fMR Processing(2)

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Today goal:
Group analysis of functional activity during Visual task in six subjects using SPM12

- Looking for average activity in group of six 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 zk84 to zk89 following the pipeline
2. Do the group statistics and display the resluts

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)

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

1. **Realignment** of functional data - spatial correction of data in time
2. **Coregister** – T1w image coregister to mean fMR data
3. **Segment** – structural T1w segmentation (WhiteMatter, GrayMatter, CSF)
4. **Normalise** – functional and structural data to a standard MNI space
5. **Smoothing** functional data with Gauss filter kernel
6. **Model specification** + **Review**
7. **Estimate Model**
8. **Results** + **Display**

DO IT FOR EACH SUBJECT zk84 – zk89

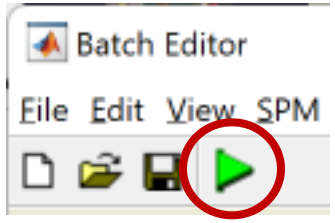
1. Realign data

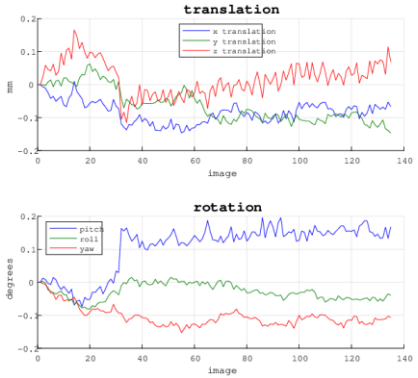
MENU: Realign (Estimate & Reslice)

BATCH EDITOR:

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

b) **Run** batch





Output:

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

2. Coregister functional and structural data

MENU: Coregister (Estimate)

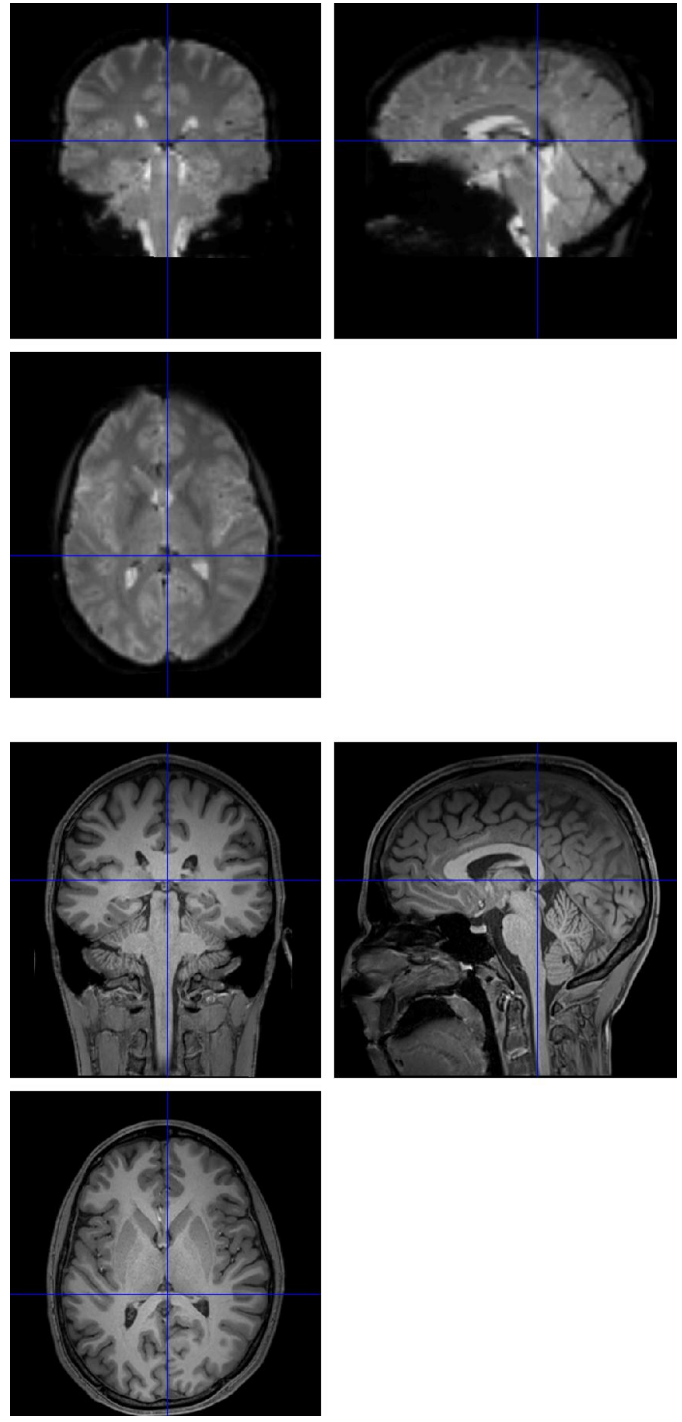
BATCH EDITOR:

a) Reference Image … select meanMF file (*meanMF*.nii*)
b) Source Image … select structural T1 data (*zkXX_T1.nii*)
c) Run batch

d) Check Reg … meanMF and zkXX_T1

This step is necessary if fMR and structural data are from different scanners or data were measured in different time

Output:
- Coregistered zkXX_T1.nii
- No additional files



3. Segment structural data

MENU: Segment

BATCH EDITOR:

a) **Volumes** … select structural T1 data (*zkXX_T1.nii*)

b) **Deformation fields** (last parameter)**...** *Forward* (transform from functional to structural)

c) All next parameters as default!

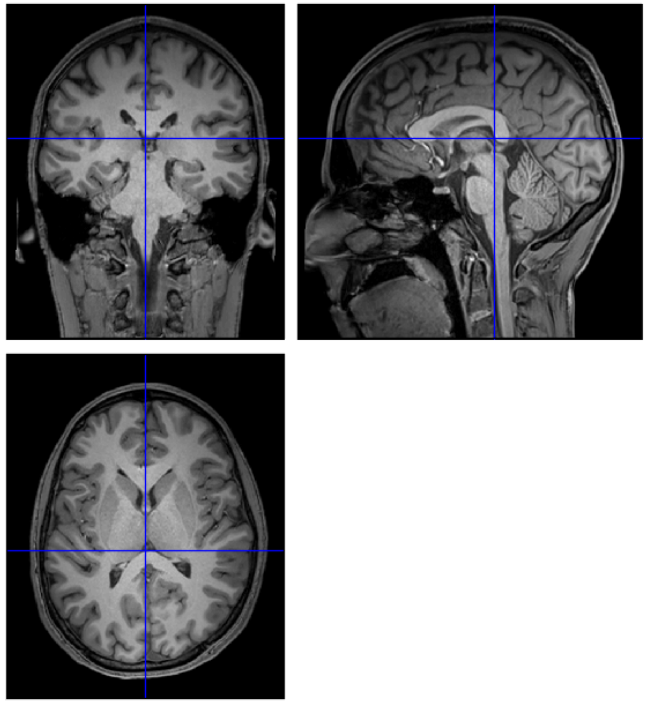
d) **Run** batch (could be time consuming little bit ☺)

