Methods & Models for fMRI Analysis 2018

TUTORIAL

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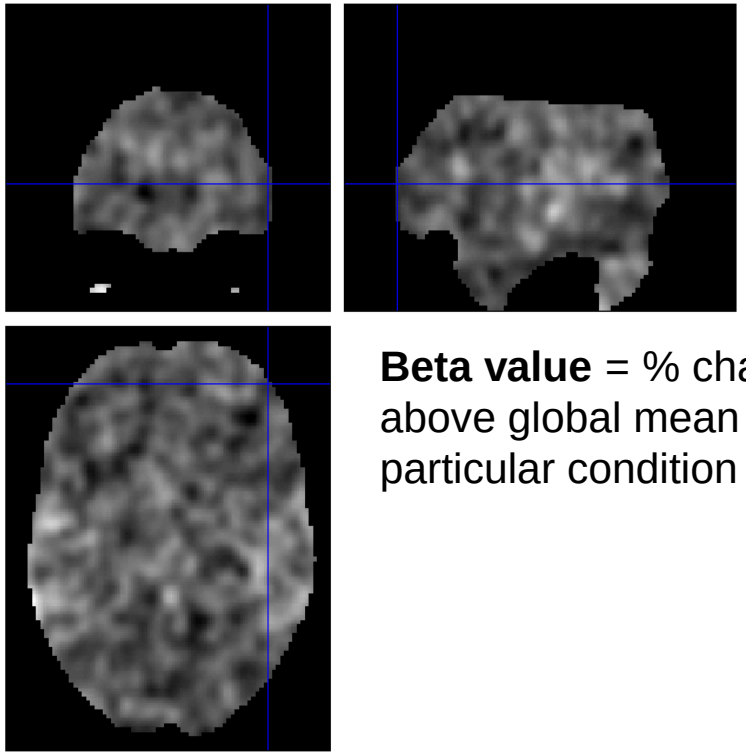
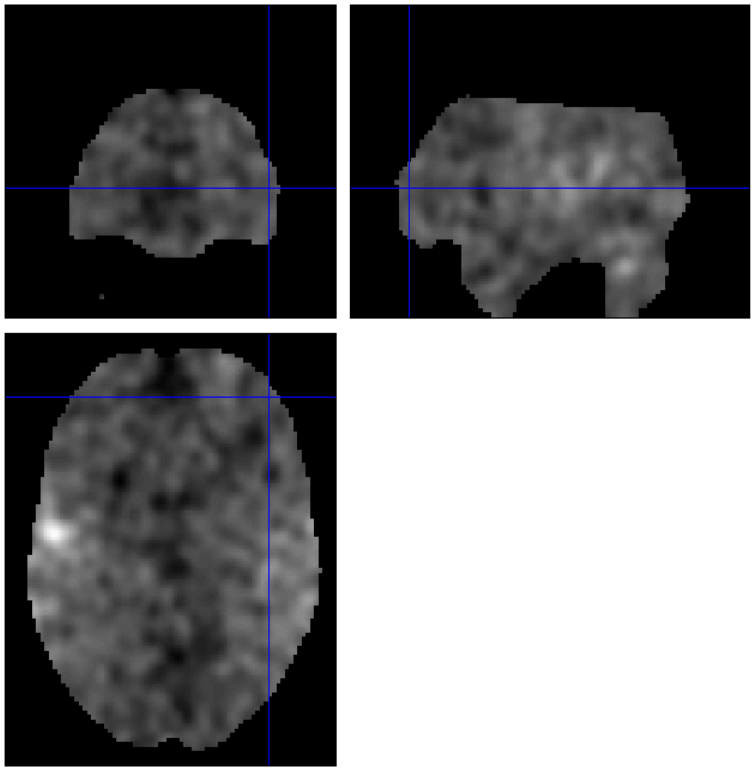
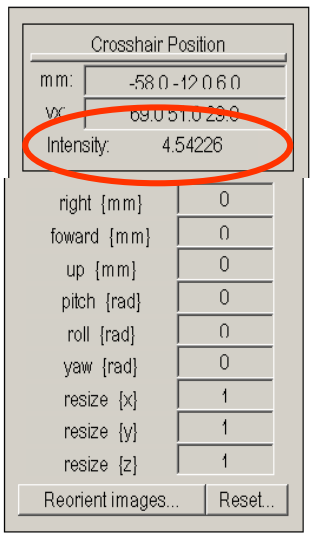
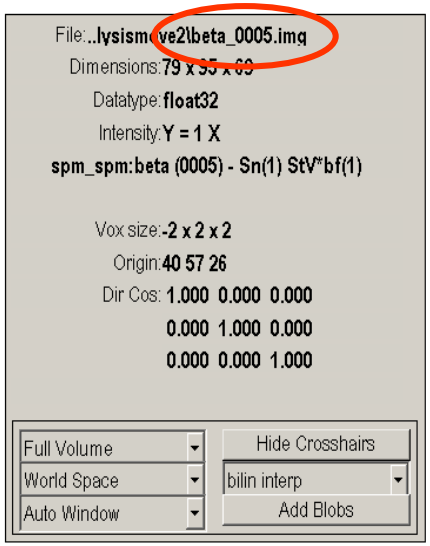
University of Zurich[UZH]
ETH Eidgenössische Technische Hochschule Zürich Swiss Federal Institute of Technology Zurich
Translational Neuromodeling Unit

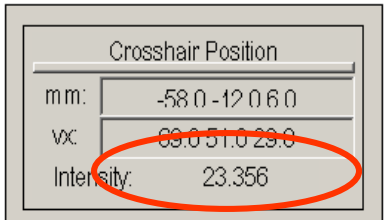


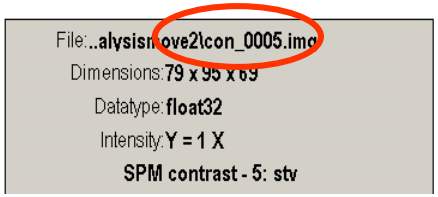
Beta value = % change above global mean for a particular condition



