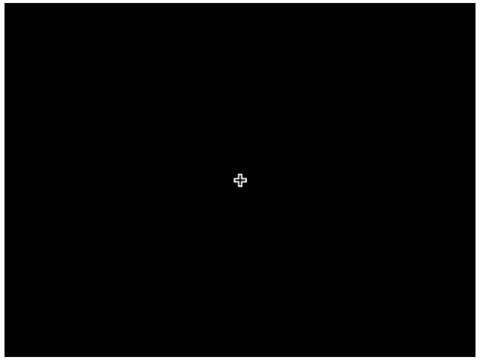
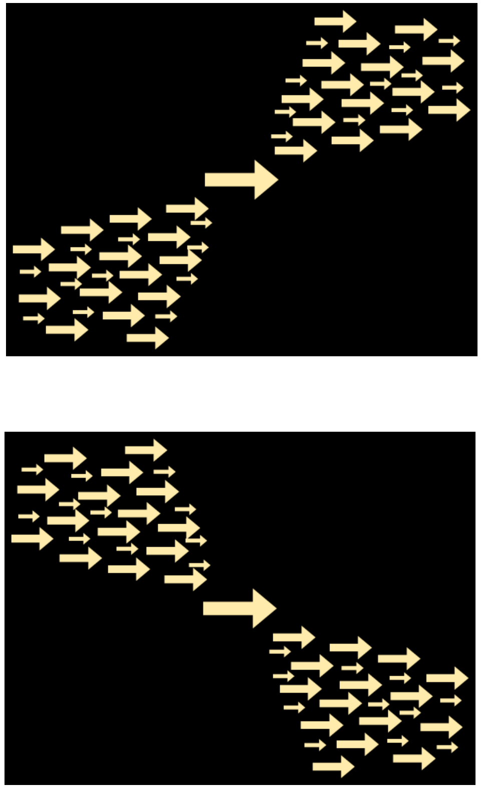
Running an entire first level SPM batch

