

fMR Processing(2)

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Today goal:

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

- Looking for average activity in group of eight 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 **subj15** 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 – subj15)

... 2nd- level analysis

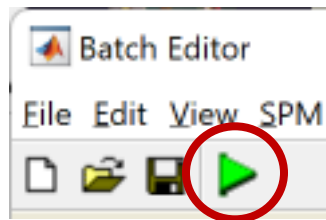
1. Realign data

MENU: Realign (Estimate & Reslice)

BATCH EDITOR:

a) **Data – Session ...** select all fMR files (*fMR*.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 mean „structural“ data

MENU: Segment

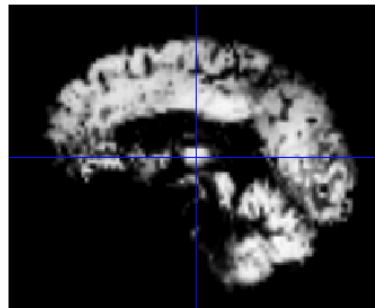
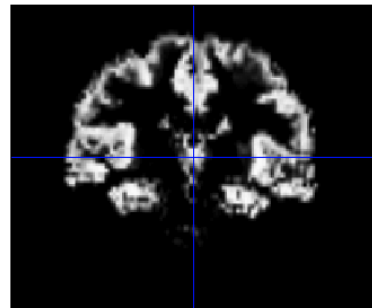
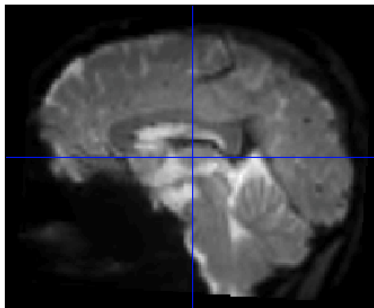
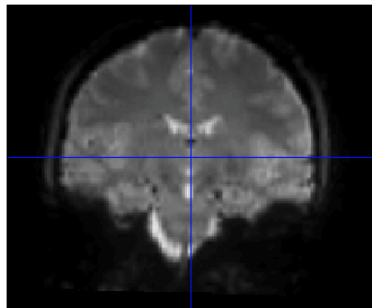
BATCH EDITOR:

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

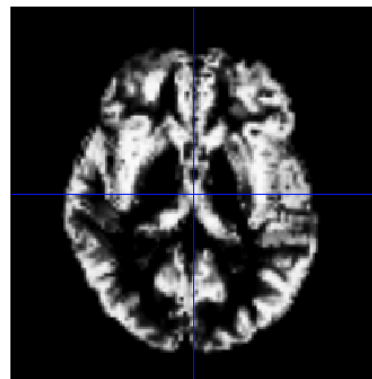
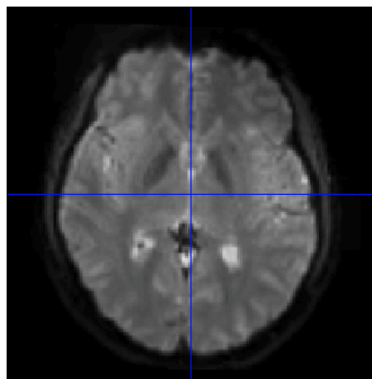
Output:

- *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)

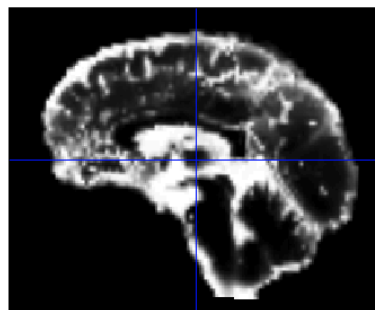
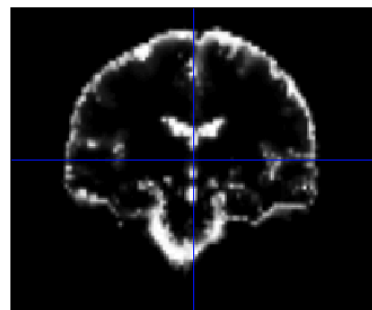
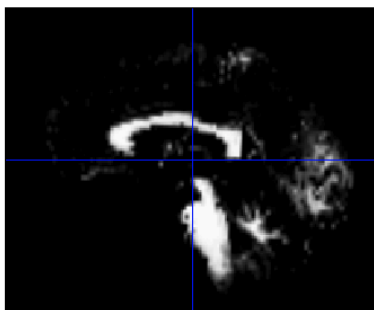
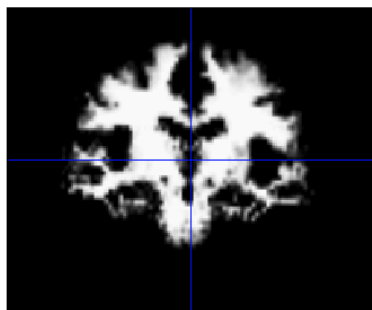
meanfMR



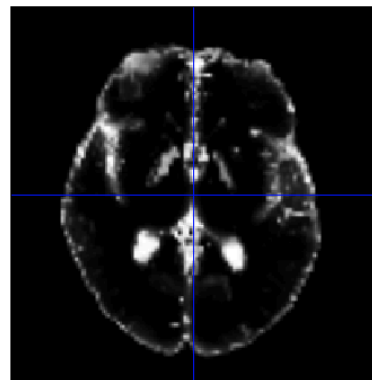
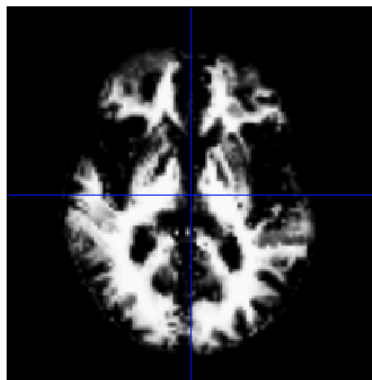
$c1^*$ = gray matter



