



fMR Processing(1)

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fMR processing (1. exercise)

Pipeline

1. **Conversion** of data: DICOM -> NIFTI  (done; *.nii suffix)
2. **Slice Timing:** temporal correction (TR vs. HRF)  (skipping this step)
3. **Realignment** of functional data - spatial correction of data in time
4. **Smooth** with Gauss filter kernel
5. **Model specification + Review**
6. **Estimate Model**
7. **Results + Display**

DICOM = Digital Imaging and Communications in Medicine
NIFTI = Neuroimaging Informatics Technology Initiative

Necessary SW: Matlab + SPM12 toolbox (Win, MacOS)

Statistical **P**arametric **M**apping

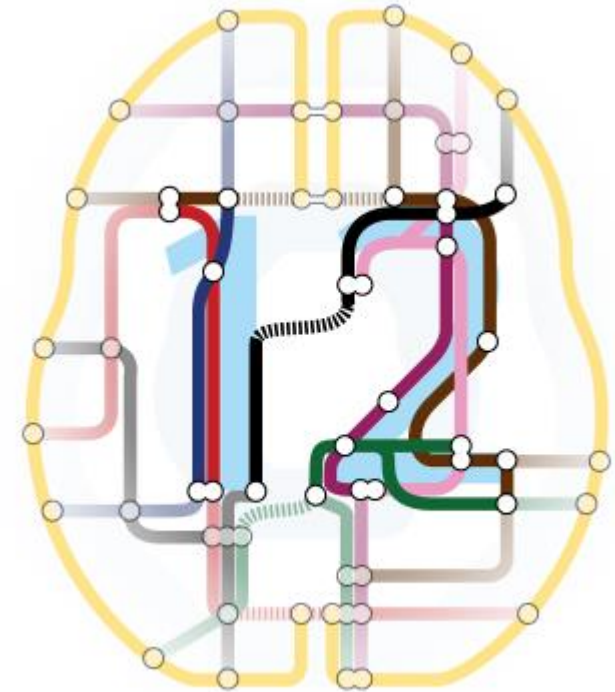
SPM12 download:

<https://www.fil.ion.ucl.ac.uk/spm/software/spm12/>

SPM12 manual:

„.../toolbox/spm12/man/manual.pdf“

4 basic SPM windows:- Menu
- Results
- Graphic
- Batch Editor



Recommended resources

SPM12

<https://www.fil.ion.ucl.ac.uk/spm/doc/>

MRicroGL

<https://www.nitrc.org/projects/mricrogl>

GLM

https://www.fil.ion.ucl.ac.uk/mfd_archive/2011/page1/mfd2011_GLM.pdf

fMR processing

Data

Paradigm:

FingerTapping (upper extremities fingers) 150vol, TR=2000ms, 60 slices

Volunteer data: folders **Subj01, Subj02, ... Subj13**

Subj09	D-S	6.3.2024
Subj10	P-B	6.3.2024
Subj11	T-T	13.3.2024
Subj12	M-L	20.3.2024
Subj13	M-H	20.3.2024

Folder structure: **fmr** (150 nii-files: “fmr_*[XXX]*.nii”)

t1 (1 nii-file: “t1.nii”)

SPM12 (7771): Menu

Spatial pre-processing

Realign (Esti... | Slice timing | Smooth

Coregister (... | Normalise (E... | Segment

Model specification, review and estimation

Specify 1st-level | Review

Specify 2nd-level | Estimate

Inference | Results

Dynamic Causal Modelling

SPM for functional MRI

Display | Check Reg | Render... | FMRI

Toolbox: | PPIs | ImCalc | DICOM Import

Help | Utils... | Batch | Quit

Copyright (c) 1991, 1994-2020

SPM12 (7771): Graphics

Help File Edit View Insert Tools Desktop Window SPM Figure

Batch Editor

File Edit View SPM BasicIO

Module List

Smooth <-X

Current Module: Smooth

Help on: Smooth

Images to smooth <-X

FWHM [8 8 8]

Data Type SAME

Implicit masking No

Filename prefix s

Current Item: Images to smooth

Specify...

Images to smooth

Specify the images to smooth.

The smoothed images are written to the same subdirectories as the original images with a configurable prefix.

SPM12 (7771): SPM(T): Results

Design Contrasts Atlas

p-values

whole brain | current cluster | small volume

Multivariate

eigenvariate | CVA | multivariate Bayes | BMS | p-value

Display

plot | overlays... | save...

Hemodynamics | clear | ext

co-ordinates

x = 0.00 y = 0.00 z = 0.00

statistic

Crosshair Position Origin

mm: 0.0 -59.4 13.7

vx: 40.0 27.3 42.9

Intensity: -0.695892

right (mm)	0
forward (mm)	0
up (mm)	0
pitch (rad)	0
roll (rad)	0
yaw (rad)	0
resize (x)	1
resize (y)	1
resize (z)	1

Set Origin Reorient...

File: .lspmT_0001.nii

Dimensions: 79 x 95 x 79

Datatype: float32

Intensity: Y = 1 X

SPM(T_[19.0]) - contrast 1: BASKET>TENIS

Vox size: -2 x 2 x 2

Origin: 40 57 36

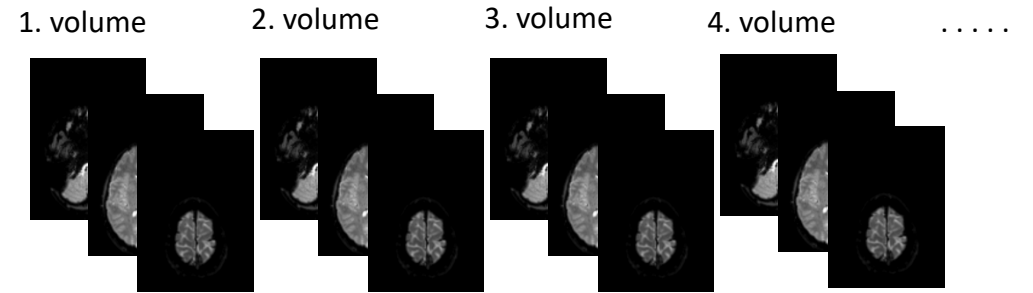
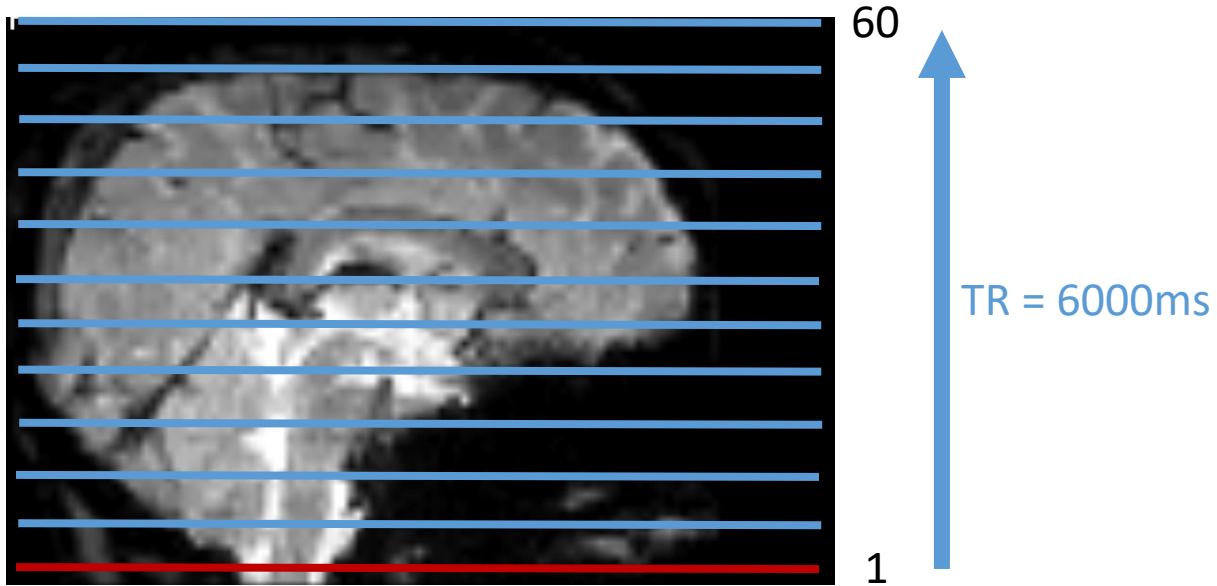
Dir Cos: 1.000 0.000 0.000
0.000 1.000 0.000
0.000 0.000 1.000

Full Volume | Hide Crosshair

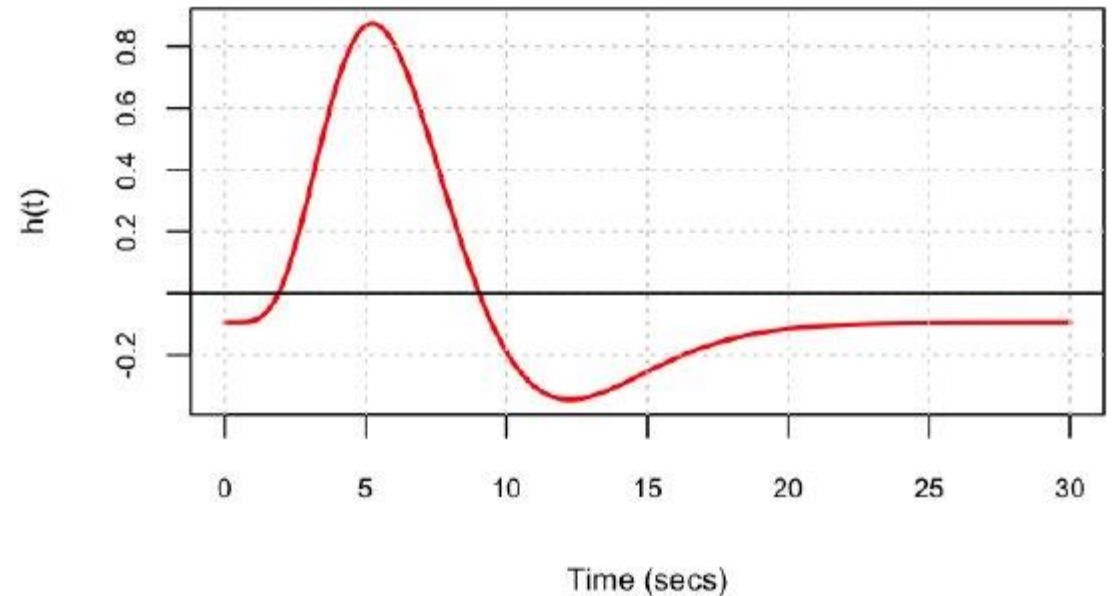
World Space | Trilinear interp.