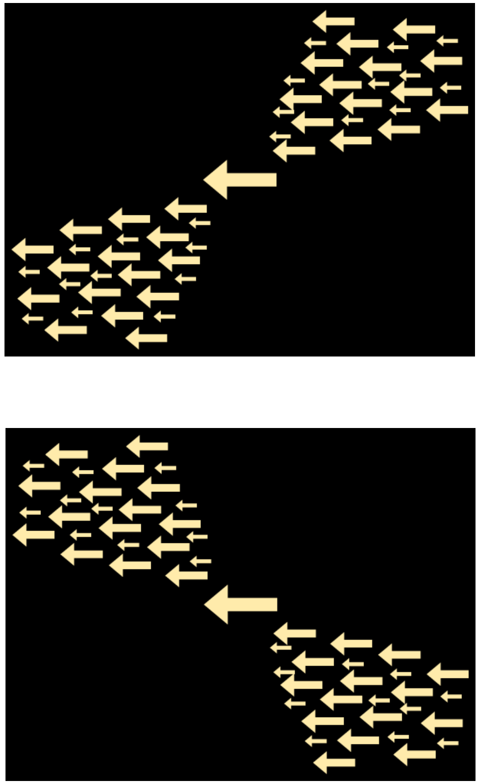
Task



Fixation



Press right

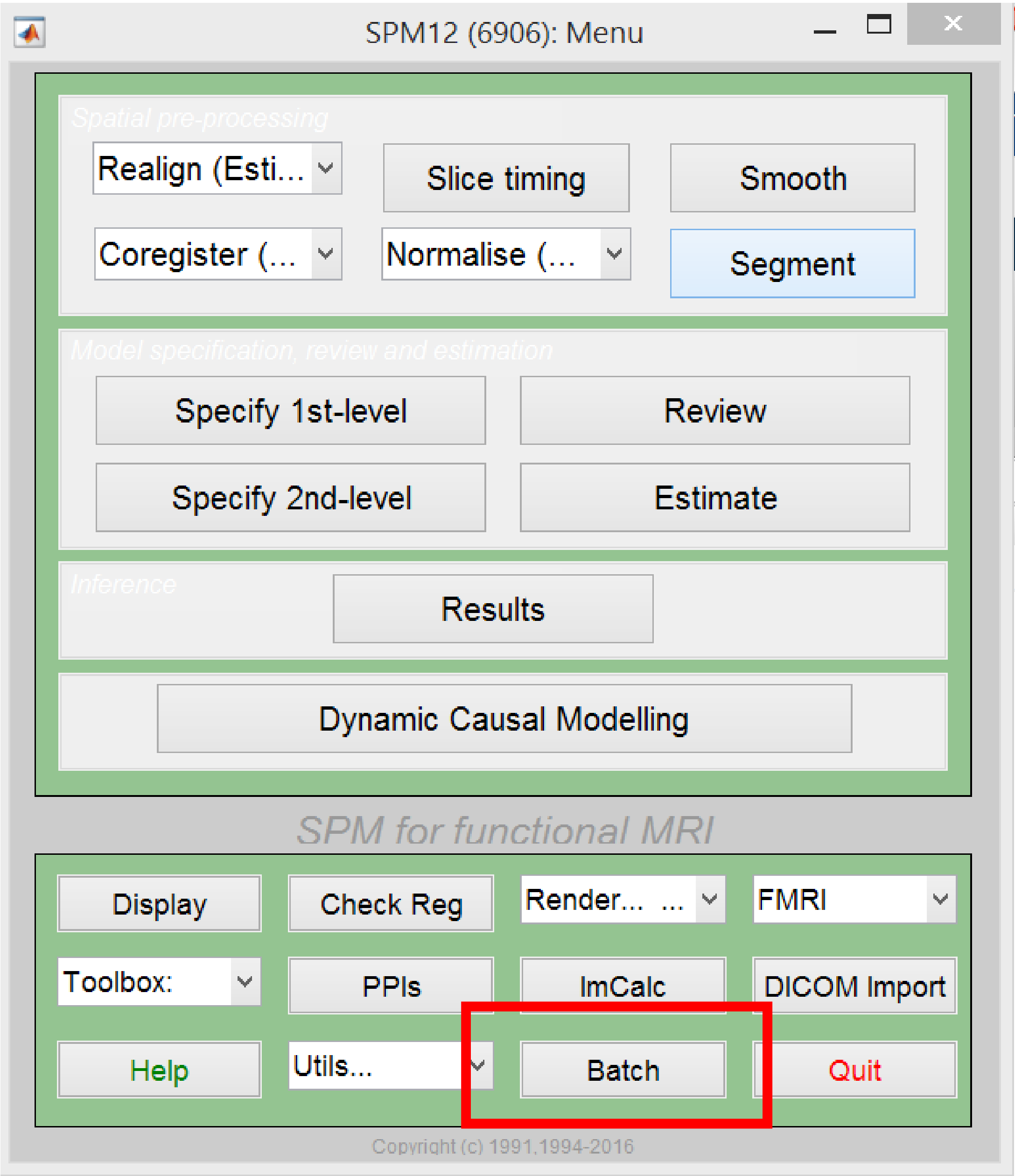


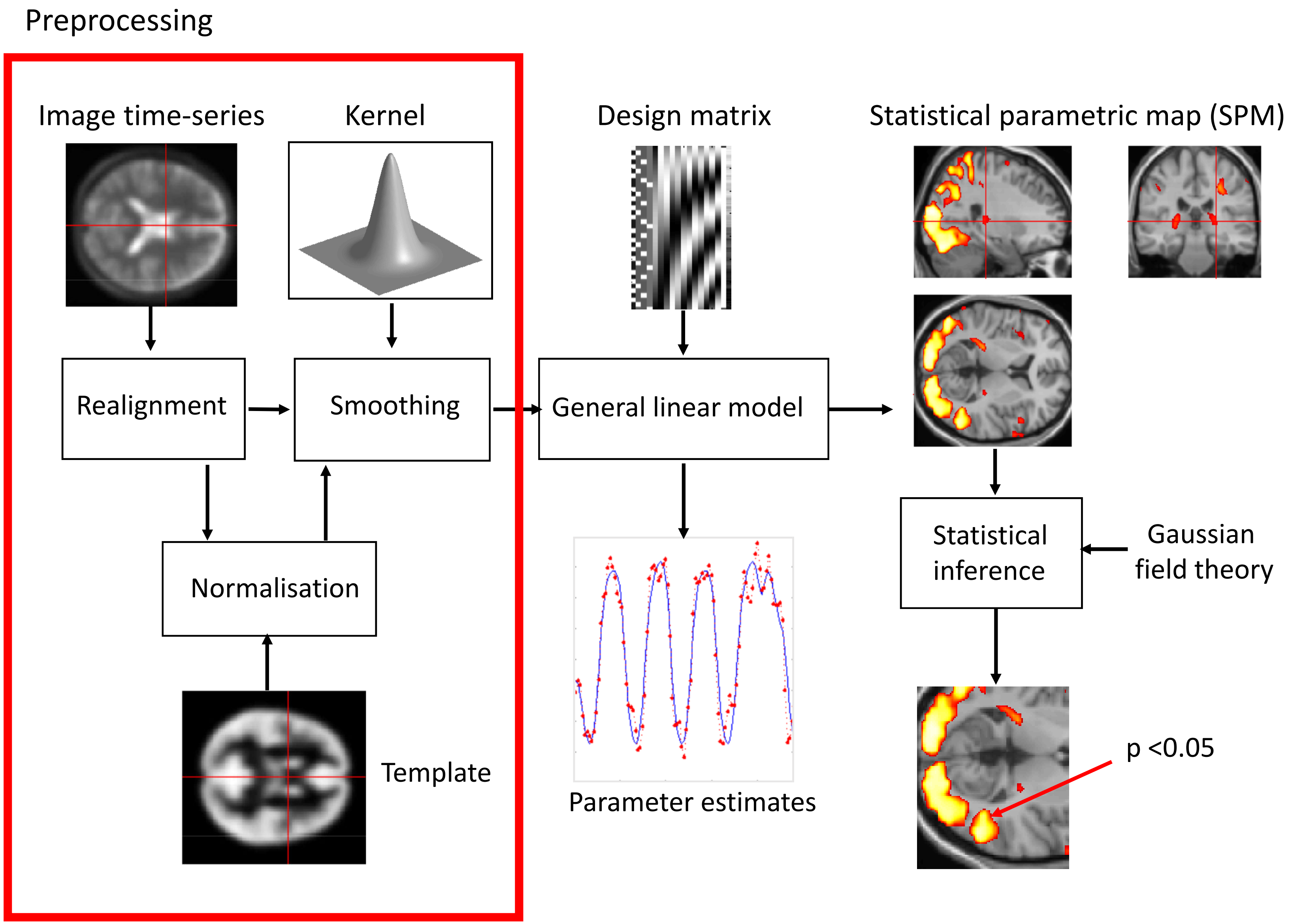
Press left

Design

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

SPM main menu





Preprocessing

Image time-series

Kernel

Realignment

Smoothing

Normalisation

Template

Design matrix

General linear model

Parameter estimates

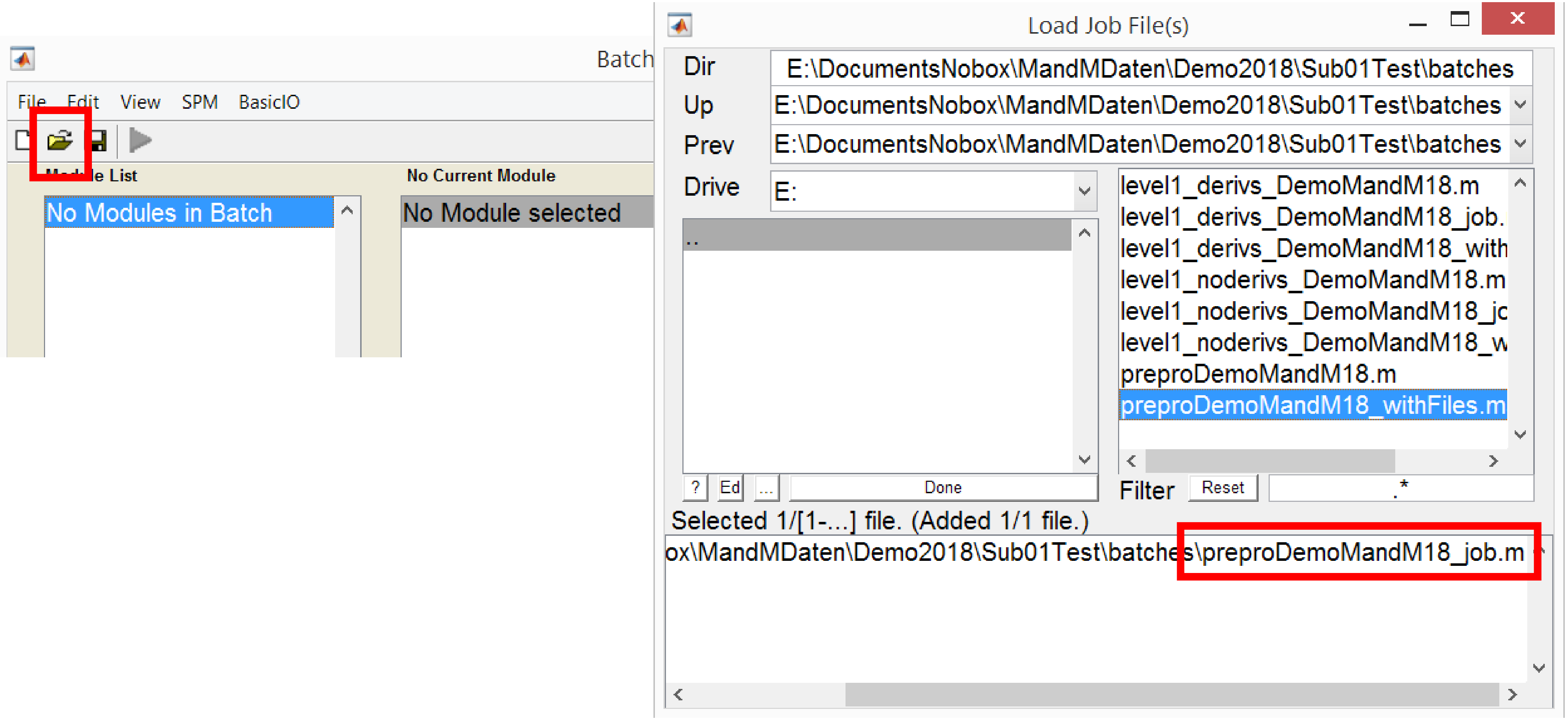
Statistical parametric map (SPM)

Statistical inference

Gaussian field theory

$p < 0.05$

Load the SPM batch



No Modules in Batch

No Module selected

Dir E:\DocumentsNobox\MandMDaten\Demo2018\Sub01Test\batches

Up E:\DocumentsNobox\MandMDaten\Demo2018\Sub01Test\batches

Prev E:\DocumentsNobox\MandMDaten\Demo2018\Sub01Test\batches

Drive E:

..

level1_derivs_DemoMandM18.m
level1_derivs_DemoMandM18_job.
level1_derivs_DemoMandM18_with
level1_noderivs_DemoMandM18.m
level1_noderivs_DemoMandM18_jc
level1_noderivs_DemoMandM18_w
preproDemoMandM18.m
preproDemoMandM18_withFiles.m

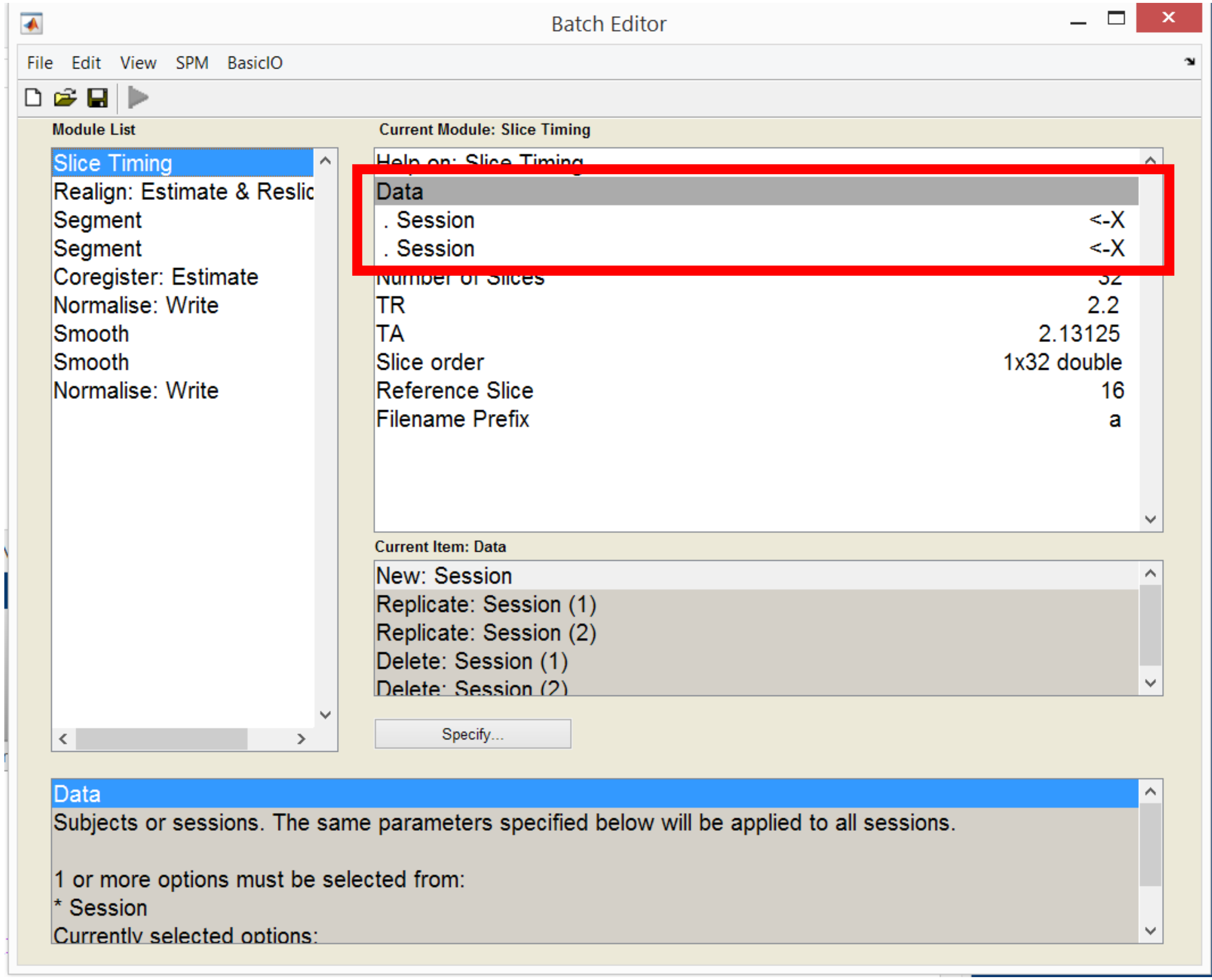
Filter .*

Selected 1/[1-...] file. (Added 1/1 file.)

ox\MandMDaten\Demo2018\Sub01Test\batches\preproDemoMandM18_job.m

Add fmri

- Select the run fmri01.nii for the first session, and fmri02.nii for the second session.
- Each contains 145 files



Slice Timing
Realign: Estimate & Reslic
Segment
Segment
Coregister: Estimate
Normalise: Write
Smooth
Smooth
Normalise: Write

Help on: Slice Timing
Data
. Session <-X
. Session <-X
Number of Slices 32
TR 2.2
TA 2.13125
Slice order 1x32 double
Reference Slice 16
Filename Prefix a

New: Session
Replicate: Session (1)
Replicate: Session (2)
Delete: Session (1)
Delete: Session (2)

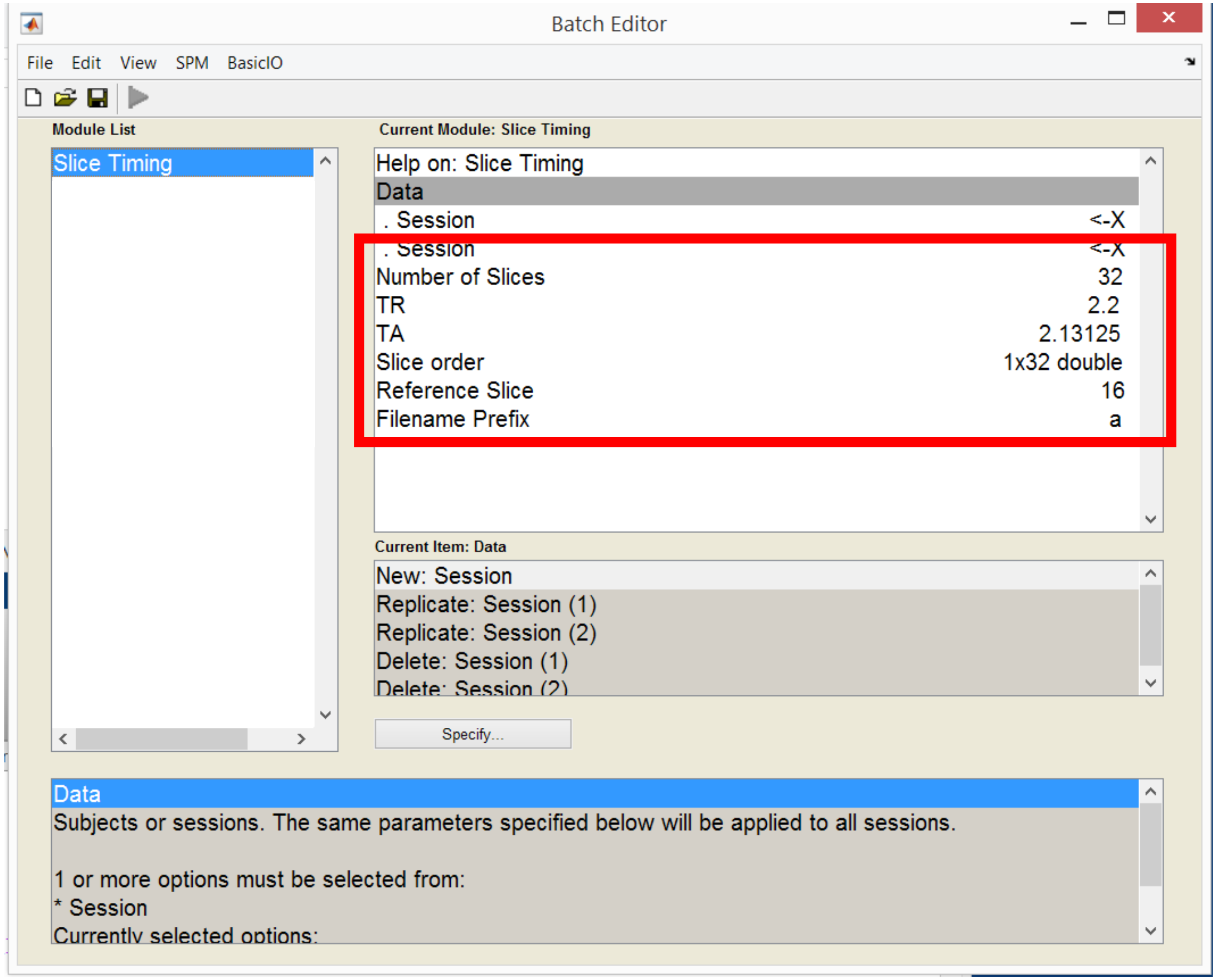
Data

Subjects or sessions. The same parameters specified below will be applied to all sessions.

1 or more options must be selected from:
* Session
Currently selected options:

Slice timing

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



Help on: Slice Timing

Data

. Session <-X

. Session <-X

Number of Slices 32

TR 2.2

TA 2.13125

Slice order 1x32 double

Reference Slice 16

Filename Prefix a

New: Session

Replicate: Session (1)

Replicate: Session (2)

Delete: Session (1)

Delete: Session (2)

Data

Subjects or sessions. The same parameters specified below will be applied to all sessions.

