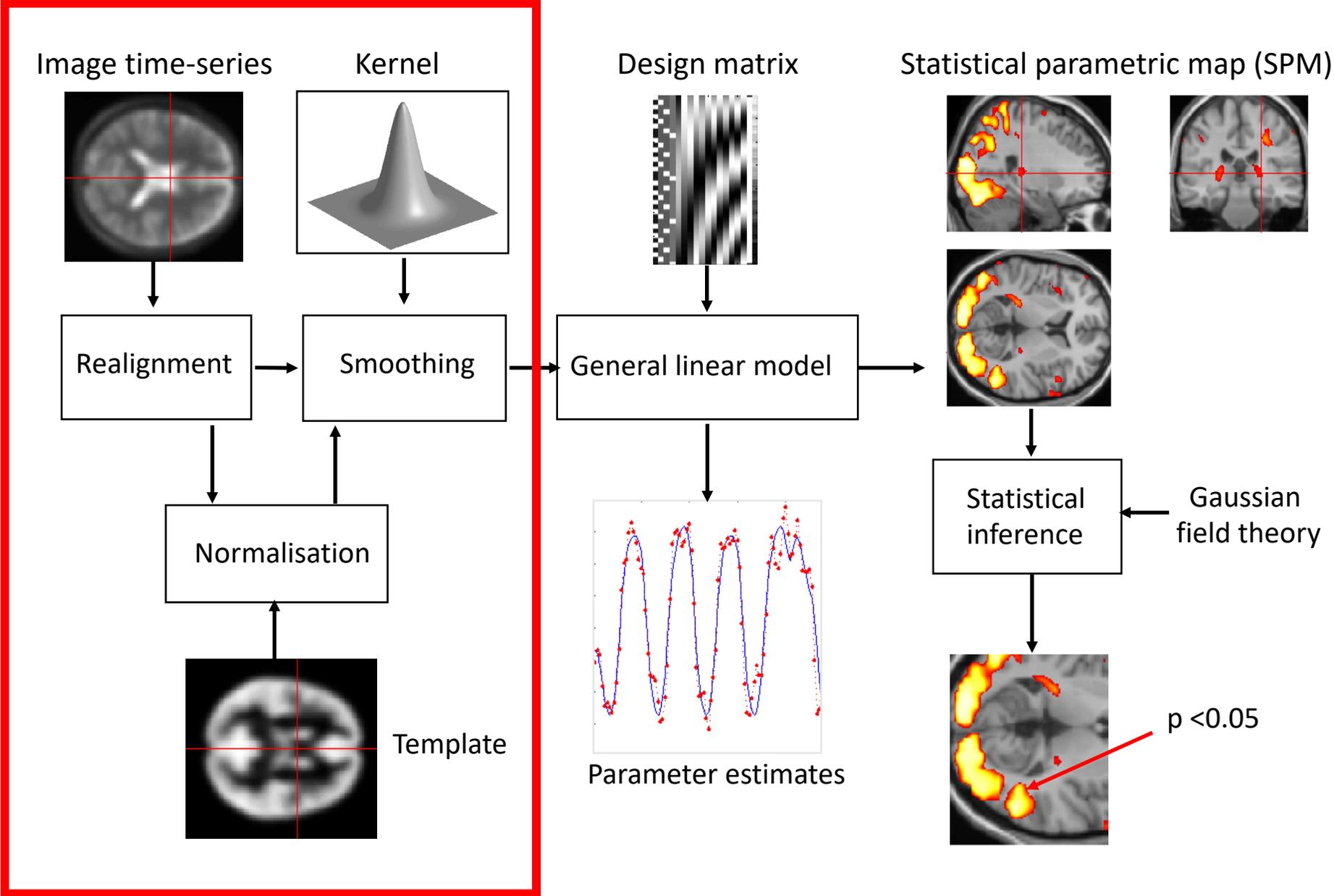
# Add fmri

- Select the run fmri01.nii for the first session, and fmri02.nii for the second session.

