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 **Subj08** following the pipeline
2. Do the group statistics and display the results

fMR processing (1. excercise) 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. excercise) 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 – Subj08
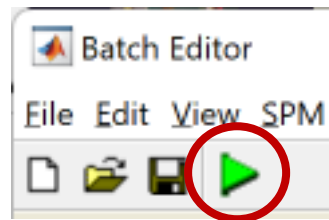
   ... 2nd- level analysis

1. Realign data

MENU: Realign (Estimate & Reslice)

BATCH EDITOR:

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

b) **Run** batch

utput:
Resliced files (prefix „**rfMR*.nii**")
„**meanfMR*.nii**" file (mean of all fMR file
Realignment parameters file „**rp_*.txt**"

2. Segment 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 ⏪)
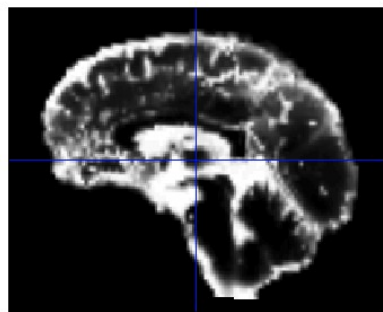
e) **Display** or **Check Reg** output files

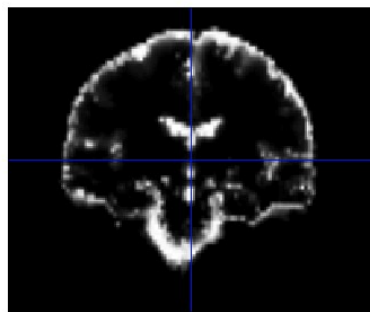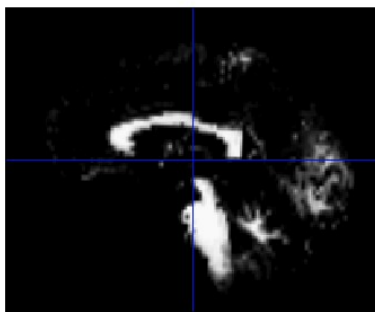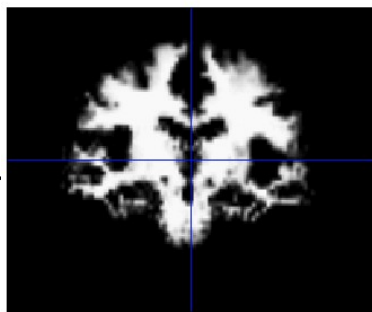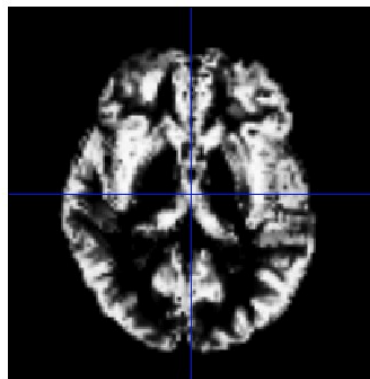**Output:**
- *c1meanfMR*.nii* (gray matter probability)
- *c2meanfMR*.nii* (white matter prob.)
- *c3meanfMR*.nii* (CSF prob.)
- *y_meanfMR*.nii* (deformation field)
- *C4mean*.nii, c5mean*.nii* (non brain tissue)

meanfMR
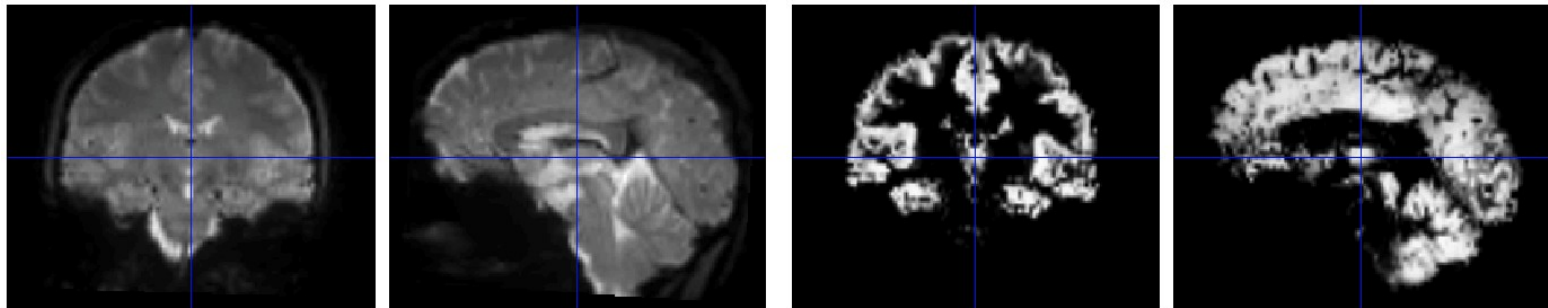
:1* = gray matter
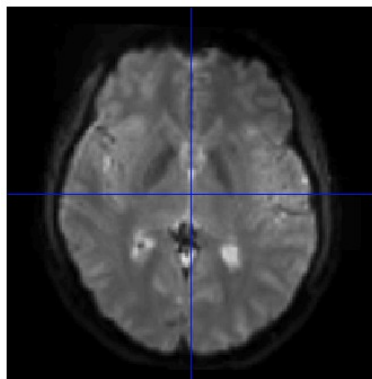
C2* = white matter