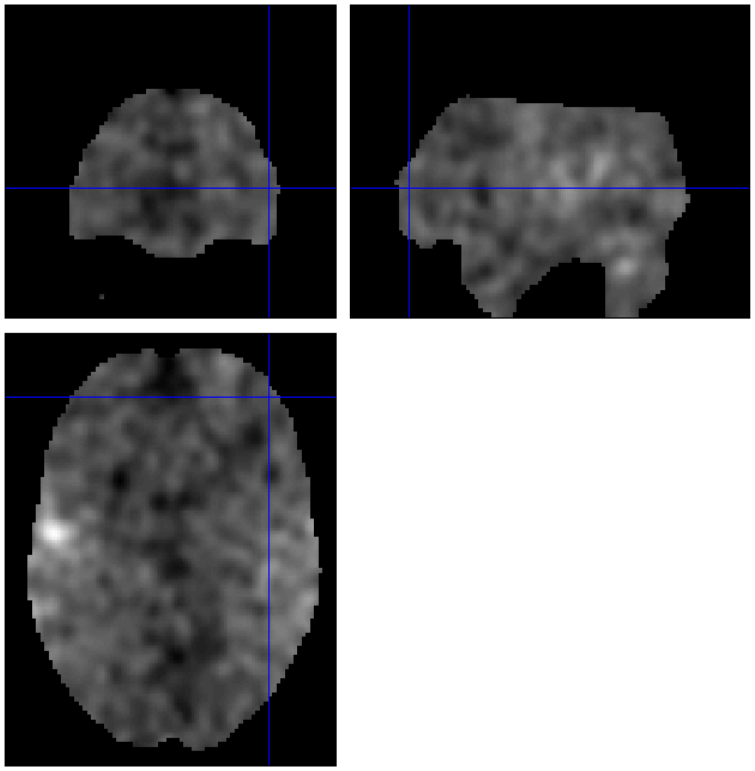


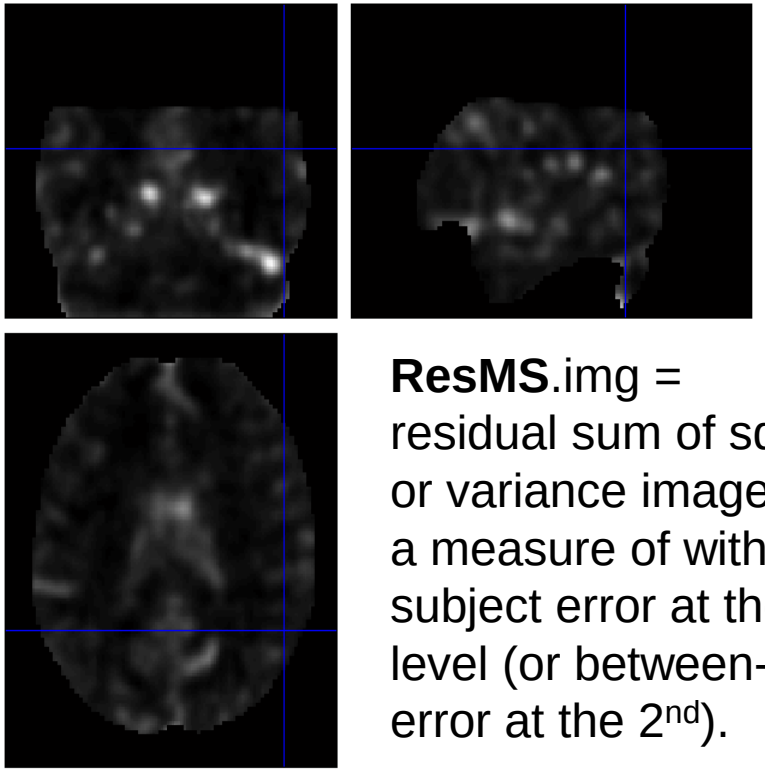




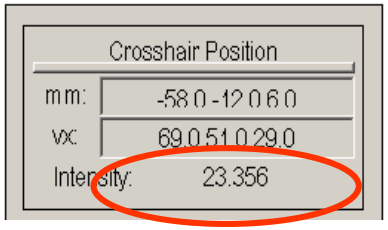


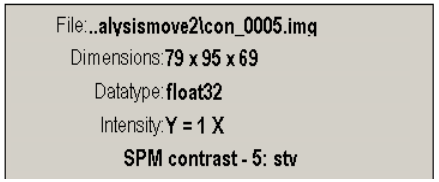
Con. value = summation of all relevant betas.



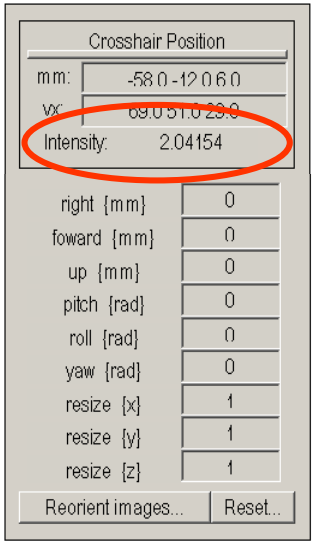


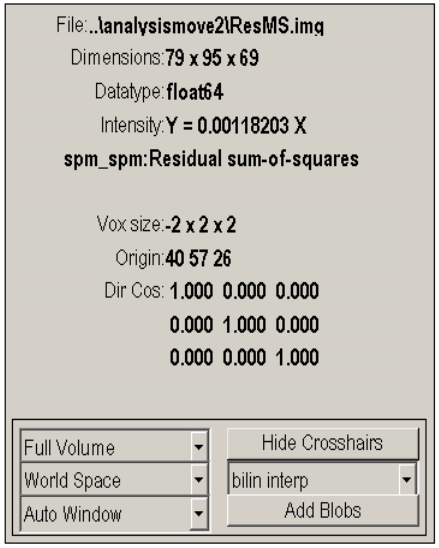
ResMS.img = $\hat{\sigma}_i^2$ residual sum of squares or variance image and is a measure of within-subject error at the 1st level (or between-subject error at the 2nd).

