

# Voxelwise statistic, two independent groups

## CONTENTS

- 1) Create a group-assignment (Excel-file)
- 2) Perform the voxelwise-T-test (independent group)
- 3) Examine Results
  - 3.1) EXPORT RESULTS-TABLE AS EXCELFILE
  - 3.2) DISPLAY RESULT TABLE IN COMMAND WINDOW
  - 3.3) EXPORT RESULTS-TABLE AS TXT-FILE
  - 3.4) SAVE THRESHOLDED IMAGE AS NIFTI-FILE
  - 3.5) EXTRACT PEAK DATA
  - 3.6) CREATE SUMMARY OF CURRENT CONTRAST
  - 3.7) Change to Cluster-based approach
- 4) Check the other contrast
- 5) CREATE BIG-SUMMARY
- 6) Define new Contrast
- 7) Work from Command line
  - 7.1) run voxelwise statistic from command line
  - 7.2) Create full report

### Scenario

-**Artificial data** for 14 animals were created, with spherical differences centered in the a) **left Primary somatosensory area mouth layer 4** and b) the **right CaudoPutamen**

Here we have two groups with 6 and 8 animals in each group. The artificially created files are stored as "vimg.nii"-image in the respective animal-folders. Note that the animal-folders are empty, except of the "vimg.nii"-image. This image is in register to the Allen mouse brain atlas ( i.e already in standard space).

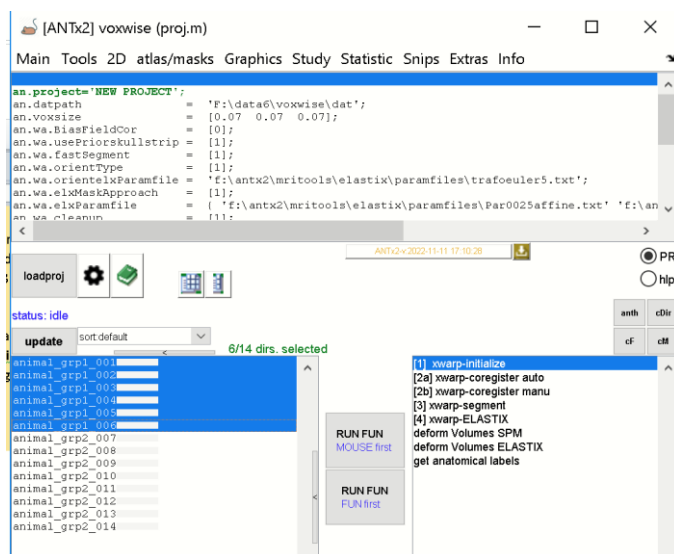
### Prerequisites

-a project with project file was created ...when doing this analysis with your own data, the image that should be analyzed using voxelwise statistic must be in the standard/template space (here : Allen mouse brain space). For instance when analyzing the gray matter image("c1t2.nii"), the image has to be transformed to standard space to make voxelwise statistic feasible.

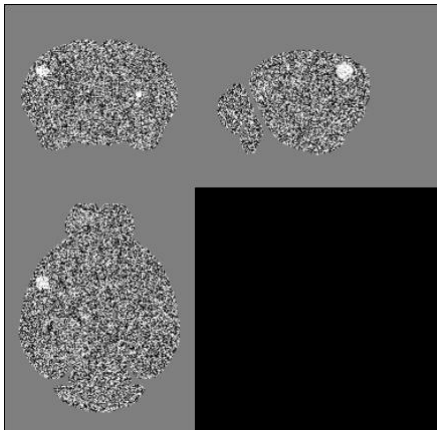
-Templates: here ,the **mouse\_Allen2017HikishimaLR'**-template is already imported in the study's templates-folder

- start ANT-gui and set current working directory to project-folder path

-load project (m-file, here proj.m)



The Figure shows the list of 14 animals (left listbox). Animals of group-1 is selected (just for displaying purpose). Note that for this animals artificial data were created.



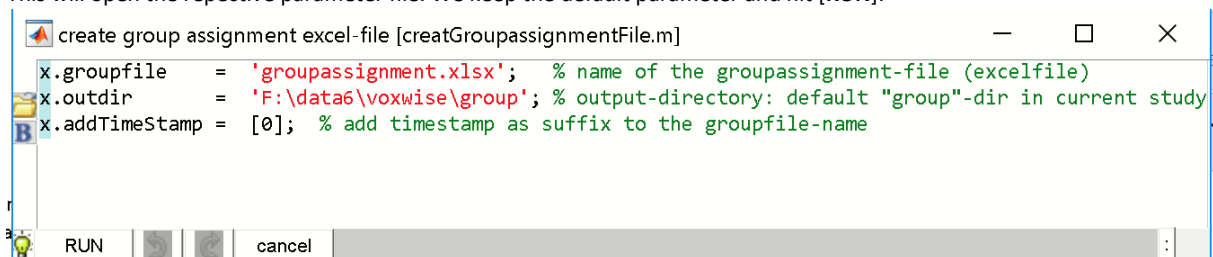
The figure shows the simulated image 'vimg.nii' (image is in standard-space) of one animal from the 2<sup>nd</sup> group with increased intensities centered at a) the left Primary somatosensory area mouth layer 4 and b) the right CaudoPutamen.

### 1) Create a group-assignment (Excel-file)

We now need a group-assignment file (Excel-file) with definitions of animals and group-assignment.

For this select: **Statistic/create group assignment file** from the **ANTx-MENU**.

This will open the respective parameter file. We keep the default parameter and hit **[RUN]**.



To this end, the Excelfile **"groupassignment.xlsx"** is created, located in the **"group"**-folder in the current study directory (**"F:\data6\voxwise\group"**).

```
.. create group-assignment file ...wait
new group-file [groupassignment.xlsx]: Explorer or open
Done!
fx >>
```

You can select the **'open'-hyperlink** in the command-window to open the Excel-file. The 1<sup>st</sup> sheet of the excelfile looks as follows:

	A	B	C	D	E	F	G	H	I
1	animal	group	group-column: please specify which animal belongs to which group as string (preferred) or numeric value avoid any spaces!!! example: "control" for "control"-animals; "ABC" for animals from "ABC-group"						
2	animal_grp1_001								
3	animal_grp1_002								
4	animal_grp1_003								
5	animal_grp1_004								
6	animal_grp1_005								
7	animal_grp1_006								
8	animal_grp2_007								
9	animal_grp2_008								
10	animal_grp2_009								
11	animal_grp2_010								
12	animal_grp2_011								
13	animal_grp2_012								
14	animal_grp2_013								
15	animal_grp2_014								
16									

The first column contains the animal-IDs of all animals of the current study. The 2<sup>nd</sup> column has to be filled with the respective group-assignment. Here the 1<sup>st</sup> 6 animals belong to the control-group, thus the 'control'-string is inserted for those animals, while the other animals belong to the "VIMG"-group, thus the "VIMG"-string is inserted in the 2<sup>nd</sup> column (see Fig. below). Note that the string-names are arbitrary. Try to avoid special characters! Save this modifications (here the same filename, "groupassignment.xlsx", is used).

