

fMR Processing(2)

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Today goal:

Group analysis of functional activity during FingerTapping task in 13 subjects using SPM12

- Looking for average activity in group of 13 measured subjects
 - Is there any common activation? Are the subject's activations on the same place in the brain
1. Do the processing of fmr data for subjects **Subj01** to **Subj13** following the pipeline
 2. Do the group statistics and display the results

fmr processing (1. exercise)

Pipeline

Conversion of data: DICOM -> NIFTI  (done; *.nii suffix)

Slice Timing: temporal correction (TR vs. HRF)  (skipping this step)

1. **Realignment** of functional data - spatial correction of data in time
2. **Smoothing** with Gauss filter kernel
3. **Model specification + Review**
4. **Estimate Model**
5. **Results + Display**

fmr processing (2. exercise)

Pipeline

Conversion of data:

DICOM -> NIFTI

✓ (done; *.nii suffix)

1. **Realignment** of functional data - spatial correction of data in time
2. **Segment** – mean fmr segmentation (WhiteMatter, GrayMatter, CSF)
3. **Normalise** – functional data to a standard MNI space (non/linear transformation)
4. **Smoothing** functional data with Gauss filter kernel
5. **Model specification + Review**
6. **Estimate Model**
7. **Results + Display**

DO IT FOR EACH SUBJECT Subj01 – Subj13

... 2nd- level analysis

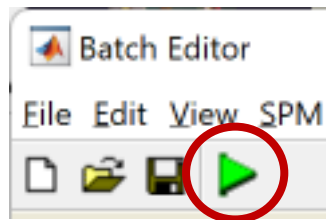
1. Realign data

MENU: Realign (Estimate & Reslice)

BATCH EDITOR:

a) **Data – Session ...** select all fmr files (*fmr_XXX*.nii*)

b) **Run batch**



Output:

- Resliced files (prefix „rfmr*.nii“)
- „meanfmr*.nii“ file (mean of all fmr files)
- Realignment parameters file „rp_*.txt“

2. Segment functional data

MENU: Segment

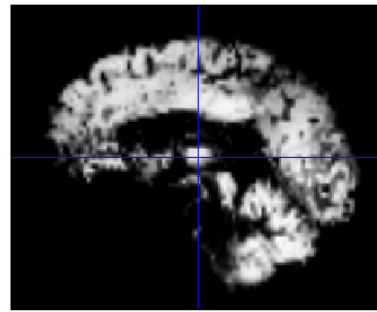
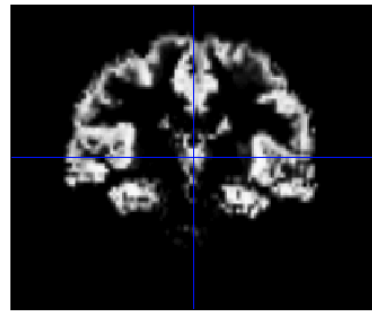
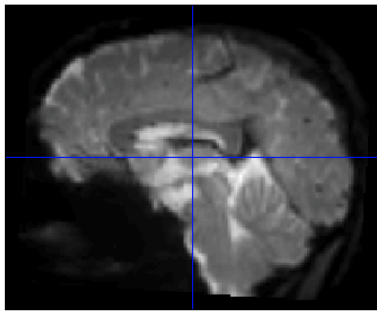
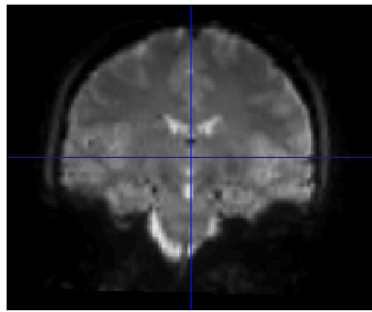
BATCH EDITOR:

- a) **Volumes** ... select mean data (*meanfmr*.nii*)
- b) **Deformation fields** (last parameter)... *Forward* (transform from functional space to MNI152)
- c) All other parameters as default!
- d) **Run batch** (could be time consuming little bit ☺)
- e) **Display or Check Reg**
output files

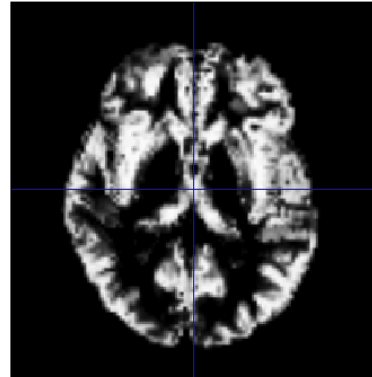
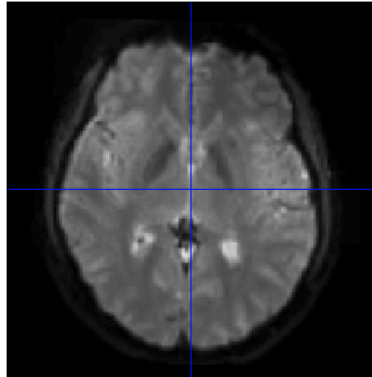
Output:

- *c1meanfmr*.nii* (gray matter probability)
- *c2meanfmr*.nii* (white matter prob.)
- *c3meanfmr*.nii* (CSF prob.)
- *y_meanfmr*.nii* (deformation field)
- *C4mean*.nii, c5mean*.nii* (non brain tissue)

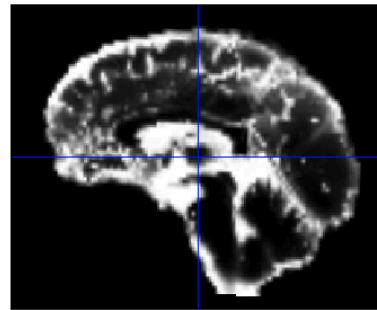
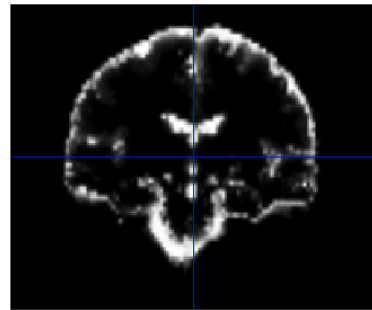
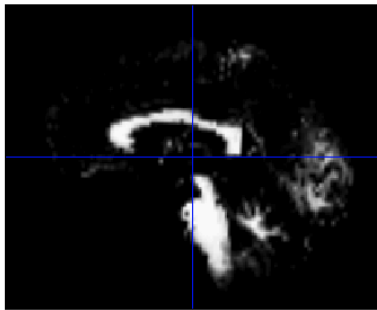
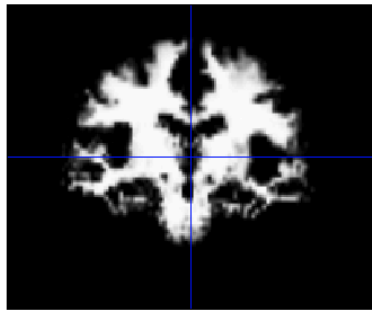
meanfmr