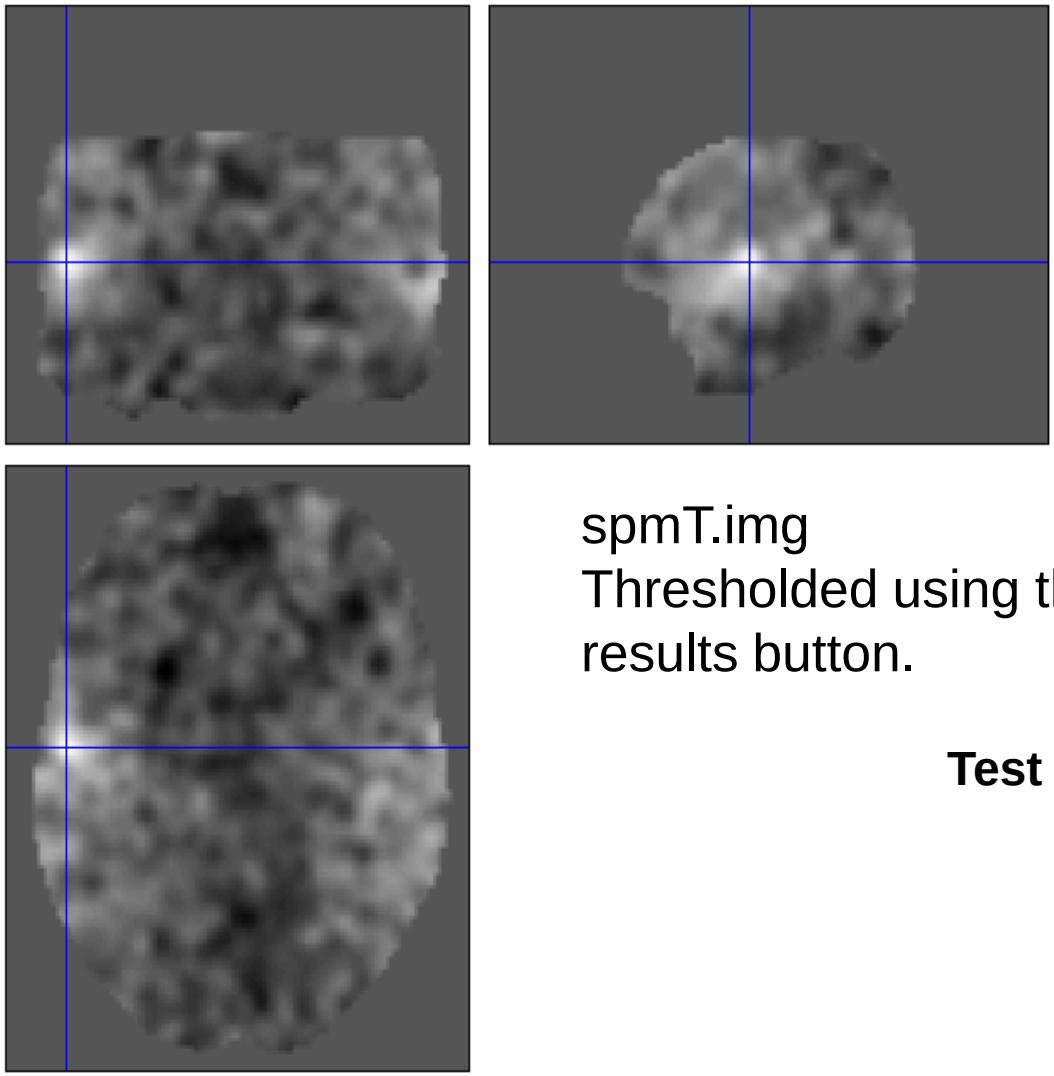




Con. value is combined with ResMS value at that voxel to produce a T statistic or spm.T.img.