e) **Display** or **Check Reg** output files

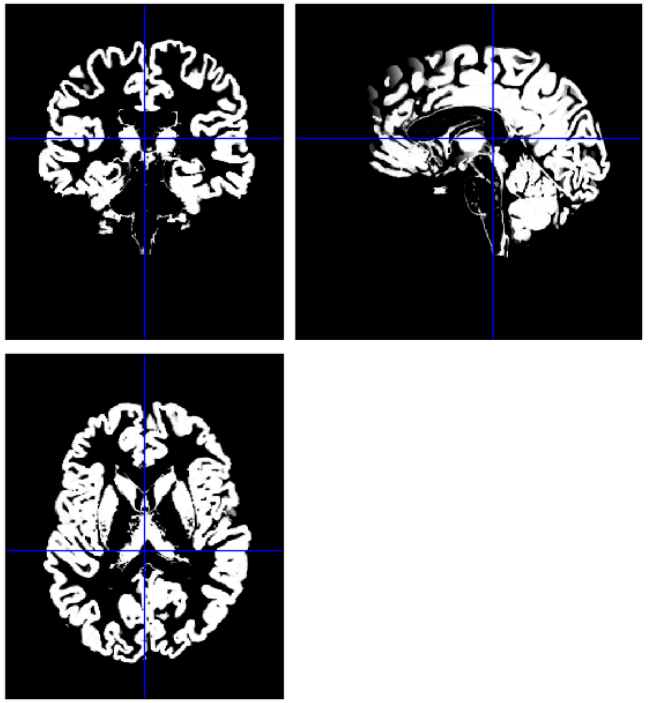
Output:

- c1zkXX_T1.nii (gray matter probability)
- c2zkXX_T1.nii (white matter prob.)
- c3zkXX_T1.nii (CSF prob.)
- y_zkXX_T1.nii (deformation field)
- c4*,c5*zkXX_T1.nii (non brain tissue)

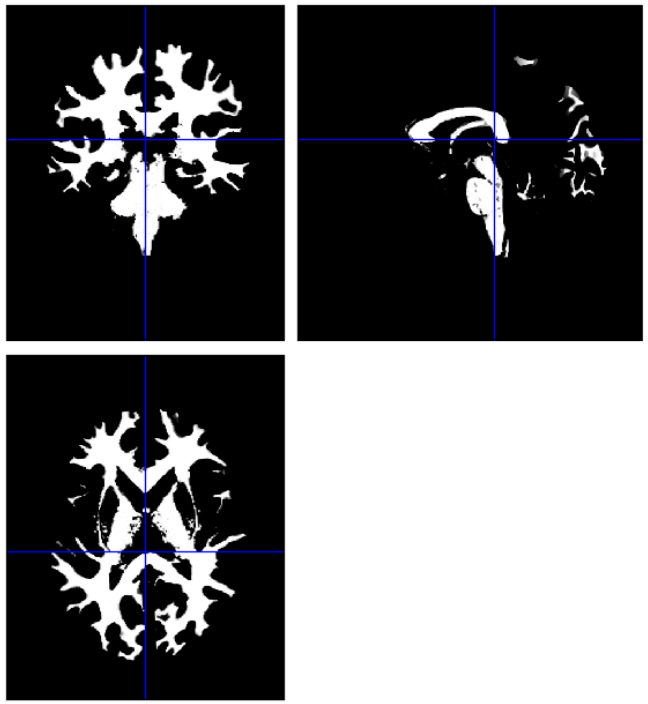
zkXX_T1.nii



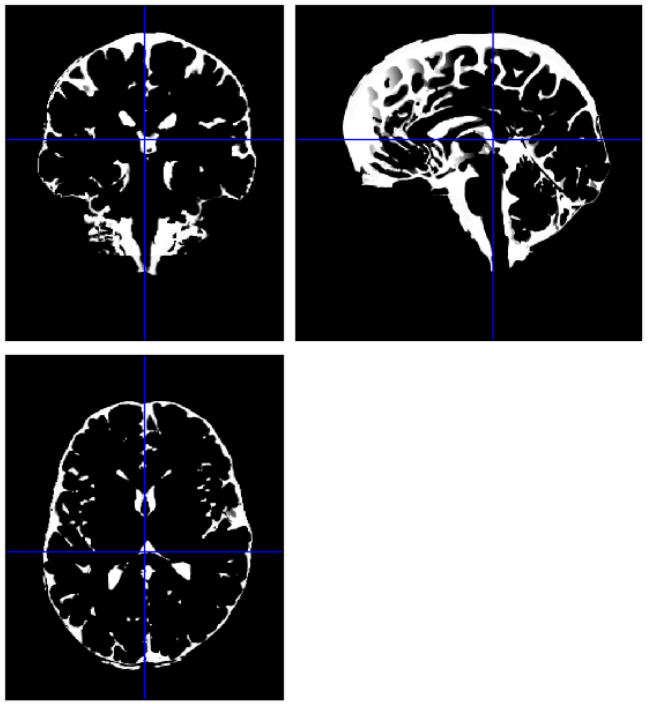
c1*.nii = gray matter



c2*.nii = white matter



c3*.nii = cerebro-spinal fluid



4a. Normalise functional data

MENU: Normalise (Write)

BATCH EDITOR:

a) **Data – Subject – Deformation Field** … select Forward deformation Field (*y_zkXX_T1.nii*)
b) **Images to Write** … all realigned functional images (*rMF*.nii*)
c) **Voxel sizes** … [2 2 2]
d) **Run batch**

e) **Display**
output files

Output:
- wrMF*.nii (functioanl data in standard ***MNI152 space***)