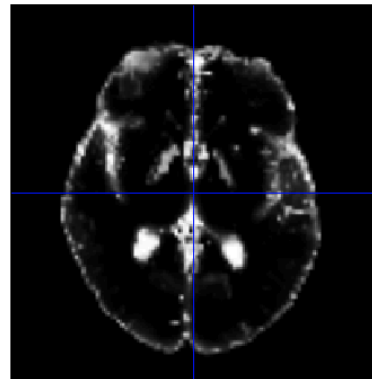
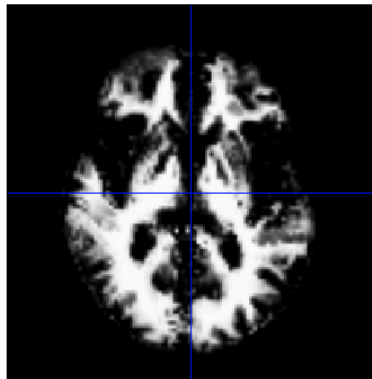
$c1^*$ = gray matter



$C2^*$ = white matter



$C3^*$ = cerebro-spinal fluid



3. Normalise functional data

MENU: Normalise (Write)

BATCH EDITOR:

- a) **Data – Subject – Deformation Field ...** select Forward deformation Field
(*y_meanfmr*.nii*)
- b) **Images to Write ...** all realigned functional images (*rfmr*.nii*)
meanfmr.nii*
- c) **Voxel sizes ...** [3 3 3]
- d) **Run batch**

- e) **Display**
output files

Output:

- 150 volumes of *wrfmr*.nii* (functional data in standard ***MNI152 space***)
- 1 volume *wmeanfmr*.nii*

4. Smooth functional data (realigned and normalised data)

MENU: Smooth

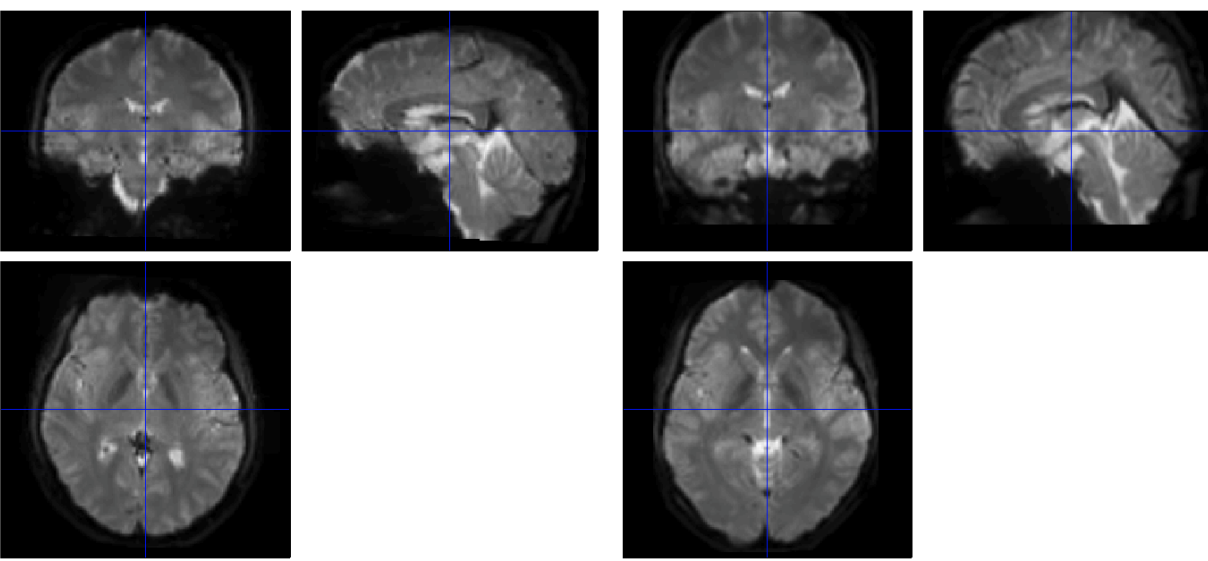
BATCH EDITOR:

- a) **Images to smooth ...** select all *wrfmr*.nii* files
- b) **FWHM ... [8 8 8]** (FWHM of the Gaussian smoothing kernel in mm)
- c) Run batch

Output:

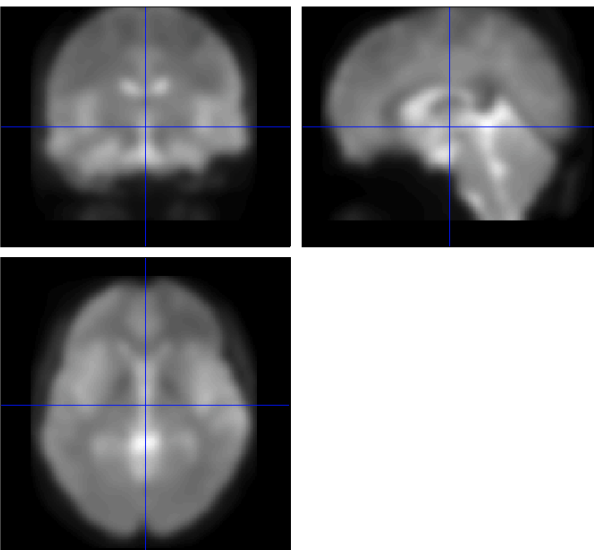
- Smoothed functional files (all with prefix „**swrfmr*.nii**“)

meanfmr



wmeanfmr

swmeanfmr



5. Model specification (1st-level)

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 *swr*.nii* data
 - b) **Conditions**
 - a) **Condition**
 - a) **Name** ... name of processed paradigm, for example LeftHandFingerTapping / RightHandFingerTapping
 - b) **Onset** ... vector of scans where the activations begin
 - c) **Durations** ... duration of activation (in scans)
- e) **Run batch**