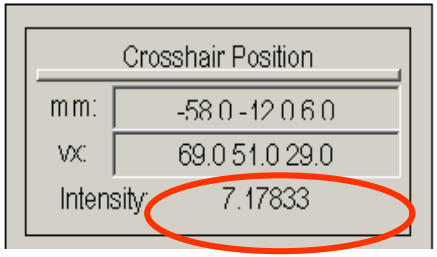


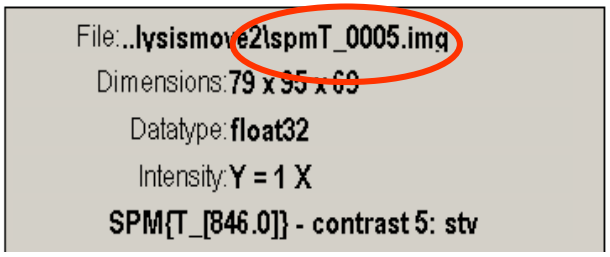


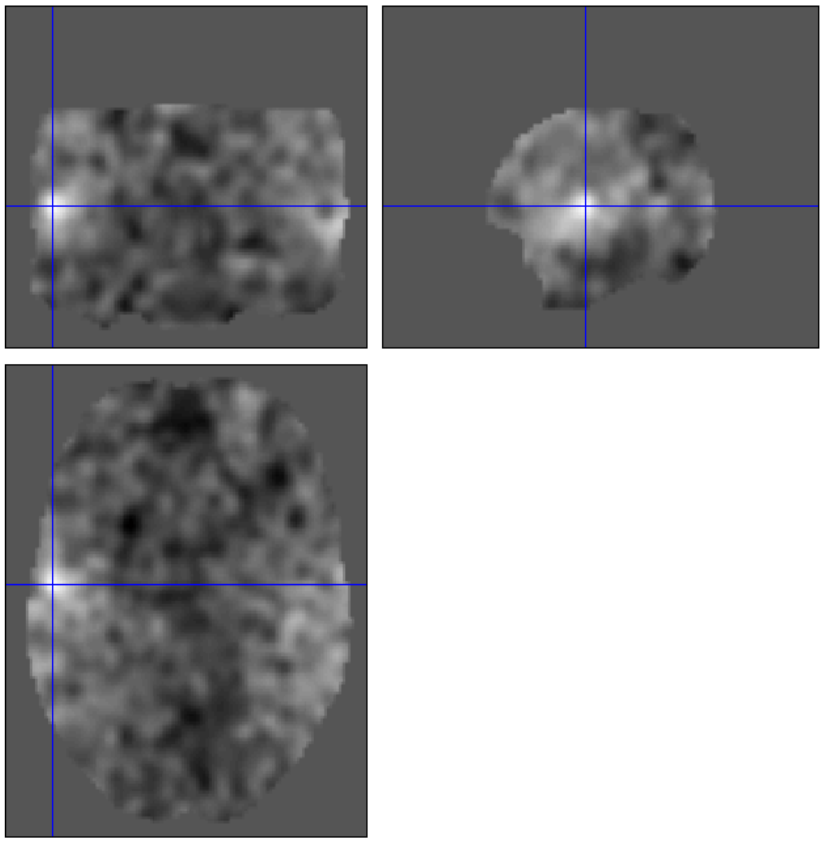
spmT.img
Thresholded using the results button.

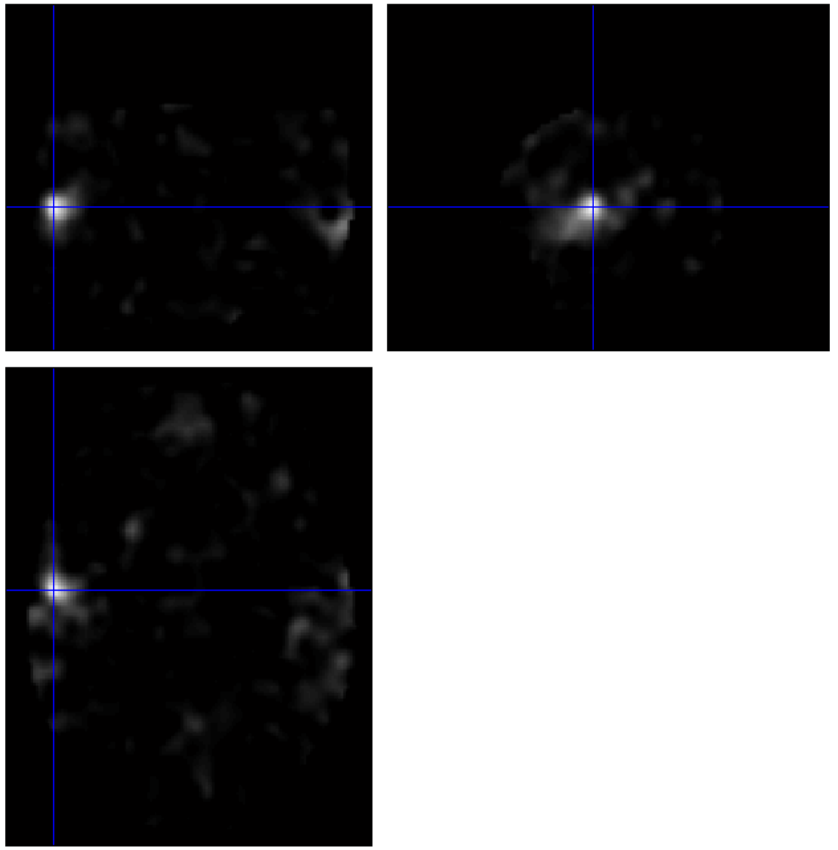
Test statistic:

$$T = \frac{\textbf{contrast of estimated parameters}}{\sqrt{\textbf{variance estimate}}}$$









Crosshair Position
mm: -58.0 -12.0 6.0
vx: 69.0 51.0 29.0
Intensity: 7.17833

File: ..lysismove2\spmT_0005.img
Dimensions: 79 x 95 x 69
Datatype: float32
Intensity: Y = 1 X
SPM{T_[846.0]} - contrast 5: stv

Crosshair Position
mm: -58.0 -12.0 6.0
vx: 69.0 51.0 29.0
Intensity: 51.5284

File: ..lysismove2\spmF_0032.img
Dimensions: 79 x 95 x 69
Datatype: float32
Intensity: Y = 1 X
SPM{F_[1.0,846.0]} - contrast 32: stvF

spmT.img and corresponding spmF.img

Worth to check:

Translational Neuromodeling Unit

Review Design
- Matrix
- Orthogonality

Explore Design:
- Sessions

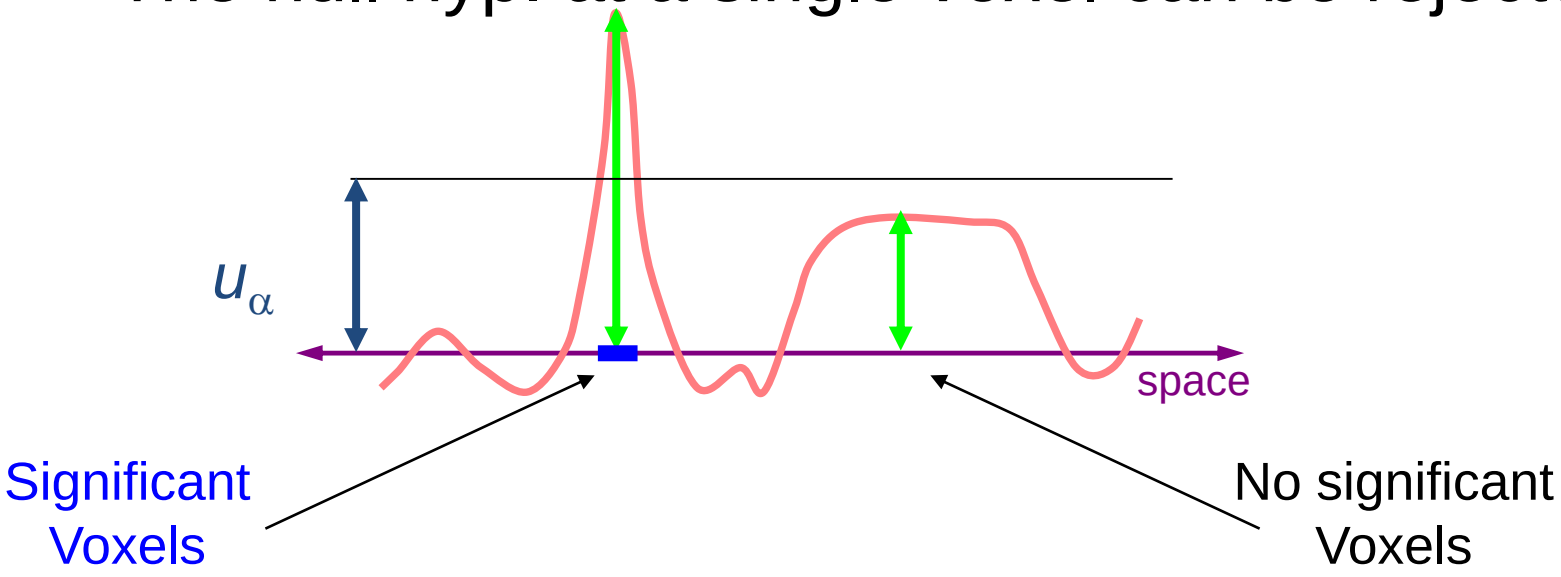
mask.nii

Correlation among regressors:

```
%% SPM.xX.xKXs.X: matrix of trials and betas (columns) in each trial
%%  R=corrcoef(X) calculates a matrix R of correlation coefficients
corr_pre=corrcoef(SPM.xX.X);
figure; imagesc(corr_pre, [-1 1]);colorbar
%% after whitening:
corr=corrcoef(SPM.xX.xKXs.X);
figure; imagesc(corr, [-1 1]);colorbar
```

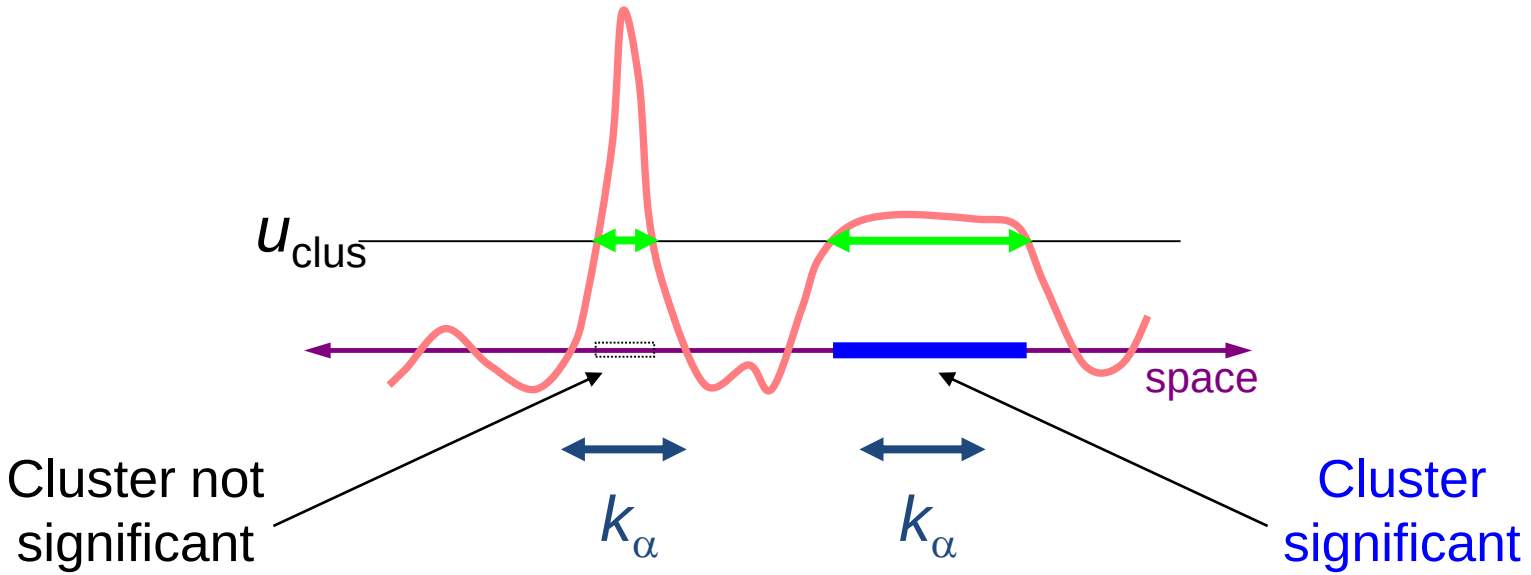
Voxel-level Inference

- Retain voxels above α-level threshold u_α
  - Signal magnitude
- Gives best spatial specificity
  - The null hyp. at a single voxel can be rejected