- Each contains 145 volumes (i.e. files)
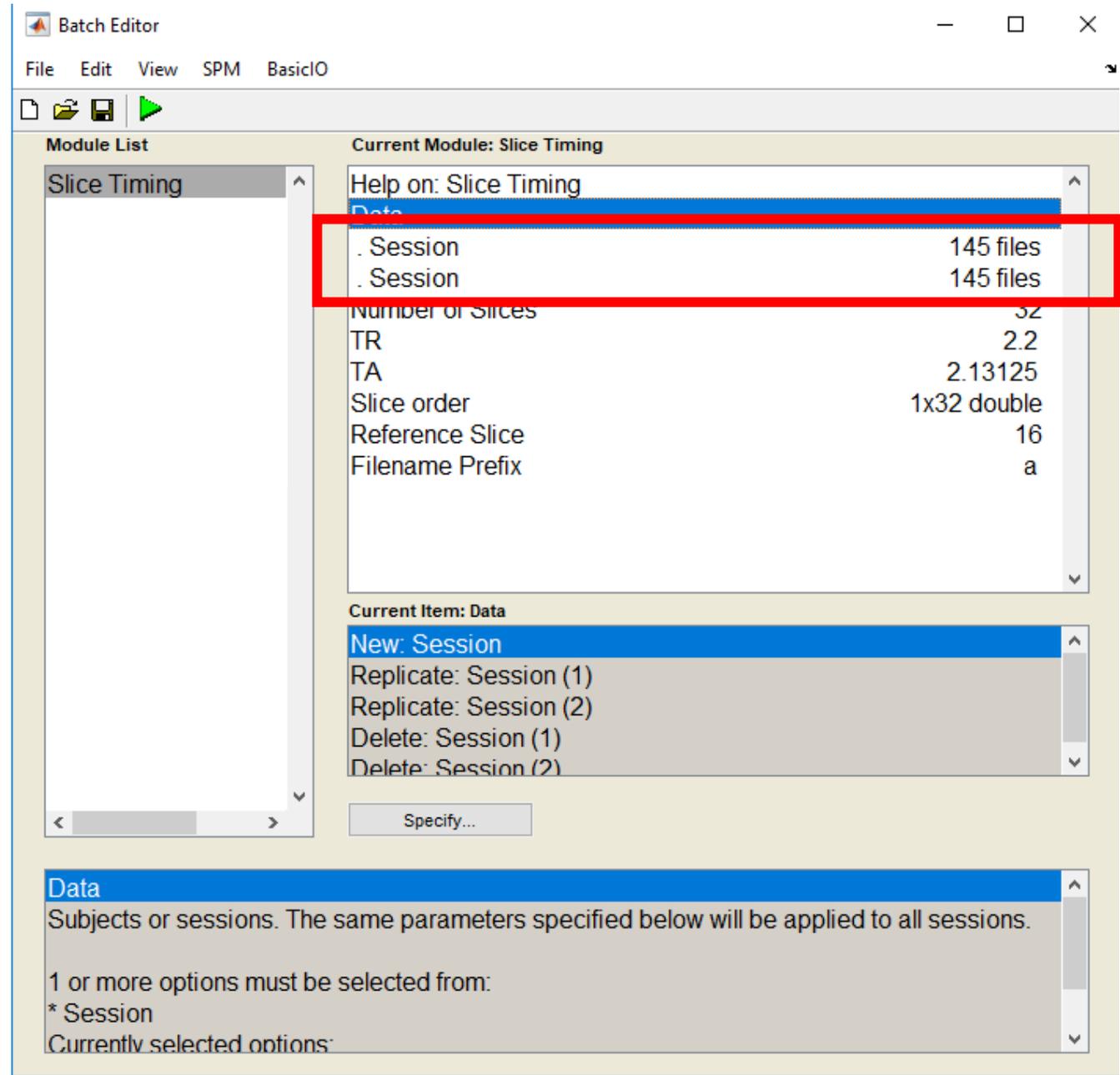
# Slice timing

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

Image time-series | Kernel | Design matrix | Statistical parametric map (SPM)

Realignment → Smoothing → General linear model

Normalisation

Template

Parameter estimates

Statistical inference ← Gaussian field theory

p <0.05

# Realignment

- Use result of «Slice Timing» using Dependencies

- Keep all default parameters.