:3* = cerebro-spinal luid
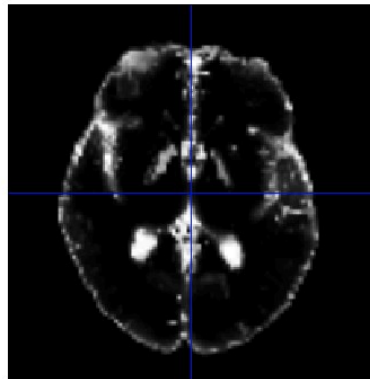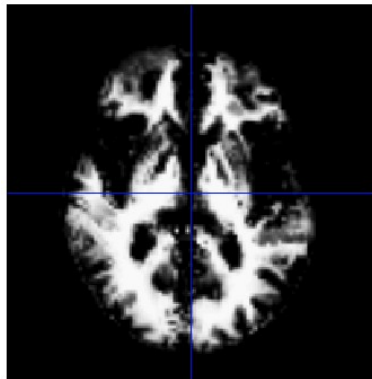
3. Normalise functional data

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:

a) **Images to smooth** ... select all *wrfMR*.nii* f

b) FWHM ... [8 8 8] (FWHM of the Gaussian smoothing kernel in mm)

c) Run batch
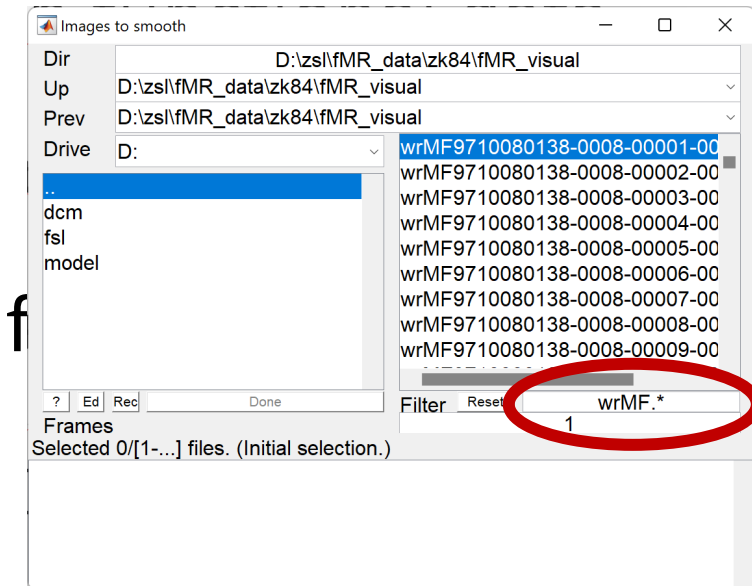
Output:
- Smoothed functional files (all with prefix „**swrfMR*.ni**
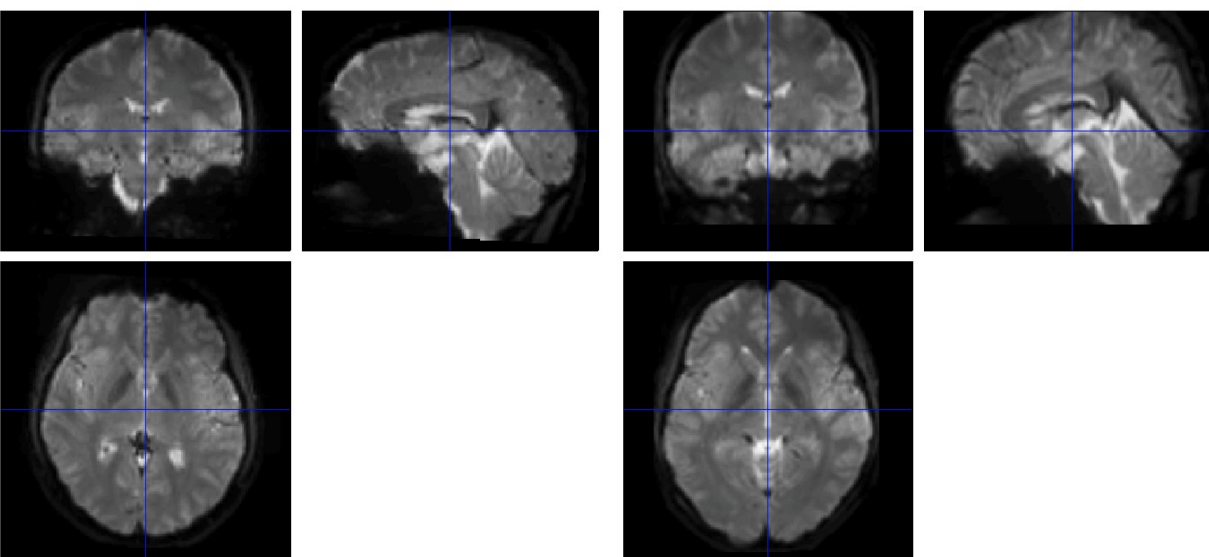
meanfMR