$C2^*$ = 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 ...** [2 2 2]
- d) **Run batch**

- e) **Display**
output files

Output:

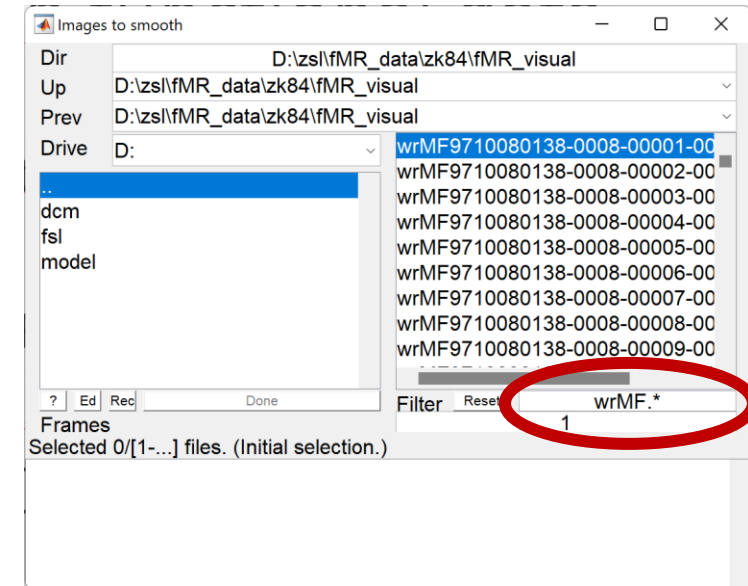
- 150 volumes of *wrfMR*.nii* (functional data in standard ***MNI152 space***)
- 1 volume *wmeanfMR*.nii*

4. Smooth functional data (realigned and normalised data)

MENU: Smooth

BATCH EDITOR:

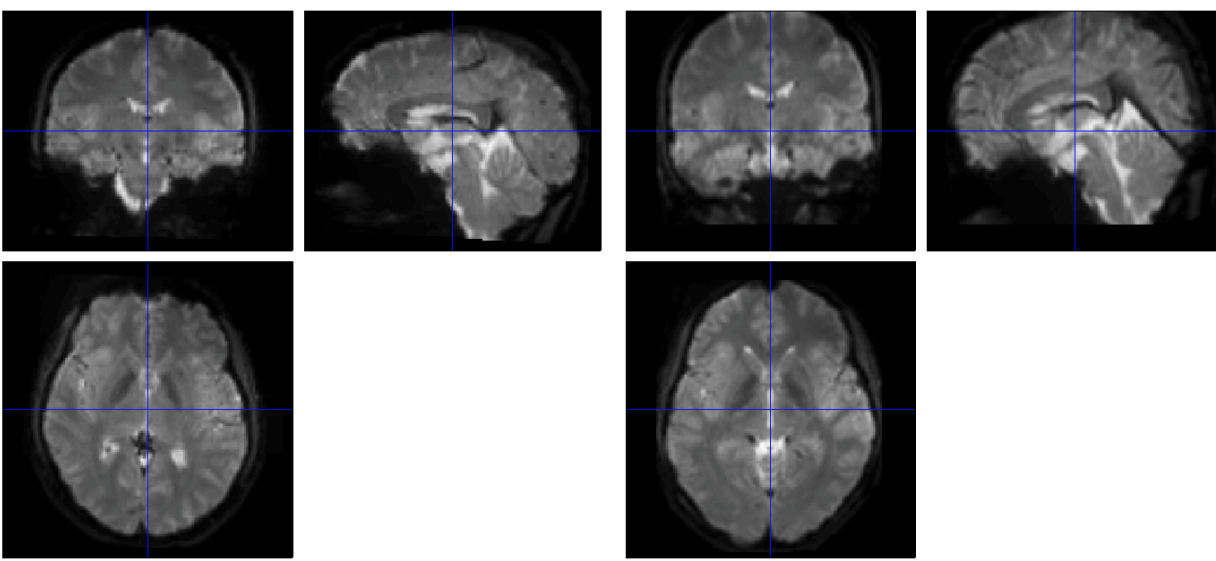
- Images to smooth ...** select all *wrfMR*.nii* files
- FWHM ... [8 8 8]** (FWHM of the Gaussian smoothing kernel in mm)
- Run batch**



Output:

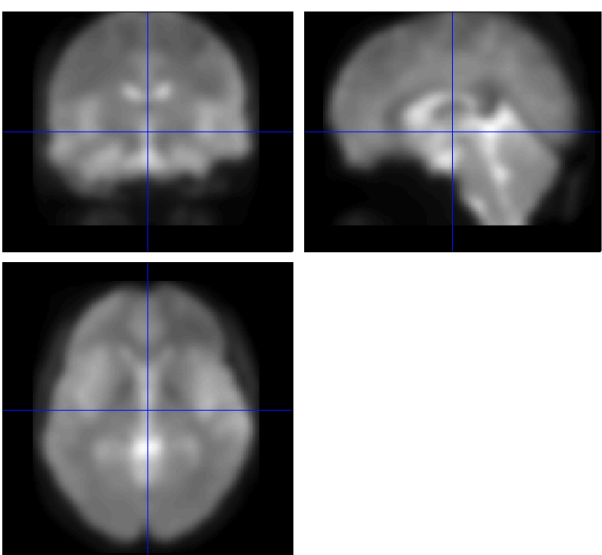
- Smoothed functional files (all with prefix „**swrfMR*.nii**“)

meanfMR



wmeanfMR

swmeanfMR



5. Model specification (1st-level)

MENU: Specify 1st-level

BATCH EDITOR:

- a) **Directory** ... select folder 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

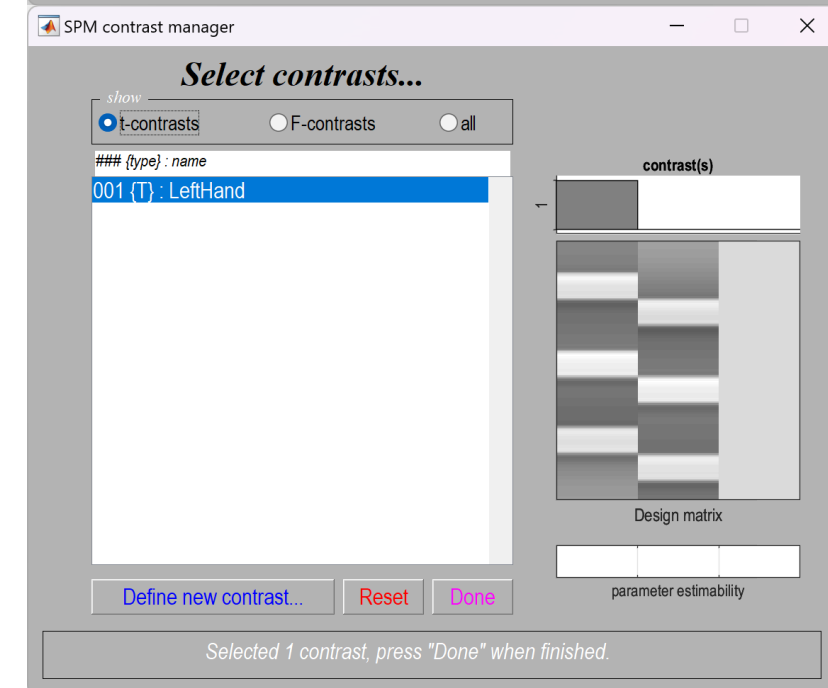
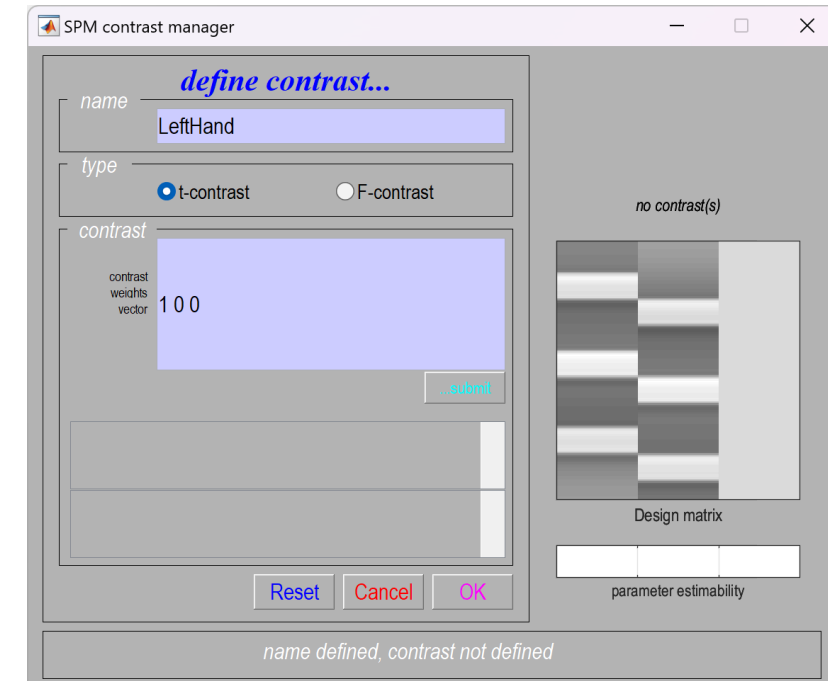
Name: **LeftHand** / **RightHand**