1 or more options must be selected from:

* Session

Currently selected options:

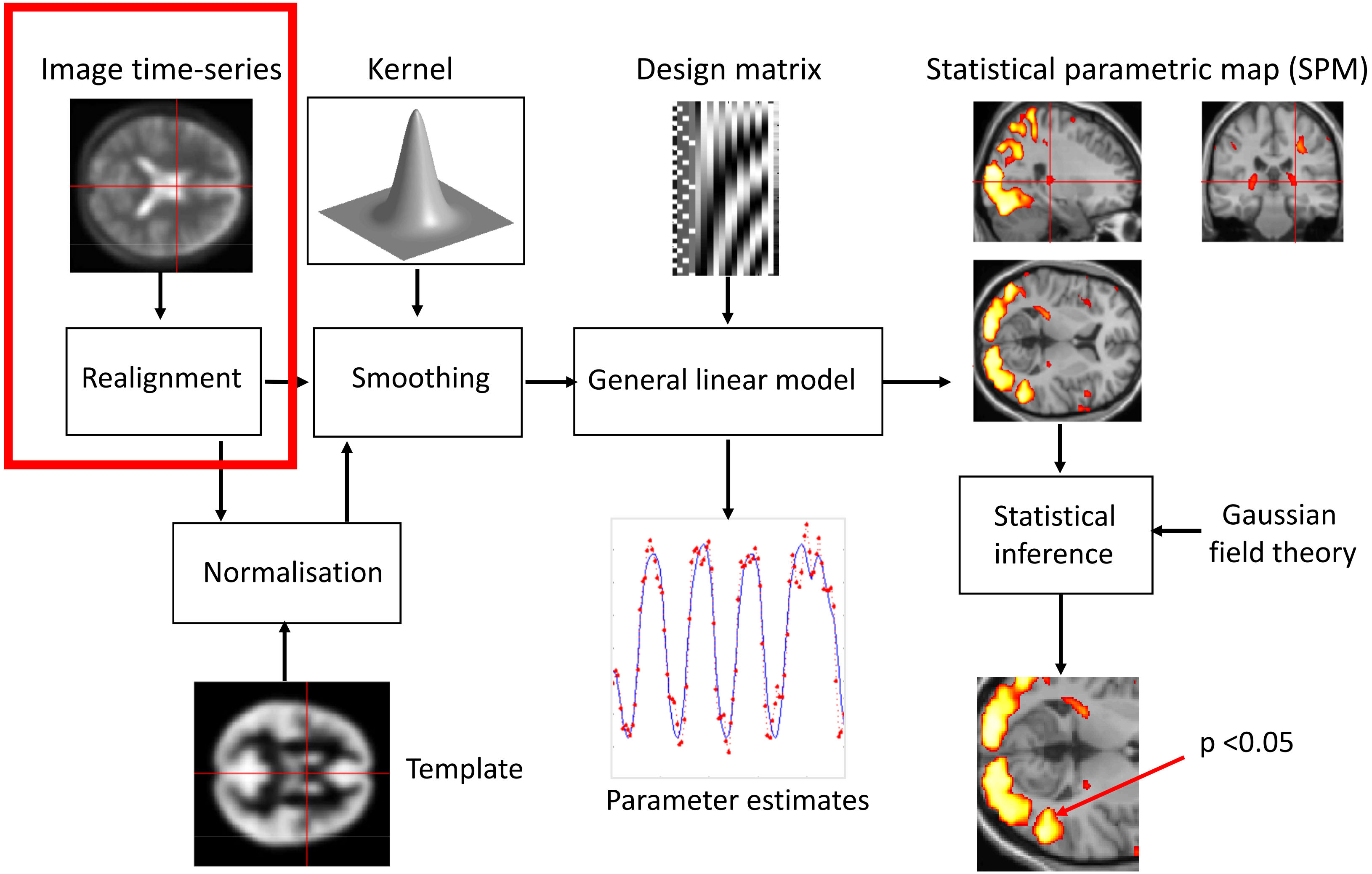


Image time-series

Kernel

Design matrix

Statistical parametric map (SPM)

Realignment

Smoothing

General linear model

Normalisation

Template

Parameter estimates

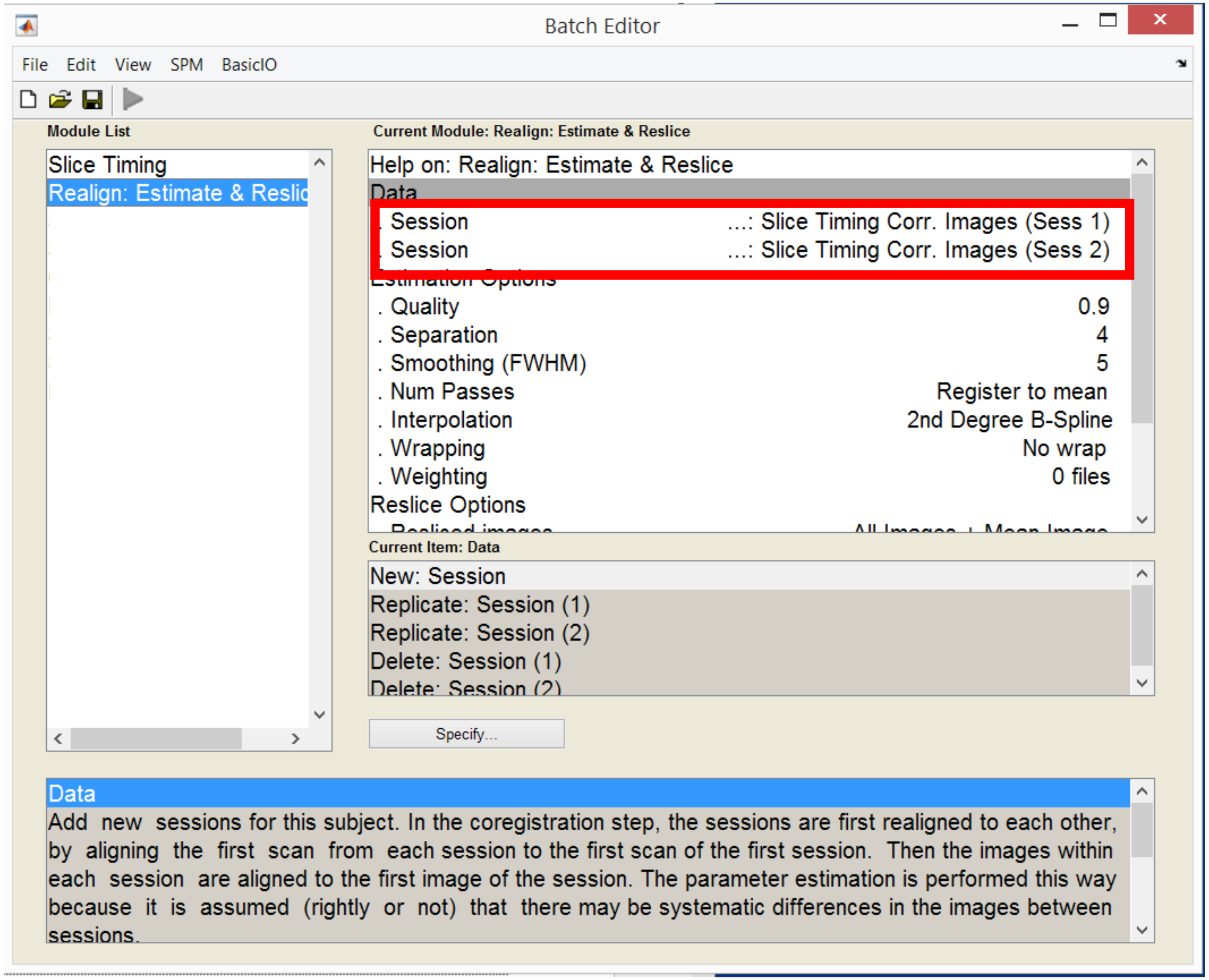
Statistical inference

Gaussian field theory

$p < 0.05$

Realignment

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



Help on: Realign: Estimate & Reslice

Data

. Session ...: Slice Timing Corr. Images (Sess 1)

. Session ...: Slice Timing Corr. Images (Sess 2)

Estimation Options

. Quality 0.9

. Separation 4

. Smoothing (FWHM) 5

. Num Passes Register to mean

. Interpolation 2nd Degree B-Spline

. Wrapping No wrap

. Weighting 0 files

Reslice Options

. Resliced images All Images + Mean Image

New: Session

Replicate: Session (1)

Replicate: Session (2)

Delete: Session (1)

Delete: Session (2)

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.

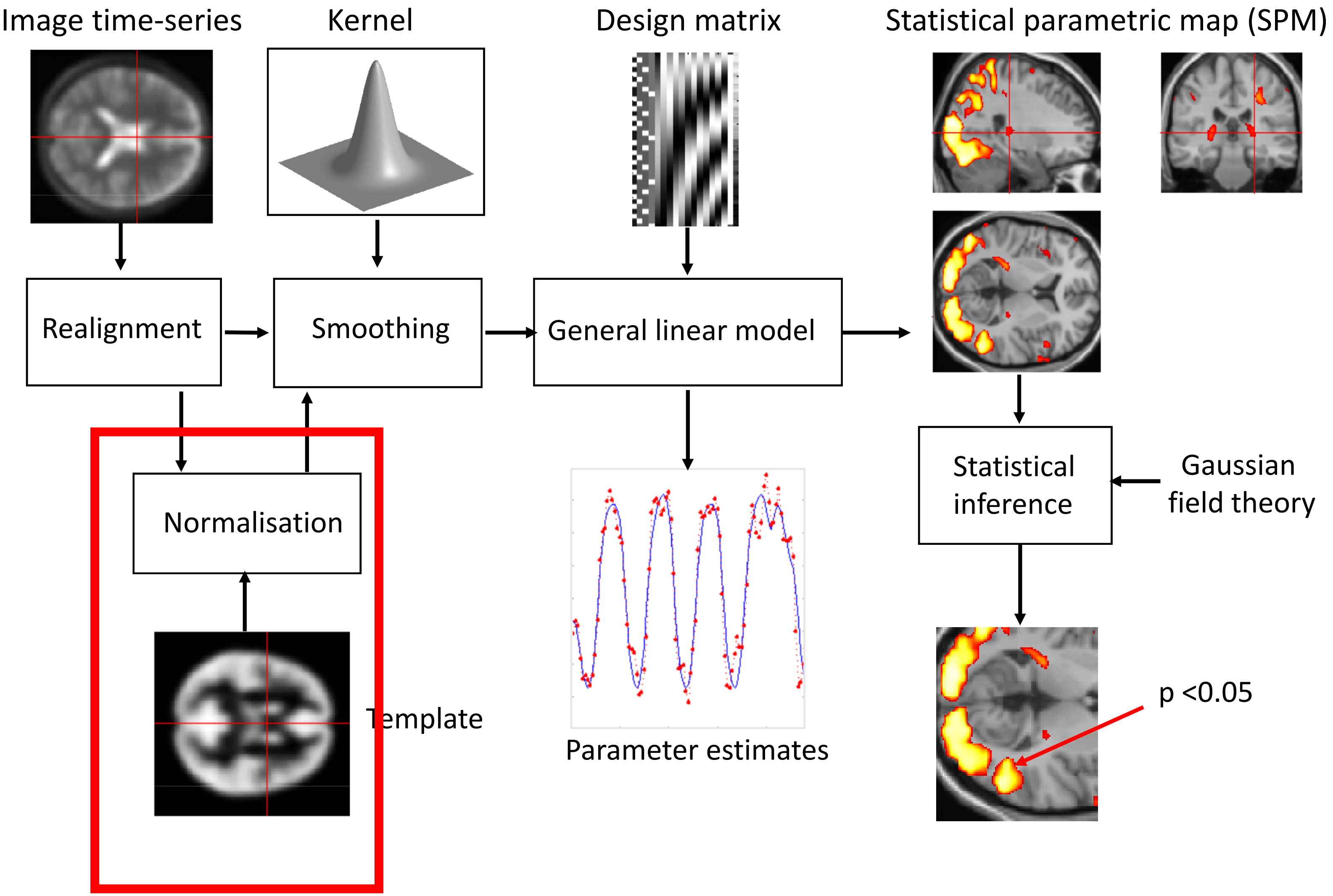


Image time-series

Kernel

Design matrix

Statistical parametric map (SPM)