wmeanfMR

swmeanfMR
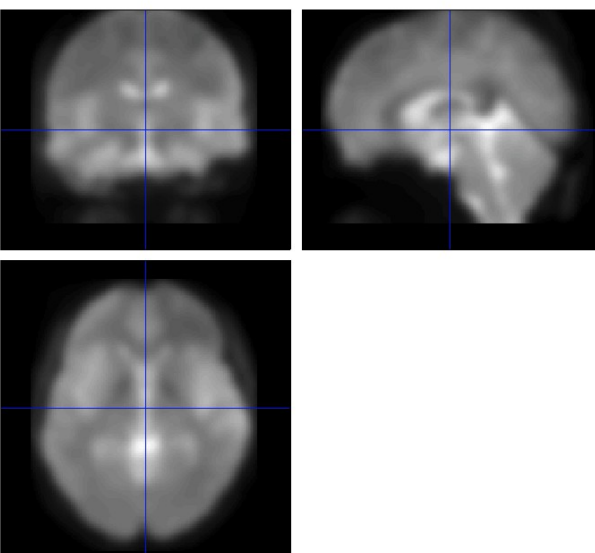
5. Model specification (1st-level)

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
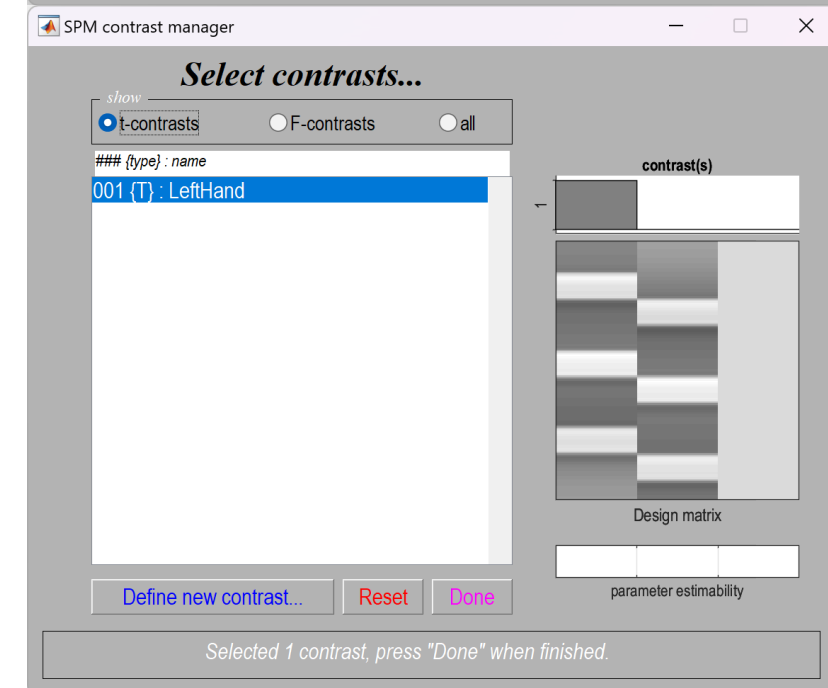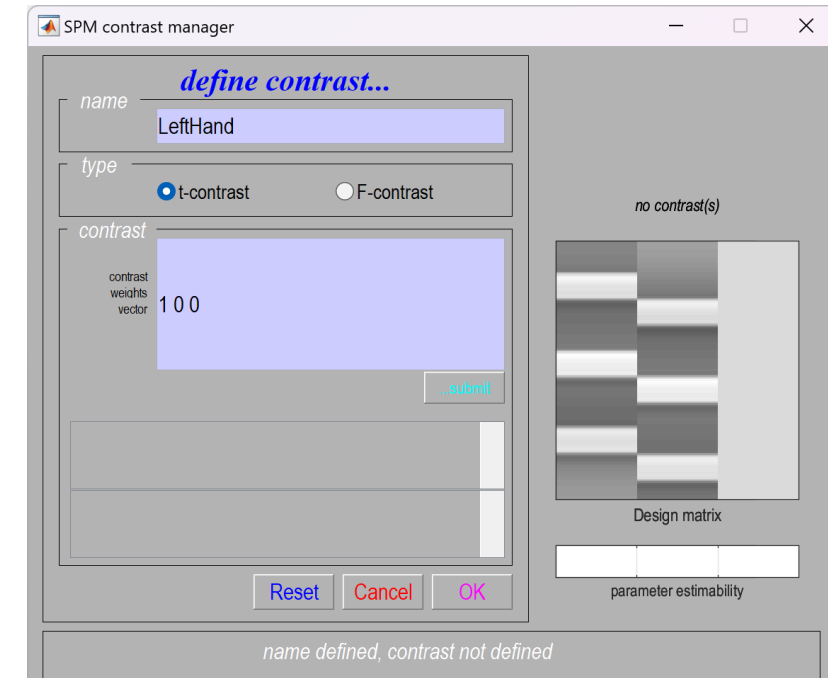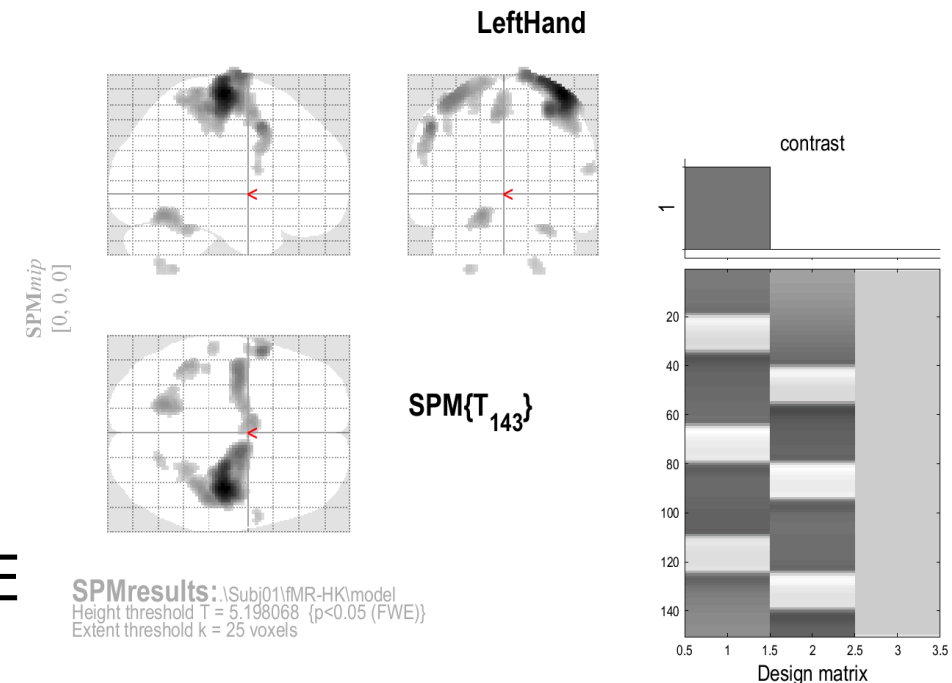
    & extent threshold {voxels} ... 25

LeftHand

SPMmip [0, 0, 0]

SPM{T$_{143}$}

contrast