Kommentar 4									
	A	B	C	D	E	F	G	H	I
1	animal	group	group-column: please specify which animal belongs to which group as string (preferred) or numeric value avoid any spaces!!! example: "control" for "control"-animals; "ABC" for animals from "ABC-group"						
2	animal_grp1_001	control							
3	animal_grp1_002	control							
4	animal_grp1_003	control							
5	animal_grp1_004	control							
6	animal_grp1_005	control							
7	animal_grp1_006	control							
8	animal_grp2_007	VIMG							
9	animal_grp2_008	VIMG							
10	animal_grp2_009	VIMG							
11	animal_grp2_010	VIMG							
12	animal_grp2_011	VIMG							
13	animal_grp2_012	VIMG							
14	animal_grp2_013	VIMG							
15	animal_grp2_014	VIMG							
16									

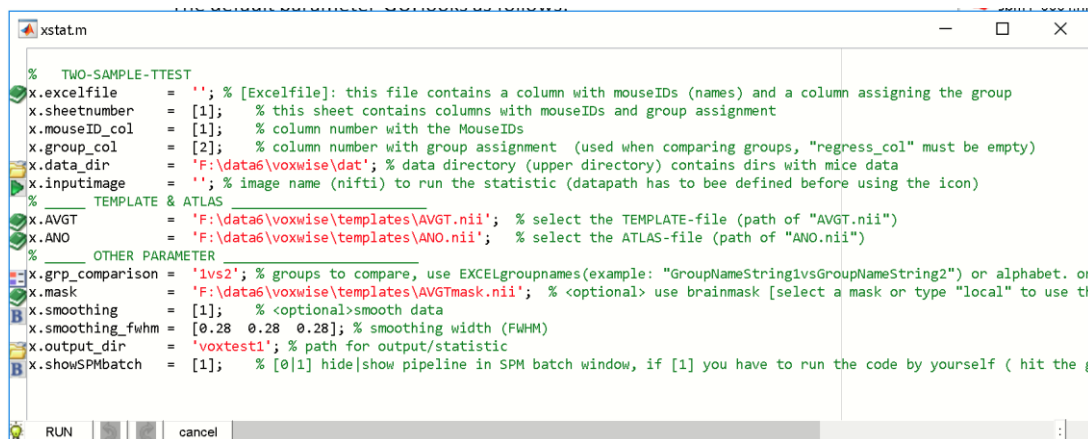
## 2) Perform the voxelwise-T-test (independent group)

We now want to run the independent voxelwise t-test comparing the two groups for the "vimg.nii"-image.

For this select: **Statistic/SPM-statistic** from the **ANTx -MENU**. This will call the main GUI (from the function [xstat.m](#)):

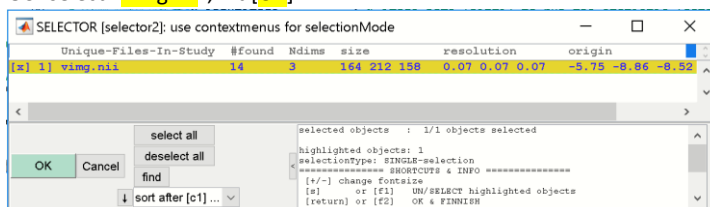


Next, select the [**indepStat**]-button to open the parameter-GUI for the voxelwise independent t-test (TWO-SAMPLE-TTEST). The default parameter-GUI looks as follows:



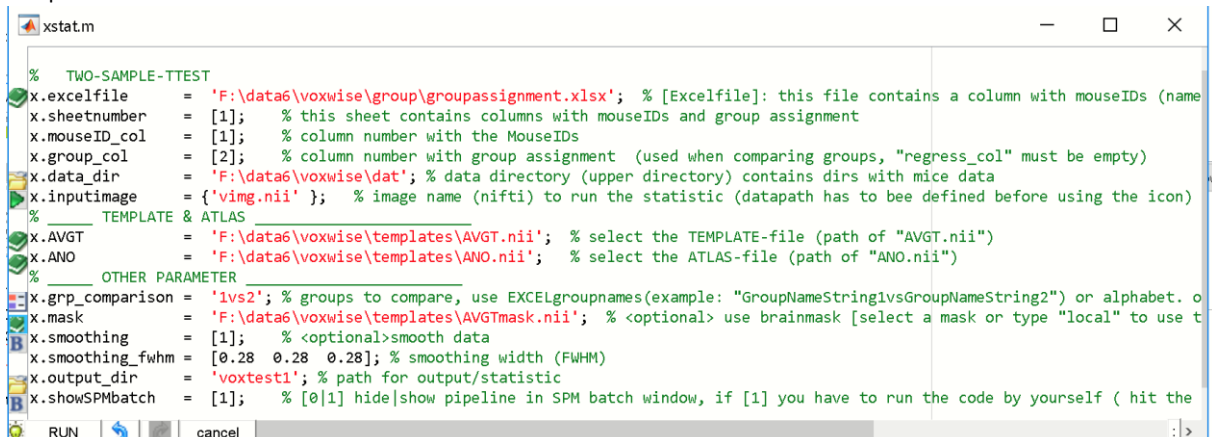
We now need to modify (or check) some parameters:

- “**x.excelfile**”: click the left icon and select the group-assignment-file (“groupassignment.xlsx”) located in the group-folder.
- “**x. data\_dir**”: click the left icon and select the study’s dat-folder (This folder contain the animals-data and the image that should be statistically tested).
- “**x. inputimage**”: click the left icon and select the image that should be statistically tested: Specifically in the file-selector GUI select “**vimg.nii**”, hit [OK].



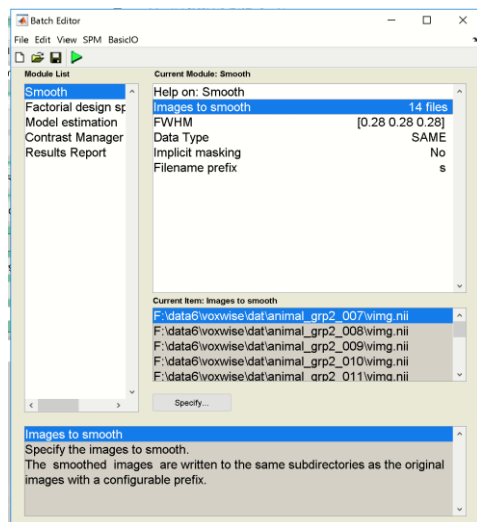
- “**x. AVGT**”: click the left icon and select the AVGT-image (“AVGT.nii”) from the study’s templates-folder.
- “**x. ANO**”: click the left icon and select the ANO-image (“ANO.nii”, i.e. the Atlas) from the study’s templates-folder.
- “**x. mask**”: click the left icon and select the AVGTmask-image (“AVGTmask.nii”) from the study’s templates-folder. Note that the animal-folders only contain the ‘vimg.nii’-image. Thus we have to assign the brain-mask (“AVGTmask.nii”) from the templates-folder.
- “**x.output\_dir**”: define the output-folder for the voxelwise statistic, here “**voxtest1**”.

The parameter-Gui should now looks as follows:



Note that the image ‘vimg.nii’ will be smoothed (“x.smoothing” is set to [1]) by the triple of the voxel-resolution (“x.smoothing\_fwhm” is [0.28 0.28 0.28]). Note also, that “x.showSPMbatch” is set to [1]. This parameter will open the SPM-batch-GUI, when hitting the [RUN]-button, allowing for final post-parameter configurations.

Hit [RUN]-button to run the voxelwise statistic. Because the parameter “x.showSPMbatch” was set to [1], the SPM-batch-GUI will pop-up, allowing for specific post-parameter configurations and final checks (see Fig. below).