4b. Normalise structural data

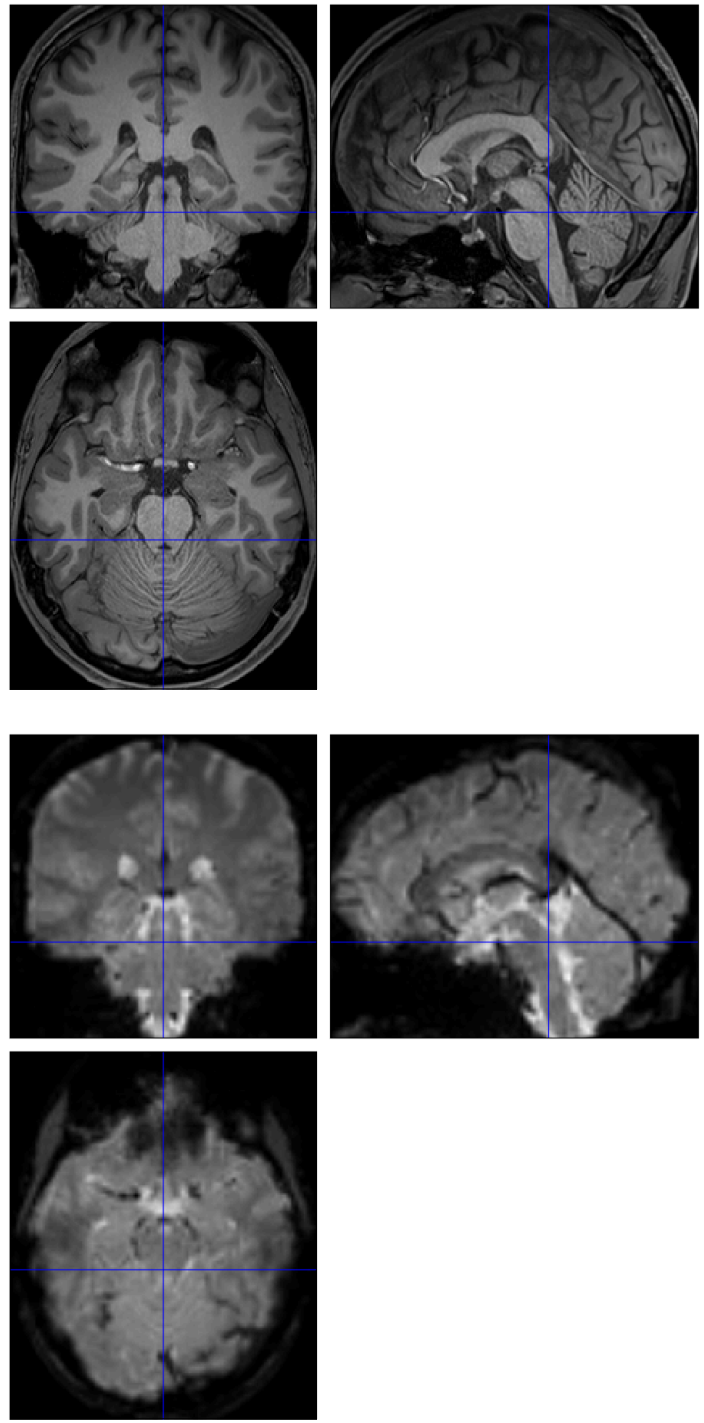
MENU: Normalise (Write)

BATCH EDITOR:

a) **Data – Subject – Deformation Field** … select Forward deformation Field (*y_zkXX_T1.nii*)
b) **Images to Write** … select structural T1 (*zkXX_T1.nii*)
c) **Voxel sizes** … [0.75 0.75 0.75]
d) **Run batch**

e) **Display**
output files

Output:
- wzkXX_T1.nii (structural data in standard ***MNI152 space***)



5. Smooth functional data (realigned and normalised)

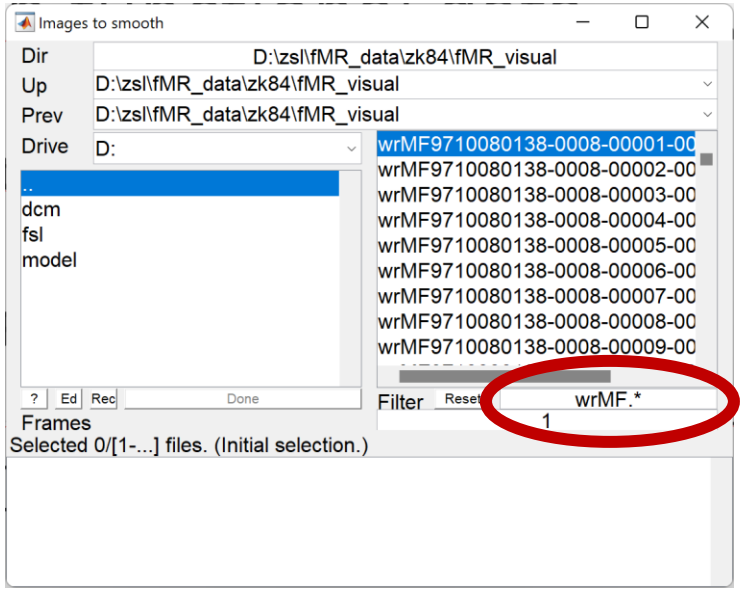
MENU: Smooth

BATCH EDITOR:

a) **Images to smooth** … select all *wrMF*.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 „**swr*.nii**“)

6. Model specification

MENU: Specify 1st-level

BATCH EDITOR:

a) **Directory** … select (pre-created) folder to store model and statistics results (*„model“*)

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 VISUAL
         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)

6. Model specification

1. Condition NEUROTRACKER
   - Name … NEUROTRACKER
   - Onset … [11 36 61 86 111]
   - Durations … 10

2. Condition 2-BACK
   - Name … 2BACK
   - Onset … [11 36 61 86]
   - Durations … 15

3. Condition VISUAL
   - Name … VISUAL
   - Onset … [16 46 76 106]
   - Durations … 15

7. Model estimation

MENU: Estimate

BATCH EDITOR:

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

8. Results (define contrast)

MENU: Results

Select SPM.mat

SPM contrast manager:

a) Define new contrast

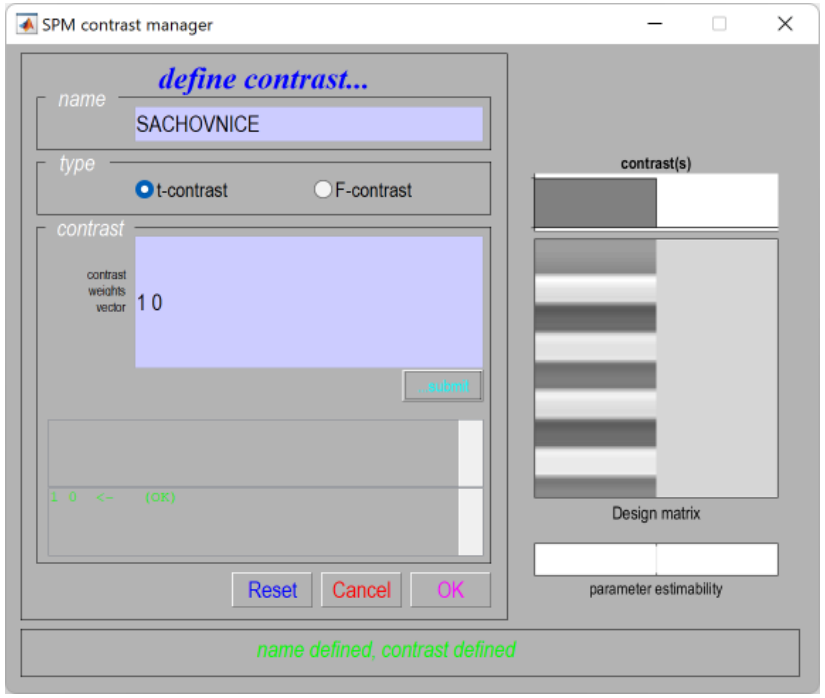
Name: SACHOVNICE (NEUROTRACKER / 2BACK)