Design matrix

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	$p_{FWE\text{-}corr}$	$q_{FDR\text{-}corr}$	k_E	p_{uncorr}	$p_{FWE\text{-}corr}$	$q_{FDR\text{-}corr}$	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 te~~ images from the

%SPM12%/canonical/avg*.nii
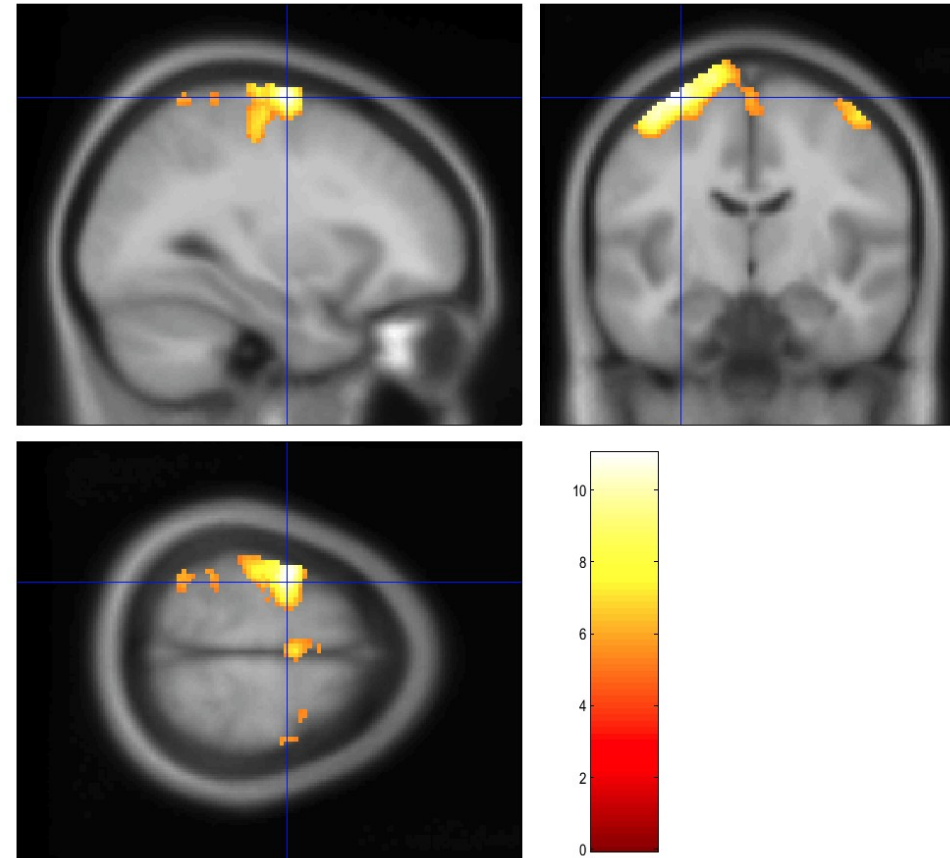
... do the preview pipeline for subjects