Here, everything seems to be ok and no further changes will be made. Hit **[RUN BATCH]**-button (green triangle) to execute this batch. The process will take a couple of minutes.

When done, you can obtain the **xstat-batch**, by typing: **“char(anth)”** in Matlab-cmd window or clicking the **[anth]**-button from the **ANTx-main GUI**:

```

%% #g FUNCTION:      [xstat.m]
%% #b info :         xstat: voxelwise statistic [SPM-statistic] for normalized data (nifti volumes)
%% =====
z=[];
z.stattype           = 'twosamplettest';           %% STATISTICAL TEST
z.excelfile           = 'F:\data6\voxwise\group\groupassignment.xlsx'; %% [Excelfile]: this file contains a column
                                                    %% with mouseIDs (names) and a column
                                                    %% assigning the group
                                                    %% this sheet contains columns with mouseIDs
z.sheetnumber         = [1];
and group assignment
z.mouseID_col         = [1];                       %% column number with the MouseIDs
z.group_col           = [2];                       %% column number with group assignment(used
when comparing groups, "regress_col"

                                                    %% must be empty)
z.data_dir             = 'F:\data6\voxwise\dat';    %% data directory (upper directory) contains
dirs with mice data
z.inputimage          = 'vimg.nii';                %% image name (nifti) to run the statistic
(datapath has to be defined before

                                                    %% using the icon)
z.AVGT                 = 'F:\data6\voxwise\templates\AVGT.nii'; %% select the TEMPLATE-file (path of
"AVGT.nii")
z.ANO                  = 'F:\data6\voxwise\templates\ANO.nii';  %% select the ATLAS-file (path of "ANO.nii")
z.grp_comparison       = '1vs2';                   %% groups to compare, use

                                                    %% or alphabet. order (example: "1vs2"), or
                                                    %% <optional> use brainmask [select a mask or type "local" to use the AVGTmask.nii
                                                    %% from the templates folder]
                                                    %% <optional>smooth data
                                                    %% smoothing width (FWHM)
                                                    %% path for output/statistic
                                                    %% [0|1] hide|show pipeline in SPM batch window, if [1] you have to run the code
                                                    %% by yourself ( hit the green driangle), [0] pipes runs automatically

EXCELgroupnames (example: "GroupName1vsGroupName2")

z.mask                 = 'F:\data6\voxwise\templates\AVGTmask.nii';

z.smoothing             = [1];
z.smoothing_fwhm        = [0.28 0.28 0.28];
z.output_dir            = 'voxtest1';
z.showSPMbatch          = [1];

xstat(1,z); %% RUN

```

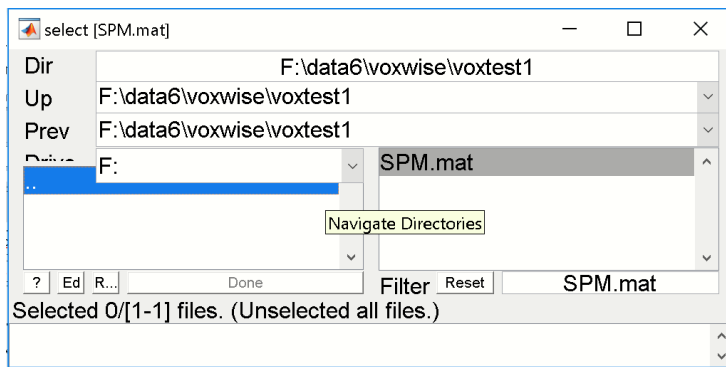
To rerun the analysis just re-run the code above.

### 3) Examine Results

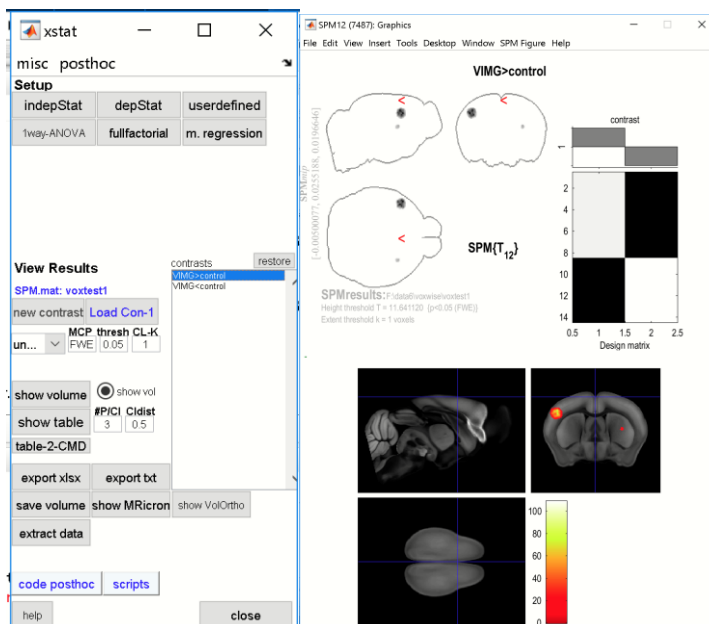
If the xstat-GUI is closed, type **xstat** in the cmd-window or select: **Statistic/SPM-statistic** from the **ANTx-MENU**.

Next, hit the **[load CON1]**-button (below the xstat-“View Results” section) to load the 1<sup>st</sup> contrast from the analysis.

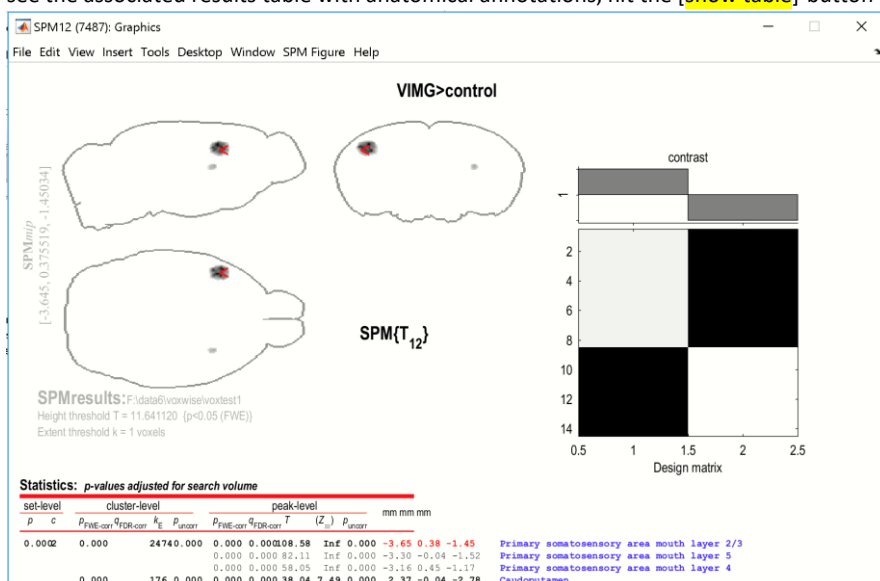
Next, select the path of the voxelwise analysis-folder (**'voxtest1'**) and the respective **SPM.mat**-file (In the below Fig: Select **SPM.mat** from the right listbox, which than appears in the lower listbox, finally hit **[Done]**).



Basically, for the independent t-statistic two contrasts will be calculated by default ('A>B' and 'A<B'). Executing the **load CON1**-button displays the 1<sup>st</sup> contrast ('VIMG>control').