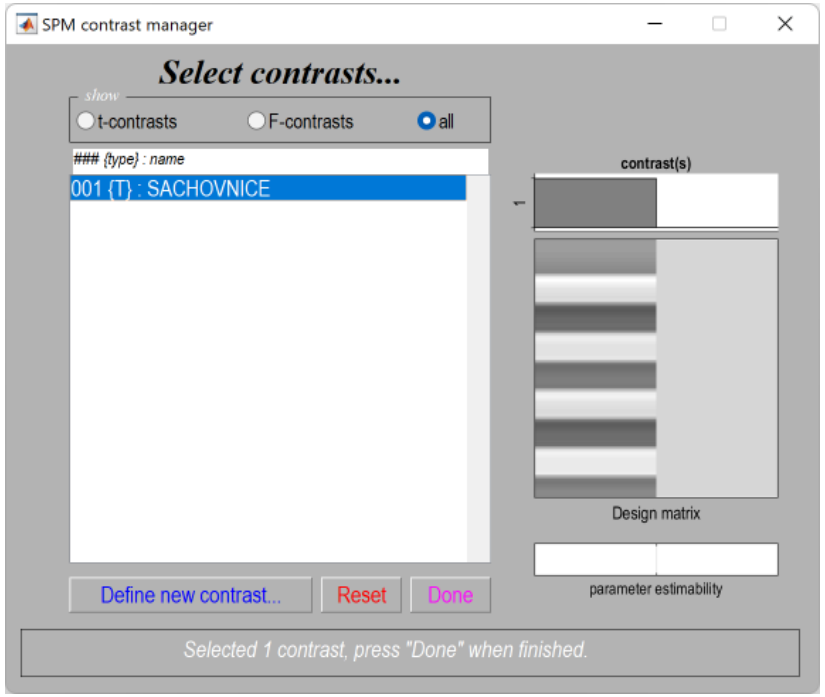
type: t-contrast

contrast: 1 0 …submit

b) OK

c) Done, Done





8. Results

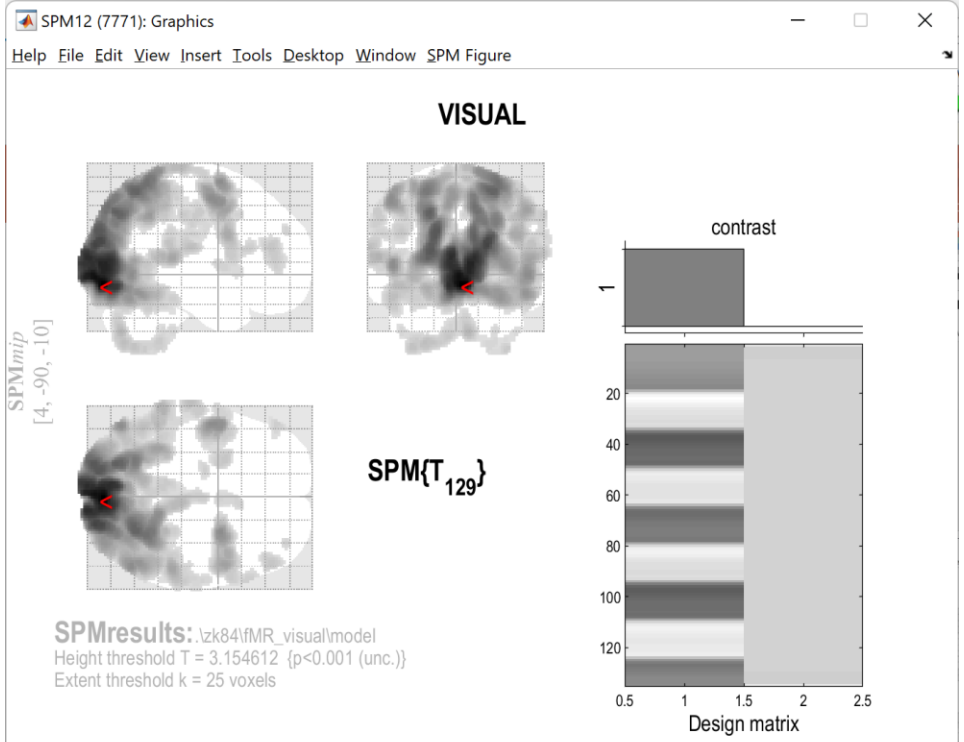
RESULTS:

apply masking … none

P value adjustment to control … none

Threshold {T or p value} … 0.001

& extent threshold {voxels} … 25



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	14	0.000	0.000	29690	0.000	0.000	0.000	22.28	Inf	0.000	4	-90	-10
						0.000	0.000	20.44	Inf	0.000	0	-96	-4
						0.000	0.000	18.91	Inf	0.000	8	-90	4
		0.000	0.000	2328	0.000	0.000	0.000	9.87	Inf	0.000	28	0	66
						0.000	0.000	8.20	7.34	0.000	52	2	46
						0.000	0.000	7.77	7.03	0.000	44	6	26
		0.000	0.000	1023	0.000	0.000	0.000	8.07	7.24	0.000	56	-36	10
						0.006	0.001	5.67	5.35	0.000	56	-40	22
						0.124	0.010	4.90	4.68	0.000	64	-28	42
		0.000	0.000	1037	0.000	0.000	0.000	6.69	6.19	0.000	8	-76	-44
						0.003	0.000	5.83	5.48	0.000	-26	-74	-52
						0.004	0.000	5.77	5.43	0.000	-36	-66	-56
		0.000	0.000	324	0.000	0.025	0.002	5.33	5.06	0.000	50	38	18
						0.055	0.004	5.12	4.88	0.000	50	40	10
		0.004	0.001	200	0.000	0.135	0.010	4.87	4.66	0.000	38	-58	-56
						0.877	0.113	4.09	3.95	0.000	26	-44	-52
						0.963	0.171	3.94	3.82	0.000	28	-36	-42
		0.065	0.007	110	0.003	0.219	0.016	4.72	4.53	0.000	-52	44	8
						1.000	0.651	3.36	3.29	0.001	-50	40	24
		0.534	0.069	50	0.030	0.396	0.031	4.52	4.35	0.000	-18	-12	70
		0.032	0.004	131	0.001	0.471	0.038	4.45	4.29	0.000	-60	-38	30

table shows 3 local maxima more than 8.0mm apart

Height threshold: T = 3.15, p = 0.001 (1.000)
Extent threshold: k = 25 voxels, p = 0.109 (0.940)
Expected voxels per cluster, <k> = 10.064
Expected number of clusters, <c> = 2.81
FWEp: 5.147, FDRp: 4.396, FWEc: 121, FDRc: 110

Degrees of freedom = [1.0, 129.0]
FWHM = 9.1 9.1 8.6 mm mm mm; 4.6 4.6 4.3 {voxels}
Volume: 1889184 = 236148 voxels = 2452.5 resels
Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 89.82 voxels)
Page 1