Subj01
Subj02
Subj03
Subj04
Subj05
Subj06
Subj07
Subj08

File structure for each subject

- **SubjXX**
  - **fMR_hk**
    - *fMR_hk*.nii   (150 origin files)*
    - *rfMR _hk*.nii   (150 realigned files)*
    - *rp_fMR _hk*.txt 1 realignment parameters txt-file*
    - *meanfMR _hk*.nii   1 mean functioanl file*
    - *wrfMR _hk*.nii   (150 realigned and normalised files)*
    - *swrfMR _hk*.nii (150 realigned, normalised and smoothed files)*
    - **model**
      - *beta_0001.nii   beta values of GLM model, for first predictor (predictor of acitavtions)*
      - *beta_0002.nii   beta values of GLM model, for second predictor (predictor of acitavtions)*
      - *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 binar mask file, created automaticaly*
      - *ResMS.nii   residuals file, errors of the GLM model*
      - *RPV.nii   ressels per voxel file*
      - *SPM.matmat-file, where GLM model is stored*
      - *spmT_0001.nii   t-statistics T-values*
  - **t1**
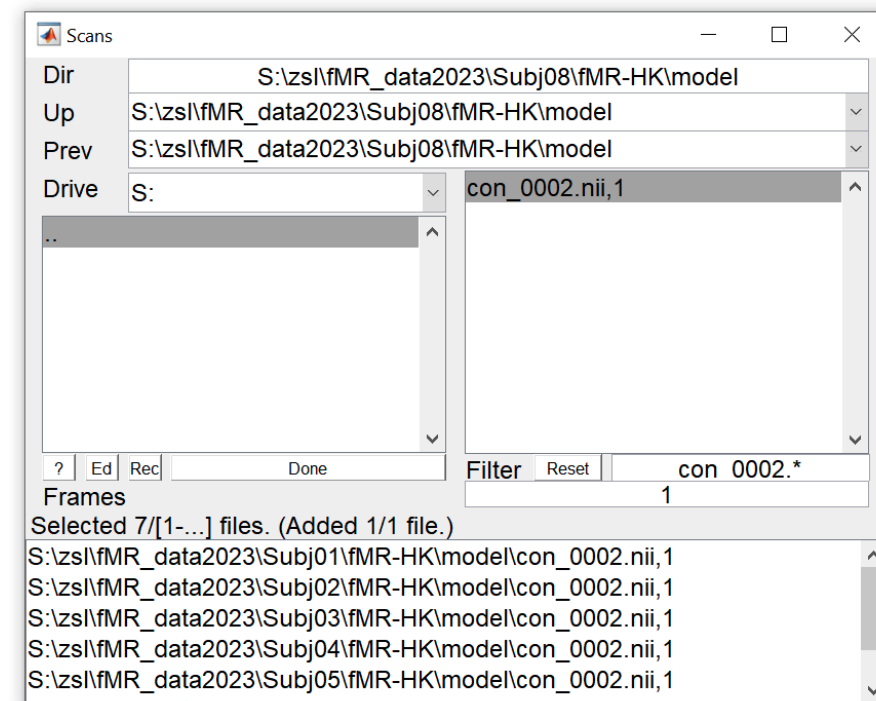   - *t1.nii   1 structural t1-weighted image*