The SPM-graphics window will show the voxelwise results for the 1<sup>st</sup> contrast 'VIMG>control' with the parameters, FWE at  $p=0.05$ , with min. survival spatial cluster (aka clustersize / sl-k) = 1 voxel. As expected, there are two significant 'blobs'. To see the associated results table with anatomical annotations, hit the **show table**-button from the xstat-GUI.

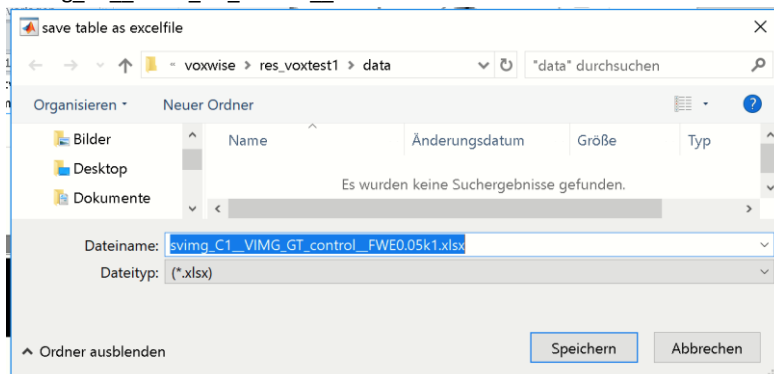


Because, the number of peaks per cluster (**#p/Cl**) is set to 3 and the cluster distance (**CLdist**) is set to 0.5 mm we see three peak clusters within the large left-hemispheric blob. You can change the respective settings for **"#p/Cl"** and **"CLdist"** in the xstat-GUI and **update** the graphic window by hitting the **VIMG>control**-contrast from the xstat-listbox. Again, to **update** any changes in the parameters just select the respective contrast from the xstat contrast listbox.

To show the volume again, hit the **[show volume]**-button.

### 3.1) EXPORT RESULTS-TABLE AS EXCELFILE

To export the results as Excel table, hit the **[export xlsx]**-button. The GUI will prompt you for a path and a proper filename of the Excel file. Note that per default, the output-path is predefined (new folder: 'res\_'+name of the analysis-folder), here: "**res\_voxtest1**" is the output-folder, which again contains a subfolder "data" that will contain the output. Also, the filename is predefined, based on the image, contrast-number, contrast-name, method, p-value and clustersize. Thus the filename is: "**svimg\_C1\_VIMG\_GT\_control\_FWE0.05k1.xlsx**".



Without changing the path and filename, just hit the **[save]**-button.

```
...export table..wait..  
voxSTAT-excelfile [svimg_C1_VIMG_GT_control_FWE0.05k1.xlsx]: Explorer or open  
DONE!  
fx >>
```

When done click the **"open"**-hyperlink to open the Excel file. The Excel file contains two sheets.

The "voxstat"-sheet contains the results-table:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	set	set	cluster	cluster	cluster	peak	peak	peak	peak	peak	x	y	z	Labels			
2	p	c	p(FWE-cor)	p(FDR-cor)	equik	p(unc)	p(FWE-cor)	p(FDR-cor)	T	equiZ	p(unc)	mm	mm	mm	-		
3	1.91226E-05	2	0		2474	6.7698E-301	0	0	108.5761719	65535	4.44089E-16	-3.645000398	0.375518739	-1.450335264	Primary somatosensory area mouth layer 2/3	img: svimg.nii	
4							0	0	82.11476898	65535	4.44089E-16	-3.295000434	-0.044481218	-1.520335257	Primary somatosensory area mouth layer 5	cmd: VMDs-control	
5						3.27609E-10	9.98809E-13	58.04750824		65535	4.44089E-16	-3.155000448	0.445518732	-1.170335293	Primary somatosensory area mouth layer 4	MCP: FWE	
6			0		176	2.91252E-52	5.15985E-08	4.81779E-11	38.04288864	7.487144601	3.51941E-14	2.374998987	-0.044481218	-2.780335128	Caudoputamen	TR: 0.05	
7																k: 1	

The "info"-sheet contains information to backtrack the statistical results:

1	Field	value
2	Image	svimg.nii
3	contrast	VIMG>control
4	MCP	FWE
5	Threshold	p<0.05
6	Clustersize	k=1
7	contrastName	VIMG>control
8	contrastNo	No-1
9	statstic	T
10	contrastDir	[1 -1]
11	dir	F:\data6\voxwise\voxtest1
12	INPUT-DATA***	
13	ANIMAL/Dir	Path
14	animal_grp2_007	F:\data6\voxwise\dat\animal_grp2_007\svimg.nii
15	animal_grp2_008	F:\data6\voxwise\dat\animal_grp2_008\svimg.nii
16	animal_grp2_009	F:\data6\voxwise\dat\animal_grp2_009\svimg.nii
17	animal_grp2_010	F:\data6\voxwise\dat\animal_grp2_010\svimg.nii
18	animal_grp2_011	F:\data6\voxwise\dat\animal_grp2_011\svimg.nii
19	animal_grp2_012	F:\data6\voxwise\dat\animal_grp2_012\svimg.nii
20	animal_grp2_013	F:\data6\voxwise\dat\animal_grp2_013\svimg.nii
21	animal_grp2_014	F:\data6\voxwise\dat\animal_grp2_014\svimg.nii
22	animal_grp1_001	F:\data6\voxwise\dat\animal_grp1_001\svimg.nii
23	animal_grp1_002	F:\data6\voxwise\dat\animal_grp1_002\svimg.nii
24	animal_grp1_003	F:\data6\voxwise\dat\animal_grp1_003\svimg.nii
25	animal_grp1_004	F:\data6\voxwise\dat\animal_grp1_004\svimg.nii
26	animal_grp1_005	F:\data6\voxwise\dat\animal_grp1_005\svimg.nii
27	animal_grp1_006	F:\data6\voxwise\dat\animal_grp1_006\svimg.nii
28	ADDITIONAL INFO***	
29		table shows 3 local maxima more than 0.5mm apart
30		Height threshold: T = 11.64, p = 0.000 (0.050)
31		Extent threshold: k = 1 voxels, p = 0.023 (0.006)

### 3.2) DISPLAY RESULT TABLE IN COMMAND WINDOW

Select **[table-2-CMD]**-button display the results-table in the command window:

```
Command Window
[VIMG>control] Result:
=====
set      set      cluster  cluster  cluster  cluster  peak    peak    peak    peak
p        c        p(FWE-corr) p(FDR-corr) equivk  p(unc)  p(FWE-corr) p(FDR-corr) T      equivk
=====
1.9123e-05 2          0          2474  6.7698e-301      0          0      108.576  Ir
|
|          0          176  2.9125e-52  3.2761e-10  9.9881e-13  58.048  Ir
|
|          0          176  2.9125e-52  5.1598e-08  4.8178e-11  38.043  7.4
=====
table shows 3 local maxima more than 0.5mm apart
Height threshold: T = 11.64, p = 0.000 (0.050)
Extent threshold: k = 1 voxels, p = 0.023 (0.006)
Expected voxels per cluster, <k> = 0.181
Expected number of clusters, <c> = 0.01
FWEp: 11.641, FDRp: 5.084, FWEc: 176
Degrees of freedom = [1.0, 12.0]
FWHM = 0.30 0.30 0.30 mm mm mm; 4.28 4.27 4.28 {voxels}
Volume: 506 = 1475422 voxels = 18004.8 resels
Voxel size: 0.07 0.07 0.07 mm mm mm; (resel = 78.19 voxels)
fx >>
```