Image time-series — Kernel — Design matrix — Statistical parametric map (SPM)

Realignment → Smoothing → General linear model →

Normalisation

Template

Parameter estimates

Statistical inference ← Gaussian field theory

p <0.05

# 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».
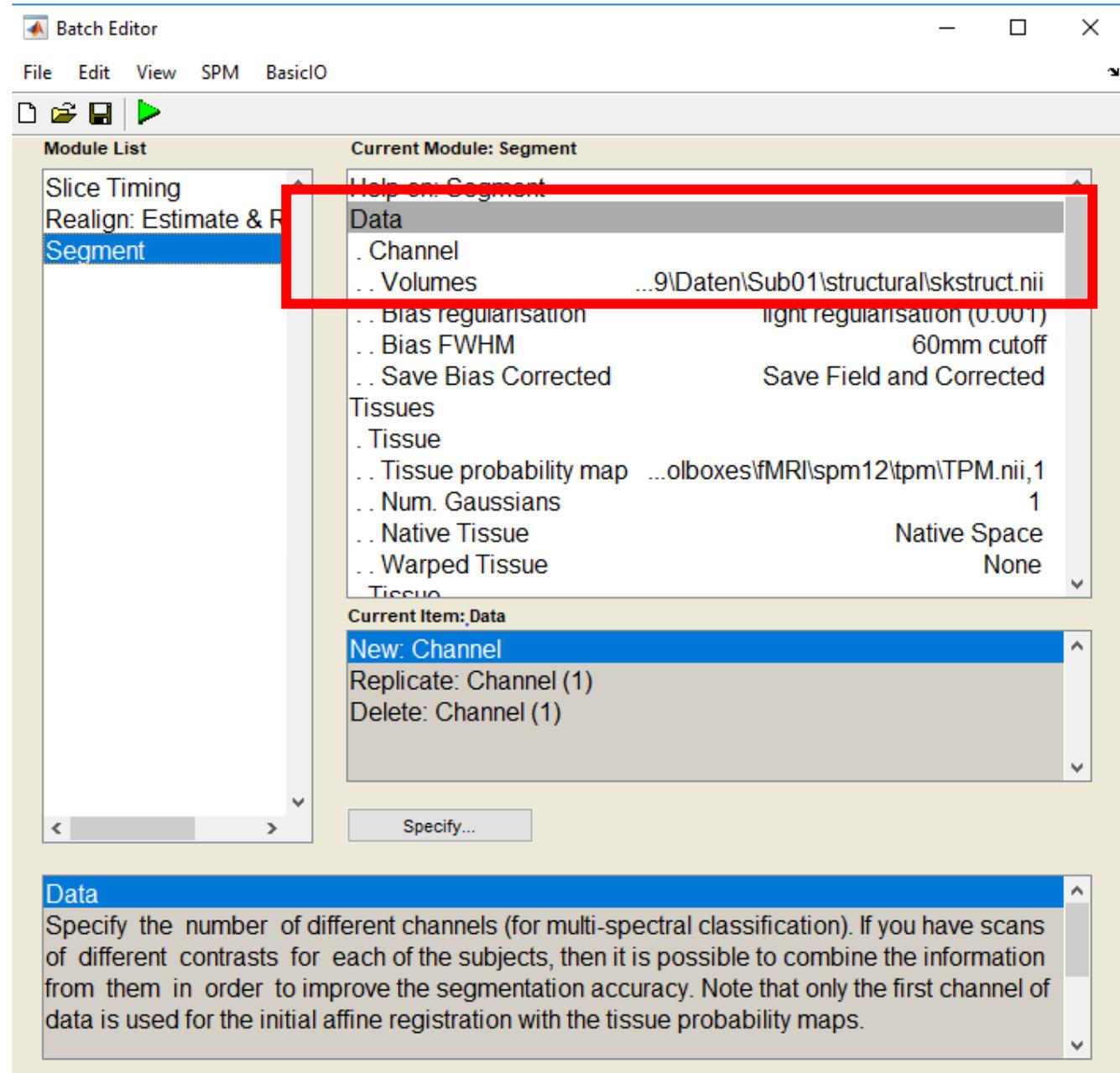


Don't forget to change Tissue Probability Maps, TPM.nii

# Coregister

- Coregister the mean functional to the anatomy (bias corrected) both selected via dependencies.