Auto Window | Add Overlay...

Slice timing (skipping this step, $TR=2s$)



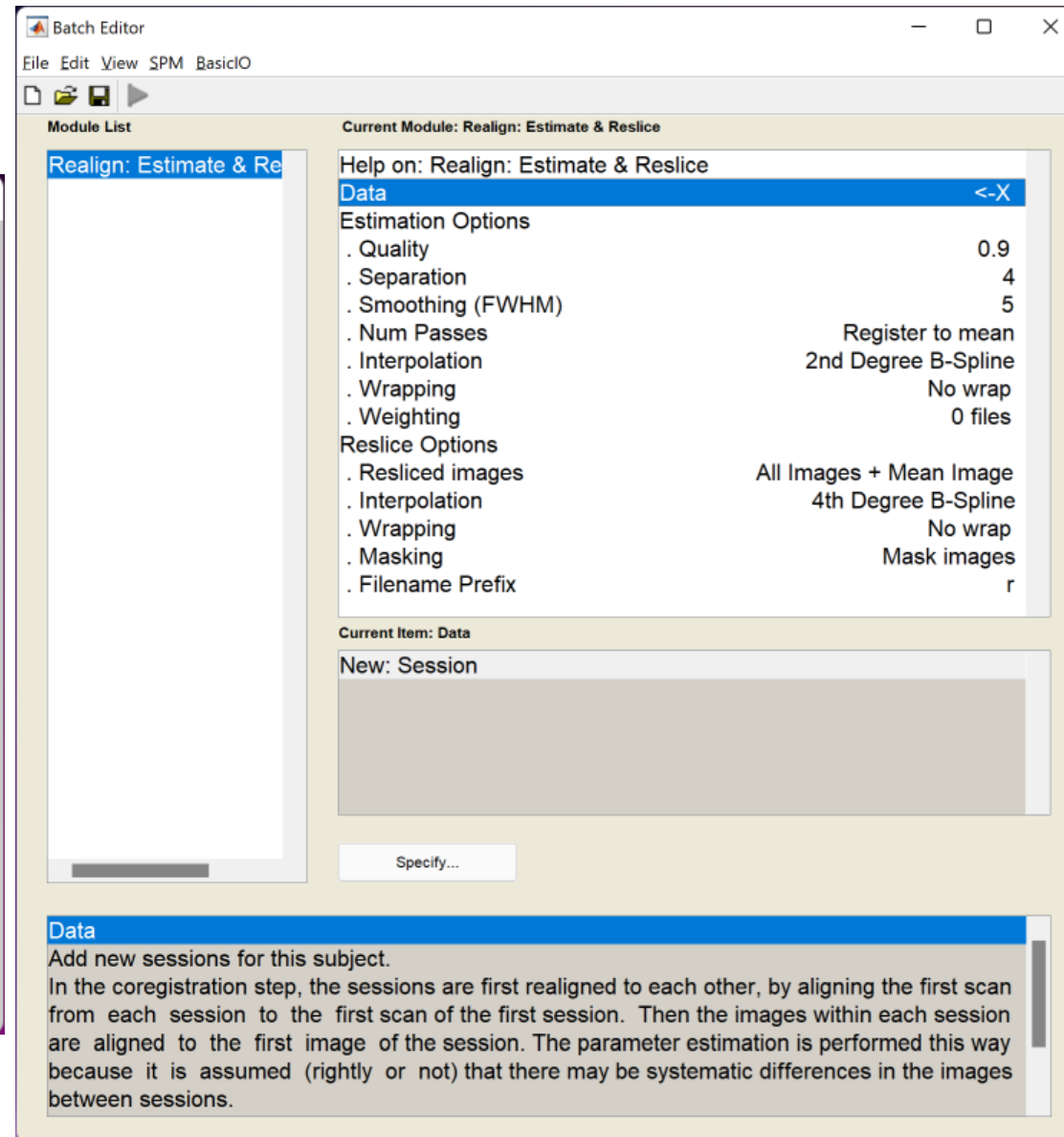
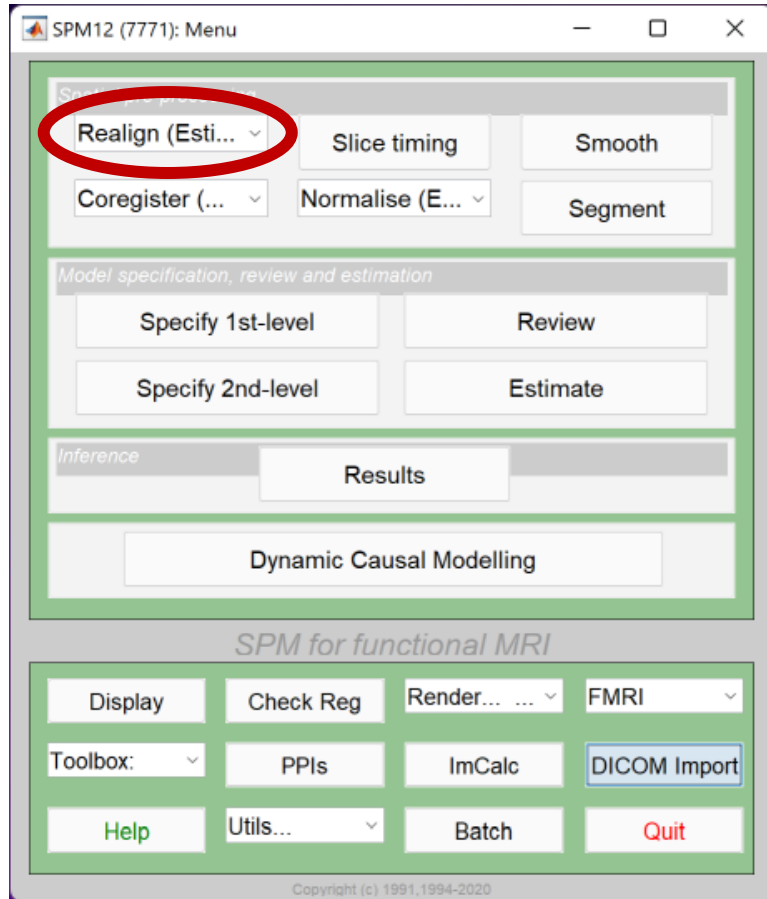
Hemodynamic Response Function



Realign data

- This routine realigns a time-series of images acquired from the same subject using a **least squares approach and a 6 parameter (rigid body) spatial transformation**. The first image in the list specified by the user is used as a reference to which all subsequent scans are realigned. The reference scan does not have to be the first chronologically and it may be wise to choose a "representative scan" in this role.
- The aim is primarily to remove movement artefact in fMRI and PET time-series (or more generally longitudinal studies). The headers are modified for each of the input images, such that they reflect the relative orientations of the data. The details of the transformation are displayed in the results window as plots of translation and rotation. A set of realignment parameters are saved for each session, named `rp_*.txt`. These can be modelled as confounds within the general linear model

Realign data

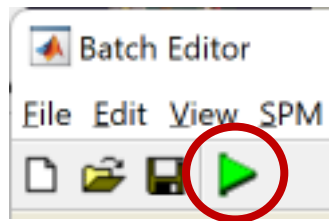


Realign data

MENU: Realign (Estimate & Reslice)

BATCH EDITOR:

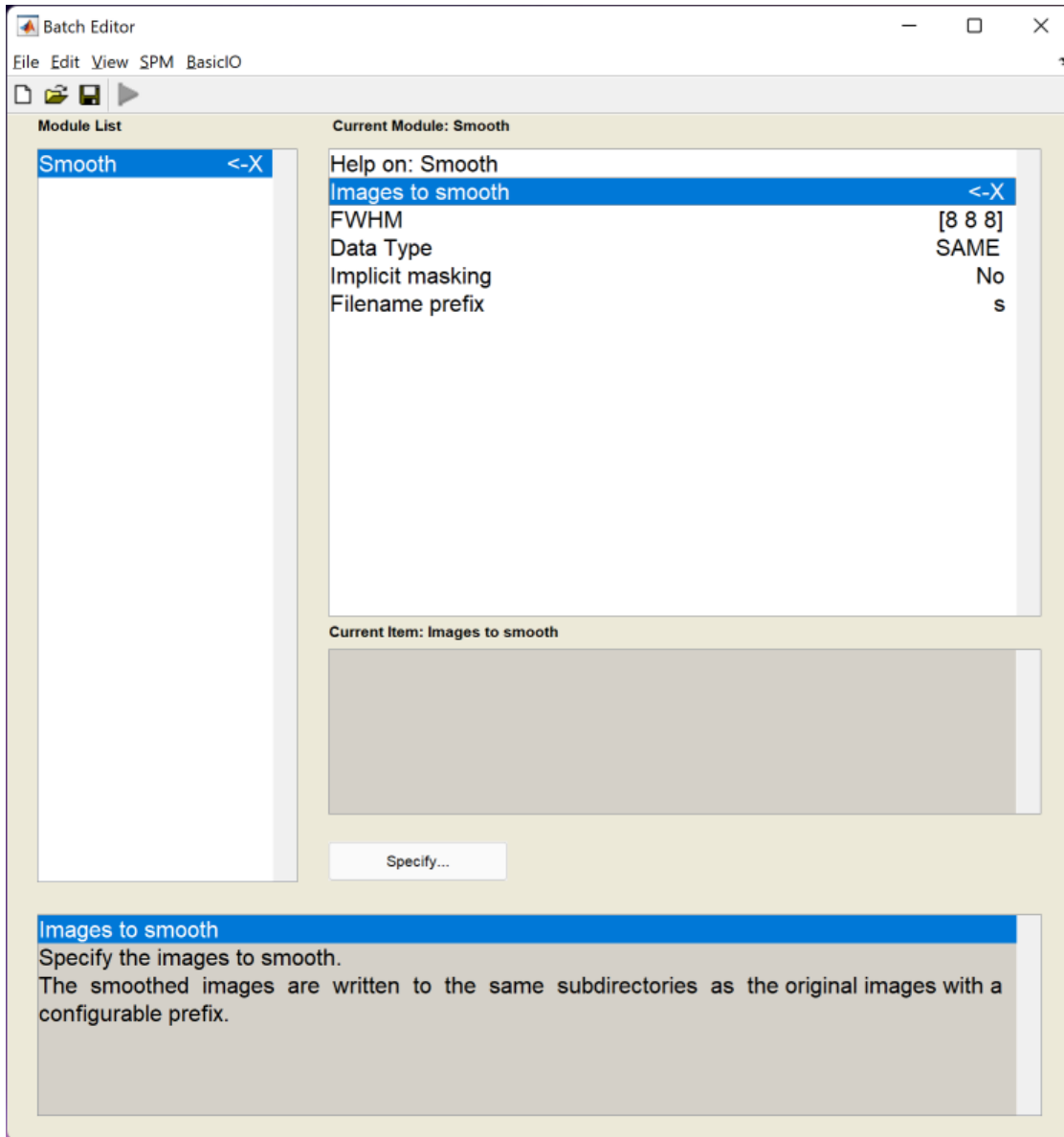
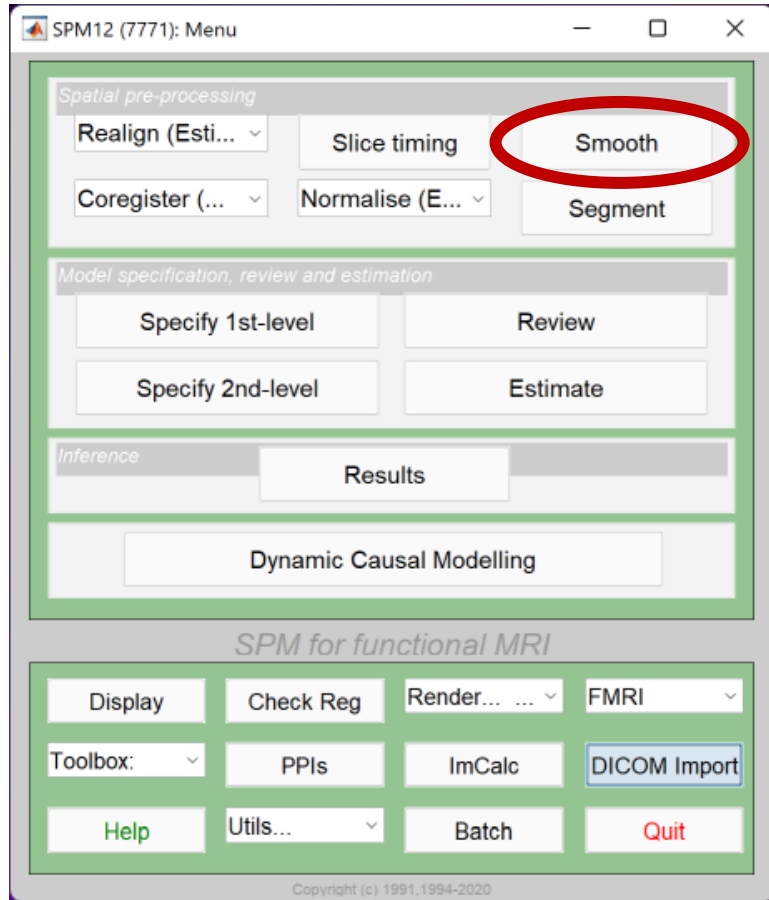
- a) Data – Session ... all fMR files
- b) Run batch



Output:

- Resliced files (prefix „r*.nii“)
- „mean*.nii“ file (mean of all fMR files)
- Realign parameters file „rp_*.txt“

Smooth

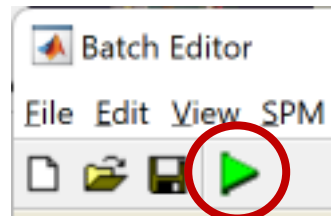


Smooth

MENU: Smooth

BATCH EDITOR:

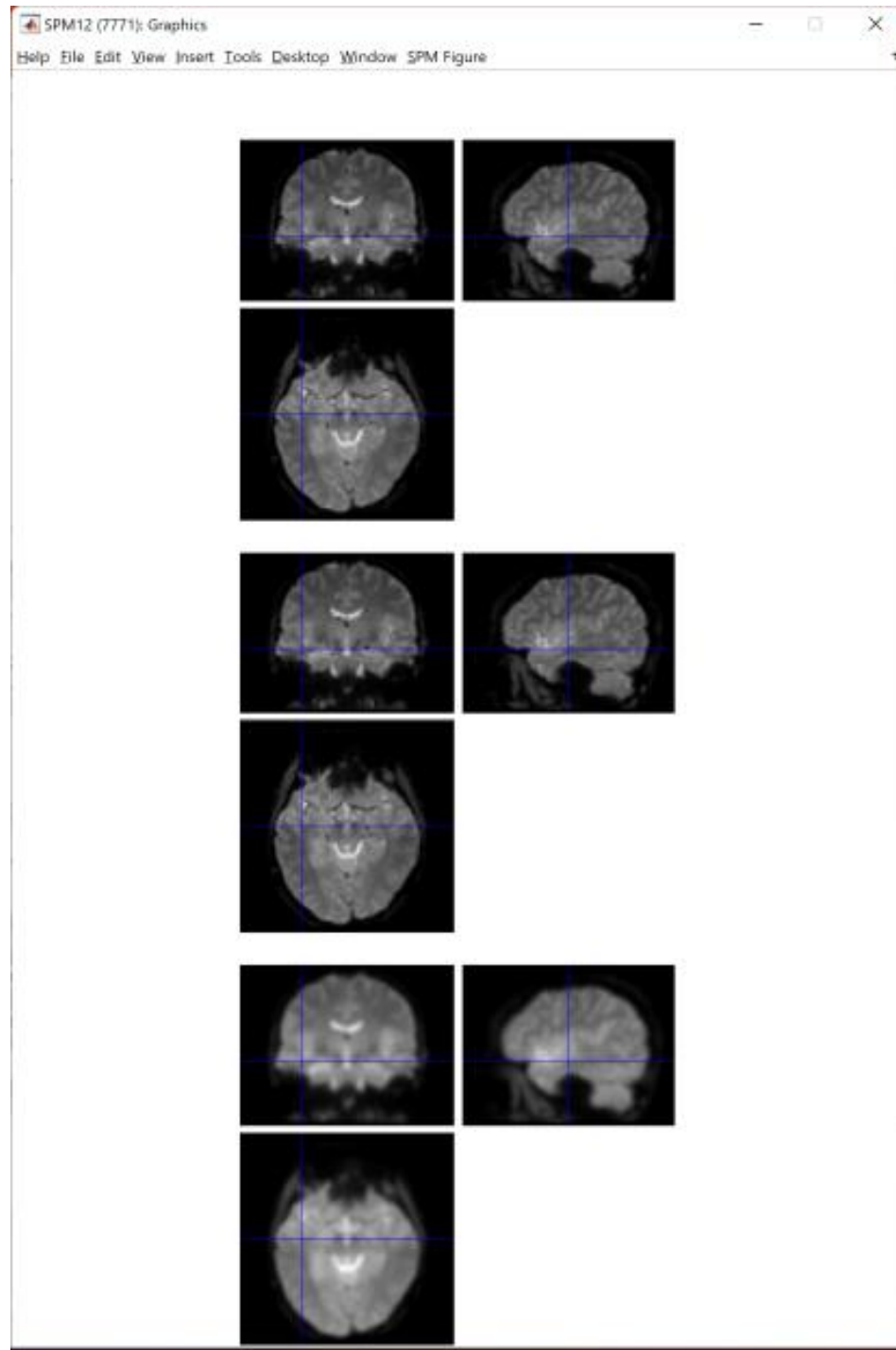
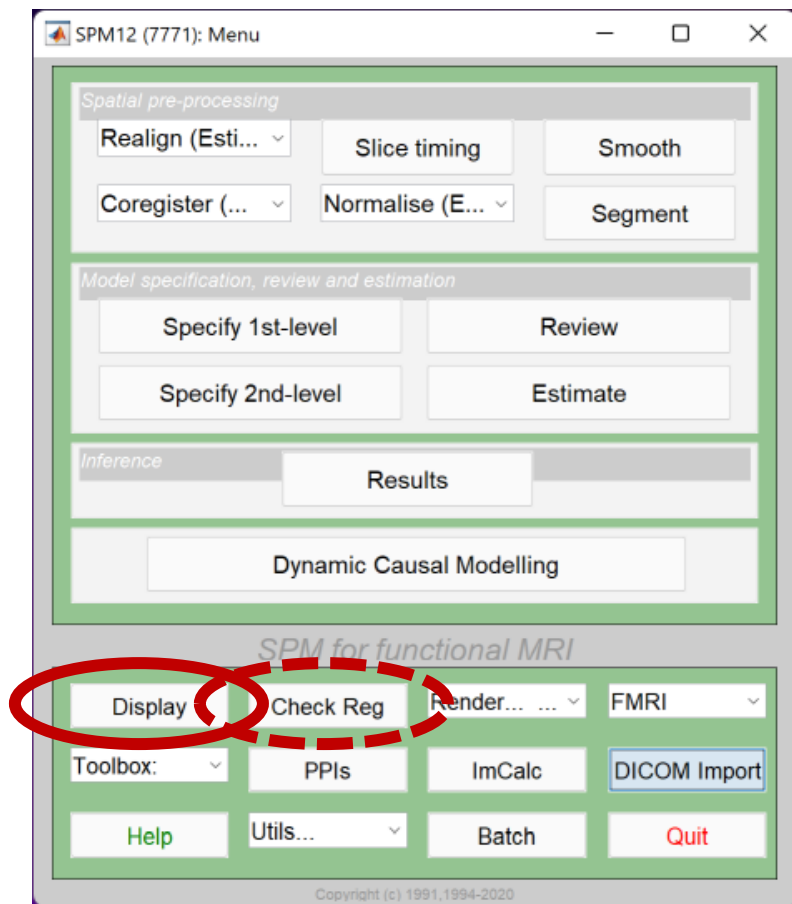
- a) Images to smooth ... select all *r*.nii* files
- b) FWHM ... **[6 6 6]** (Full width at half maximum of the Gaussian smoothing kernel in mm, doubled size of voxel recommended)
- c) Run batch