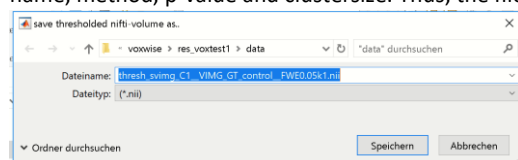
### 3.3) EXPORT RESULTS-TABLE AS TXT-FILE

To export the results as text-file, hit the **[export txt]**-button. When path/file is not changed this will save the results-table as "svimg\_C1\_VIMG\_GT\_control\_FWE0.05k1.txt" in the "res\_voxtest1\data"-folder:

```
svimg_C1_VIMG_GT_control_FWE0.05k1.txt
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
=====
set      set      cluster  cluster  cluster  cluster  peak    peak    peak    peak
p        c        p(FWE-corr) p(FDR-corr) equivk  p(unc)  p(FWE-corr) p(FDR-corr) T      equivk
=====
1.9123e-05 2          0          2474  6.7698e-301      0          0      108.576  Inf  4.4409e-16 -3.65  0.38 -1.45 Primary somatosensory area mouth layer 2/3
|
|          0          176  2.9125e-52  3.2761e-10  9.9881e-13  58.048  Inf  4.4409e-16 -3.30 -0.04 -1.52 Primary somatosensory area mouth layer 5
|
|          0          176  2.9125e-52  5.1598e-08  4.8178e-11  38.043  7.487  3.5194e-14  2.37 -0.04 -2.78 Primary somatosensory area mouth layer 4
|
|          0          176  2.9125e-52  5.1598e-08  4.8178e-11  38.043  7.487  3.5194e-14  2.37 -0.04 -2.78 Caudoputamen
=====
table shows 3 local maxima more than 0.5mm apart
Height threshold: T = 11.64, p = 0.000 (0.050)
Extent threshold: k = 1 voxels, p = 0.023 (0.006)
Expected voxels per cluster, <k> = 0.181
Expected number of clusters, <c> = 0.01
FWEp: 11.641, FDRp: 5.084, FWEc: 176
Degrees of freedom = [1.0, 12.0]
FWHM = 0.30 0.30 0.30 mm mm mm; 4.28 4.27 4.28 {voxels}
Volume: 506 = 1475422 voxels = 18004.8 resels
Voxel size: 0.07 0.07 0.07 mm mm mm; (resel = 78.19 voxels)
```

### 3.4) SAVE THRESHOLDED IMAGE AS NIFTI-FILE

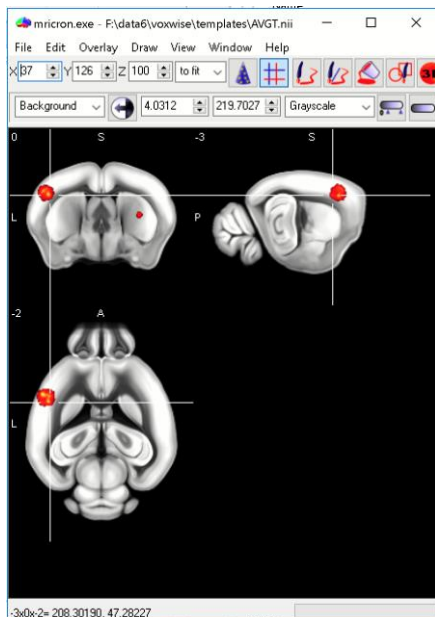
To save the thresholded (surviving) t-map as NIFTI-file hit the **[save volume]**-button. The GUI will prompt you for a path and a proper filename. Note that per default, the output-path is predefined (new folder: 'res\_'+analysis-folder), here: "res\_voxtest1" in the subfolder "data". Also, the filename is predefined, based on the image, contrast-number, contrast-name, method, p-value and clustersize. Thus, the filename is: "thresh\_svimg\_C1\_VIMG\_GT\_control\_FWE0.05k1.nii".



When done you can select the hyperlink **'MRicron'** from the command-window to open the saved statistical t-map overlaid onto the template ('AVGT.nii') via MRicron.

```
...saving volume...wait...
voxSTAT-volume [AVGT.nii - thresh_svimg_C1_VIMG_GT_control_FWE0.05k1.nii]: Explorer or MRicron
Done!
fx >>
```





Alternatively, you can hit the **[show MRicron]**-button from the xstat-GUI and select the respective NIFTI ("thresh\_svmg\_C1\_VIMG\_GT\_control\_FWE0.05k1.nii").

### 3.5) EXTRACT PEAK DATA

To extract the single data (for each animal) of the surviving peak-data of the results-table hit the **[extract data]** button. The GUI will prompt you for a path and a proper filename of the file. Note that per default, the output-path is predefined (new folder: 'res\_'+analysis-folder), here: "res\_voxtest1" in the subfolder "data". Also, the filename is predefined, based on the image, contrast-number, contrast-name, method, p-value and clustersize. Thus the filename is:

"svm\_g\_C1\_VIMG\_GT\_control\_FWE0.05k1\_NPC3\_SINGLEDATA.xlsx". Thus, just hit **[save]**.

```
..Extracting data ...wait...DONE!
data extracted [svm_g_C1_VIMG_GT_control_FWE0.05k1_NPC3_SINGLEDATA.xlsx]: Explorer or open
fx >>
```

When done, hit the **"open"**-hyperlink from the cmd-window to open the Excelfile:

animal					
A1	A	B	C	D	E
1	animal	group	Primary somatosensory area mouth layer 2/3	Primary somatosensory area mouth layer 5	Primary somatosensory area mouth layer 4
2			[-3.645,0.37552,-1.4503]	[-3.295,-0.044481,-1.5203]	[-3.155,0.44552,-1.1703]
3	animal_grp2_007	VIMG	1.726580307	1.583499897	1.03667339
4	animal_grp2_008	VIMG	1.726013138	1.523868497	1.047932843
5	animal_grp2_009	VIMG	1.732084074	1.623216213	1.031859421
6	animal_grp2_010	VIMG	1.756582342	1.609011189	0.995671776
7	animal_grp2_011	VIMG	1.661035182	1.618879633	0.984121443
8	animal_grp2_012	VIMG	1.689820455	1.649107412	1.045689146
9	animal_grp2_013	control	1.65941989	1.512732024	1.113033319
10	animal_grp2_014	control	1.645523203	1.575806608	1.1022894
11	animal_grp1_001	control	-0.437822931	-0.412956494	-0.254568327
12	animal_grp1_002	control	-0.364898759	-0.367373546	-0.250484564
13	animal_grp1_003	control	-0.433699804	-0.320627867	-0.334920369
14	animal_grp1_004	control	-0.383939185	-0.434580515	-0.232331362
15	animal_grp1_005	VIMG	-0.403700956	-0.37832031	-0.239073993
16	animal_grp1_006	VIMG	-0.40903667	-0.393954919	-0.268529537
17					
18					

The file contains the single-values from each animal (with animal-id and group-assignment) for the 4 observed peaks.