Realignment

Smoothing

General linear model

Normalisation

Template

Parameter estimates

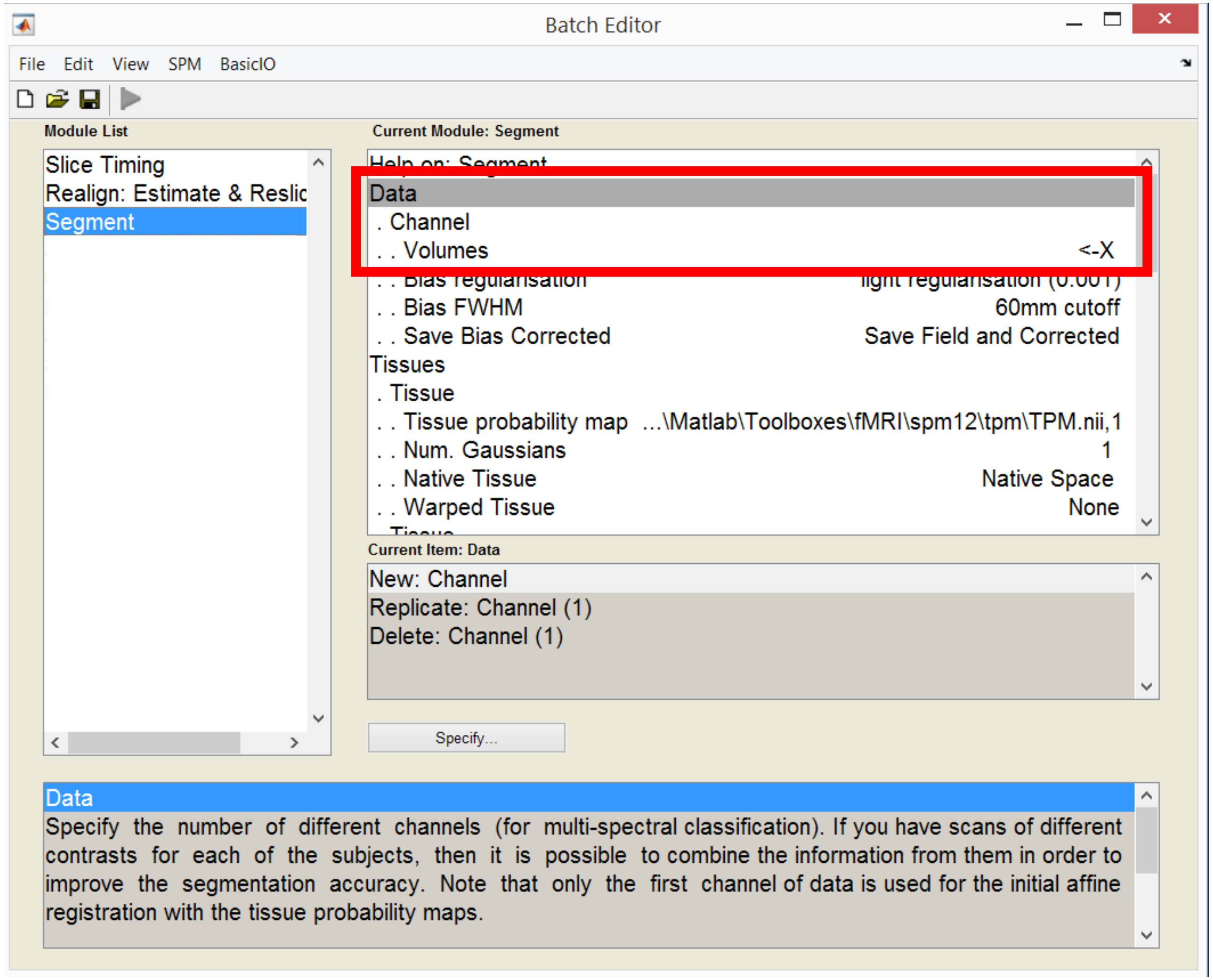
Statistical inference

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».



```
Help on: Segment
Data
 . Channel
 . . Volumes                                            <-X
 . . Bias regularisation             light regularisation (0.001)
 . . Bias FWHM                                   60mm cutoff
 . . Save Bias Corrected              Save Field and Corrected
Tissues
 . Tissue
 . . Tissue probability map  ...\Matlab\Toolboxes\fMRI\spm12\tpm\TPM.nii,1
 . . Num. Gaussians                                        1
 . . Native Tissue                                Native Space
 . . Warped Tissue                                        None
 . Tissue
```

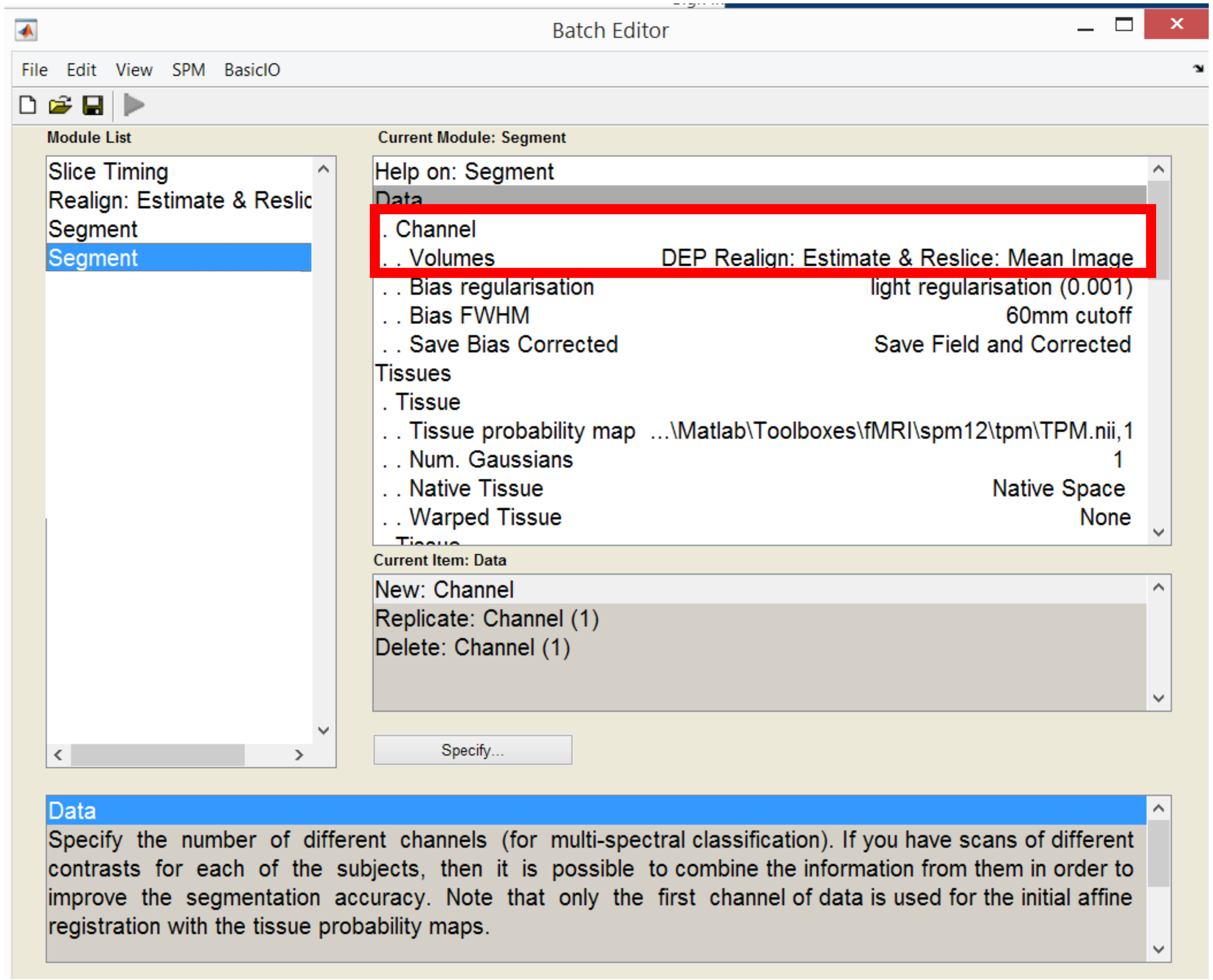
Data

Specify the number of different channels (for multi-spectral classification). If you have scans of different contrasts for each of the subjects, then it is possible to combine the information from them in order to improve the segmentation accuracy. Note that only the first channel of data is used for the initial affine registration with the tissue probability maps.

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

Segment

- Use mean functional via Dependencies.
- This will segment the mean functional and correct it for bias fields (save bias corrected) and compute «Deformation fields» (not needed later on).



Slice Timing
Realign: Estimate & Reslic
Segment
Segment

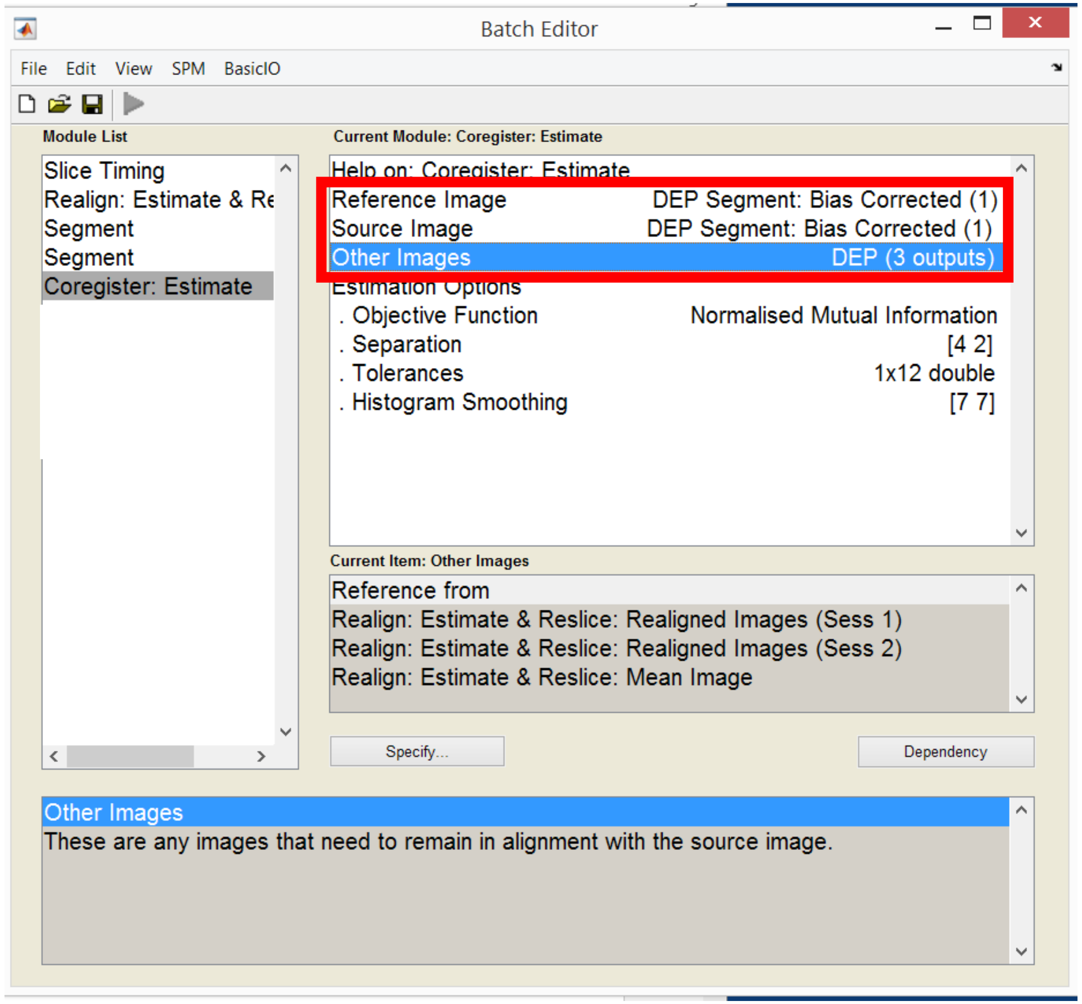
Help on: Segment
Data
. Channel
. . Volumes DEP Realign: Estimate & Reslice: Mean Image
. . Bias regularisation light regularisation (0.001)
. . Bias FWHM 60mm cutoff
. . Save Bias Corrected Save Field and Corrected
Tissues
. Tissue
. . Tissue probability map ...\Matlab\Toolboxes\fMRI\spm12\tpm\TPM.nii,1
. . Num. Gaussians 1
. . Native Tissue Native Space
. . Warped Tissue None

New: Channel
Replicate: Channel (1)
Delete: Channel (1)

Data
Specify the number of different channels (for multi-spectral classification). If you have scans of different contrasts for each of the subjects, then it is possible to combine the information from them in order to improve the segmentation accuracy. Note that only the first channel of data is used for the initial affine registration with the tissue probability maps.