Output:

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

fmr Statistics

5. Model specification - Conditions

1. Condition **LeftHand**

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

2. Condition **RightHand**

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

6. Model estimation

MENU: Estimate

BATCH EDITOR:

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

7. Results (define contrast)

MENU: Results

Select SPM.mat

SPM contrast manager:

a) Define new contrast

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

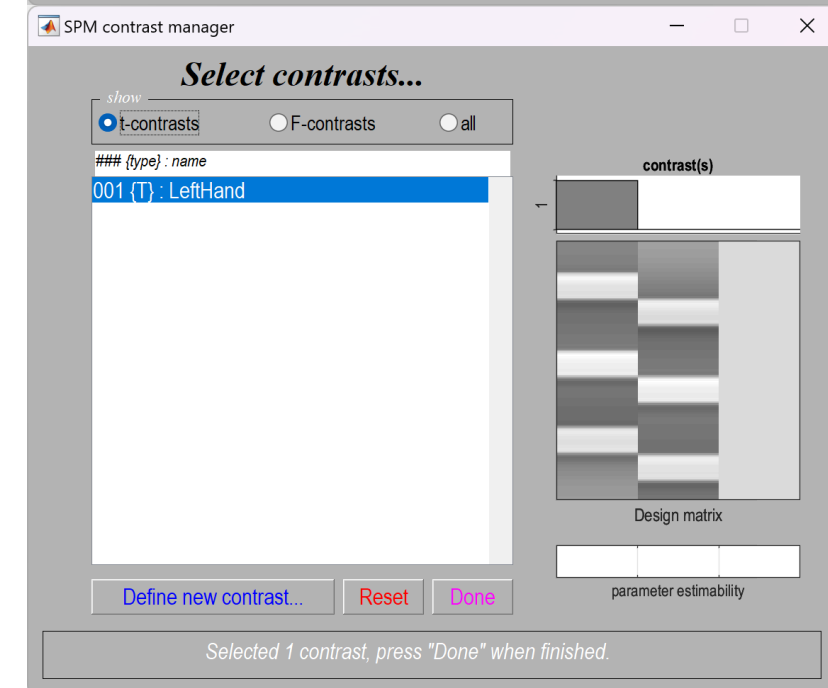
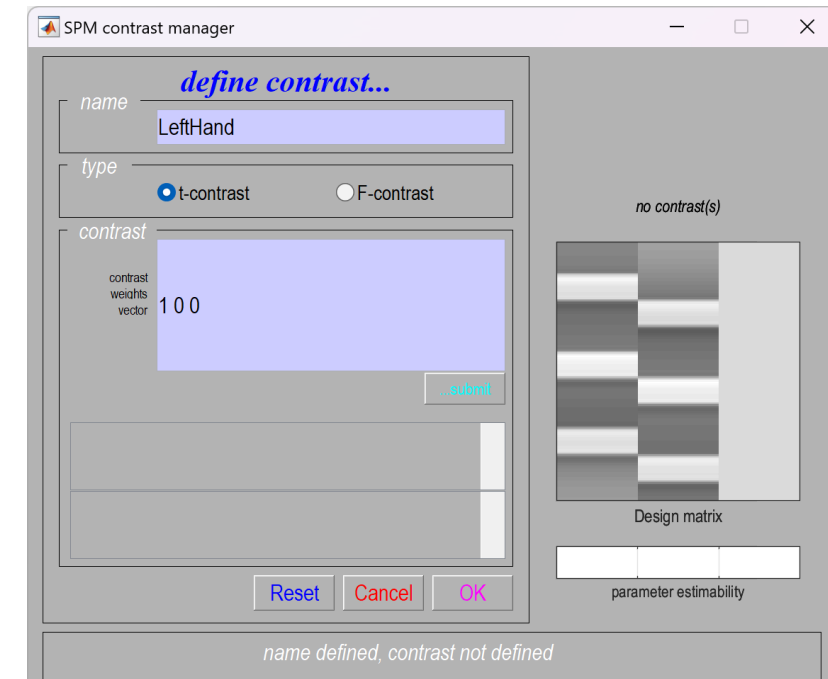
type: **t-contrast**

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

...submit

b) OK

c) Done



8. Results

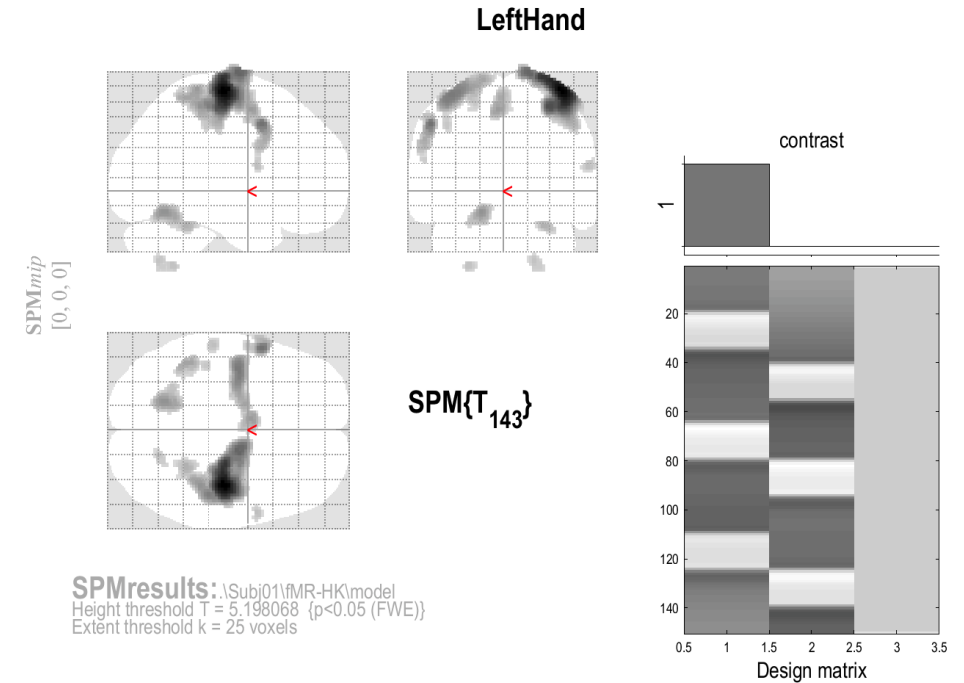
RESULTS:

apply masking ... none

P value adjustment to control ... none/FWE

Threshold {T or p value} ... 0.001/0.05

& extent threshold {voxels} ... 25



SPMresults: \Subj01\fmr-HK\model
Height threshold T = 5.198068 (p<0.05 (FWE))
Extent threshold k = 25 voxels