Output:

- Smoothed files (all with prefix „s*.nii“)

Data check (!)



GLM – General Linear Model

$$y = X\beta + e$$

Dependent variable

BOLD signal in particular voxels

Independent variable (Predictor)

Experiment conditions

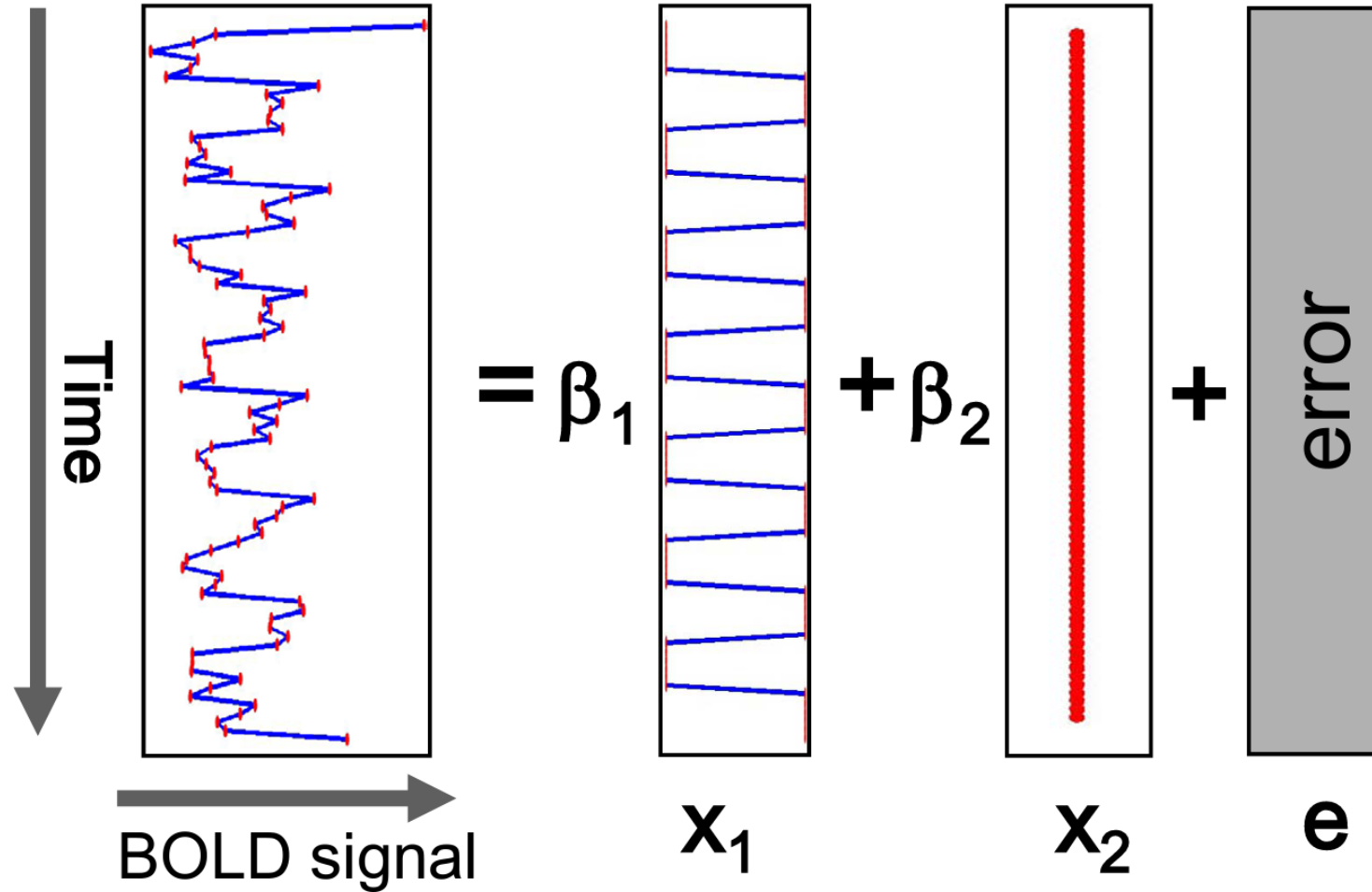
Beta parameters (regression coeff.)

Quantifies how much each predictor (X) independently influences the dependent variable (Y)

Error (Residuals)

Variance in the data (y), which is not explained by the linear combination of predictors (x)