- Apply same transformation to all realigned fmri images (via dependencies).

# Normalize fmri

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

Image time-series | Kernel | Design matrix | Statistical parametric map (SPM)

Realignment → Smoothing → General linear model

Normalisation

Template

Parameter estimates

Statistical inference ← Gaussian field theory

p <0.05
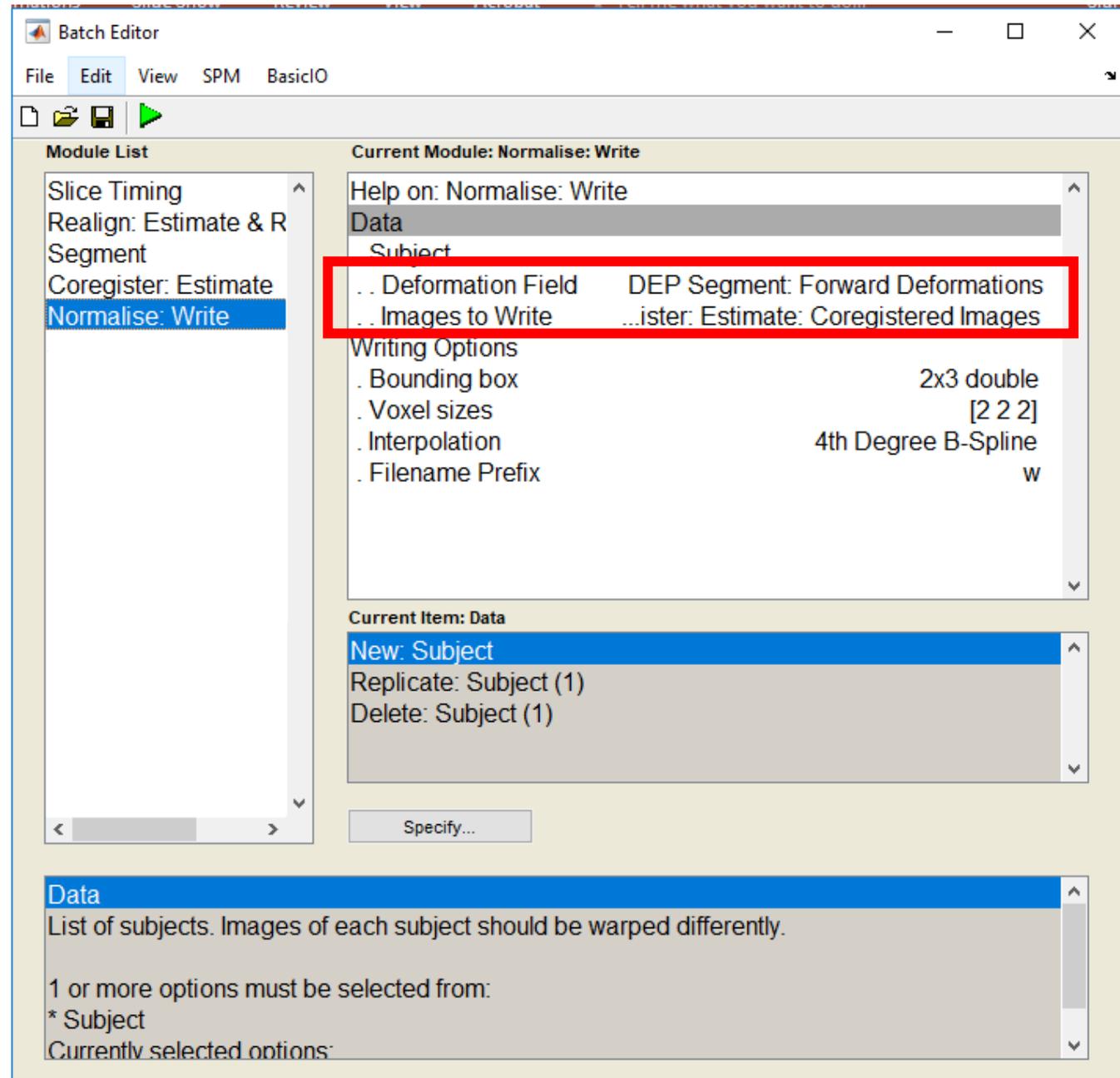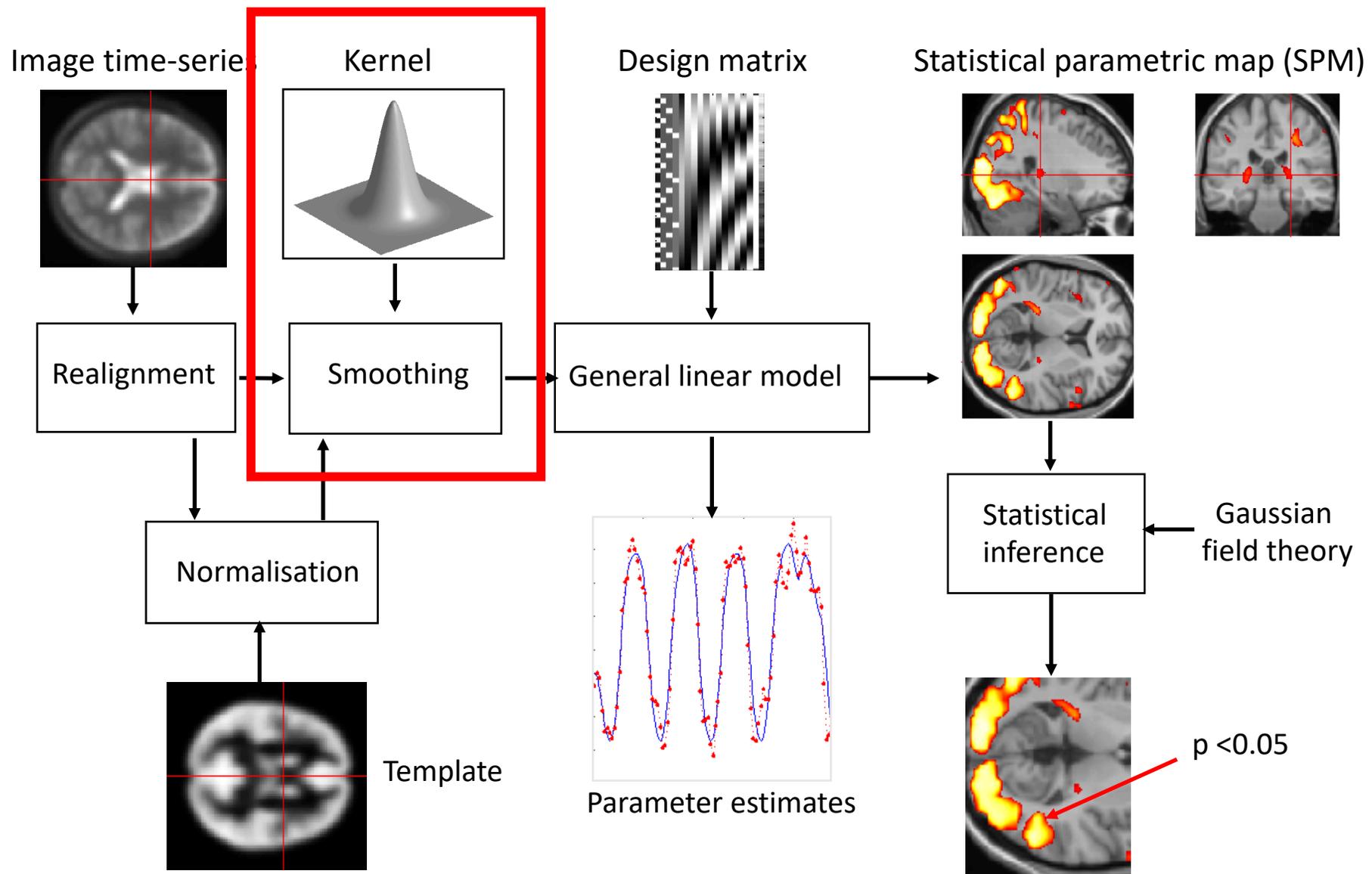
# Smoothing