Statistics: p-values adjusted for search volume

set-level		cluster-level				peak-level					mm mm mm		
p	c	p _{FWE-corr}	q _{FDR-corr}	k _E	p _{uncorr}	p _{FWE-corr}	q _{FDR-corr}	T	(Z _E)	p _{uncorr}			
0.000	12	0.000	0.000	2169	0.000	0.000	0.000	14.82	Inf	0.000	40	-18	66
						0.000	0.000	10.87	Inf	0.000	32	-24	56
						0.000	0.000	9.77	Inf	0.000	16	-10	80
		0.000	0.000	233	0.000	0.000	0.000	9.34	Inf	0.000	-54	8	44
						0.000	0.009	6.41	6.00	0.000	-56	-2	48
						0.004	0.102	5.81	5.49	0.000	-58	6	20
		0.000	0.000	582	0.000	0.000	0.000	9.00	Inf	0.000	-38	-8	64
						0.000	0.000	7.27	6.70	0.000	-16	-4	74
						0.001	0.027	6.16	5.79	0.000	-24	-12	60
		0.000	0.000	269	0.000	0.000	0.000	7.99	7.25	0.000	-18	-60	-16
		0.000	0.000	221	0.000	0.000	0.000	7.65	6.99	0.000	-6	0	54
						0.000	0.000	7.13	6.59	0.000	-4	-2	62
		0.000	0.000	124	0.000	0.000	0.000	7.29	6.71	0.000	-44	-44	62
						0.023	0.484	5.40	5.14	0.000	-34	-48	68
		0.000	0.000	83	0.000	0.000	0.002	6.79	6.31	0.000	28	-46	-26
		0.000	0.000	32	0.000	0.000	0.016	6.29	5.90	0.000	58	4	16
		0.000	0.000	39	0.000	0.001	0.020	6.23	5.85	0.000	-56	-26	48
		0.000	0.000	28	0.000	0.001	0.032	6.11	5.75	0.000	-26	-56	-52
		0.000	0.000	50	0.000	0.001	0.040	6.05	5.70	0.000	20	-66	-50
		0.000	0.000	33	0.000	0.003	0.071	5.91	5.58	0.000	-42	-32	44

table shows 3 local maxima more than 8.0mm apart

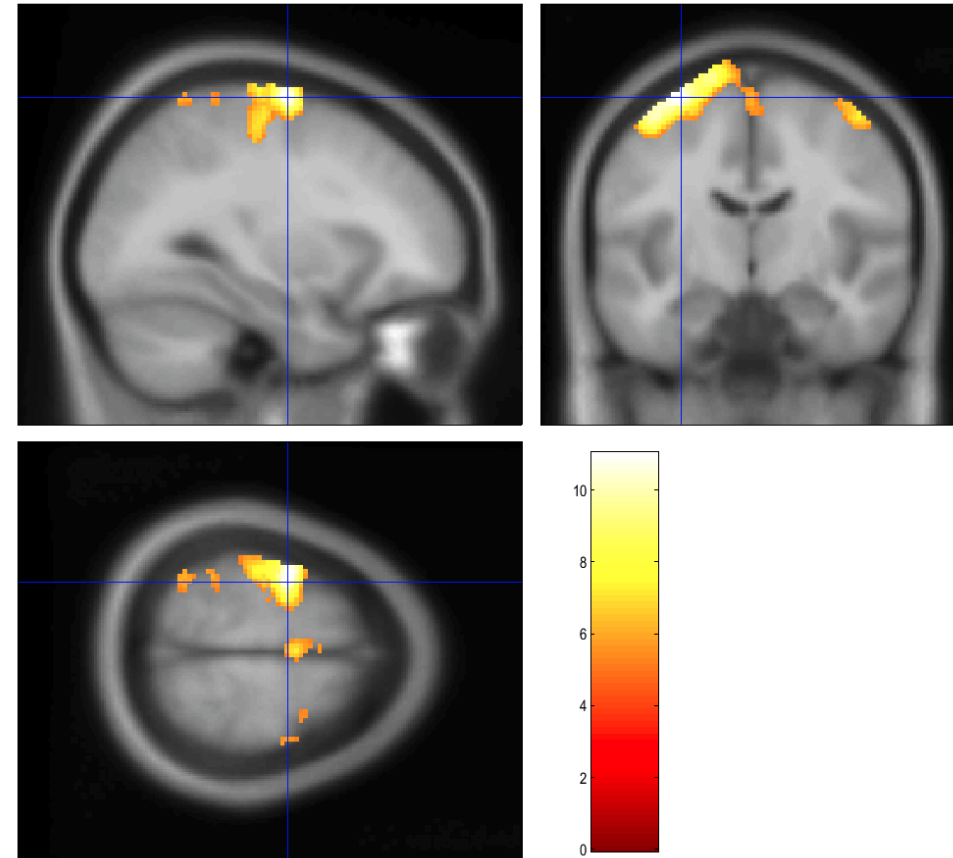
Height threshold: T = 5.20, p = 0.000 (0.050)
Extent threshold: k = 25 voxels, p = 0.001 (0.000)
Expected voxels per cluster, <k> = 1.588
Expected number of clusters, <c> = 0.00
FWEp: 5.198, FDRp: 6.052, FWEc: 1, FDRc: 10

Degrees of freedom = [1.0, 143.0]
FWHM = 8.1 8.1 7.9 mm mm mm; 4.1 4.0 3.9 {voxels}
Volume: 1882440 = 235305 voxels = 3393.1 resels
Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 64.76 voxels)

Display Results

Results can be displayed with **overlay** command
(in results window, Slices, Section, Montage)

As a background image use the MNI template
images from the
`%SPM12%/canonical/avg*.nii`



... do the preview pipeline for all subjects (batch editor?)

Subj01

Subj02

Subj03

Subj04

Subj05

Subj06

...