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 (8x con_0001.nii)

c) **Run** batch

Help File Edit View Insert Tools Desktop Window SPM Figure

Statistical analysis: Design

mean

..k84/fMR_visual/model/con_0001.nii

..k85/fMR_visual/model/con_0001.nii

..k86/fMR_visual/model/con_0001.nii

images

..k87/fMR_visual/model/con_0001.nii

..k88/fMR_visual/model/con_0001.nii

..k89/fMR_visual/model/con_0001.nii

parameters

(gray $\rightarrow$ β not uniquely specified)

parameter estimability
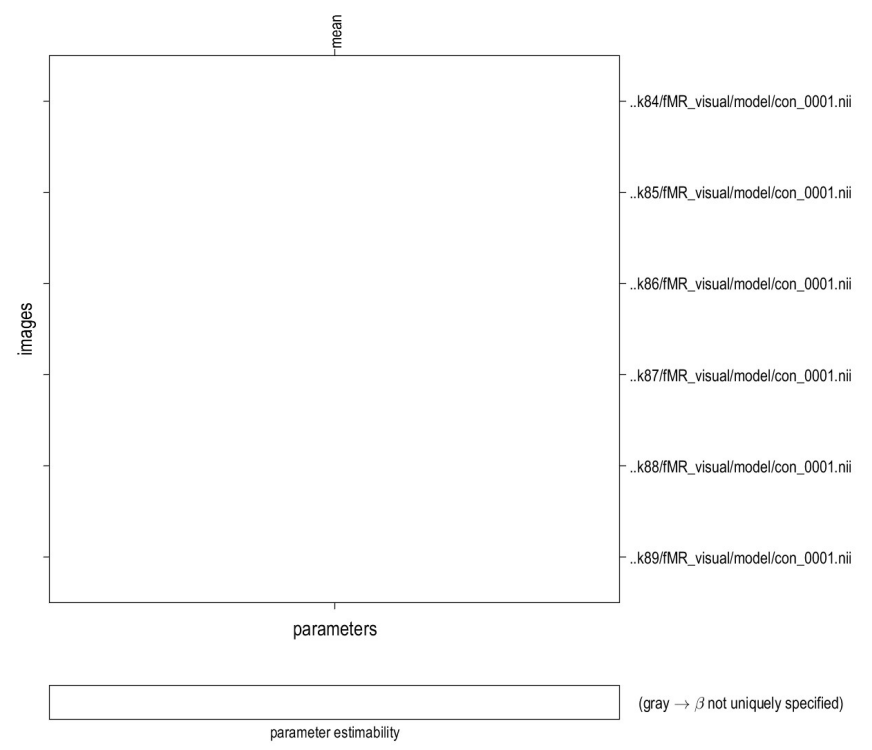
Design description...

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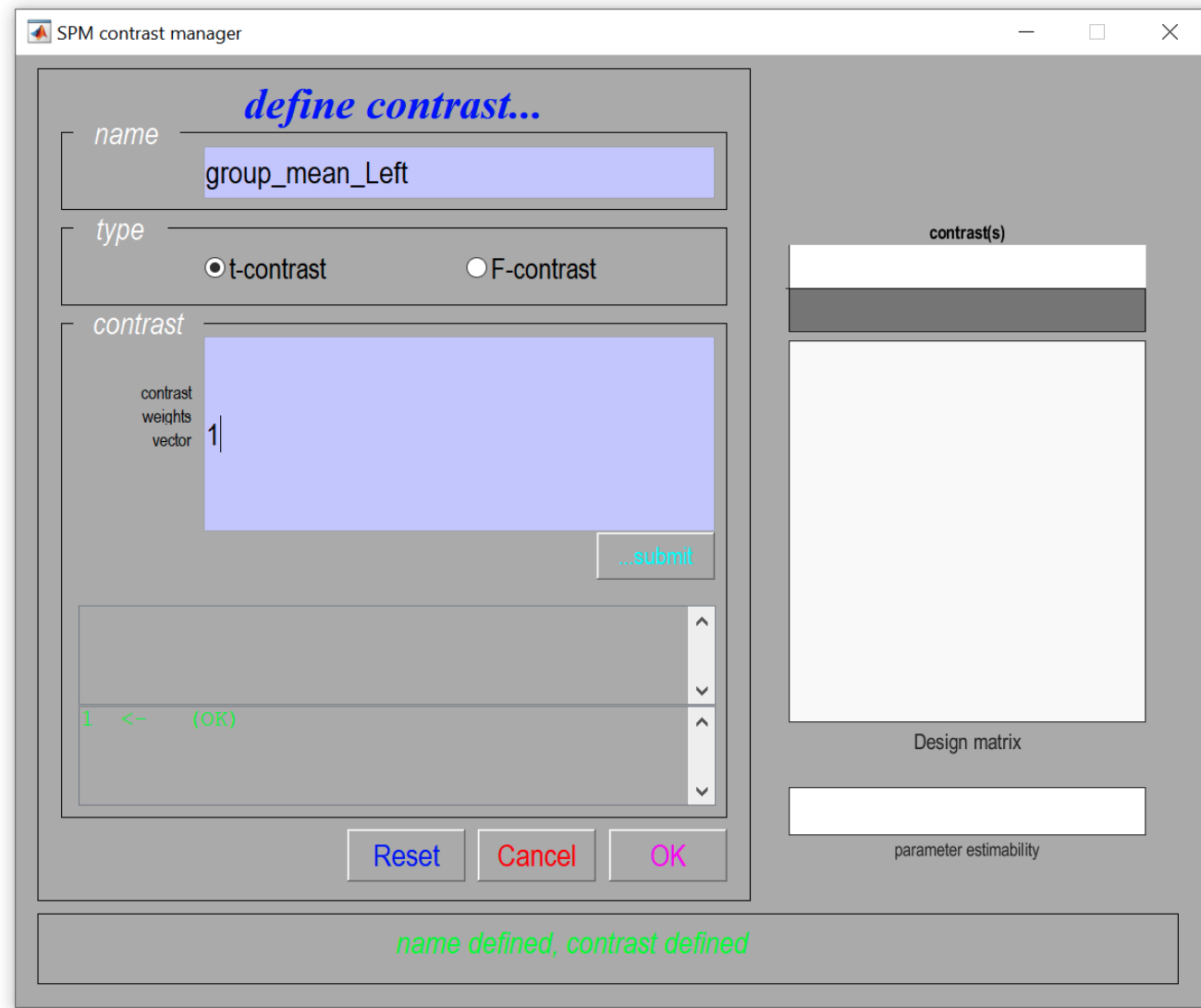a) Select SPM.mat ... select *SPM.mat*
b) Run batch