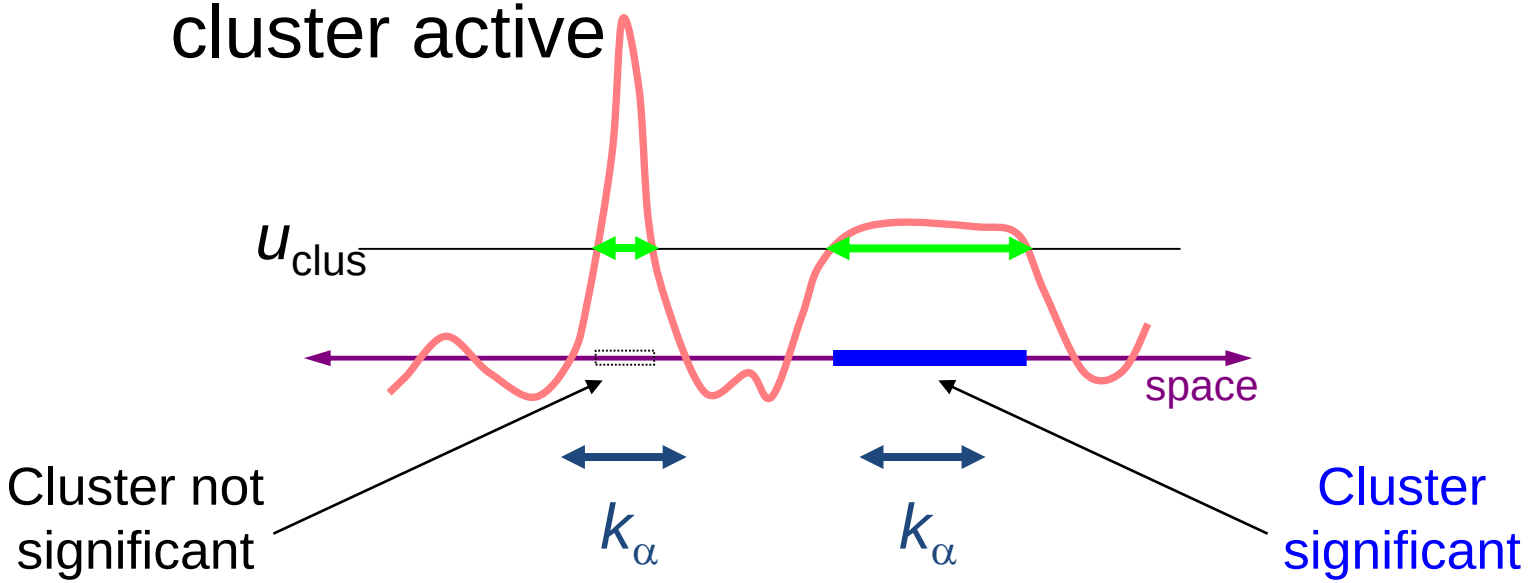
Cluster-level Inference

- Two step-process
  - Define clusters by threshold u_{clus}
  - Retain clusters larger than α-level threshold k_α: Spatial extent



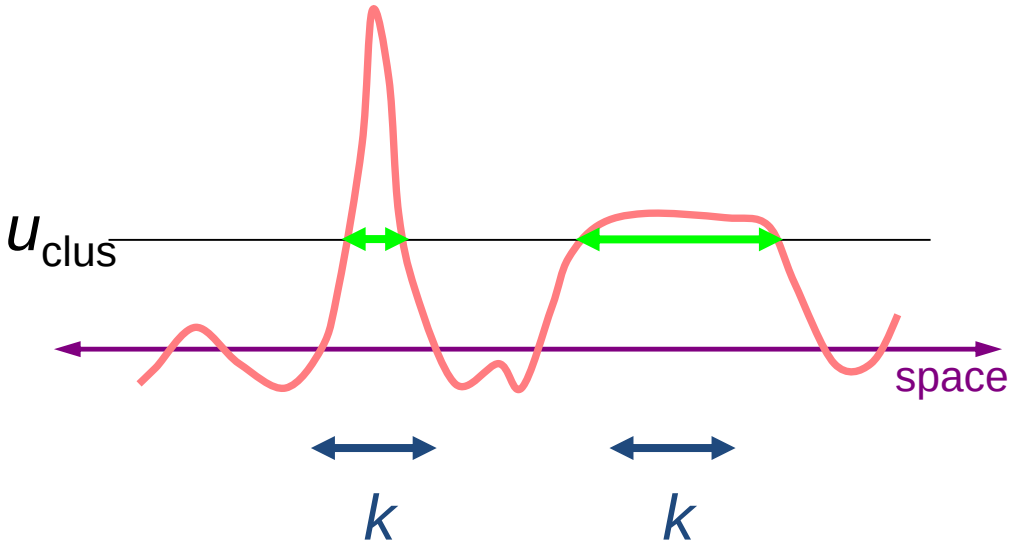
Cluster-level Inference

- Typically better sensitivity
- Worse spatial specificity
  - The null hyp. of entire cluster is rejected
  - Only means that *one or more* of voxels in cluster active



Set-level Inference

- Count number of blobs *c*
  - Minimum blob size *k*
- Worst spatial specificity
  - Only can reject global null hypothesis