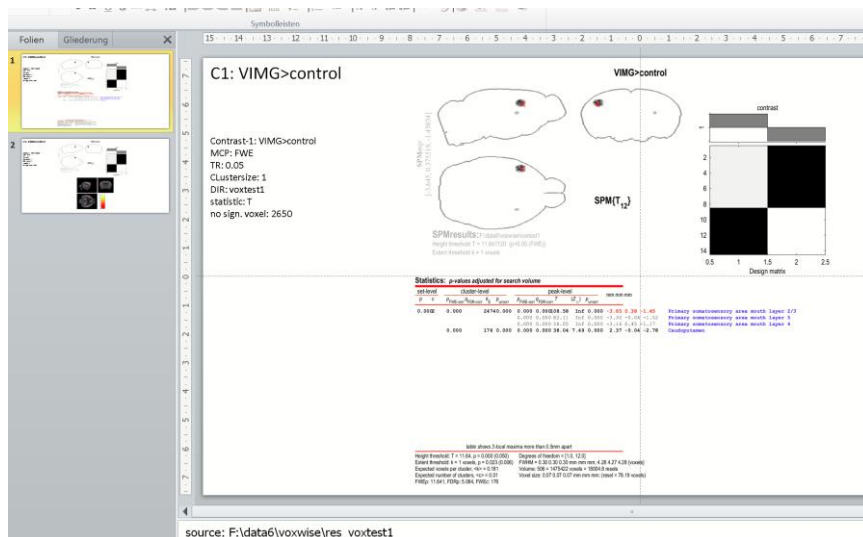
### 3.6) CREATE SUMMARY OF CURRENT CONTRAST

To obtain a fast summary of the current contrast, select from the xstat-MENU: **posthoc/create summary of current contrast**. This will create a Powerpoint-file with the summary for the 1<sup>st</sup> contrast. Note that the current settings from the xstat-GUI (MCP, thresh, CL-I, "#p/CI" and "CLdist") are used.

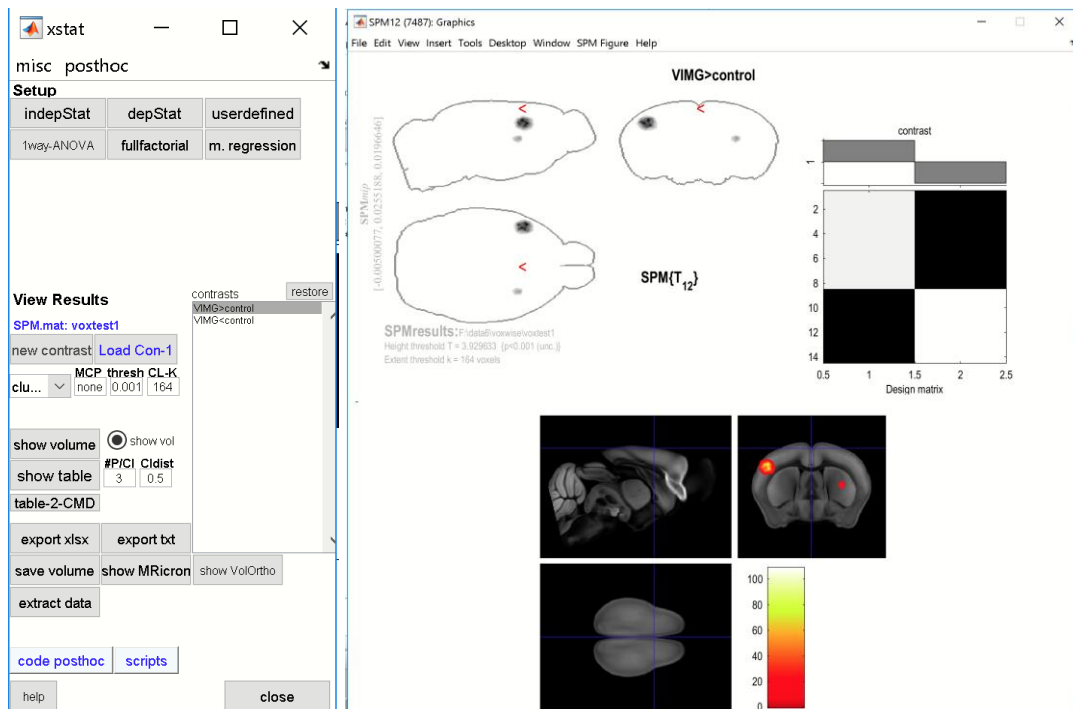
```
summary saved [sum_svmg_con1_VIMG_GT_control_FWE0.05k1.pptx]: Explorer or open
fx >>
```

When done, hit the **"open"**-hyperlink from the cmd-window to open the PPT-file:

Note that the PPT-file is directly stored in the "res\_voxtest1"-folder ('res\_'+analysis-folder).



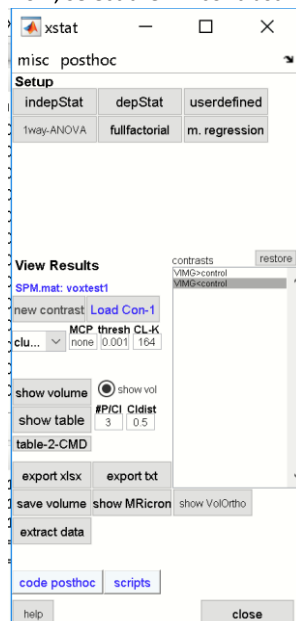
When selected the cluster-based approach will automatically run, and first set the p-value to 0.001, uncorrected and estimates the spatial threshold, i.e. the minimum number of neighboring voxels mandatory for a significant cluster. Next, this spatial threshold is used for the cluster-based approach. Here, a significant cluster-based height threshold at  $p=0.001$  needs 164 neighboring voxels to survive.



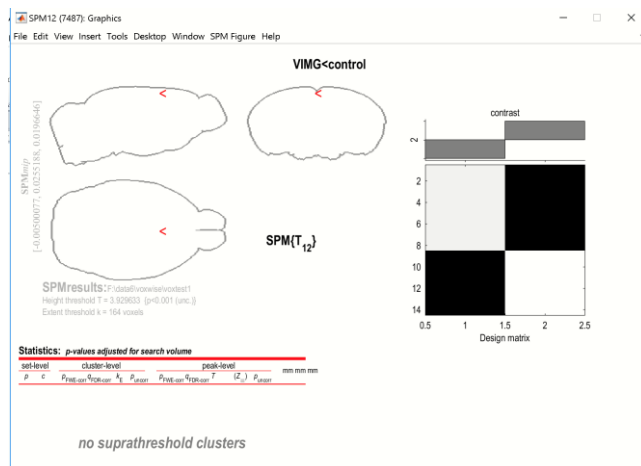
For the cluster-based approach, the results are quite similar compared to the FWE-approach.

#### 4) Check the other contrast

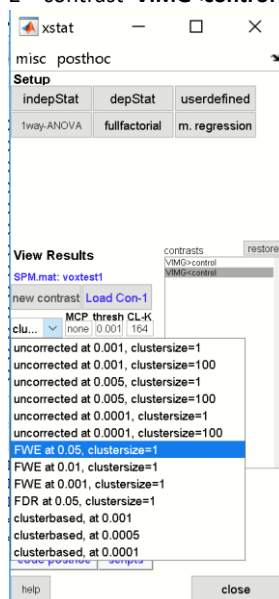
Now, select the 2<sup>nd</sup> contrast 'VIMG<control' from the xstat-contrast listbox.