type: **t-contrast**

contrast: **1 0 0** / **0 1 0** ...submit

b) OK

c) Done



8. Results

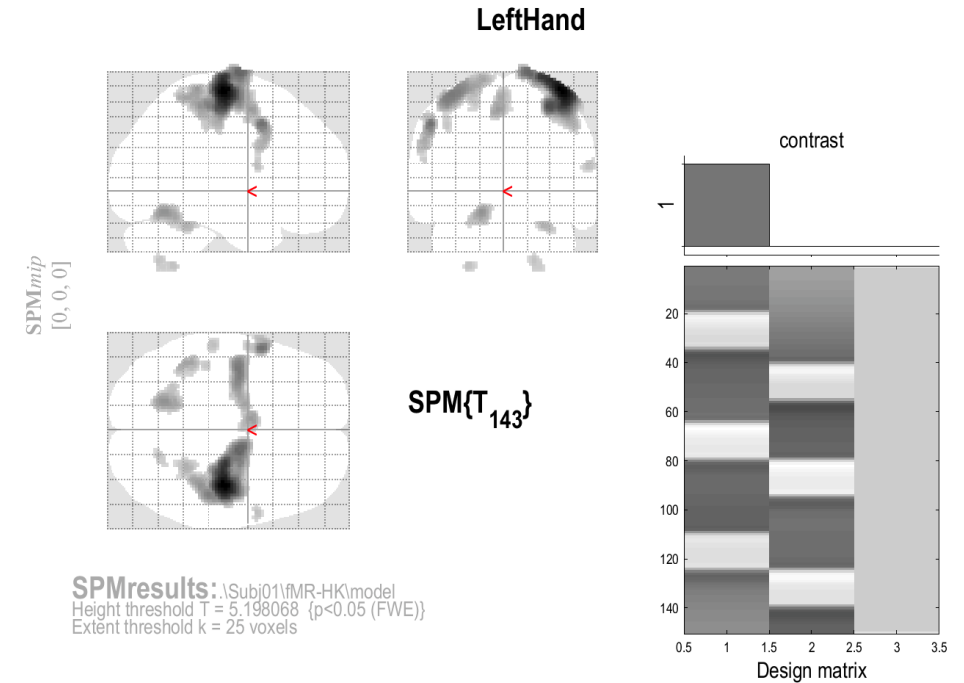
RESULTS:

apply masking ... none

P value adjustment to control ... none/FWE

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

& extent threshold {voxels} ... 7



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, <c> = 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)

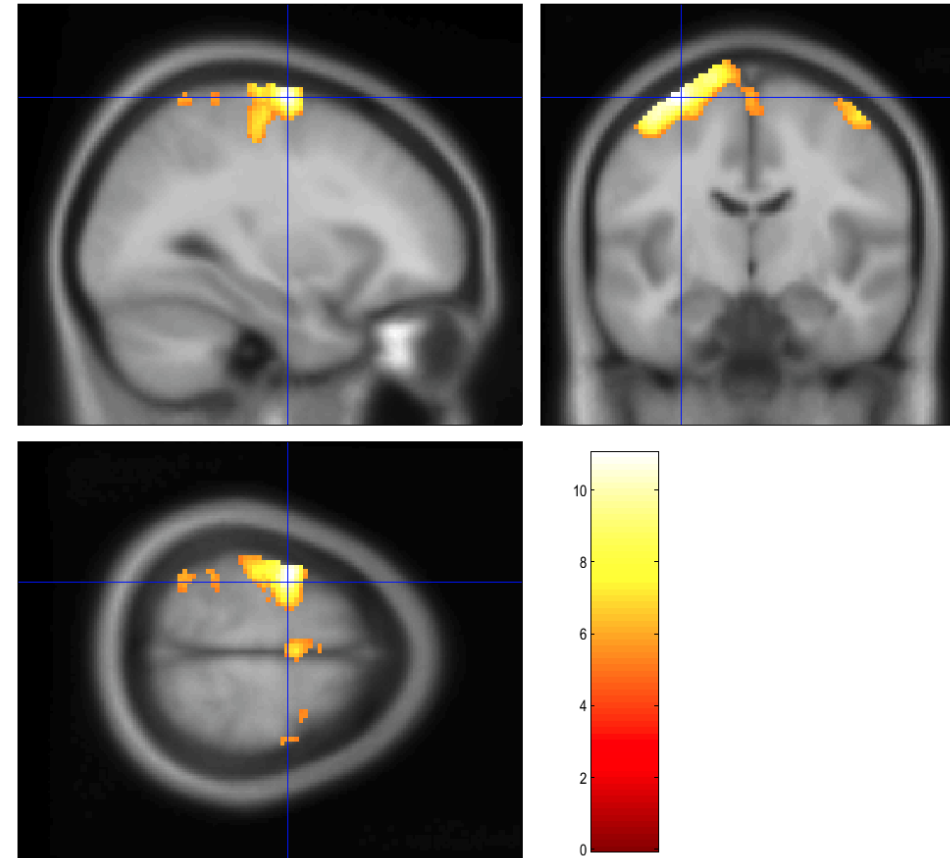
Display Results

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

Use the MNI template as a background image

file from the

`%SPM12%/canonical/avg*.nii`



... do the preview pipeline for subjects

Subj01

Subj02

Subj03

Subj04

Subj05

Subj06

Subj07

Subj08

Subj09

Subj10

Subj11

Subj12

Subj13

Subj14

Subj15

File structure for each subject

- **subjXX**

- *fMR_*.nii* (150 origin files)
- *rfMR_*.nii* (150 realigned files)
- *rp_fMR_*.txt* 1 realignment parameters txt-file
- *meanfMR_*.nii* 1 mean functional file
- *wrfMR_*.nii* (150 realigned and normalised files)
- *swrfMR_*.nii* (150 realigned, normalised and smoothed files)