Coregister

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



Current Module: Coregister: Estimate

Help on: Coregister: Estimate

Reference Image	DEP Segment: Bias Corrected (1)
Source Image	DEP Segment: Bias Corrected (1)
Other Images	DEP (3 outputs)
Estimation Options	
. Objective Function	Normalised Mutual Information
. Separation	[4 2]
. Tolerances	1x12 double
. Histogram Smoothing	[7 7]

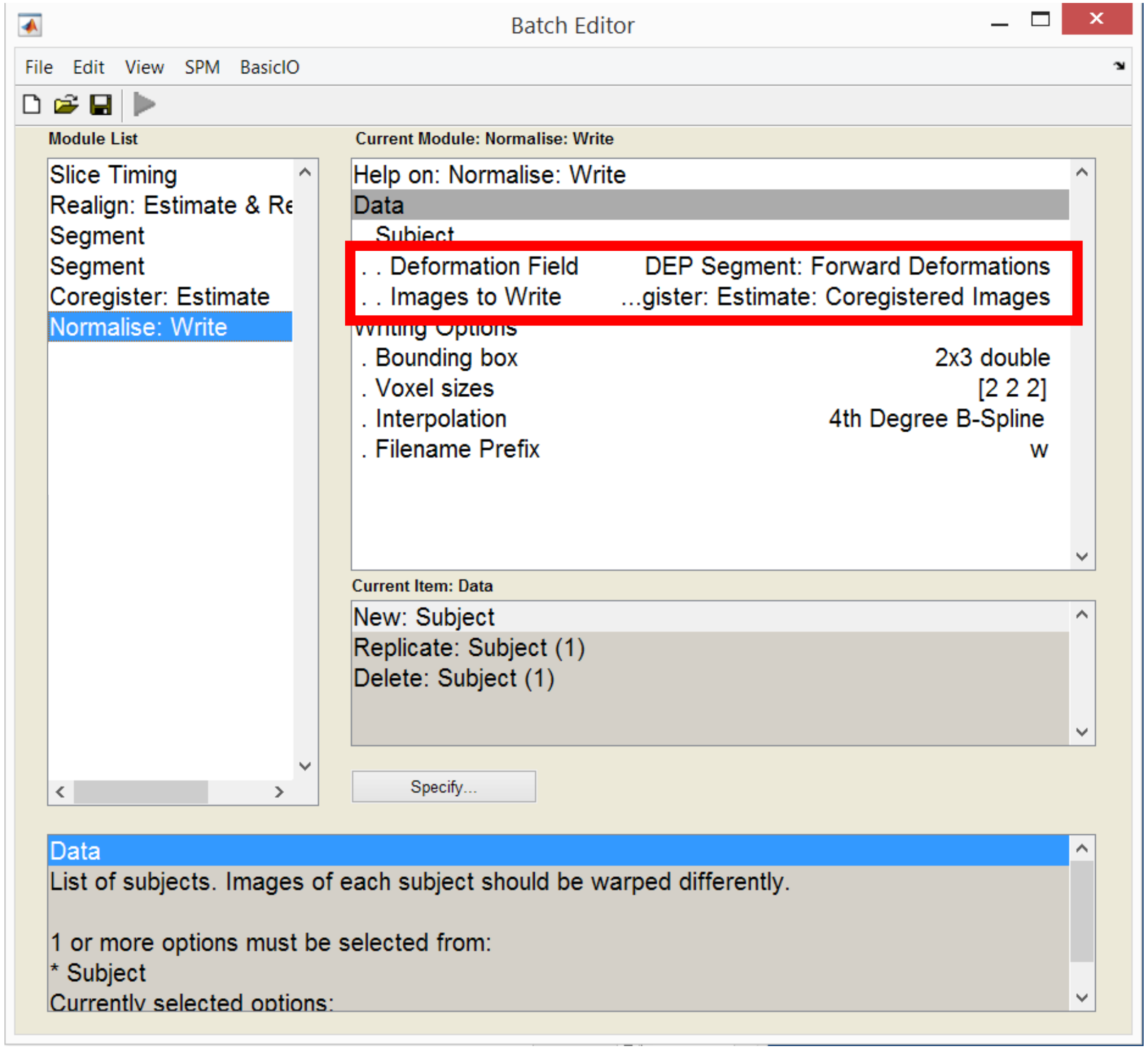
Current Item: Other Images

Reference from
Realign: Estimate & Reslice: Realigned Images (Sess 1)
Realign: Estimate & Reslice: Realigned Images (Sess 2)
Realign: Estimate & Reslice: Mean Image

Other Images
These are any images that need to remain in alignment with the source image.

Normalize fmri

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



Slice Timing
Realign: Estimate & Re
Segment
Segment
Coregister: Estimate
Normalise: Write

Help on: Normalise: Write
Data
Subject
. . Deformation Field DEP Segment: Forward Deformations
. . Images to Write ...gister: Estimate: Coregistered Images
Writing Options
. Bounding box 2x3 double
. Voxel sizes [2 2 2]
. Interpolation 4th Degree B-Spline
. Filename Prefix w

New: Subject
Replicate: Subject (1)
Delete: Subject (1)

Data
List of subjects. Images of each subject should be warped differently.

1 or more options must be selected from:
* Subject
Currently selected options:

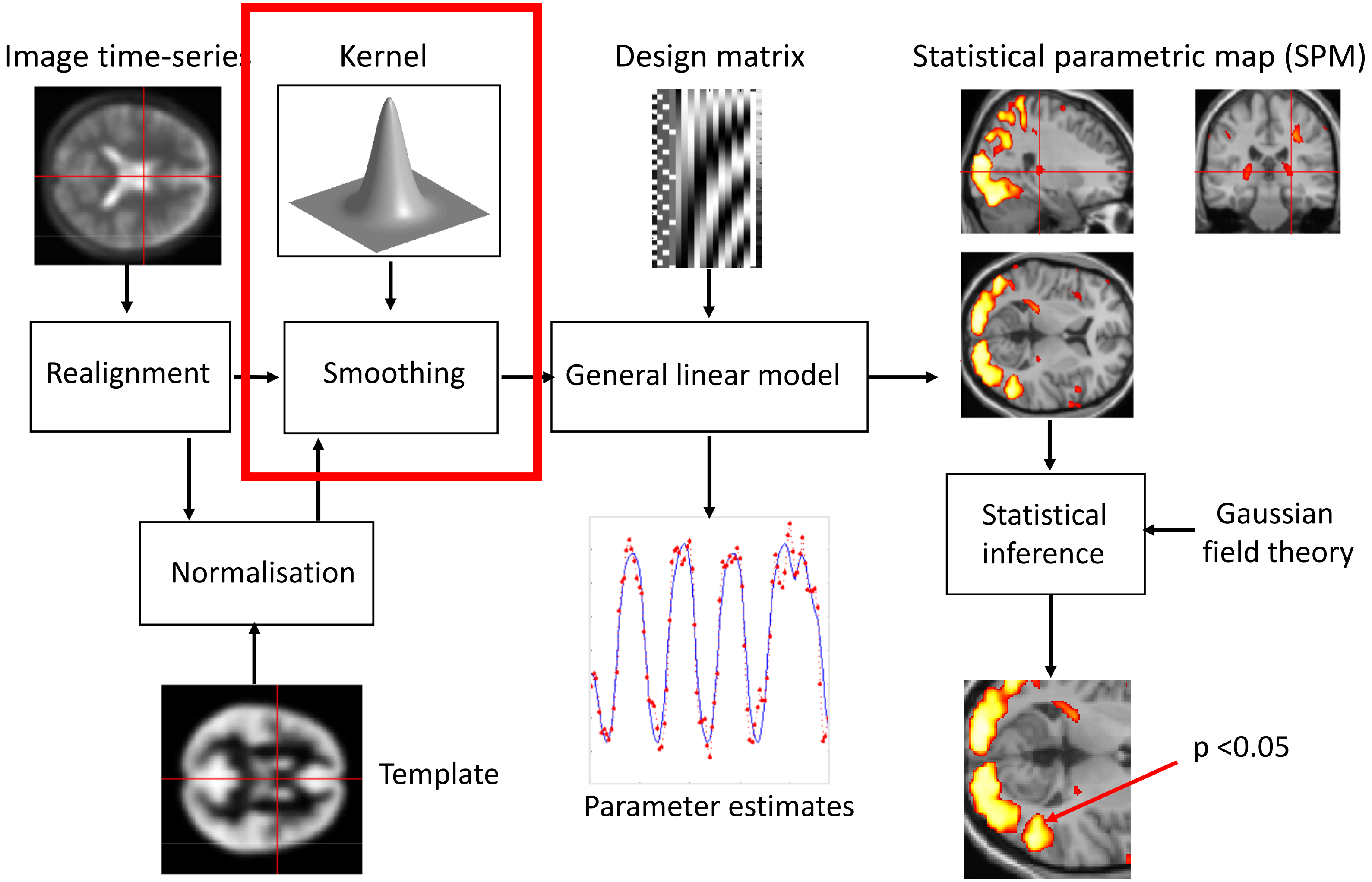


Image time-series

Kernel

Design matrix

Statistical parametric map (SPM)

Realignment

Smoothing

General linear model

Normalisation

Template

Parameter estimates

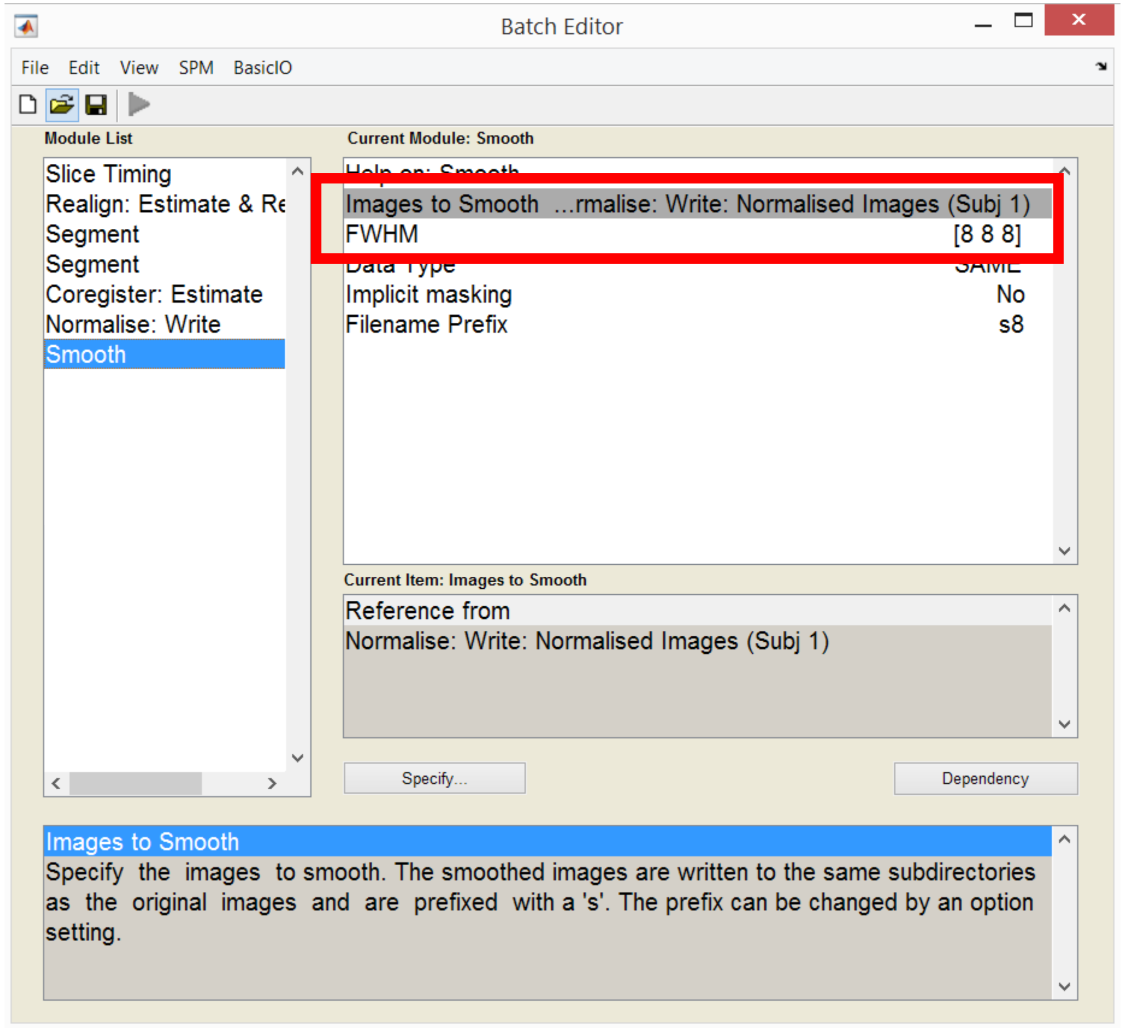
Statistical inference

Gaussian field theory

$p < 0.05$

Smoothing

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



Module List:
- Slice Timing
- Realign: Estimate & Re
- Segment
- Segment
- Coregister: Estimate
- Normalise: Write
- Smooth