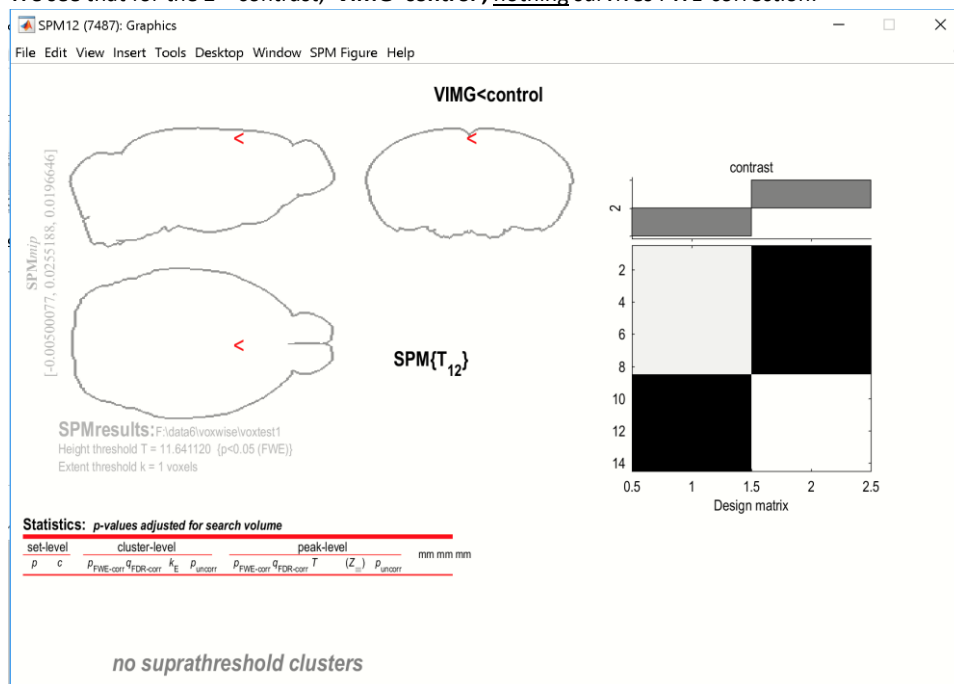
Based on the previous settings, the cluster-based approach shows no significant clusters.



Now, select '**FWE at 0.05, clustersize=1**' from the xstat-pulldown MENU and **update** the graphics-window by selecting the 2<sup>nd</sup> contrast '**VIMG<control**' from the **contrast-listbox**



We see that for the 2<sup>nd</sup> contrast, '**VIMG<control**', **nothing** survives FWE-correction:



## 5) CREATE BIG-SUMMARY

Sometimes it is useful to obtain a summary for all existing contrasts and all methods (uncorrected, FEW and cluster-based approach). For this, select from the **xstat-MENU**: **posthoc/all methods summary & export tables all contrasts**. This will create three PowerPoint-files in the “**res\_voxtest1**”-folder and also export the resulting tables as Excel-files and will store the respective t-maps as NIFTI-files.

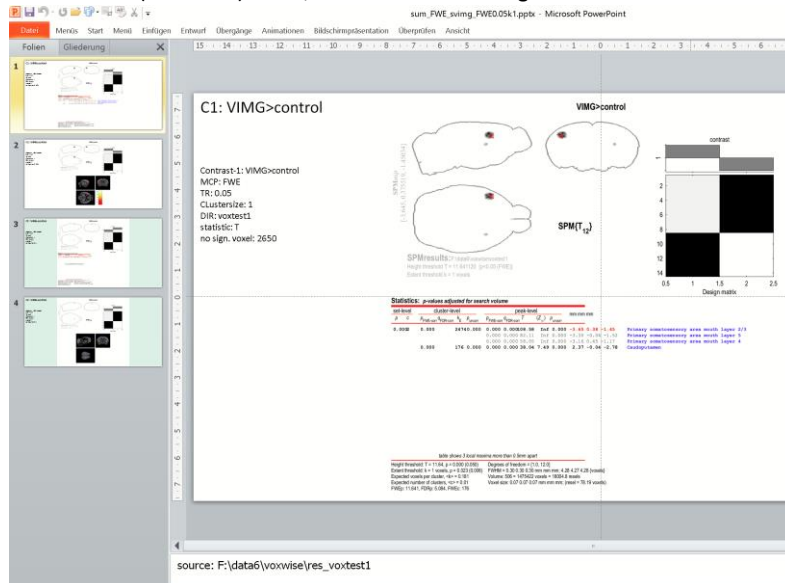
**The procedure will create three PPT-files:**

‘sum\_UNCOR\_svimg\_none0.001k1.pptx’ -uncorrected at  $p=0.001$

‘sum\_FWE\_svimg\_FWE0.05k1.pptx’ -using the FWE approach

‘sum\_CLUST\_svimg\_CLUST0.001k164.pptx’ -using the cluster-based approach

The below figure displays the summary of the FWE approach. This Powerpoint-file contains the table (or first part of the table, depending on the table size) and displays the volume with surviving voxels for the 1st contrast (slides 1-2) and the 2nd contrast (slides 3-4). Note, there are no surviving voxels for the 2nd contrast.

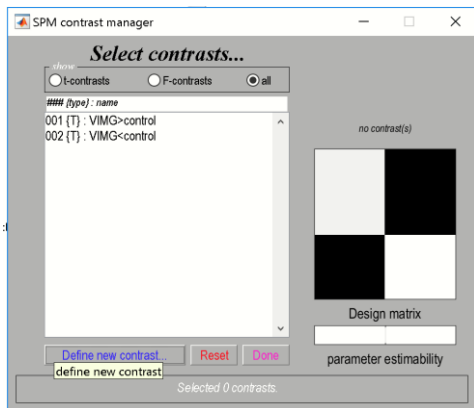


Note that this routine also creates the NIFTI-files and result-tables (Excel-files) for all contrast. The folder “**..\res\_voxtest1\data**” contains these files:

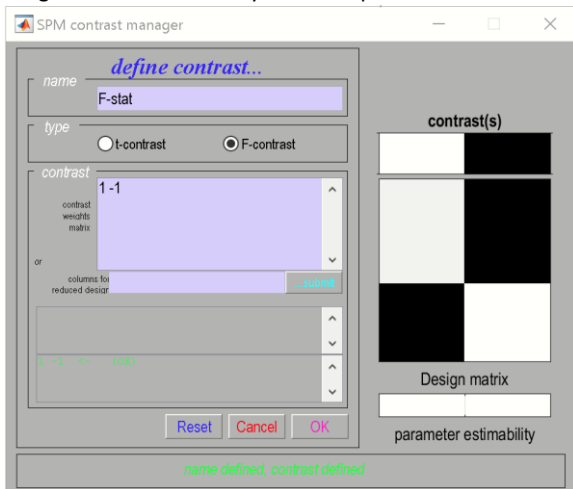
Name	Änderungsdatum	Typ
svimg_C1_VIMG_GT_control_CLUST0.001k164.nii	23.11.22 11:55	Nii
svimg_C1_VIMG_GT_control_CLUST0.001k164.xlsx	23.11.22 11:55	Mi
svimg_C1_VIMG_GT_control_FWE0.05k1.nii	23.11.22 11:55	Nii
svimg_C1_VIMG_GT_control_FWE0.05k1.txt	23.11.22 10:45	TX
svimg_C1_VIMG_GT_control_FWE0.05k1.xlsx	23.11.22 11:56	Mi
svimg_C1_VIMG_GT_control_none0.001k1.nii	23.11.22 11:53	Nii
svimg_C1_VIMG_GT_control_none0.001k1.xlsx	23.11.22 11:53	Mi
svimg_C2_VIMG_LT_control_CLUST0.001k164.nii	23.11.22 11:55	Nii
svimg_C2_VIMG_LT_control_CLUST0.001k164.xlsx	23.11.22 11:55	Mi
svimg_C2_VIMG_LT_control_FWE0.05k1.nii	23.11.22 11:56	Nii
svimg_C2_VIMG_LT_control_FWE0.05k1.xlsx	23.11.22 11:56	Mi
svimg_C2_VIMG_LT_control_none0.001k1.nii	23.11.22 11:54	Nii
svimg_C2_VIMG_LT_control_none0.001k1.xlsx	23.11.22 11:54	Mi