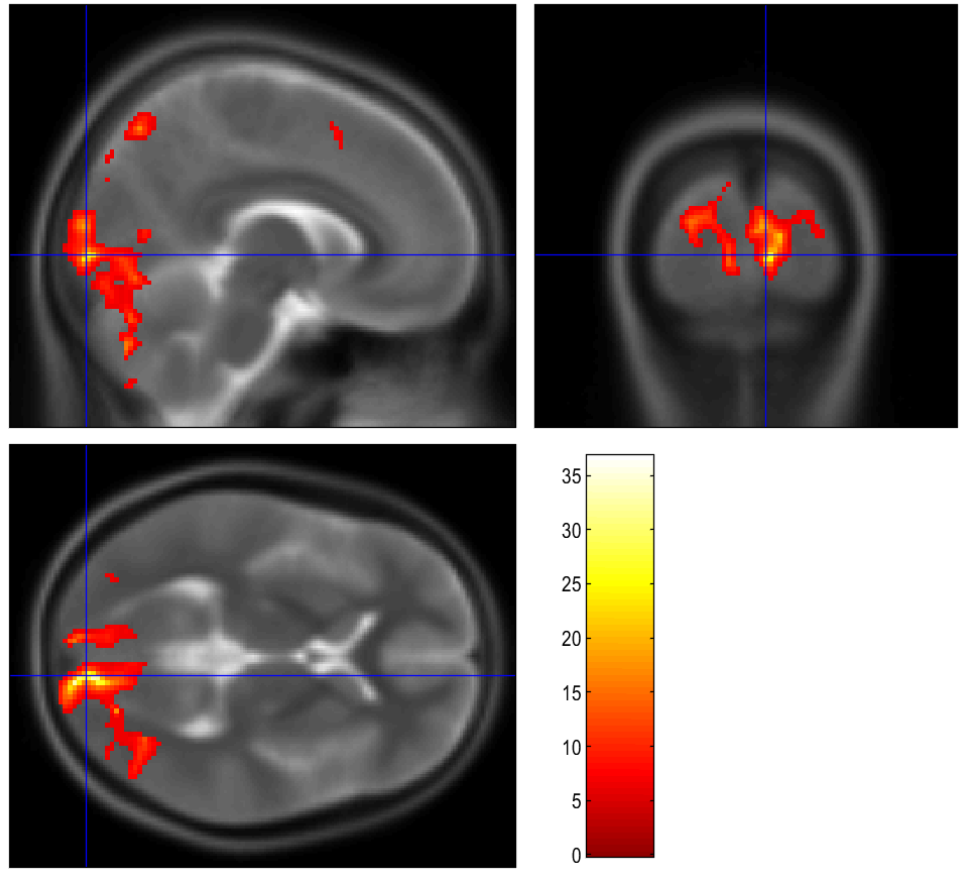
Display Results

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 subjects

zk84

zk85

zk86

zk87

zk88

zk89

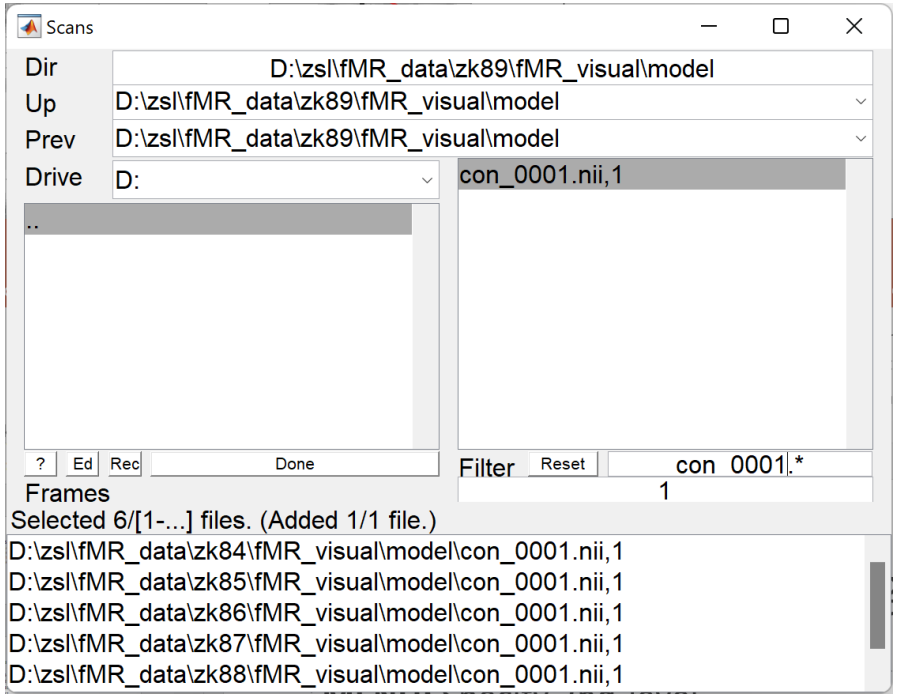
File structure for each subject

- **zkXX**
  - **fMR_2back**
  - **fMR_neurotracker**
  - **fMR_visual**
    - *MF*.nii* — *(135 origin files)*
    - *rMF*.nii* — *(135 realigned files)*
    - *rp_MF*.txt* — *1 realignment parameters txt-file*
    - *meanMF*.nii* — *1 mean functioanl file*
    - *wrMF*.nii* — *(135 realigned and normalised files)*
    - *swrMF*.nii* — *(135 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 (constant predictor)*
      - *con_0001.nii* — *contrast file for first 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.mat* — *mat-file, where GLM model is stored*
      - *spmT_0001.nii* — *t-statistics T-values*
  - **t1**
    - *c1*.nii* — *1 gray matter probability file*
    - *c2*.nii* — *1 white matter probability file*
    - *c3*.nii* — *1 cerebro-spinal fluid probability file*
    - *y_*.nii* — *1 forward deformation field (from structural to MNI space)*
    - *w*.nii* — *1 normalised structural data*

2nd- level
(GROUP ANALYSIS)

9. Model specification (group mean)

MENU: Specify 2nd-level



BATCH EDITOR:

a) **Directory** … select (pre-created) folder (for example *„group_mean“*)