- *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

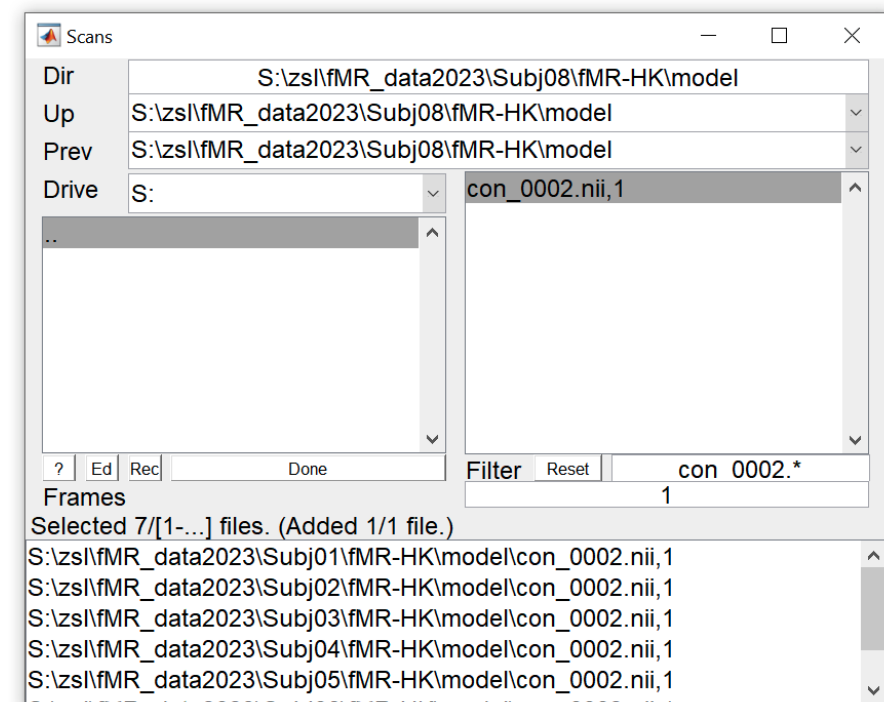
2nd-level
(GROUP ANALYSIS)

8. Model specification (group mean)

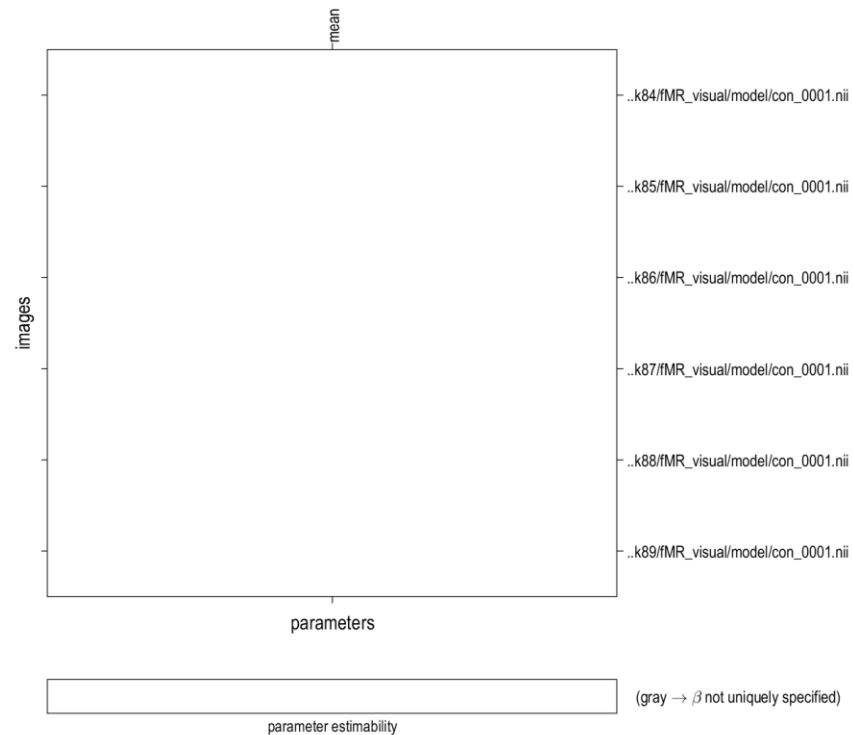
MENU: Specify 2nd-level

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 (8x *con_0001.nii*)
- c) **Run batch**



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 5 degrees of freedom from 6 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