Subj13

File structure for each subject

- **SubjXX**

- **fmr**

- *fmr*.nii* (150 origin files)
 - *rfmr *.nii* (150 realigned files)
 - *rp_fmr*.txt* 1 realignment parameters txt-file
 - *meanfmr*.nii* 1 mean function file
 - *wrfmr*.nii* (150 realigned and normalised files)
 - *swrfmr*.nii* (150 realigned, normalised and smoothed files)

- **model**

- *beta_0001.nii* beta values of GLM model, for first predictor (predictor of activations)
 - *beta_0002.nii* beta values of GLM model, for second predictor (predictor of activations)
 - *beta_0003.nii* beta values of GLM model, for third predictor (constant predictor)
 - ***con_0001.nii*** contrast file for first predictor **IMPORTANT FOR GROUP ANALYSIS!!!**
 - ***con_0002.nii*** contrast file for second predictor **IMPORTANT FOR GROUP ANALYSIS!!!**
 - *mask.nii* binary mask file, created automatically
 - *ResMS.nii* residuals file, errors of the GLM model
 - *RPV.nii* residuals per voxel file
 - *SPM.mat* mat-file, where GLM model is stored
 - *spmT_0001.nii* t-statistics T-values

- **t1**

- *t1.nii* 1 structural t1-weighted image

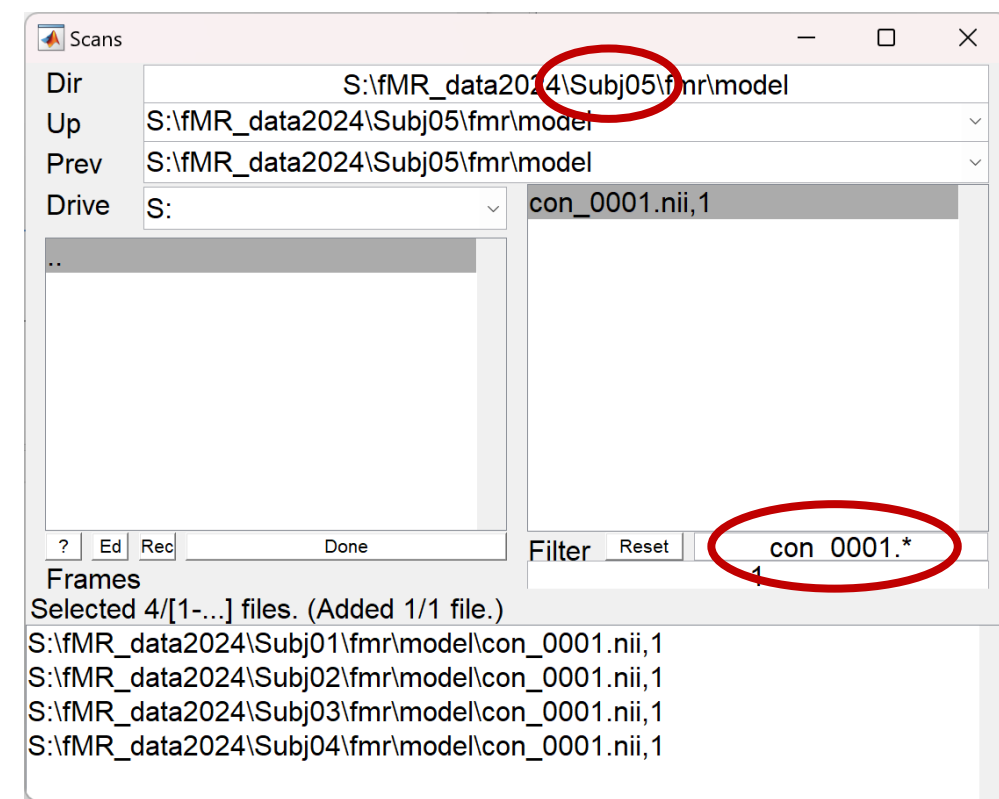
2nd-level
(GROUP ANALYSIS)

8. Model specification (group mean)

MENU: Specify 2nd-level

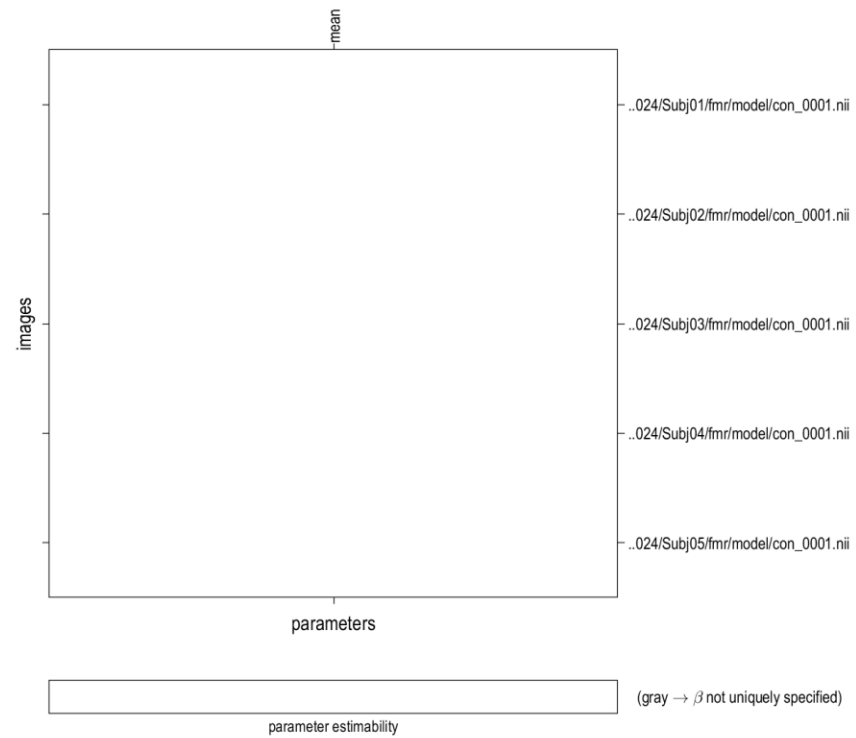
BATCH EDITOR:

- a) **Directory** ... select folder (for example „*group_mean_Left*“)
- b) **Design – One-sample t-test – Scans** ... select all *con_0001.nii* files from model folder of each subject (13x *con_0001.nii*)
- c) **Run batch**



con_0001.nii ... LeftHand
con_0002.nii ... RightHand

Statistical analysis: Design



Design description...