Current Module: Smooth

Help on: Smooth

Images to Smooth	...rmalise: Write: Normalised Images (Subj 1)
FWHM	[8 8 8]
Data Type	SAME
Implicit masking	No
Filename Prefix	s8

Current Item: Images to Smooth

Reference from
Normalise: Write: Normalised Images (Subj 1)

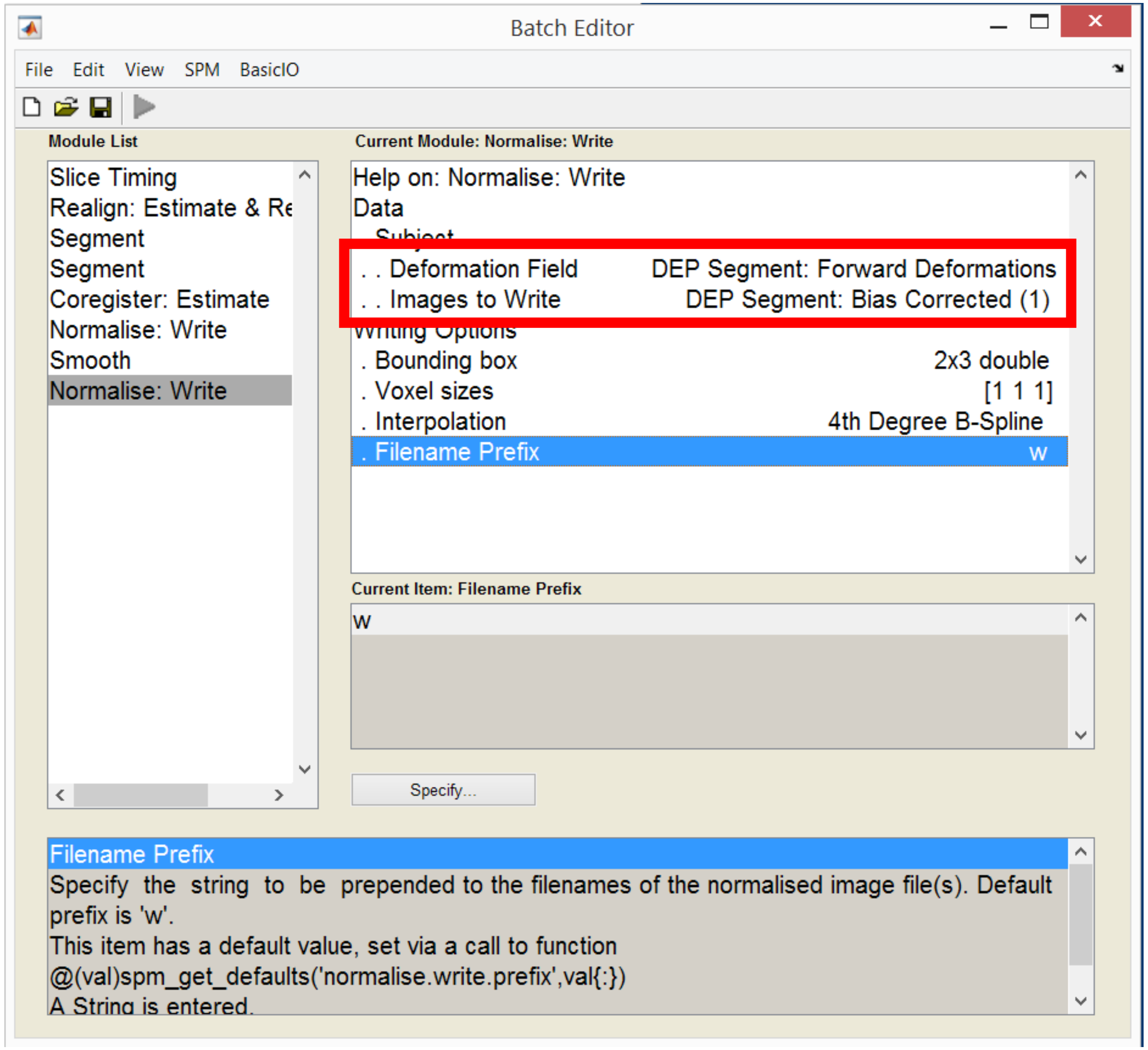
Images to Smooth

Specify the images to smooth. The smoothed images are written to the same subdirectories as the original images and are prefixed with a 's'. The prefix can be changed by an option setting.

Normalize anatomy

- Deform skstruct.nii image to standard space (use coregistered image and deformation field from anatomy). -> Dependencies

- Mainly used for display purposes later on.



Module List

- Slice Timing
- Realign: Estimate & Re
- Segment
- Segment
- Coregister: Estimate
- Normalise: Write
- Smooth
- Normalise: Write

Current Module: Normalise: Write

Help on: Normalise: Write
Data
. Subject
. . Deformation Field DEP Segment: Forward Deformations
. . Images to Write DEP Segment: Bias Corrected (1)
Writing Options
. Bounding box 2x3 double
. Voxel sizes [1 1 1]
. Interpolation 4th Degree B-Spline
. Filename Prefix w

Current Item: Filename Prefix

w

Filename Prefix
Specify the string to be prepended to the filenames of the normalised image file(s). Default prefix is 'w'.
This item has a default value, set via a call to function
@(val)spm_get_defaults('normalise.write.prefix',val{:})
A String is entered.

Run the preprocessing batch

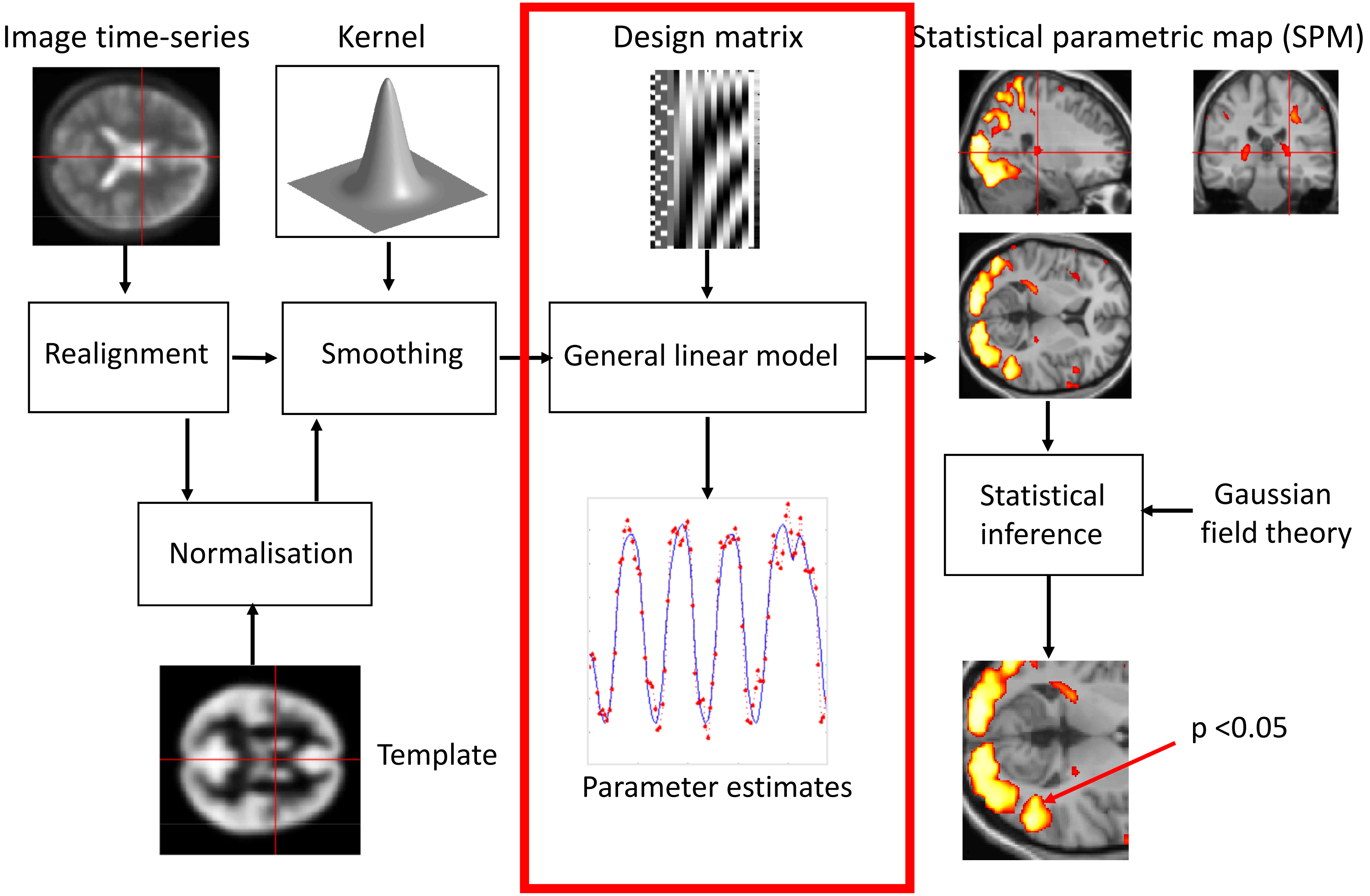


Image time-series

Kernel

Design matrix

Statistical parametric map (SPM)