## 6) Define new Contrast

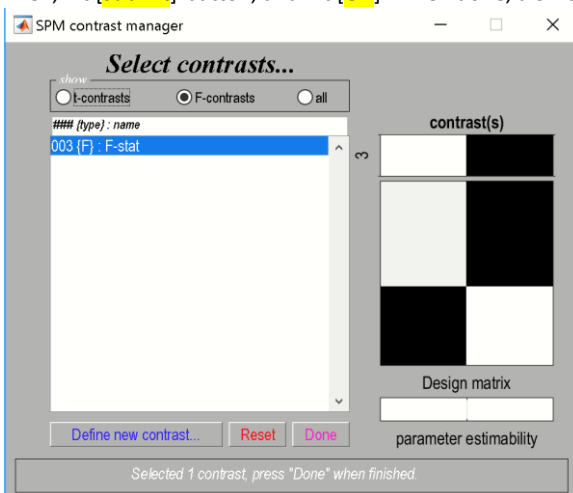
To define a new contrast hit **[new contrast]**-button from the **xstat-GUI**. When asked, select the specific **SPM.mat** from the voxelwise analysis-folder. In the SPM contrast-manager, select **[Define new contrast]**:



Here we select an F-contrast (radio: F-contrast). Enter 'F-stat' in the name-field and enter [1 -1] in the field 'contrast weights matrix'. Please try to avoid special characters for the contrast-name.

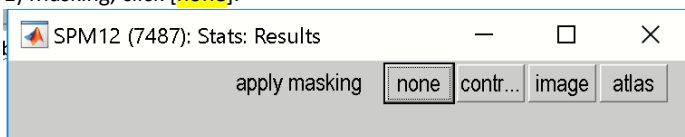


Then, hit [submit]-button, and hit [OK]. When done, a 3<sup>rd</sup> contrast (F-contrast) with name "F-stat" is created.

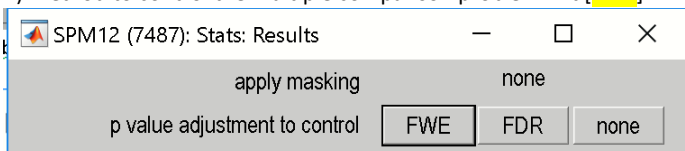


Hit [Done]-button. Next, you have to enter some parameters:

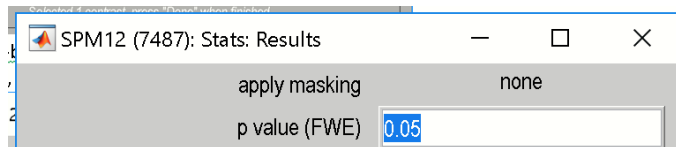
1) Masking, click [none].



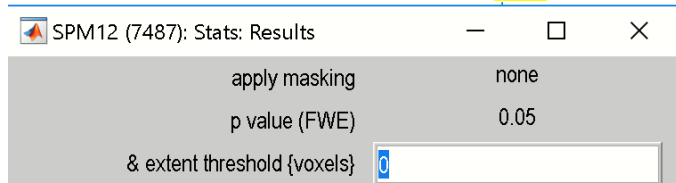
2) Method to control the multiple comparison problem: hit [FWE].



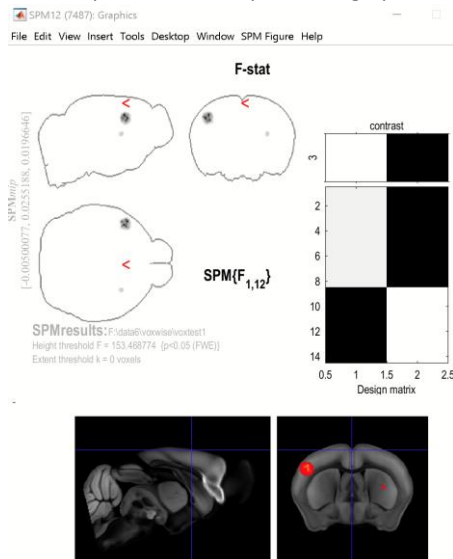
3) p-value: (keep 0.05), just hit the [enter]-key.



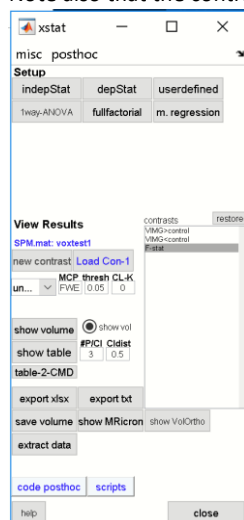
4) Extend/spatial threshold: (keep 0), just hit the **[enter]**-key.



This will produce the output in the graphic window for the F-contrast:



Note also that the contrast list box in the xstat-GUI will be updated (now containing 3 contrasts):



From here you can modify the parameters and **update** the graphic window by selecting a contrast (such as the 3<sup>rd</sup> contrast) from the contrast-listbox.

## 7) Work from Command line

### 7.1) run voxelwise statistic from command line

```
z=[];
z.stattype      = 'twosamplettest';           %STATISTICAL TEST
z.excelfile     = 'F:\data6\voxwise\group\groupassignment.xlsx'; %[Excelfile] containing mouseIDs and group
z.sheetnumber   = [1];                       %sheet with columns mouseIDs and group
z.mouseID_col   = [1];                       %column index with the MouseIDs
z.group_col     = [2];                       %column index with group assignment
z.data_dir      = 'F:\data6\voxwise\dat';    %data directory (upper directory)
```

```

z.inputimage      = 'vimg.nii';           %image name (nifti) to run the statistic
z.AVGT            = 'F:\data6\voxwise\templates\AVGT.nii'; % TEMPLATE-file (in templates-folder)
z.ANO             = 'F:\data6\voxwise\templates\ANO.nii';  % ATLAS-file (in templates-folder)
z.grp_comparison  = '1vs2';               %groups to compare (do not modify)
z.mask            = 'F:\data6\voxwise\templates\AVGTmask.nii'; %<optional> "brainmask
z.smoothing       = [1];                  %<optional>smooth data: [0]no,[1]yes
z.smoothing_fwhm  = [0.28 0.28 0.28];    %smoothing kernel (FWHM)
z.output_dir      = 'voxtest2';           %path for output-folder for statistic
z.showSPMbatch    = [0];                  %hide|show pipeline in SPM-batch-manager
xstat(1,z);          %RUN

```

execute this code to re-run the voxelwise statistic.

## 7.2) Create full report

```

xstat('loadspm','F:\data6\voxwise\voxtest2'): % open xstat-GUI and load SPM.mat-file
xstat('fullreport'); % create full report, i.e. three PPTfiles (uncorrected, FWE, cluster-based) + export result tables and statistical maps as NIFTI-files

```

For more information, see scripts [\[scripts\]](#)-button and help of xstat.