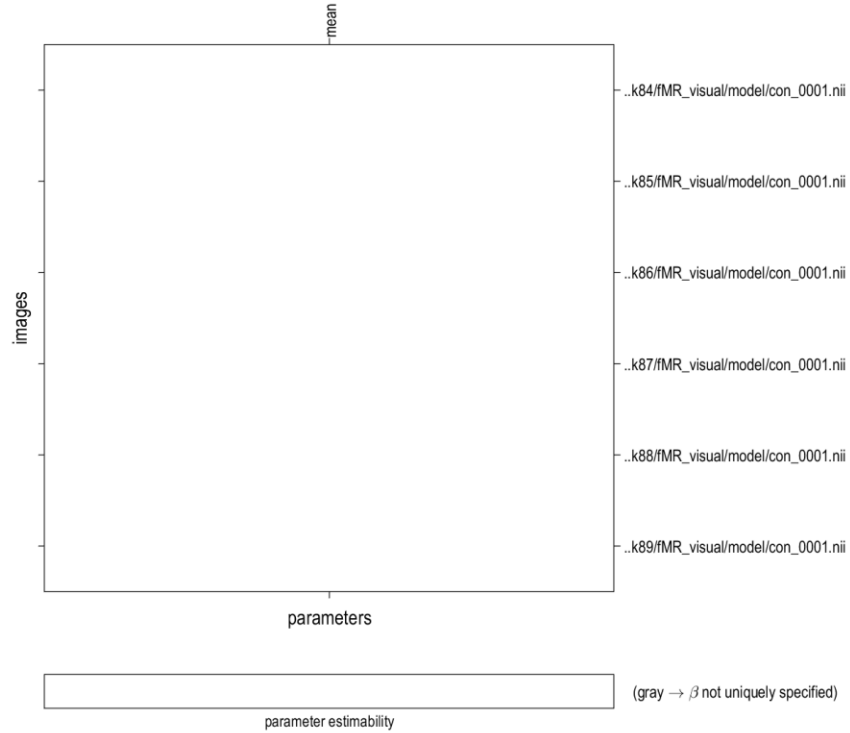
b) **Design – One-sample t-test – Scans** … select all *con_0001.nii* files from model folder of each subject (6x con_0001.nii)

c) **Run** batch

SPM12 (7771): Graphics

Help File Edit View Insert Tools Desktop Window SPM Figure

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

10. Model estimation (group mean)

MENU: Estimate

BATCH EDITOR:

a) Select SPM.mat … select *SPM.mat*

b) Run batch

11. Results – define contrast (group mean)

MENU: Results

Select SPM.mat

SPM contrast manager:

a) Define new contrast

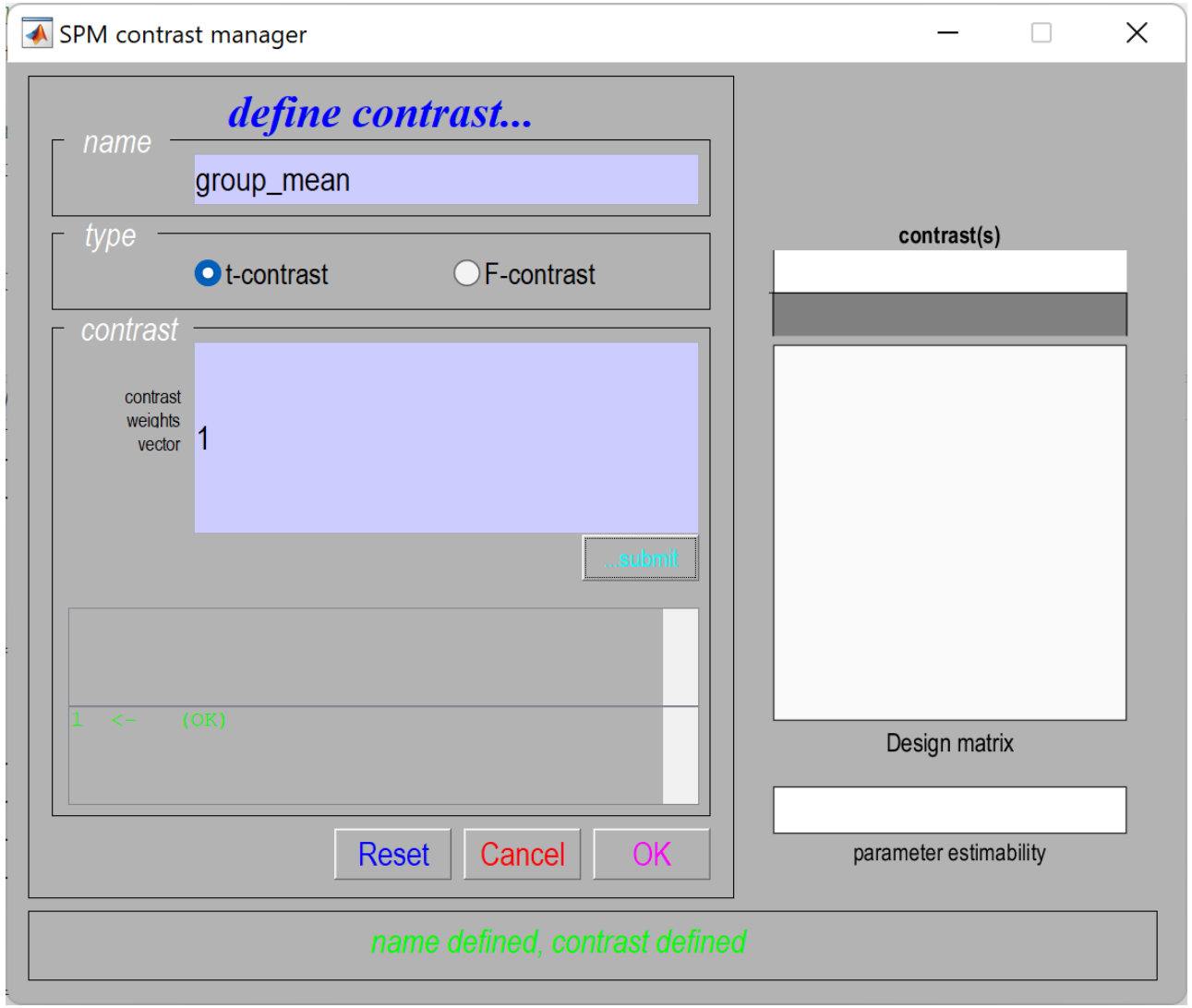
Name: *GROUP_MEAN*

type: *t-contrast*

contrast: *1* …submit

b) OK

c) Done



11. Results (group mean)

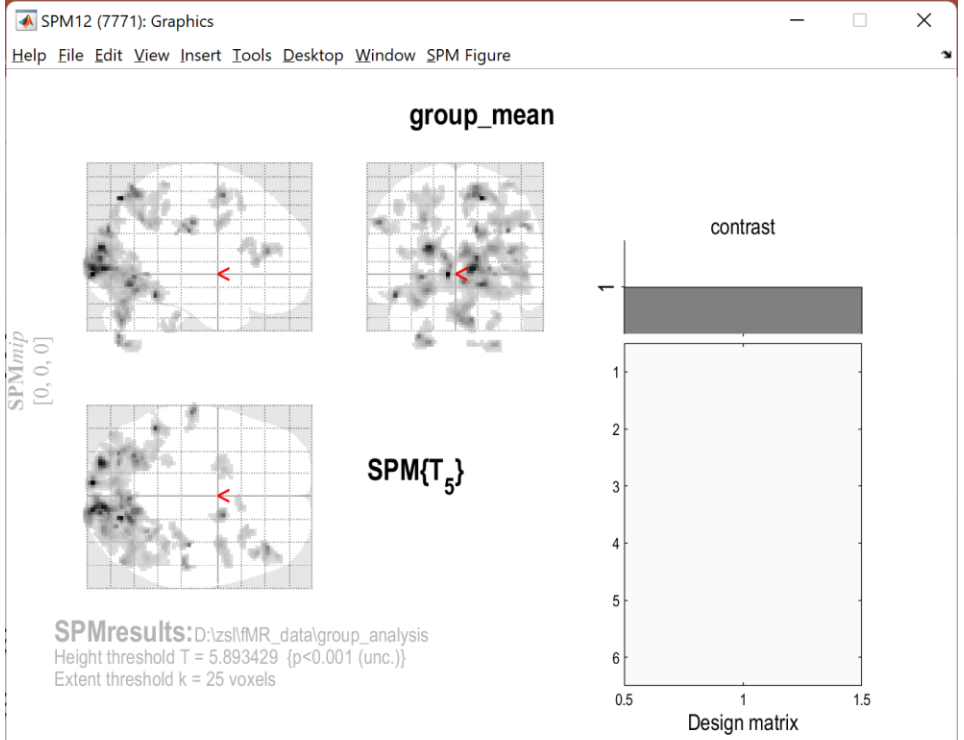
RESULTS:

apply masking … none

P value adjustment to control … none

Threshold {T or p value} … 0.001

& extent threshold {voxels} … 25



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	19	0.000	0.000	5257	0.000	0.029	0.962	36.68	5.13	0.000	-8	-98	-2
						0.052	0.962	32.70	5.03	0.000	12	-98	2
						0.052	0.962	32.66	5.02	0.000	10	-90	2
		0.000	0.000	394	0.000	0.043	0.962	33.88	5.06	0.000	18	-76	54
						0.492	0.962	20.78	4.57	0.000	12	-64	56
						0.999	0.962	12.53	4.02	0.000	6	-74	54
		0.188	0.052	64	0.007	0.425	0.962	21.41	4.60	0.000	16	2	56
		0.027	0.008	107	0.001	0.495	0.962	20.76	4.57	0.000	-60	-22	36
						1.000	0.962	7.70	3.44	0.000	-50	-24	30
		0.341	0.092	51	0.014	0.562	0.962	20.23	4.55	0.000	38	-24	30
						1.000	0.962	10.72	3.84	0.000	32	-32	30
		0.075	0.021	84	0.003	0.711	0.962	19.29	4.50	0.000	-30	-78	-48
						0.989	0.962	16.17	4.31	0.000	-22	-78	-52
		0.002	0.001	180	0.000	0.977	0.962	17.74	4.41	0.000	40	36	14
						0.999	0.962	12.55	4.02	0.000	44	28	8
						1.000	0.962	10.63	3.83	0.000	46	44	16
		0.815	0.242	28	0.058	0.993	0.962	15.52	4.26	0.000	50	-28	34
		0.000	0.000	250	0.000	0.993	0.962	15.37	4.25	0.000	-26	-60	38
						1.000	0.962	9.06	3.64	0.000	-28	-52	32
						1.000	0.962	8.86	3.61	0.000	-26	-50	44
		0.017	0.006	119	0.001	0.997	0.962	14.19	4.16	0.000	28	-72	-54

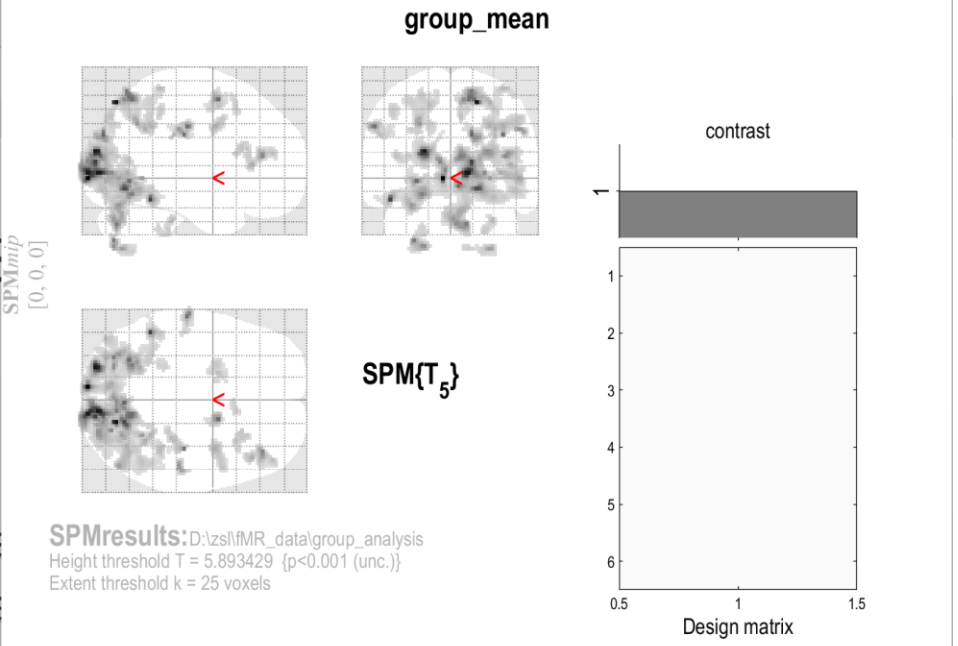
table shows 3 local maxima more than 8.0mm apart

Height threshold: T = 5.89, p = 0.001 (1.000)
Extent threshold: k = 25 voxels, p = 0.072 (0.875)
Expected voxels per cluster, <k> = 7.761
Expected number of clusters, <c> = 2.08
FWEp: 32.935, FDRp: Inf, FWEc: 107, FDRc: 84

Degrees of freedom = [1.0, 5.0]
FWHM = 15.0 14.7 13.9 mm mm mm; 7.5 7.3 7.0 {voxels}
Volume: 1649448 = 206181 voxels = 498.4 resels
Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 384.96 voxels)
Page 1