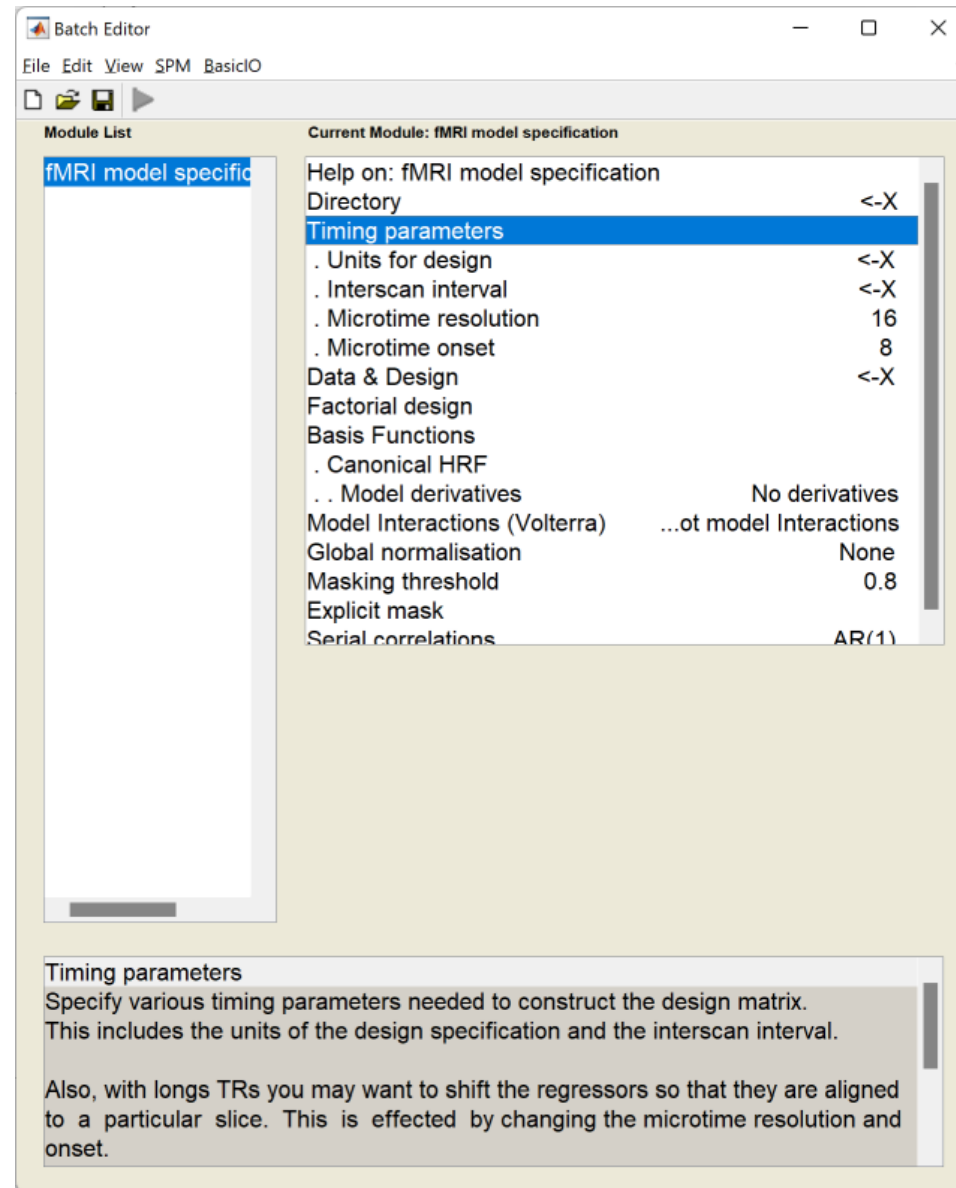
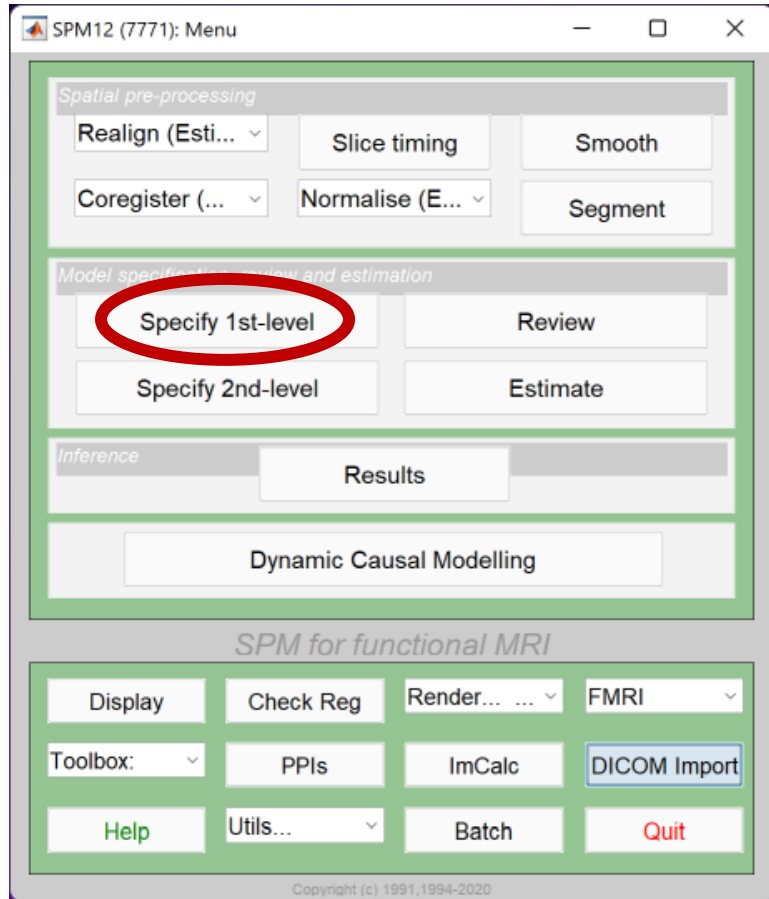
Single voxel regression model



$$y = x_1\beta_1 + x_2\beta_2 + e$$

fMRI Statistics

Model specification



fMR Statistics

Model specification

MENU: Specify 1st-level

BATCH EDITOR:

- a) Directory ... select (pre-created) folder “**model**” to store model and statistics results
- b) Units for design ... **Scans**
- c) Interscan interval ... **2** (equals to TR)
- d) Data & Design
 - a) Scans ... select **sr*.nii** data
 - b) Conditions
 - a) Condition
 - a) Name ... name of processed paradigm, for example “RightHand”, “LeftHand”
 - b) Onset ... vector of scans where the activations begins
 - c) Durations ... duration of activation (in scans)
- e) Run batch

Output:

- **SPM.mat** file (GLM model)

fMR Statistics

Model specification

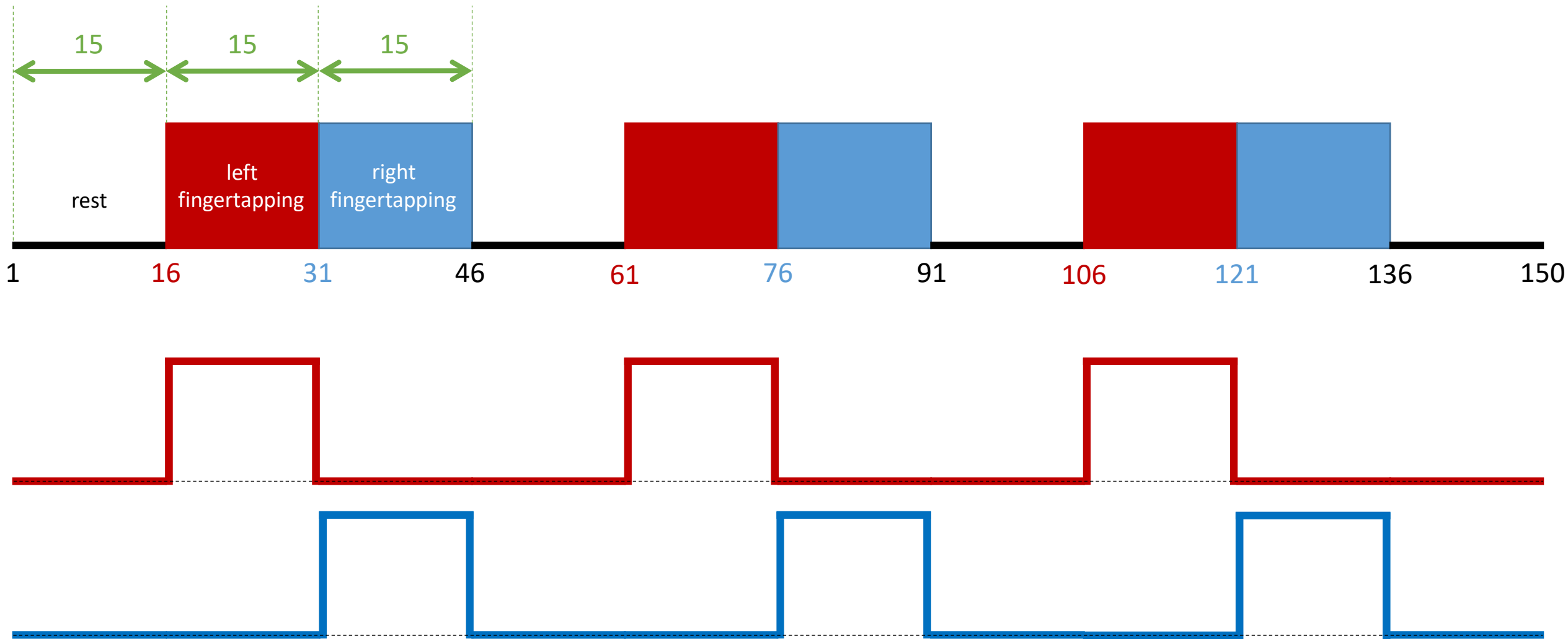
1. Condition **LeftHand**

- Name ... **LeftHandFingerTapping**
- Onset ... **[16 61 106]**
- Durations ... **15**