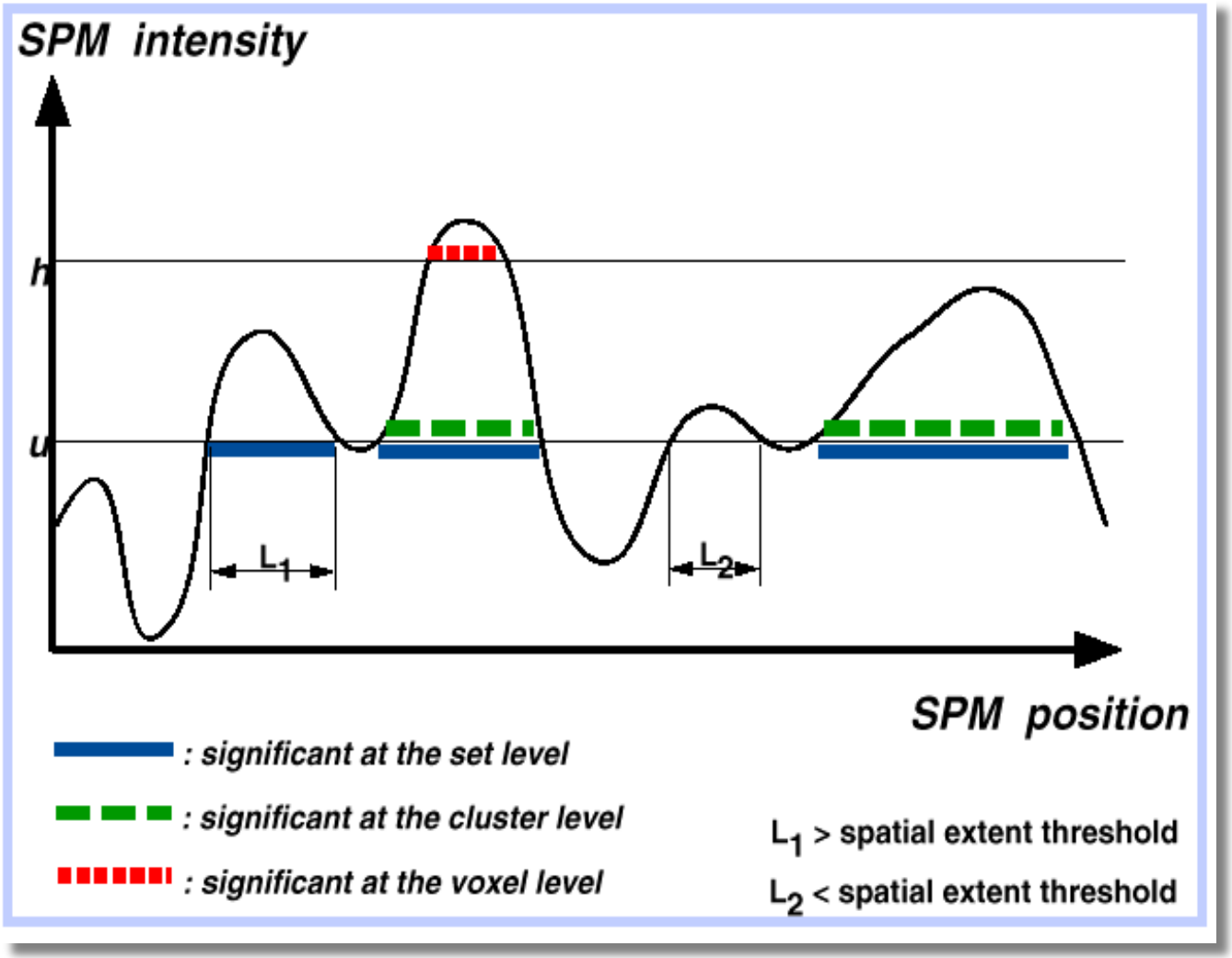
Here *c* = 1; only 1 cluster larger than k

Review: Levels of inference & power

Set level…

Cluster level…

Voxel level…



Options for displaying contrasts:

Apply masking

- none
- contrast
- image
- atlas

Maximum probability tissue labels derived from the "MICCAI 2012 Grand Challenge and Workshop on Multi-Atlas Labeling"[7] are available in files `tpm/labels_Neuromorphometrics.{nii,xml}`. These data were released under the Creative Commons Attribution-NonCommercial (CC BY-NC) with no end date. Users should credit the MRI scans as originating from the OASIS project[8] and the labeled data as "provided by Neuromorphometrics, Inc.[9] under academic subscription". These references should be included in all workshop and final publications. See `spm_templates.man` for more details about the generation of this file.

Options for displaying contrasts:

Apply masking (image) vs. small volume correction

- *p*-values will change

e.g. Positive effect of condition_1 / left middle frontal gyrus

Apply explicit mask vs. small volume correction

- *p*-values should be the same

→ can differ as your ReML-estimation will be based on the ROI

Save thresholded image

- thresholded SPM
- all clusters
- current cluster

rsfMRI - Lecture

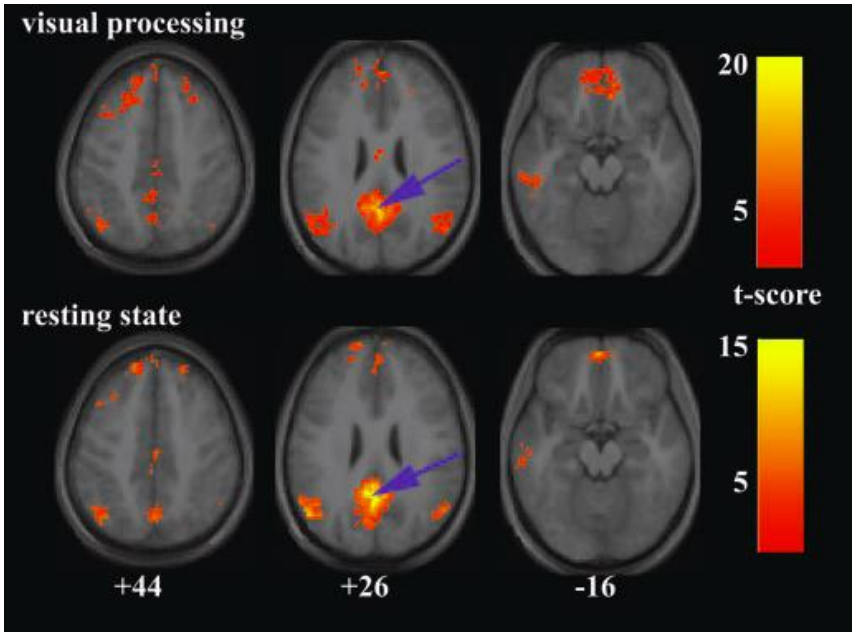
Tasks

- Resting state:
  - Eyes closed
  - do not think of anything in particular
- Visual processing
  - black-and-white radial checkerboard pattern