Design : One sample t-test
Global calculation : omit
Grand mean scaling : <no grand Mean scaling>
Global normalisation : <no global normalisation>
Parameters : 1 condition, +0 covariate, +0 block, +0 nuisance
1 total, having 1 degrees of freedom
leaving 4 degrees of freedom from 5 images

9. Model estimation (group mean)

MENU: Estimate

BATCH EDITOR:

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

10. Results – define contrast (group mean)

MENU: Results

Select SPM.mat

SPM contrast manager:

a) Define new contrast

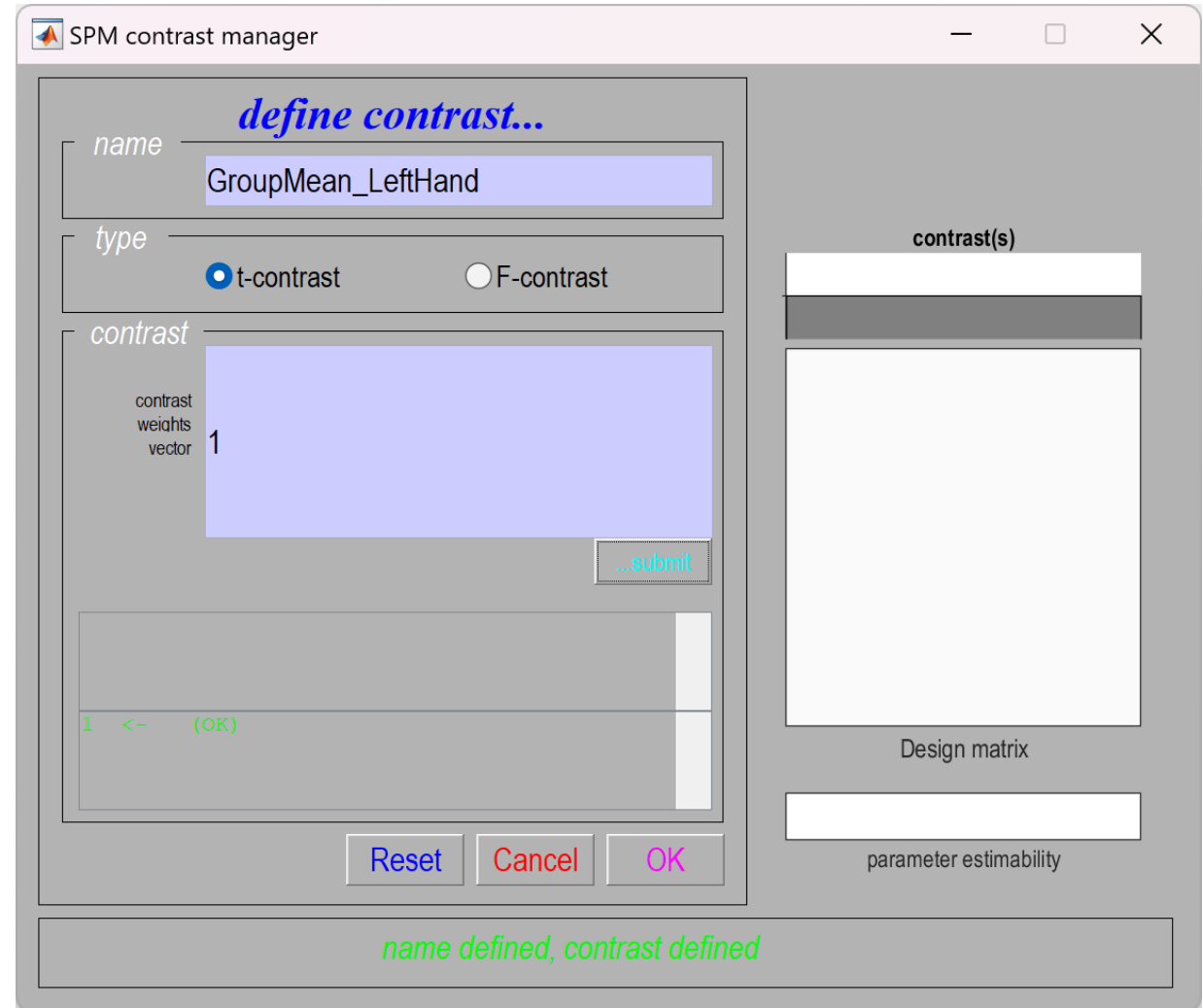
Name: *GroupMean_LeftHand*

type: *t-contrast*

contrast: *1* ...submit

b) OK

c) Done



11. Results (group mean)

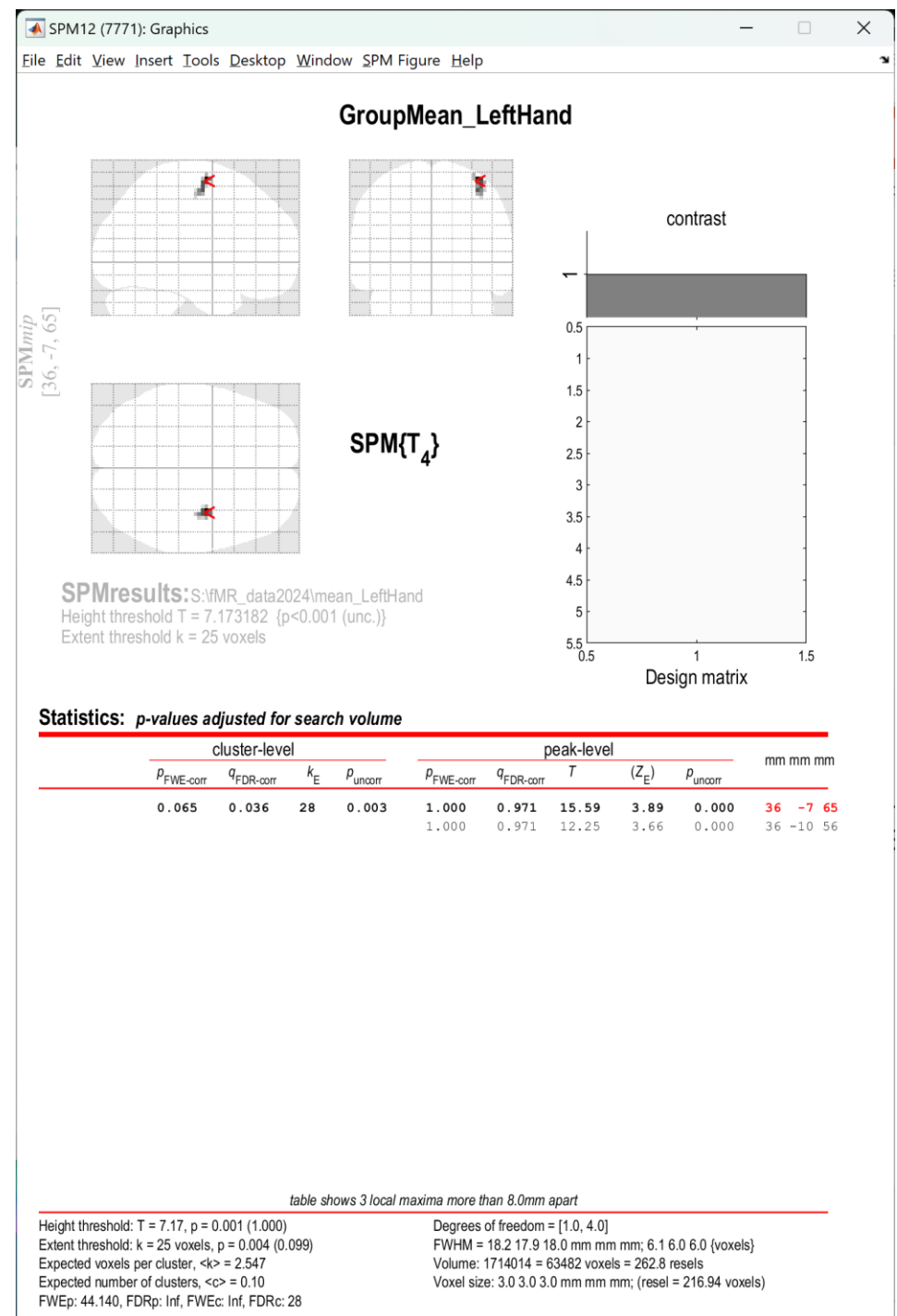
RESULTS:

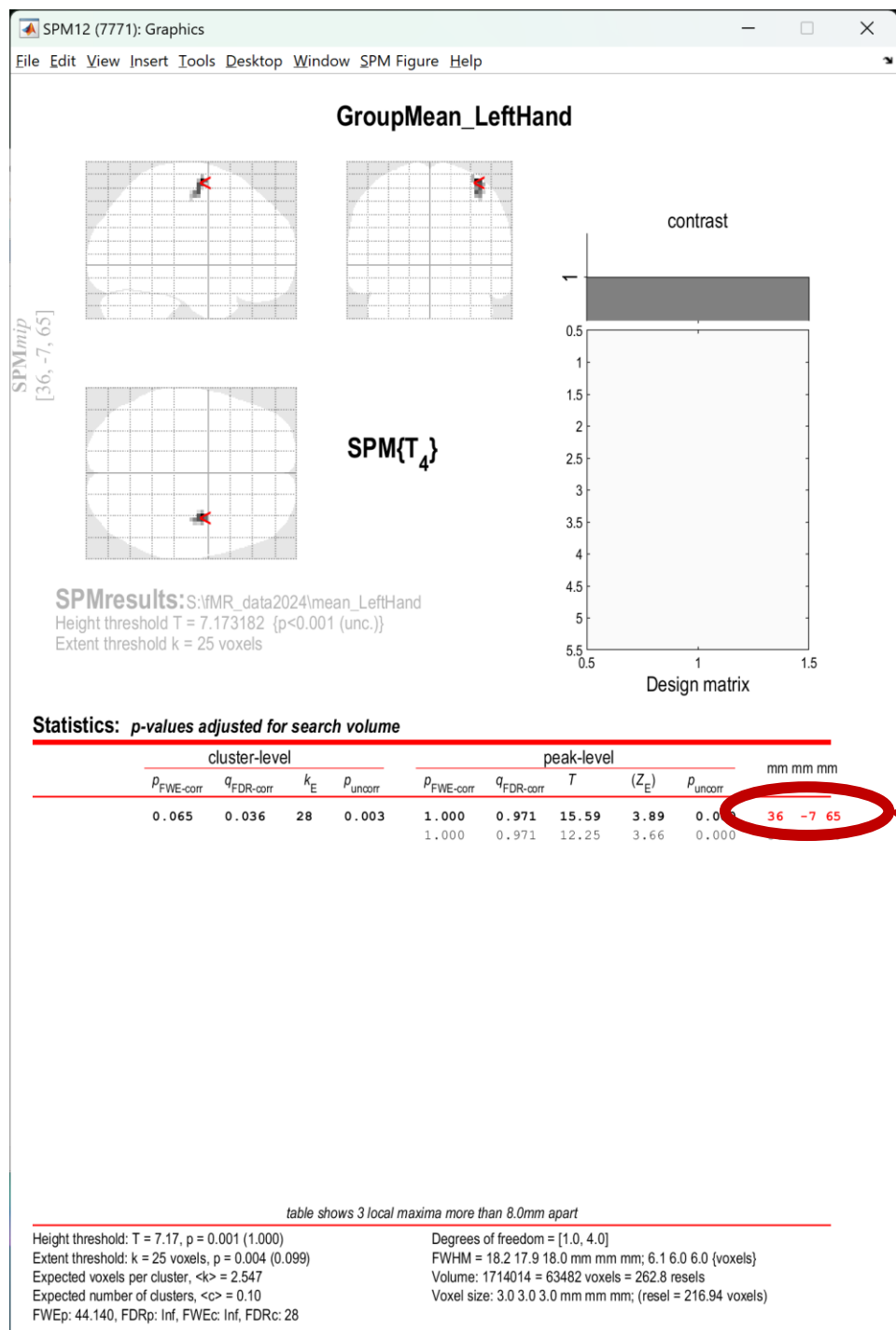
apply masking ... none

P value adjustment to control ... **none**

Threshold {T or p value} ... 0.001

& extent threshold {voxels} ... 25





Coordinates of maximal activation in MNI space

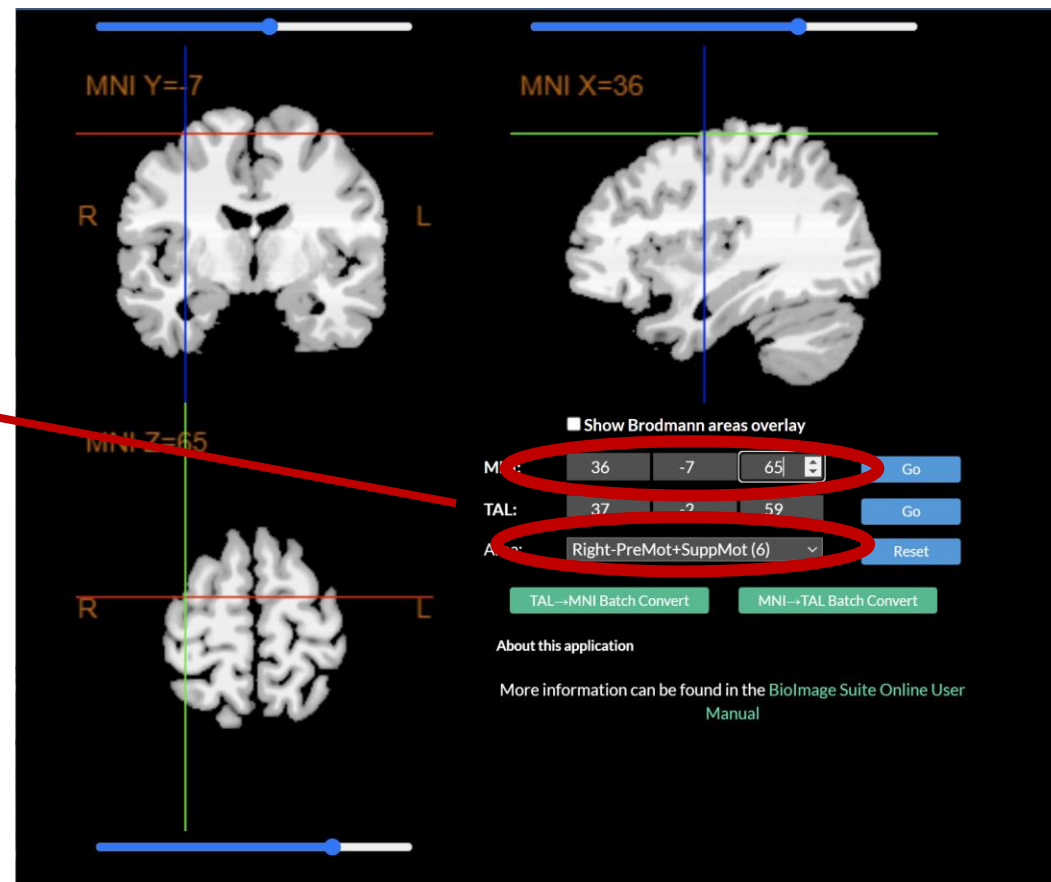
Use

<https://bioimagesuiteweb.github.io/webapp/mni2tal.html>

To find the brain area, which is activated:

List of Brodmann areas:

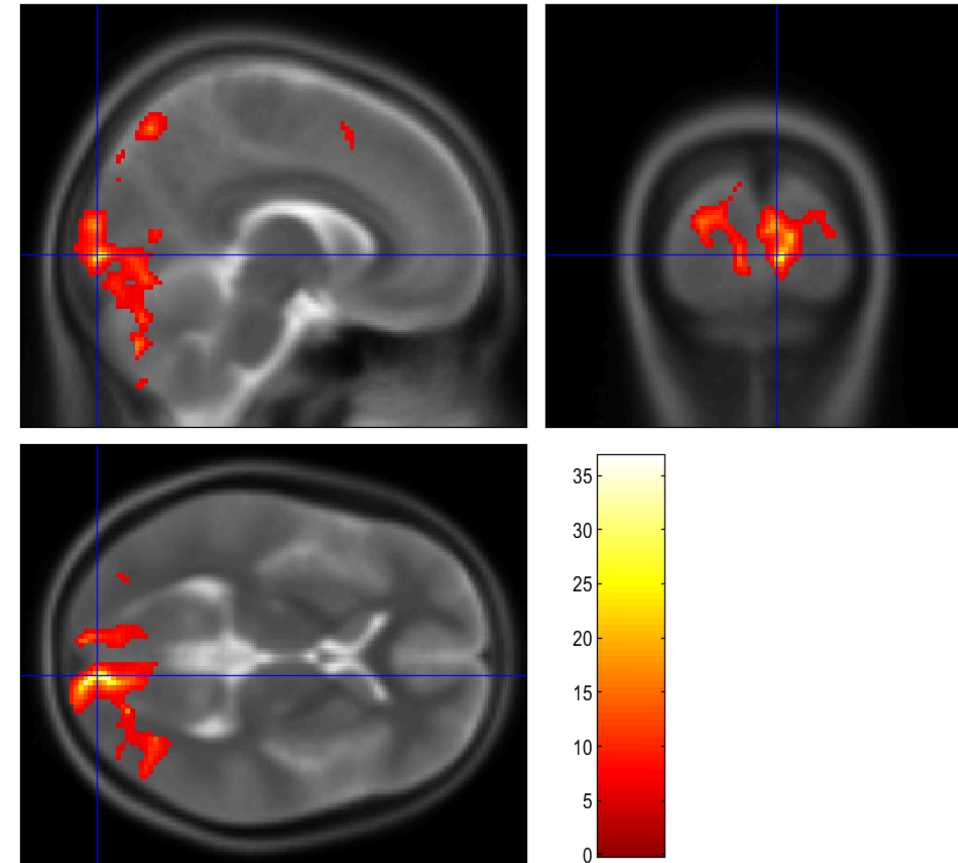
https://en.wikipedia.org/wiki/Brodmann_area



Display Results

Results can be displayed with **overlay** command
(in results window, Slices, Section, Montage)

As a background image use the MNI template
images from the
`%SPM12%/canonical/avg*.nii`



Homework

1. Do the 1st-level analysis for both hands in all 13 measured subjects. Follow the pipeline from the 2nd exercise **(2 points)**
2. Do the group analysis following the pipeline from the 2nd exercise. Show the mean activation in the group for left (con_0001) and right (con_0002) hand **(2 points)**
3. Display results of the 2nd-level analysis for both tasks **(2 points)**
4. Find main areas with statistically significant activations for both tasks (up to three main areas). Use MNI atlas by your own choice. Describe expected/real results. Consult your results with Brodmann areas atlas **(4 points)**

Homework protocol is mainly about results. Showing the 1st-level analysis is not necessary. Please use common formats (pdf, word documents, ...)

Hint: batch editor is programmable and could be helpful with the repeating commands