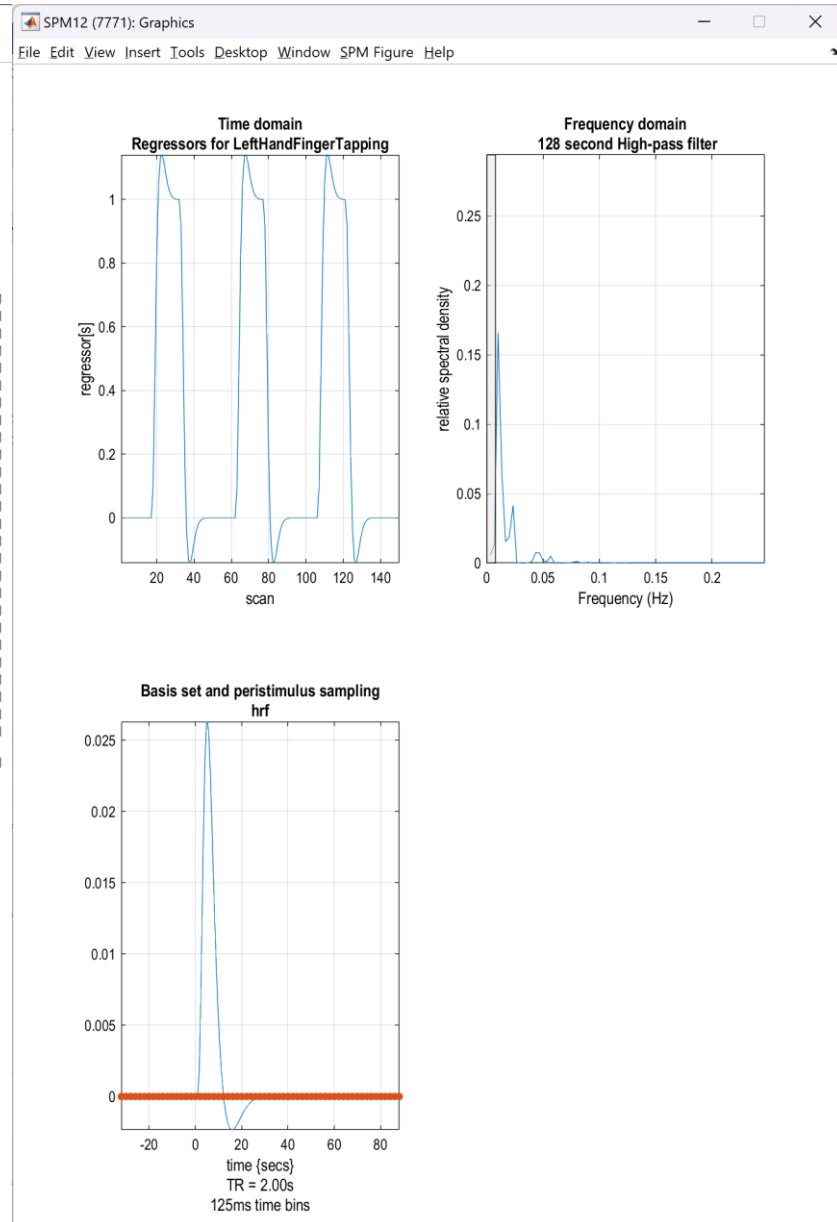
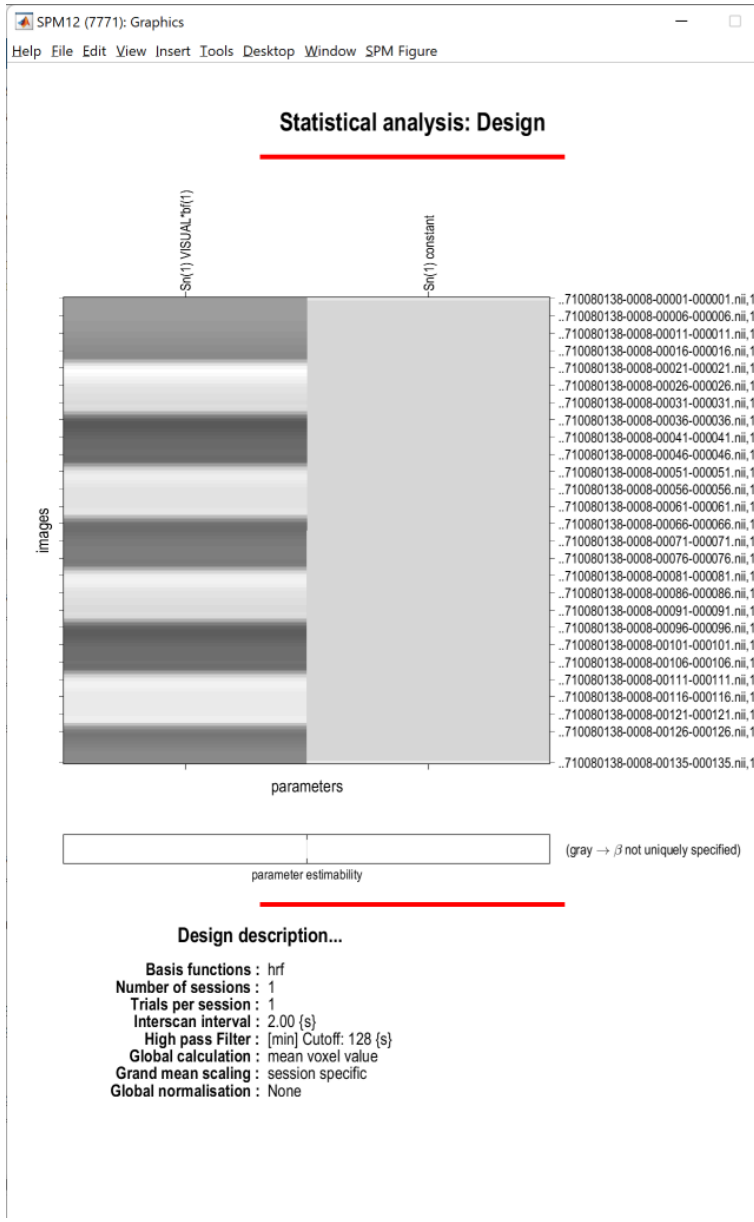
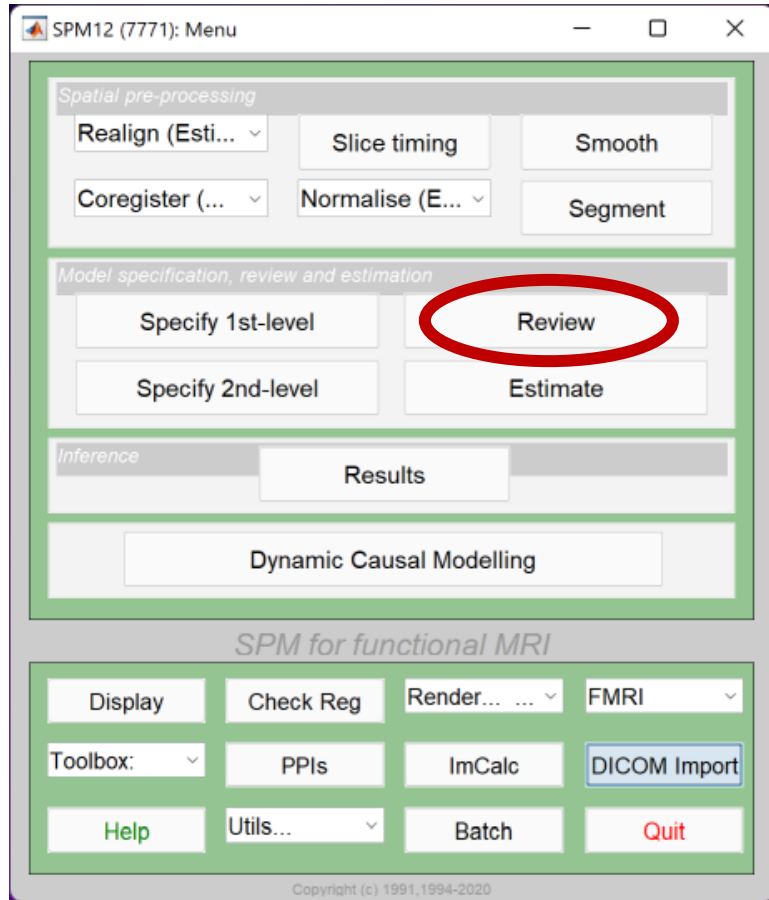
2. Condition **RightHand**

- Name ... **RightHandFingerTapping**
- Onset ... **[31 76 121]**
- Durations ... **15**

fMR Motor paradigm (in scans; scan = 2s)



fMR Statistics Model review



fMR Statistics

Model review

MENU: Review

BATCH EDITOR:

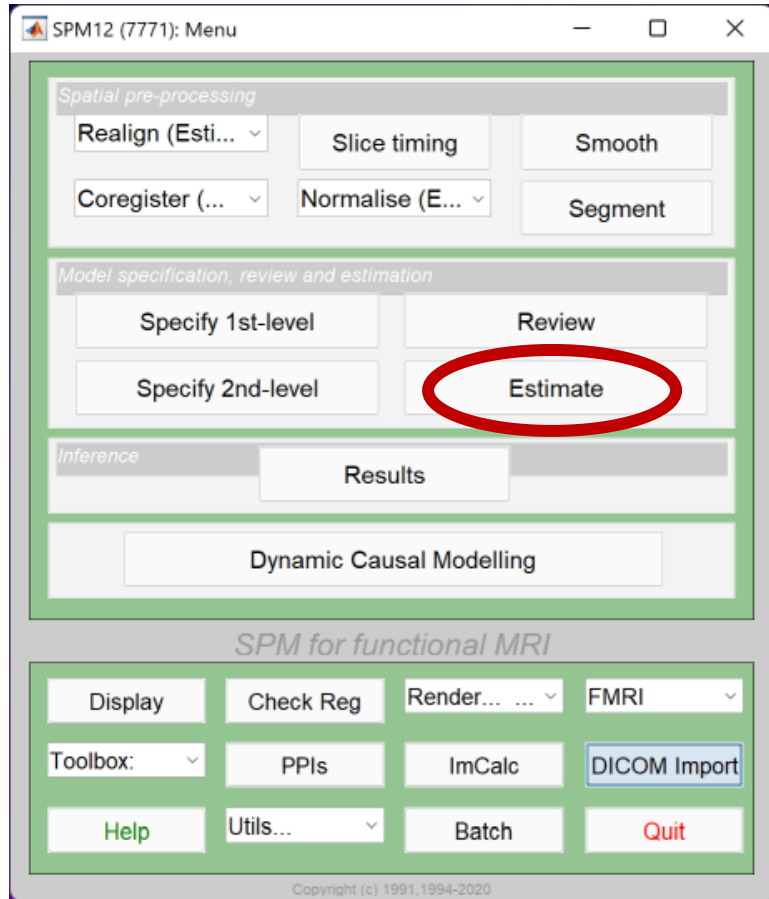
- a) Select SPM.mat ... select *SPM.mat*
- b) Run batch