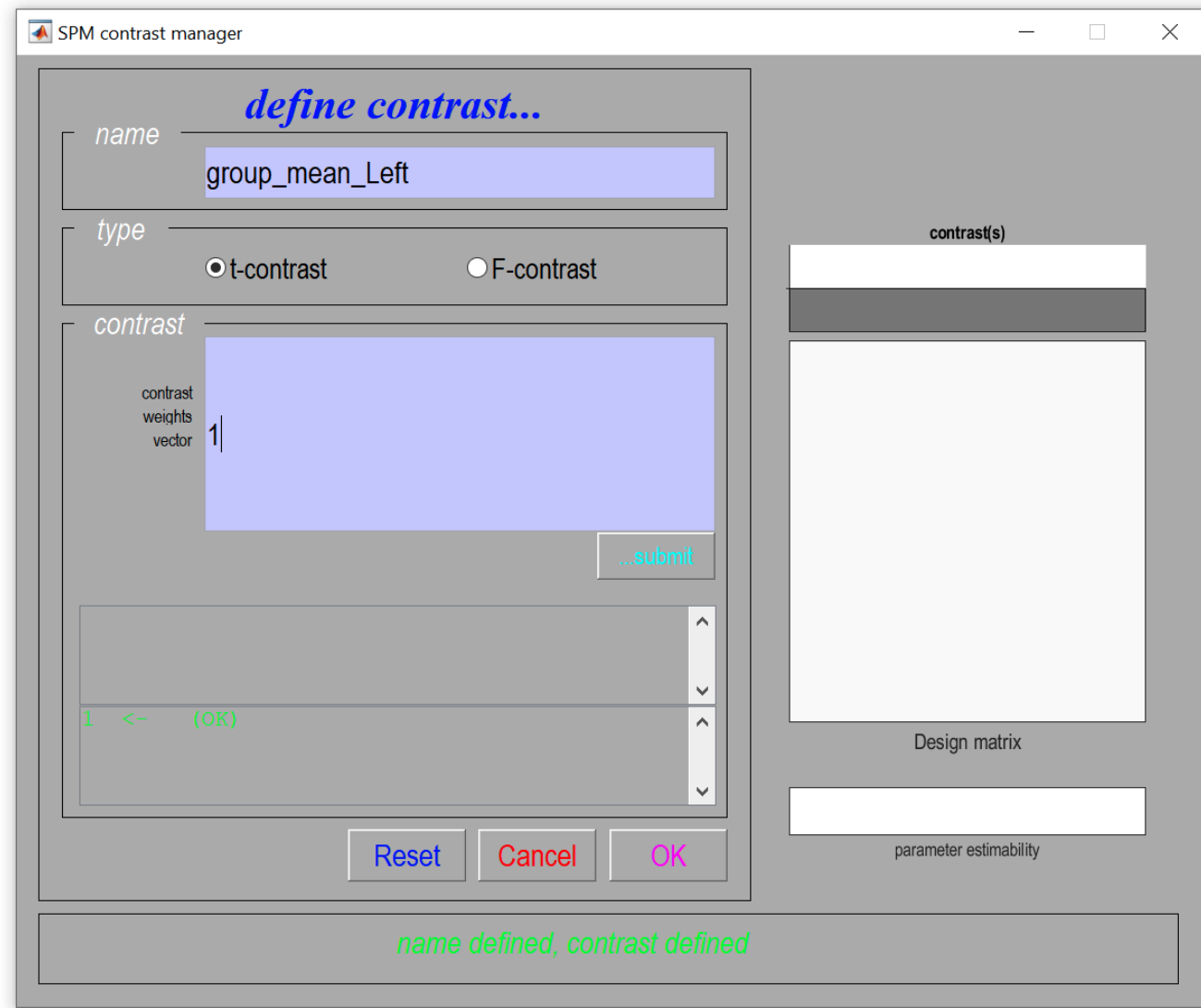
Name: *group_mean_Left*

type: *t-contrast*

contrast: *1* ...submit

b) OK

c) Done



11. Results (group mean)

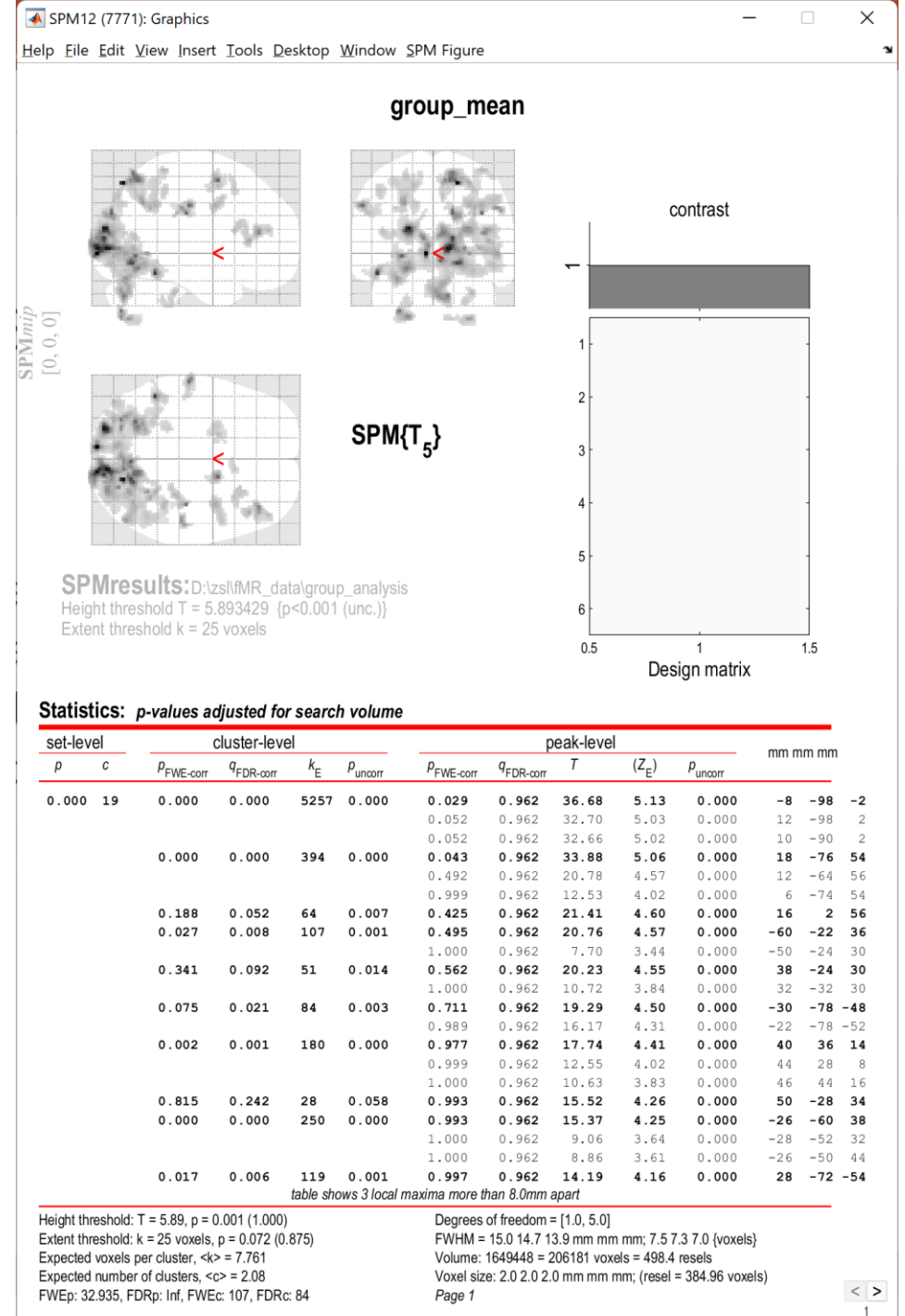
RESULTS:

apply masking ... none

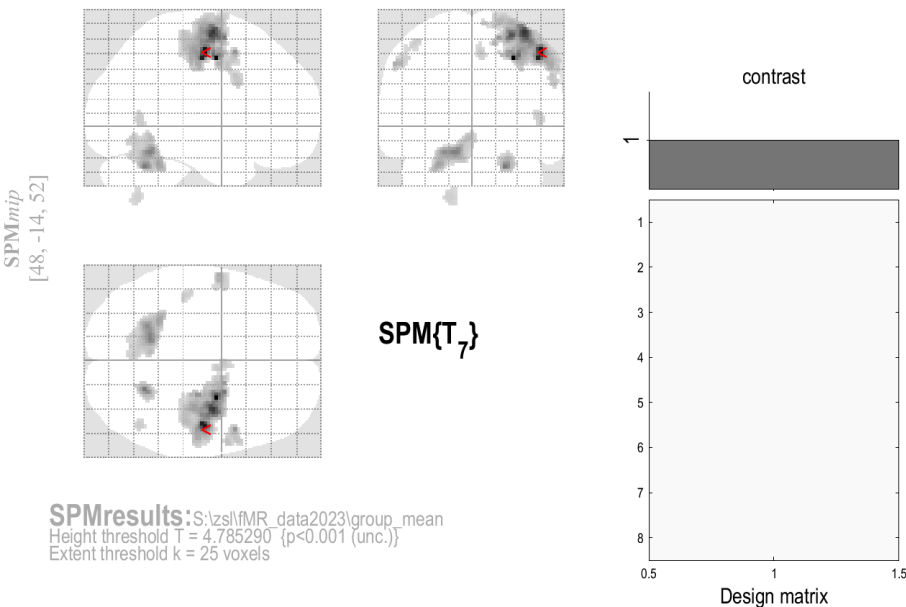
P value adjustment to control ... **none**

Threshold {T or p value} ... 0.001

& extent threshold {voxels} ... 7



group_mean_Left



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

Statistics: p-values adjusted for search volume

set-level		cluster-level				peak-level					mm mm mm
ρ	c	$p_{FWE-corr}$	$q_{FDR-corr}$	k_E	p_{uncorr}	$p_{FWE-corr}$	$q_{FDR-corr}$	T	(Z_E)	p_{uncorr}	
0.000	9	0.000	0.000	1901	0.000	0.007	0.175	23.36	5.40	0.000	28 -6 46
						0.016	0.175	20.66	5.25	0.000	
						0.048	0.208	17.65	5.04	0.000	36 -8 64
		0.014	0.005	119	0.000	0.654	0.457	12.01	4.51	0.000	22 -58 -30
		0.000	0.000	618	0.000	0.802	0.470	11.55	4.46	0.000	-14 -54 -20
						0.912	0.578	10.35	4.30	0.000	-22 -56 -20
						0.990	0.641	8.68	4.04	0.000	-26 -48 -28
		0.045	0.012	92	0.002	0.950	0.586	9.78	4.22	0.000	50 8 50
						1.000	0.854	6.61	3.61	0.000	58 10 28
						1.000	0.854	6.58	3.61	0.000	60 2 40
		0.155	0.036	66	0.006	0.996	0.694	8.22	3.95	0.000	-58 -4 42
						1.000	0.884	5.65	3.36	0.000	-50 0 46
						1.000	0.932	5.27	3.25	0.001	-48 -6 52
		0.755	0.203	30	0.046	1.000	0.868	6.07	3.48	0.000	4 0 50
		0.823	0.203	27	0.057	1.000	0.868	6.05	3.47	0.000	48 -60 0
		0.823	0.203	27	0.057	1.000	0.868	5.84	3.42	0.000	-44 -28 56
		0.457	0.108	43	0.020	1.000	0.884	5.65	3.36	0.000	-18 -62 -52