SPM12 (7771): Graphics

Help File Edit View Insert Tools Desktop Window SPM Figure



SPMresults: D:\zsl\fMR_data\group_analysis
Height threshold T = 5.893429 {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	$p_{FWE\text{-}corr}$	$q_{FDR\text{-}corr}$	k_E	p_{uncorr}	$p_{FWE\text{-}corr}$	$q_{FDR\text{-}corr}$	T	(Z_E)	p_{uncorr}	
0.000	19	0.000	0.000	5257	0.000	0.029	0.962	36.68	5.13	0.000	-8 -98 -2
						0.052	0.962	32.70	5.03	0.000	
						0.052	0.962	32.66	5.02	0.000	10 -90 2
		0.000	0.000	394	0.000	0.043	0.962	33.88	5.06	0.000	18 -76 54
						0.492	0.962	20.78	4.57	0.000	12 -64 56
						0.999	0.962	12.53	4.02	0.000	6 -74 54
		0.188	0.052	64	0.007	0.425	0.962	21.41	4.60	0.000	16 2 56
		0.027	0.008	107	0.001	0.495	0.962	20.76	4.57	0.000	-60 -22 36
						1.000	0.962	7.70	3.44	0.000	-50 -24 30
		0.341	0.092	51	0.014	0.562	0.962	20.23	4.55	0.000	38 -24 30
						1.000	0.962	10.72	3.84	0.000	32 -32 30
		0.075	0.021	84	0.003	0.711	0.962	19.29	4.50	0.000	-30 -78 -48
						0.989	0.962	16.17	4.31	0.000	-22 -78 -52
		0.002	0.001	180	0.000	0.977	0.962	17.74	4.41	0.000	40 36 14
						0.999	0.962	12.55	4.02	0.000	44 28 8
						1.000	0.962	10.63	3.83	0.000	46 44 16
		0.815	0.242	28	0.058	0.993	0.962	15.52	4.26	0.000	50 -28 34
		0.000	0.000	250	0.000	0.993	0.962	15.37	4.25	0.000	-26 -60 38
						1.000	0.962	9.06	3.64	0.000	-28 -52 32
						1.000	0.962	8.86	3.61	0.000	-26 -50 44
		0.017	0.006	119	0.001	0.997	0.962	14.19	4.16	0.000	28 -72 -54

table shows 3 local maxima more than 8.0mm apart

Height threshold: T = 5.89, p = 0.001 (1.000)
Extent threshold: k = 25 voxels, p = 0.072 (0.875)
Expected voxels per cluster, <k> = 7.761
Expected number of clusters, <c> = 2.08
FWEp: 32.935, FDRp: Inf, FWEc: 107, FDRc: 84

Degrees of freedom = [1.0, 5.0]
FWHM = 15.0 14.7 13.9 mm mm mm; 7.5 7.3 7.0 {voxels}
Volume: 1649448 = 206181 voxels = 498.4 resels
Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 384.96 voxels)

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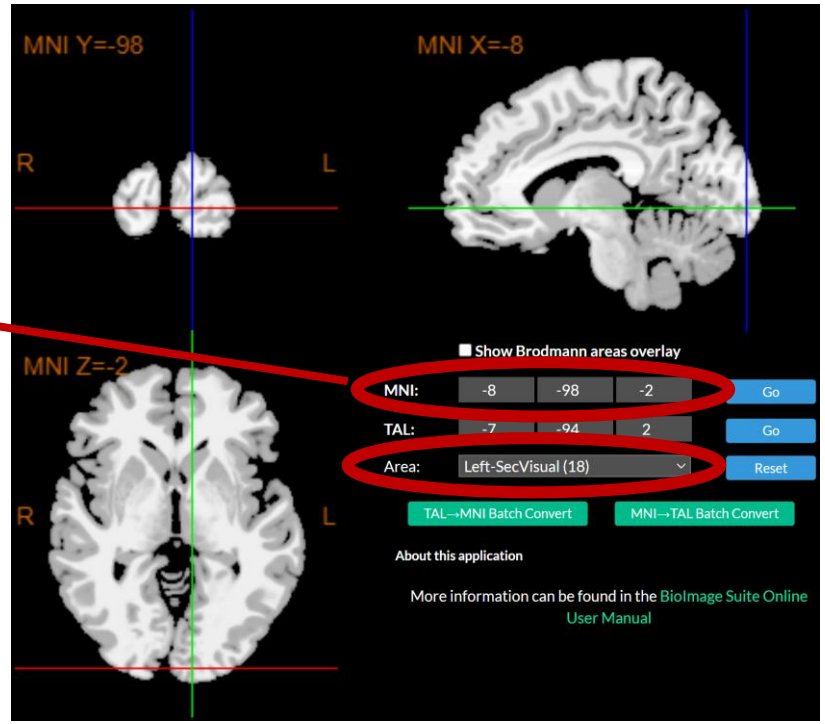
1

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



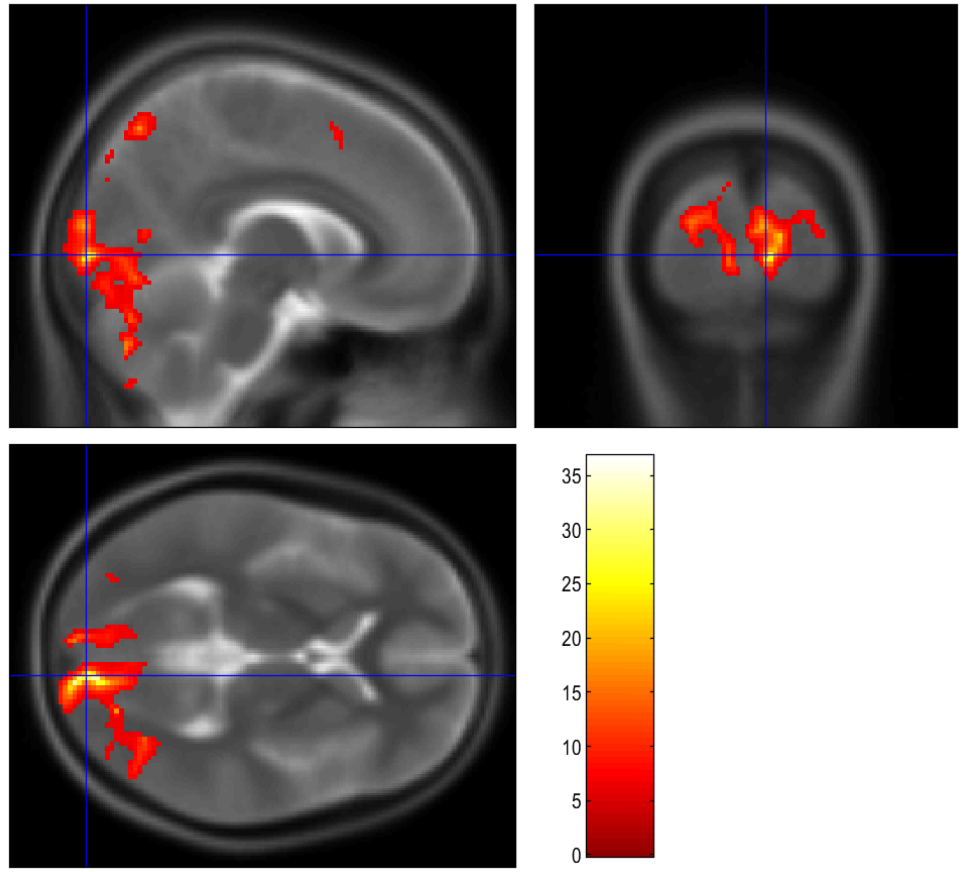
Display Results

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

- Choose one of the measured paradigm (neurotracker OR 2back OR visual) and do the processing in all six subjects folowing the pipeline from the 2nd excercise
- Do the group analysis folowing the pipeline from the 2nd excercise
- Describe and Display results of the 2nd-level analysis, find areas with statisticaly significant activation (Brodmann areas)

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