RESULTS:

- Design – Design Matrix (model design for selected parameters)
- Design – Explore – Session 1 – LeftHandFingerTapping (time and frequency domain of the model)
- Design – Explore – Session 1 – RightHandFingerTapping (time and frequency domain of the model)

fMR Statistics

Model estimation



fMR Statistics

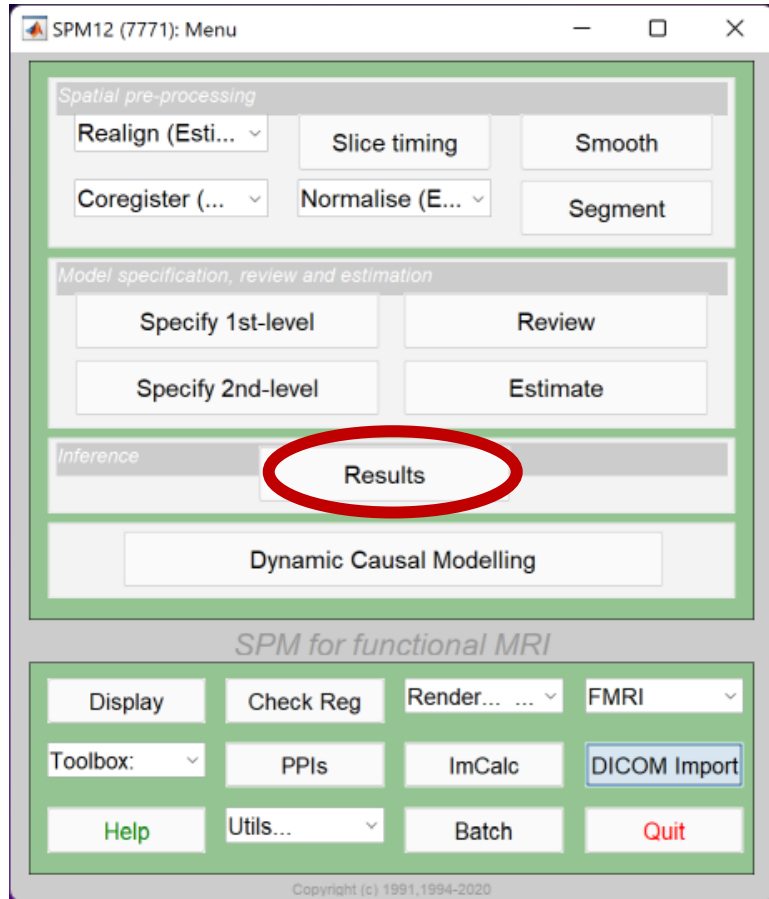
Model estimation

MENU: Estimate

BATCH EDITOR:

- a) Select SPM.mat ... select *SPM.mat*
- b) Run batch

fMR Statistics Results



fMR Statistics

Model estimation

MENU: Results

Select SPM.mat

SPM contrast manager:

a) Define new contrast

Name: **LeftHand** / **RightHand**

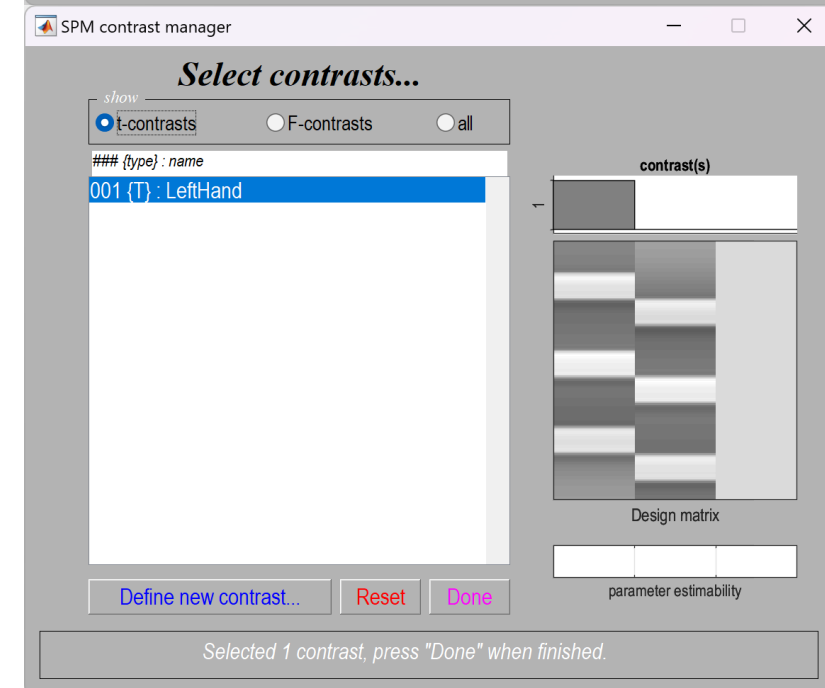
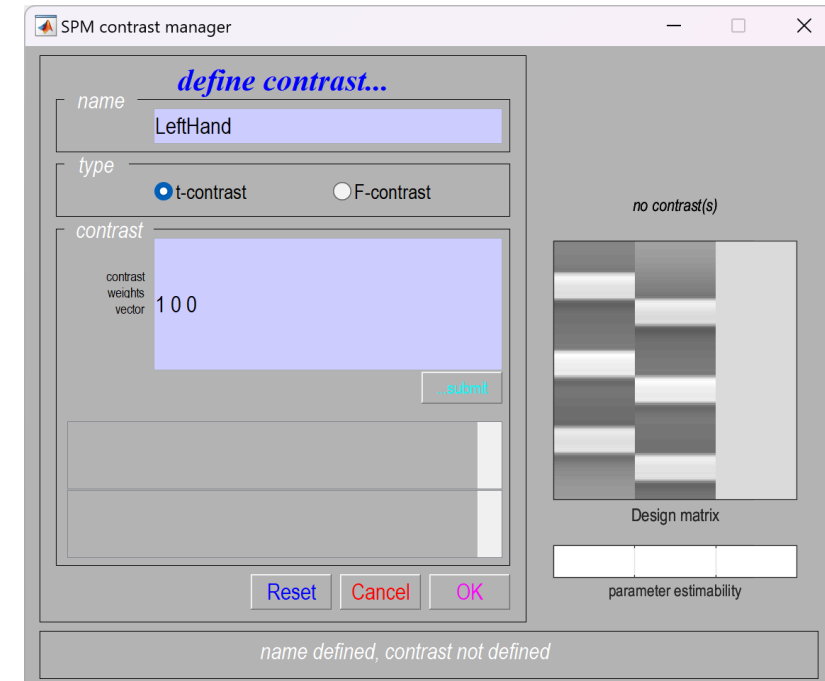
type: **t-contrast**

contrast: **1 0 0** / **0 1 0**

...submit

b) OK

c) Done



fMR Statistics

Model estimation

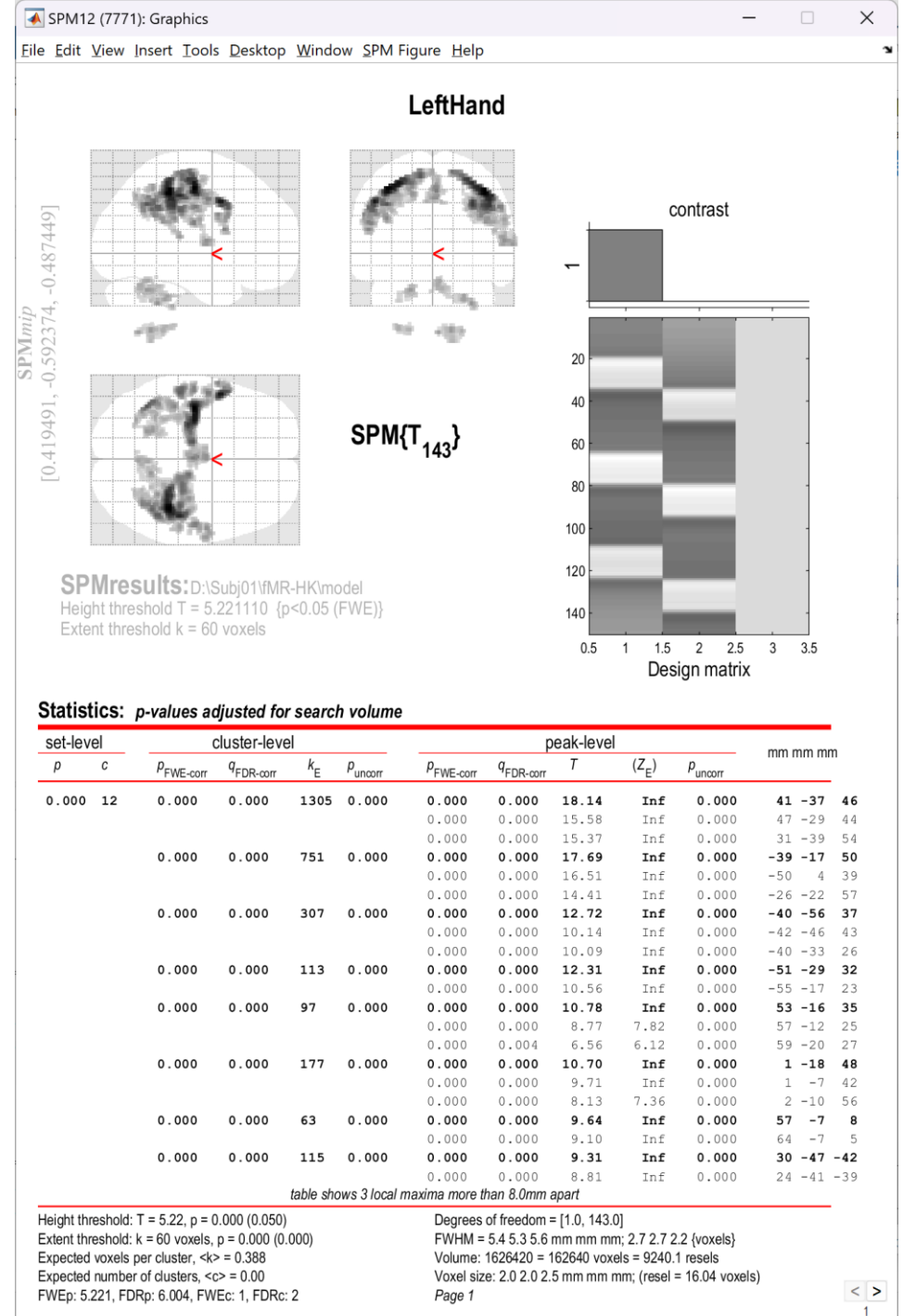
RESULTS:

apply masking ... **none**

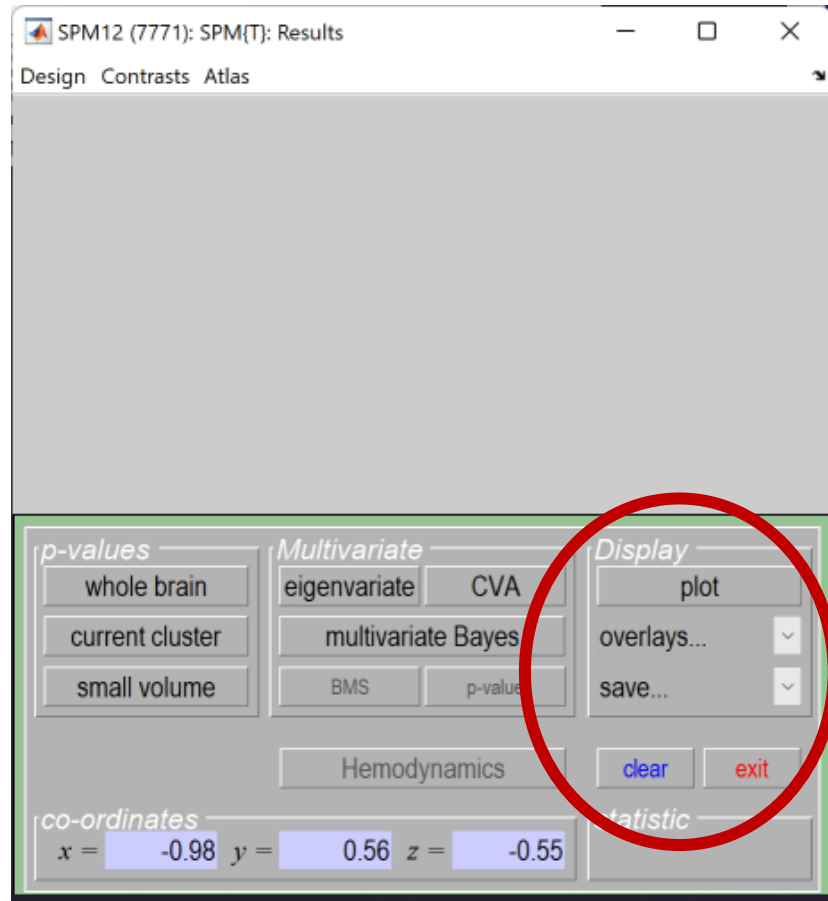
P value adjustment to control ... **FWE**

P value (FWE) ... **0.05**

& extent threshold {voxels} ... **60**



fMR Statistics Display



overlays...:

- Slices
- Sections (multiplanar)
- Montage (Axial / Coronal / Sagittal)

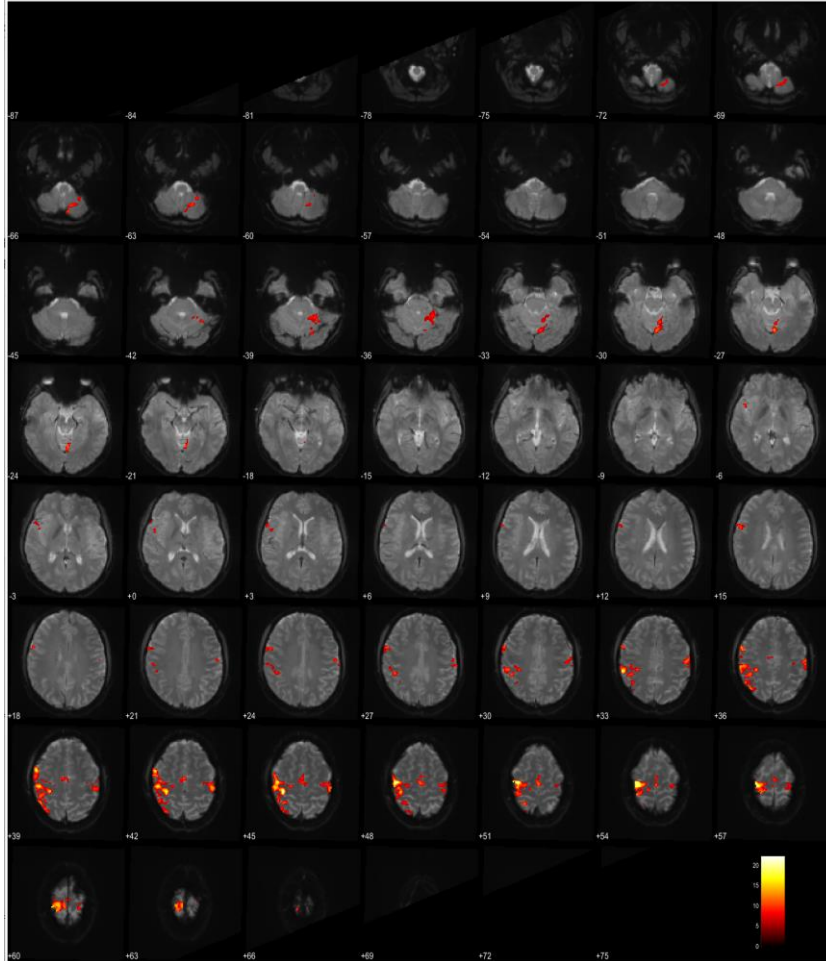
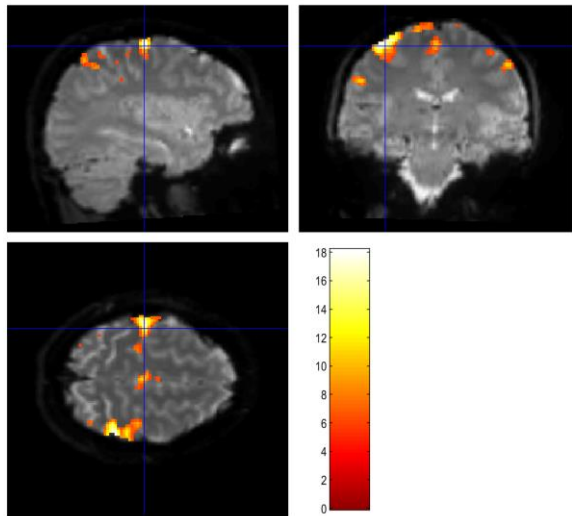
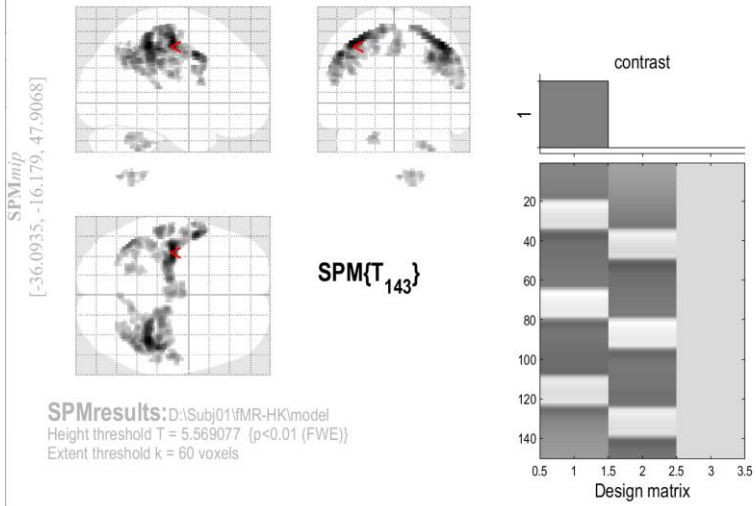
mean*.nii

plot:

Plot ... Fitted responses – adjusted

Plot against ... scan or time

LeftHand



LeftHand