Realignment

Smoothing

General linear model

Normalisation

Template

Parameter estimates

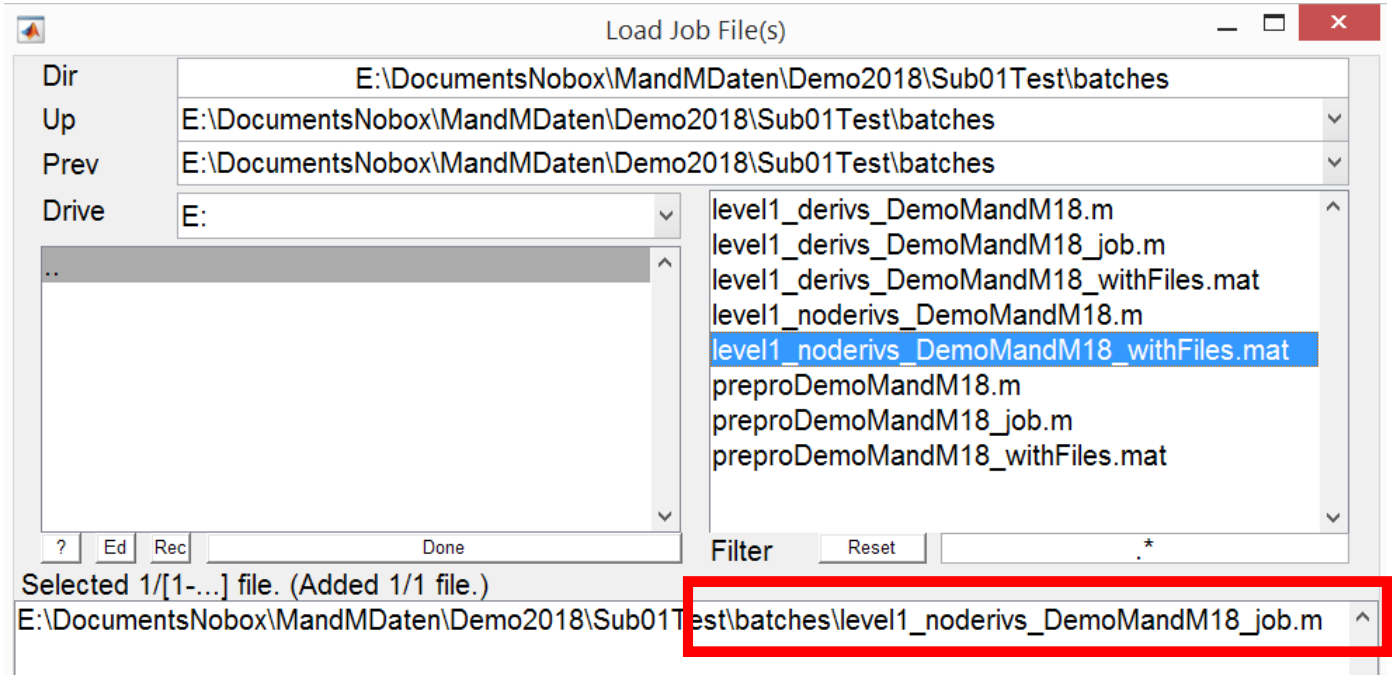
Statistical inference

Gaussian field theory

$p < 0.05$

Open new batch and load level1 batch

- Batch names:
    - level1_noderivs_DemoMandM18_job.m
    - level1_derivs_DemoMandM18_job.m



Dir E:\DocumentsNobox\MandMDaten\Demo2018\Sub01Test\batches

Up E:\DocumentsNobox\MandMDaten\Demo2018\Sub01Test\batches

Prev E:\DocumentsNobox\MandMDaten\Demo2018\Sub01Test\batches

Drive E:

..

level1_derivs_DemoMandM18.m
level1_derivs_DemoMandM18_job.m
level1_derivs_DemoMandM18_withFiles.mat
level1_noderivs_DemoMandM18.m
level1_noderivs_DemoMandM18_withFiles.mat
preproDemoMandM18.m
preproDemoMandM18_job.m
preproDemoMandM18_withFiles.mat

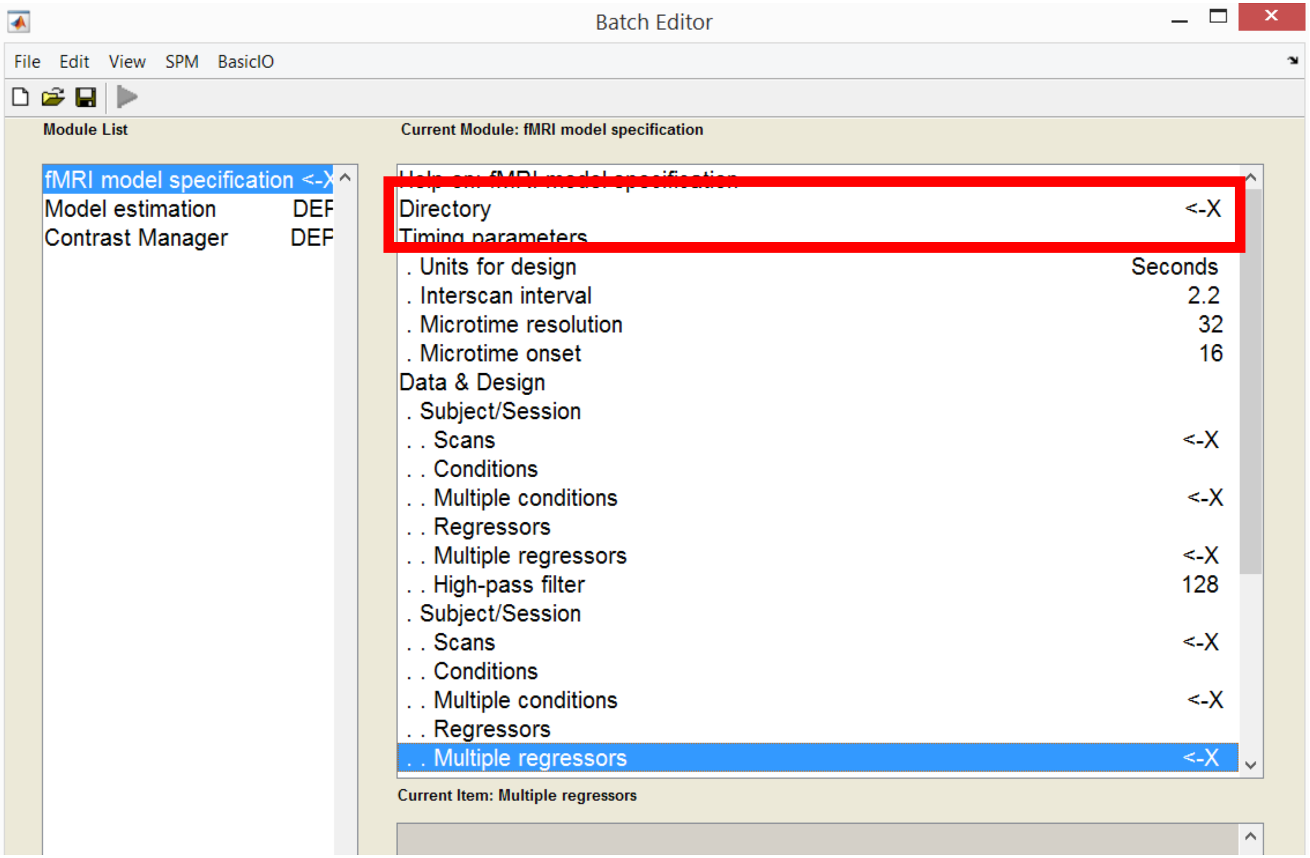
Filter .*

Selected 1/[1-...] file. (Added 1/1 file.)

E:\DocumentsNobox\MandMDaten\Demo2018\Sub01Test\batches\level1_noderivs_DemoMandM18_job.m

GLM specification

- Specify directory where you want to save the analysis (lrArrowDeriv or lrArrowNoDeriv).
    - Parameters: Units for design, TR, microtime resolution, microtime onset



Module List

fMRI model specification <-X
Model estimation DEF
Contrast Manager DEF

Current Module: fMRI model specification

Help on: fMRI model specification
Directory <-X
Timing parameters
. Units for design Seconds
. Interscan interval 2.2
. Microtime resolution 32
. Microtime onset 16
Data & Design
. Subject/Session
. . Scans <-X
. . Conditions
. . Multiple conditions <-X
. . Regressors
. . Multiple regressors <-X
. . High-pass filter 128
. Subject/Session
. . Scans <-X
. . Conditions
. . Multiple conditions <-X
. . Regressors
. . Multiple regressors <-X

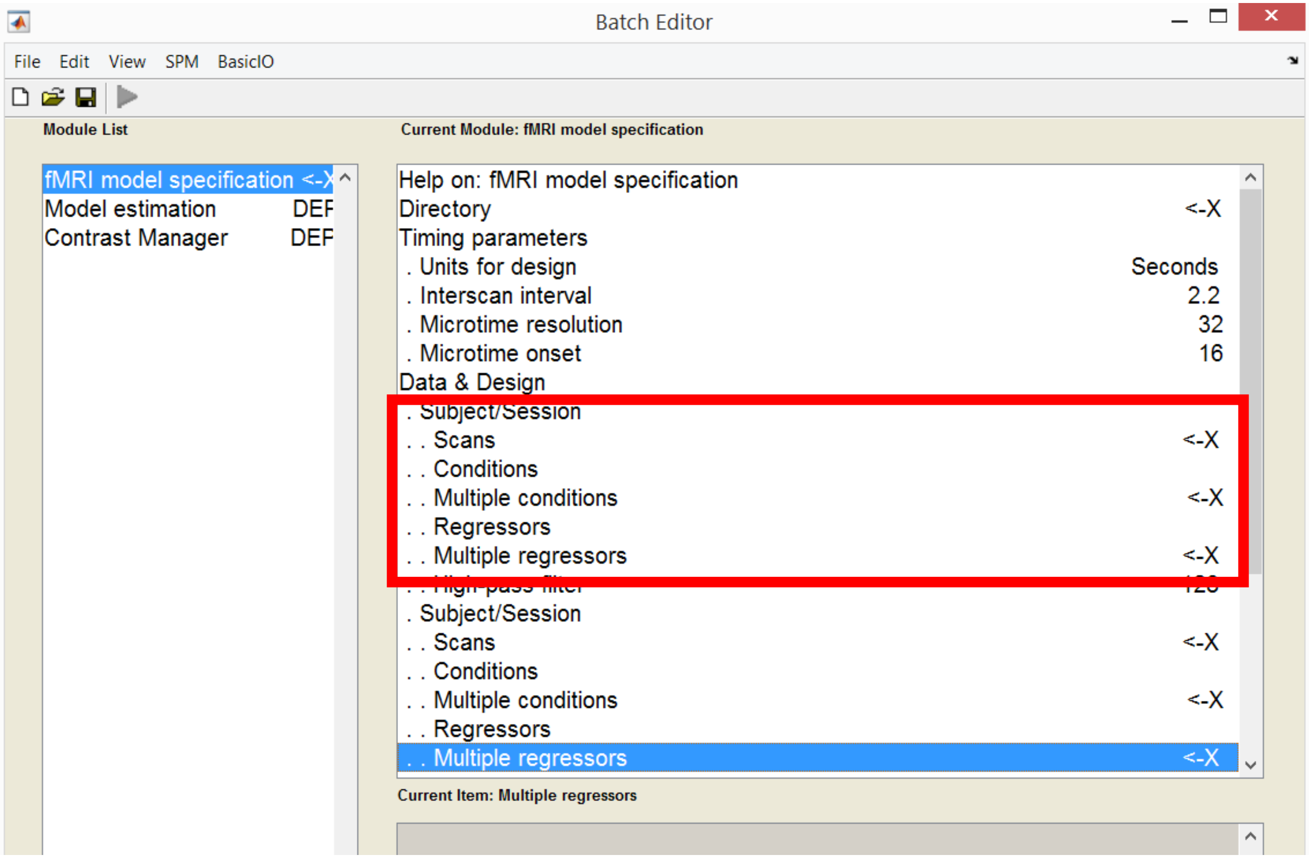
Current Item: Multiple regressors

GLM specification

- Data and paradidgm

Specify session 1:

- Scans: s8wafmri01.nii
  - 145 images
- Multiple conditions:
  - lrArrowRegs01 or lrPressRegs01
- Multiple regressors:
  - rp_afmri01.nii (Movement parameters)
- Analog for run 2.