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
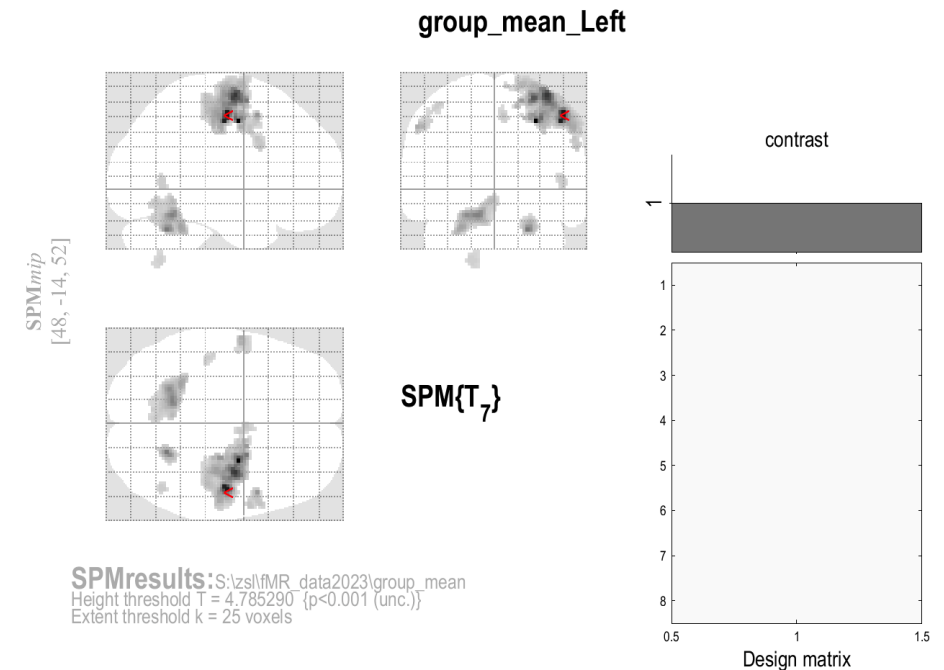
b) OK

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} ... 25

group_mean_Left

SPMmip
[48, -14, 52]

SPM{T$_7$}

contrast

Design matrix

SPMresults:S:\zsl\fMR_data2023\group_mean
Height threshold T = 4.785290 {p<0.001 (unc.)}
Extent threshold k = 25 voxels