- Apply smoothing to normalized fMRI data (via dependencies)

- Set FWHM to [8 8 8]

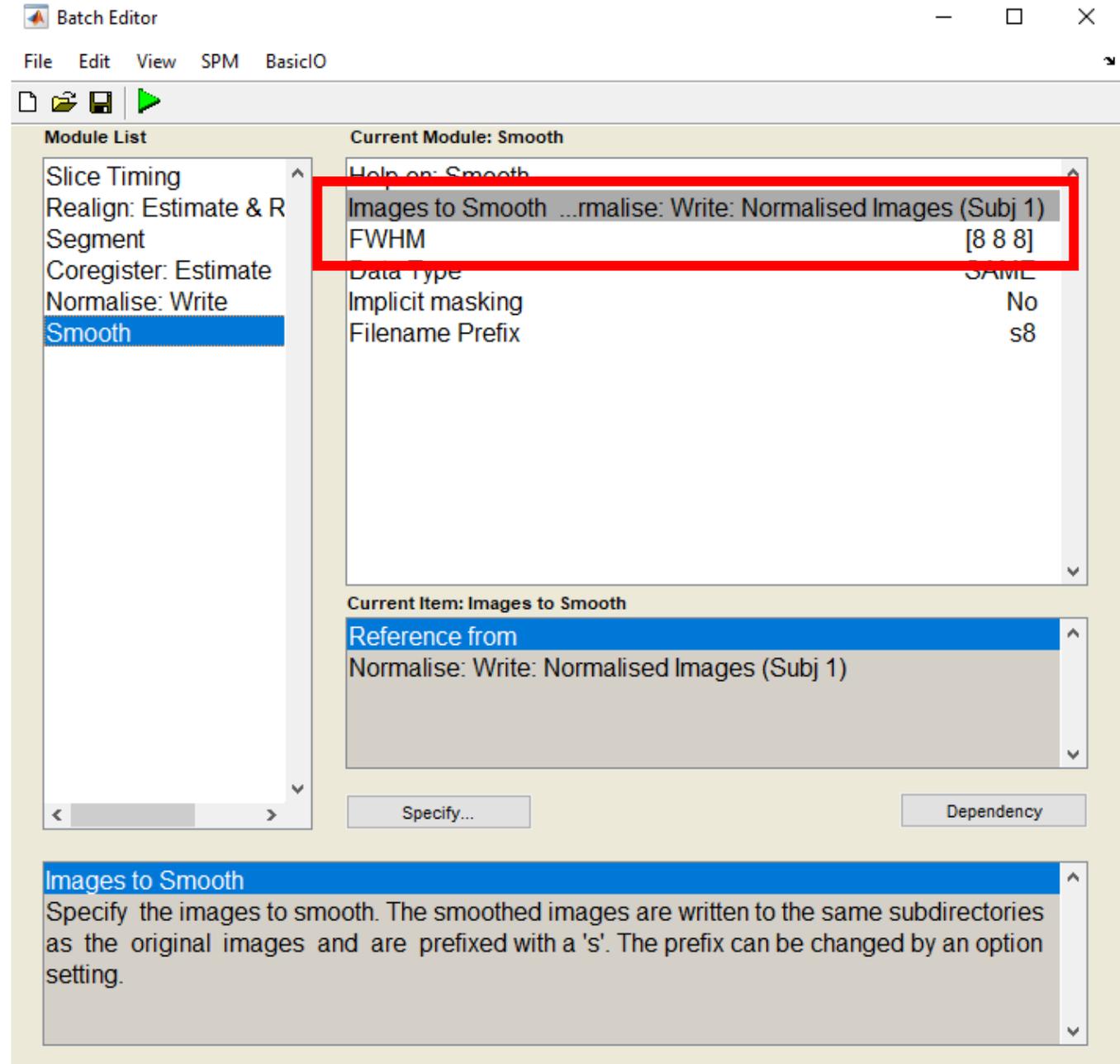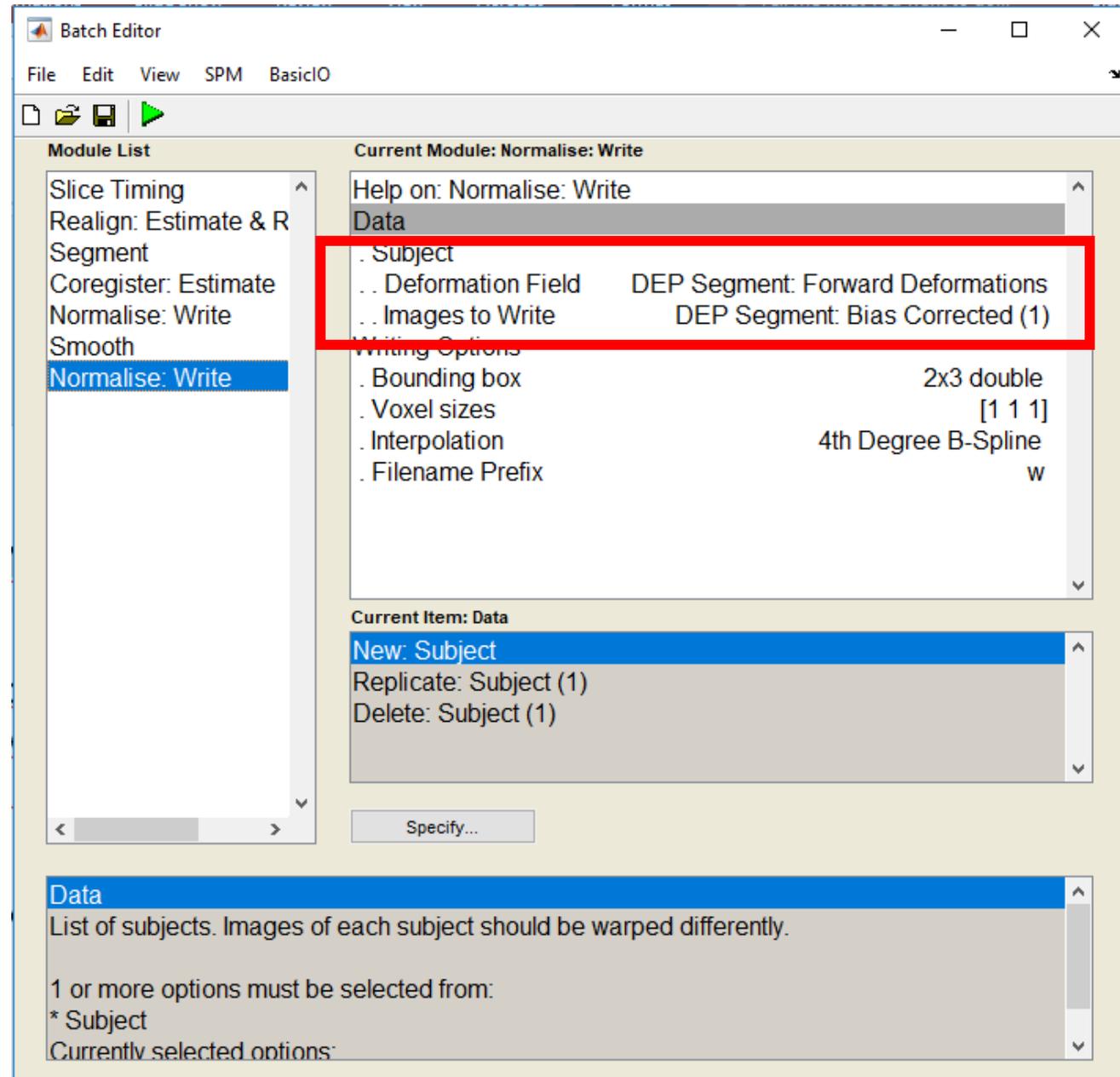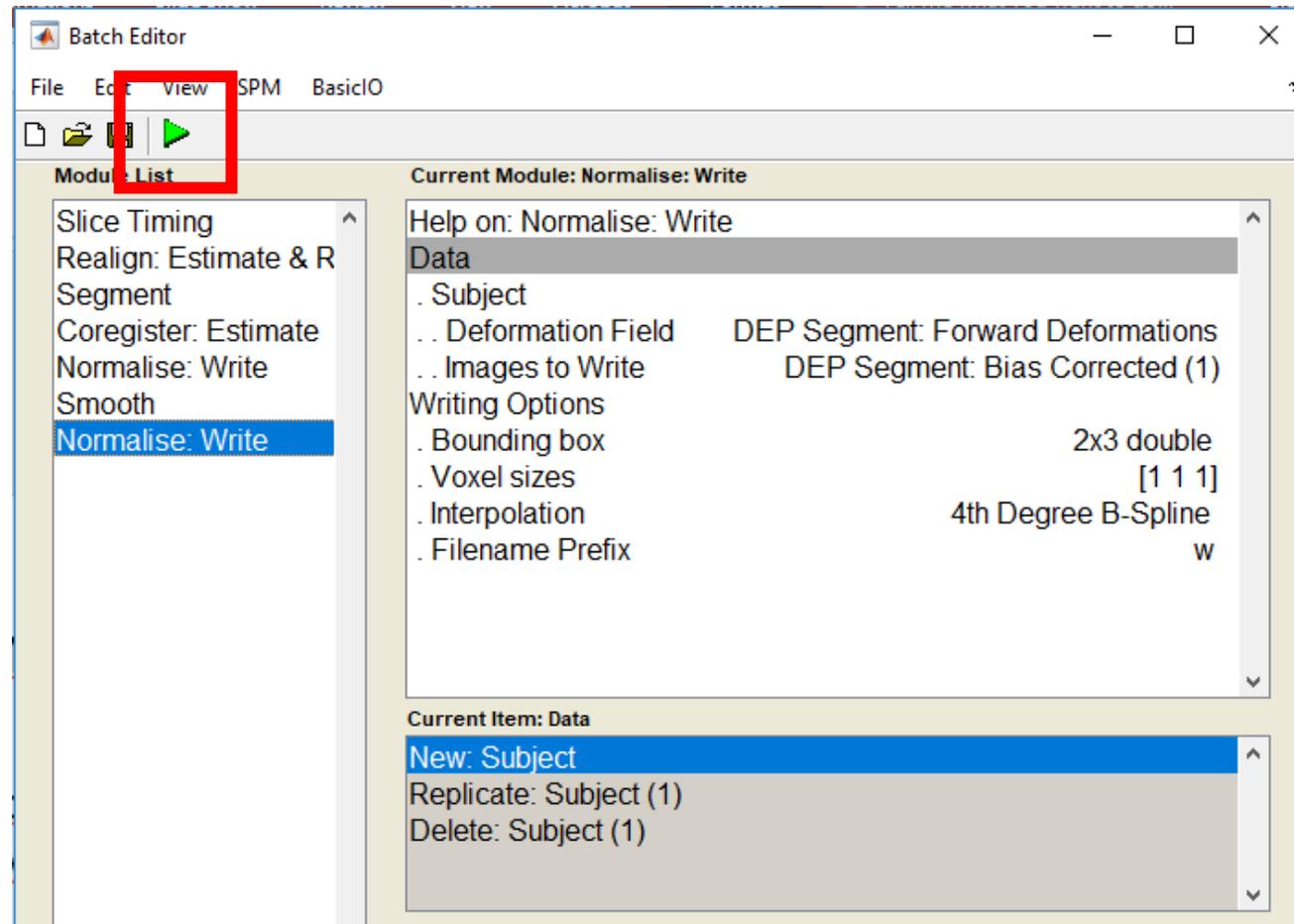# Normalize anatomy

- 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?