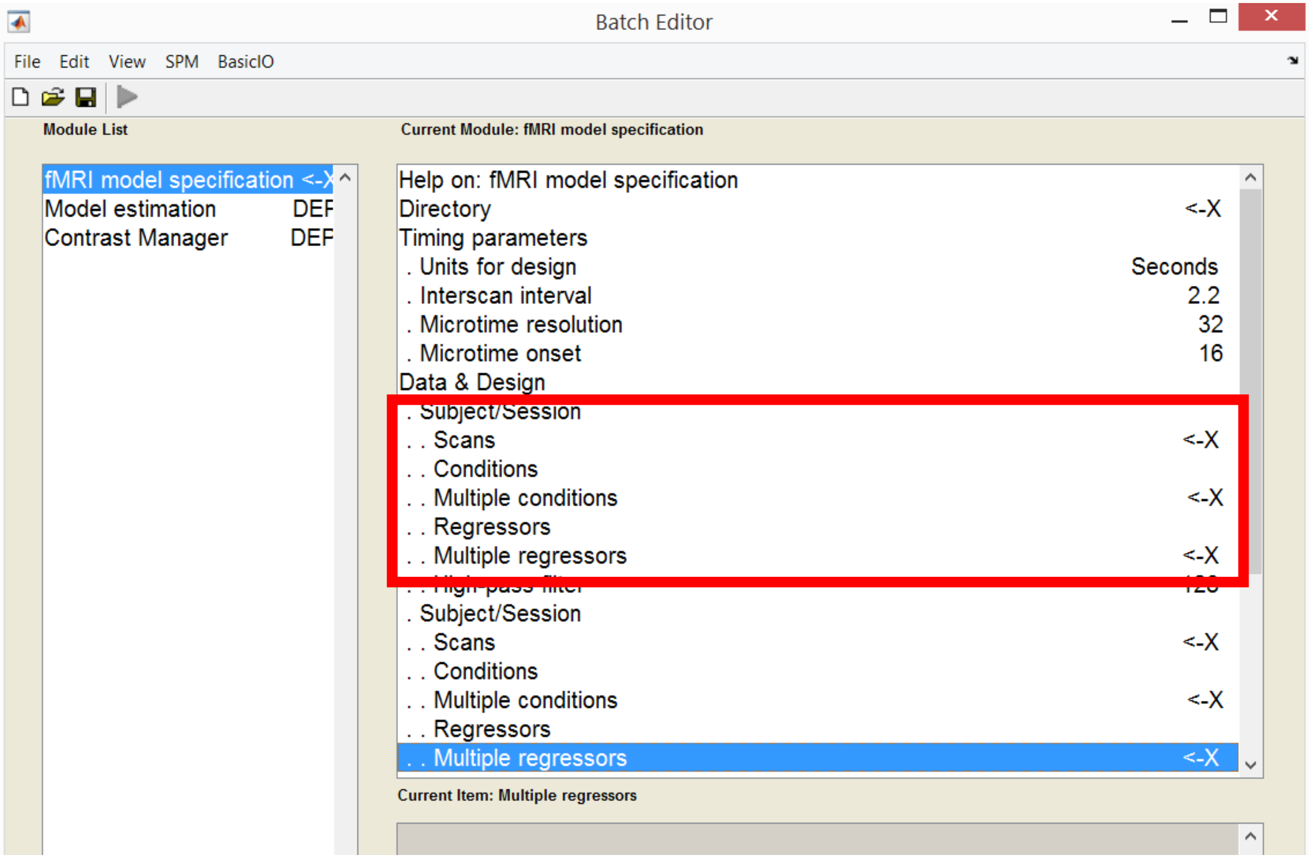
Module List	
fMRI model specification	<-X
Model estimation	DEP
Contrast Manager	DEP

Current Module: fMRI model specification	
Help on: fMRI model specification	
Directory	<-X
Timing parameters	
. Units for design	Seconds
. Interscan interval	2.2
. Microtime resolution	32
. Microtime onset	16
Data & Design	
. Subject/Session	
. . Scans	<-X
. . Conditions	
. . Multiple conditions	<-X
. . Regressors	
. . Multiple regressors	<-X
. . High-pass filter	128
. Subject/Session	
. . Scans	<-X
. . Conditions	
. . Multiple conditions	<-X
. . Regressors	
. . Multiple regressors	<-X

Current Item: Multiple regressors

GLM specification

- Have a look at the multiple conditions file.



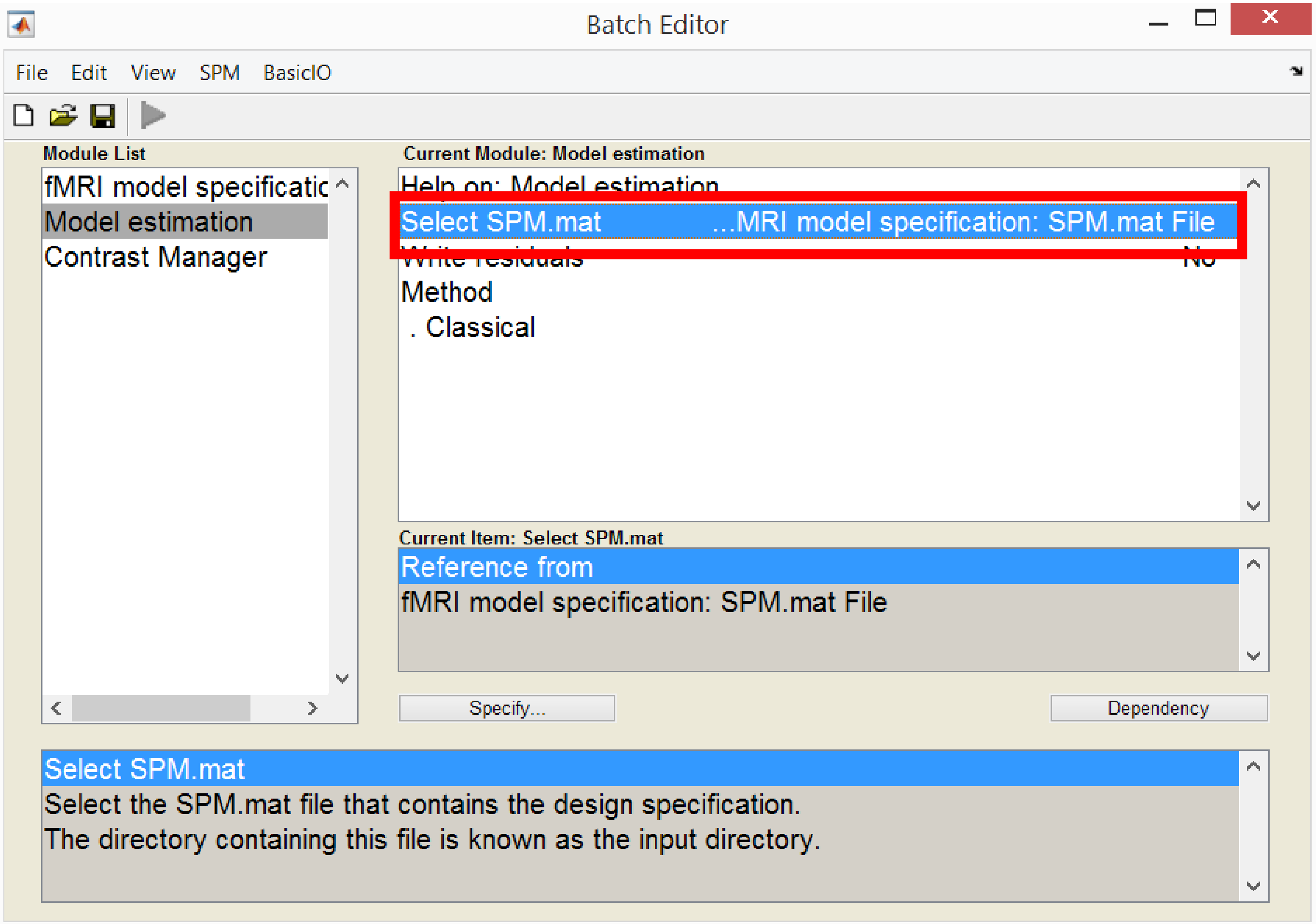
fMRI model specification <-X
Model estimation DEF
Contrast Manager DEF

Help on: fMRI model specification
Directory <-X
Timing parameters
. Units for design Seconds
. Interscan interval 2.2
. Microtime resolution 32
. Microtime onset 16
Data & Design
. Subject/Session
. . Scans <-X
. . Conditions
. . Multiple conditions <-X
. . Regressors
. . Multiple regressors <-X
. . High-pass filter 128
. Subject/Session
. . Scans <-X
. . Conditions
. . Multiple conditions <-X
. . Regressors
. . Multiple regressors <-X

Current Item: Multiple regressors

Estimate model

- Define SPM.mat via dependencies.



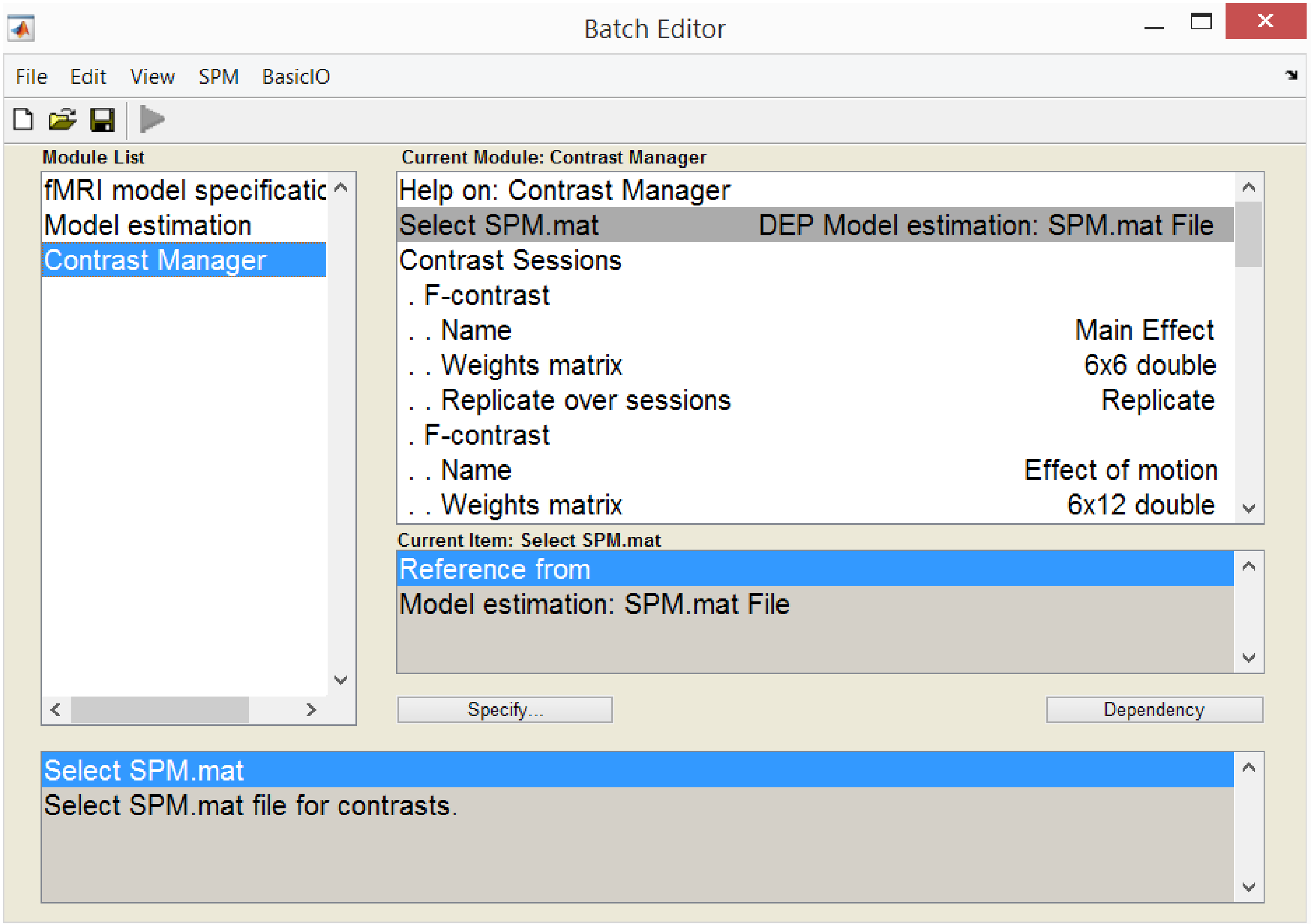
Help on: Model estimation
Select SPM.mat ...MRI model specification: SPM.mat File
Write residuals No
Method
. Classical

Current Item: Select SPM.mat
Reference from
fMRI model specification: SPM.mat File

Select SPM.mat
Select the SPM.mat file that contains the design specification.
The directory containing this file is known as the input directory.

Define contrasts

- Define SPM.mat via Dependencies.



fMRI model specificatio
Model estimation
Contrast Manager

Current Module: Contrast Manager

Help on: Contrast Manager
Select SPM.mat DEP Model estimation: SPM.mat File
Contrast Sessions
. F-contrast
. . Name Main Effect
. . Weights matrix 6x6 double
. . Replicate over sessions Replicate
. F-contrast
. . Name Effect of motion
. . Weights matrix 6x12 double

Current Item: Select SPM.mat

Reference from
Model estimation: SPM.mat File

Select SPM.mat
Select SPM.mat file for contrasts.

Look at results

- Check coregistration (use check reg)
- Check normalization (use check reg)
- Open the statistical results with «Results»