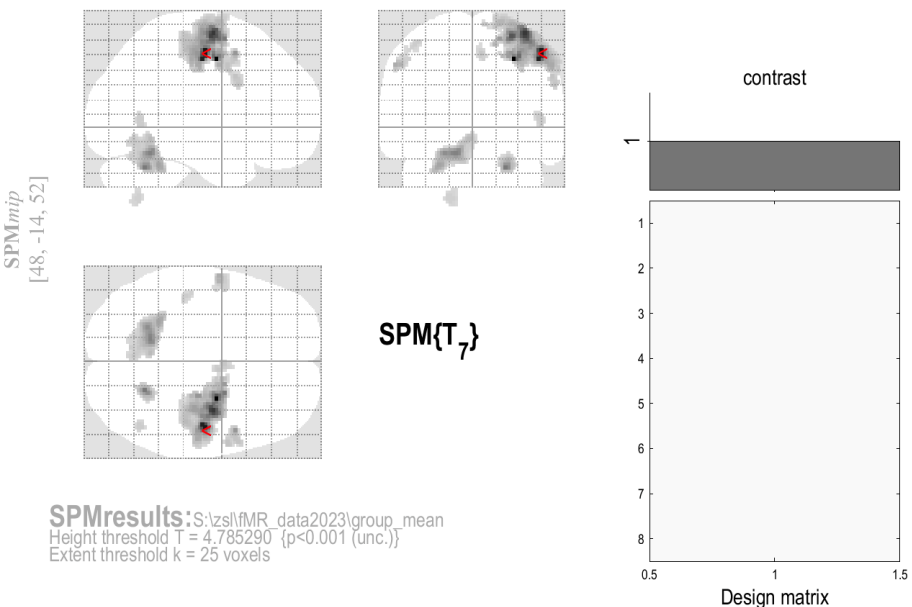**Statistics:** *p-values adjusted for search volume*

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	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	48	-14	52
						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, <k> = 7.413
Expected number of clusters, <c> = 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)

group_mean_Left

SPM$_{mip}$
[48, -14, 52]

contrast

SPM{T$_7$}

SPMresults: S:\zsl\fMR_data2023\group_mean
Height threshold T = 4.785290 {p<0.001 (unc.)}
Extent threshold k = 25 voxels

Design matrix

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	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
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		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	5.25	3.25	0.001	-48	-4	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

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Extent threshold: k = 25 voxels, p = 0.066 (0.864)
Expected voxels per cluster, <k> = 7.413
Expected number of clusters, <c> = 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)

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 ter

images from the

%SPM12%/canonical/avg*.nii
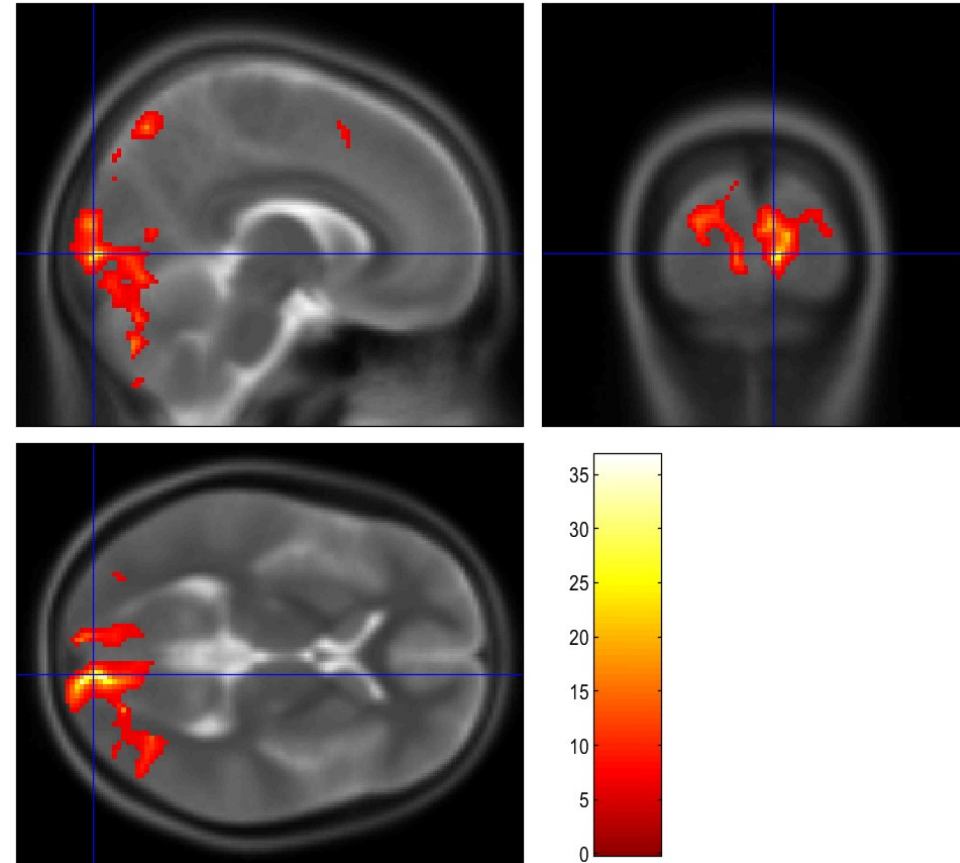
Homework

- Do the 1st-level analysis for both hands in all eight measured subjects. Folow the pipeline from the 2nd excercise.

- Do the group analysis folowing the pipeline from the 2nd excercise. Show the mean activation in the group for left (con_ 0001) and right (con_0002) hand.

- Describe and Display results of the 2nd-level analysis, find main areas with statisticaly significant activations (up to three main areas). Use MNI atlas by your own choice.

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