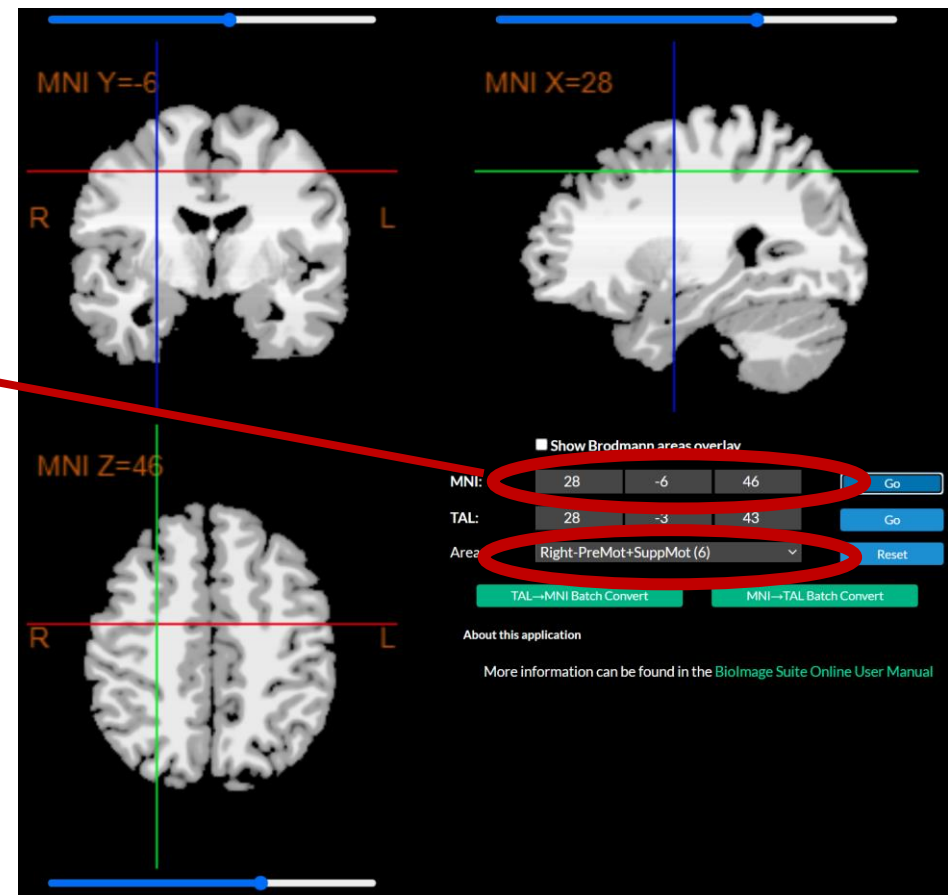


table shows 3 local maxima more than 8.0mm apart

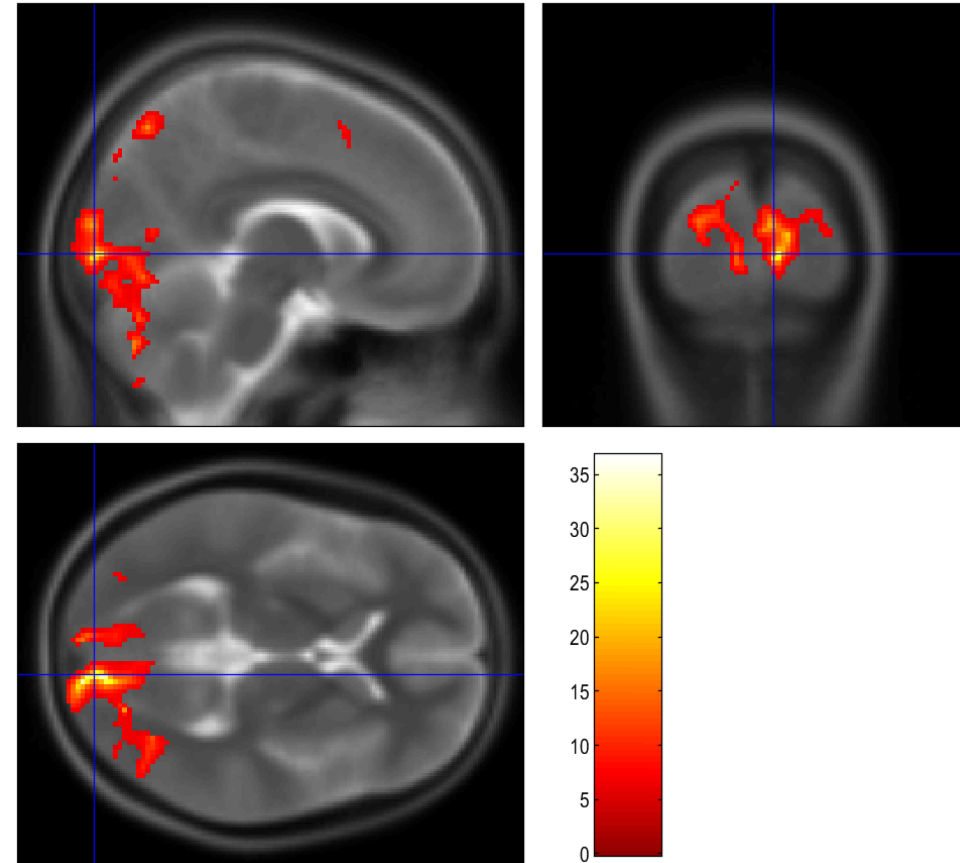
Height threshold: $T = 4.79$, $p = 0.001$ (1.000)
 Extent threshold: $k = 25$ voxels, $p = 0.066$ (0.864)
 Expected voxels per cluster, $\langle c \rangle = 7.413$
 Expected number of clusters, $\langle c \rangle = 2.00$
 FWEp: 17.528, FDRp: Inf, FWEc: 92, FDRc: 66

Degrees of freedom = [1.0, 7.0]
 FWHM = 12.0 11.9 11.5 mm mm mm; 6.0 6.0 5.8 (voxels)
 Volume: 1651312 = 206414 voxels = 926.2 resels
 Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 207.23 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`



Homework

1. Do the 1st-level analysis for both hands in all (15) 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