→ not highly demanding cognitive task

Visual processing and resting-state neural connectivity for the PCC

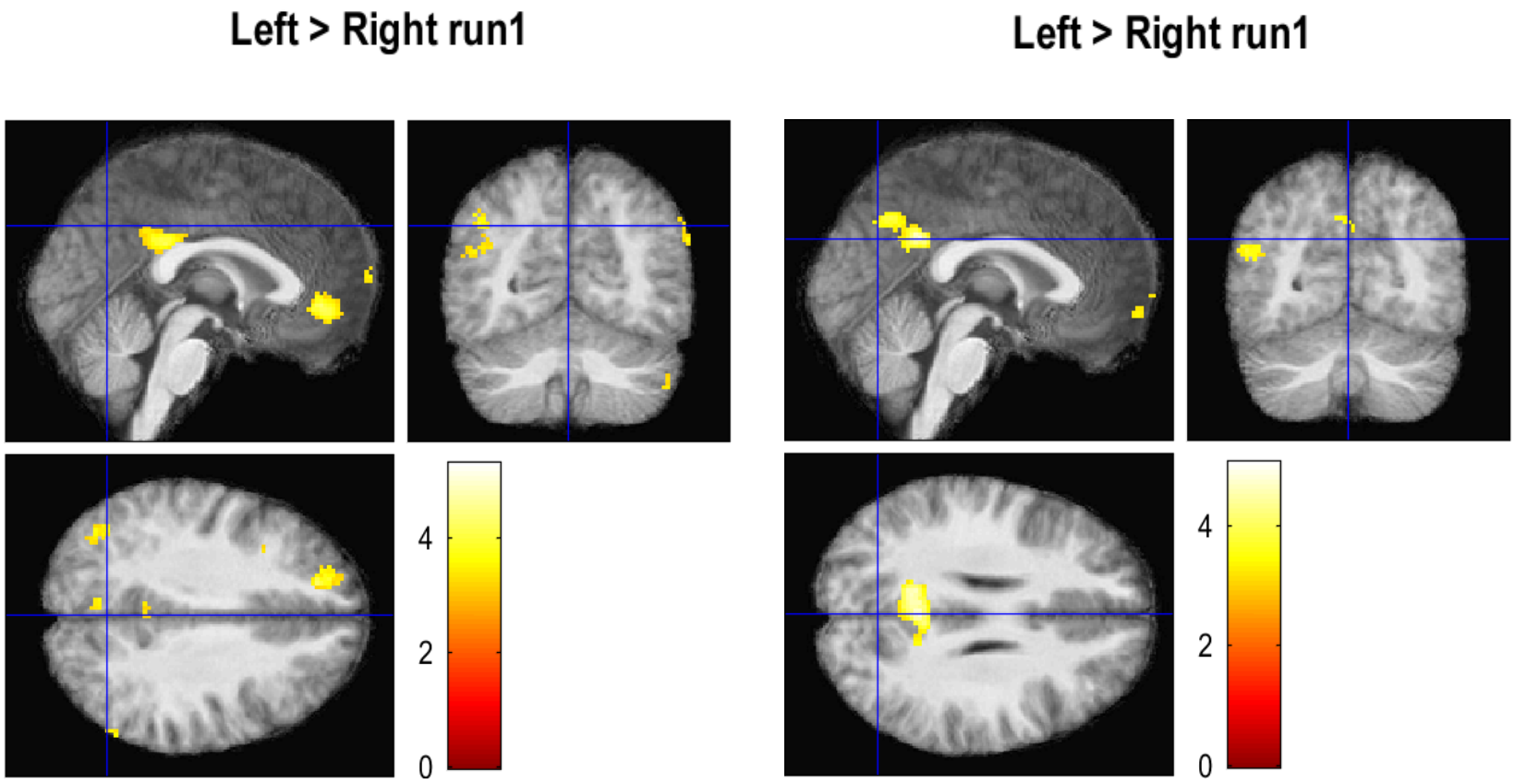
[-2 -51 27]



Greicius et al. (2003), *PNAS*

Sub03 and Sub04

Translational Neuromodeling Unit



Methods & Models 2018

p<0.05 FWE at cluster-level, with CDT:p<0.001

SPM interface: factorial design specification

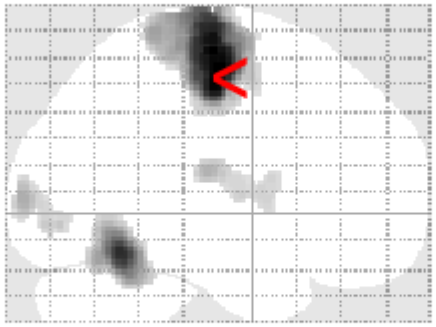
Options:

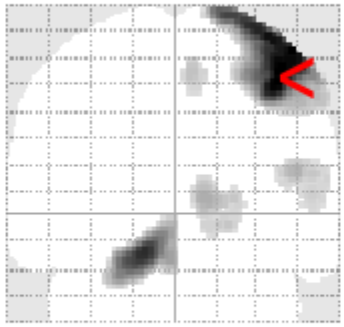
- FFX
- One-sample t-test
- Paired t-test
- One-way ANOVA – within subject
- Flexible factorial

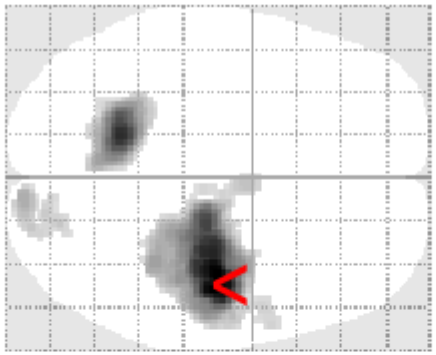
FFX:

Translational Neuromodeling Unit

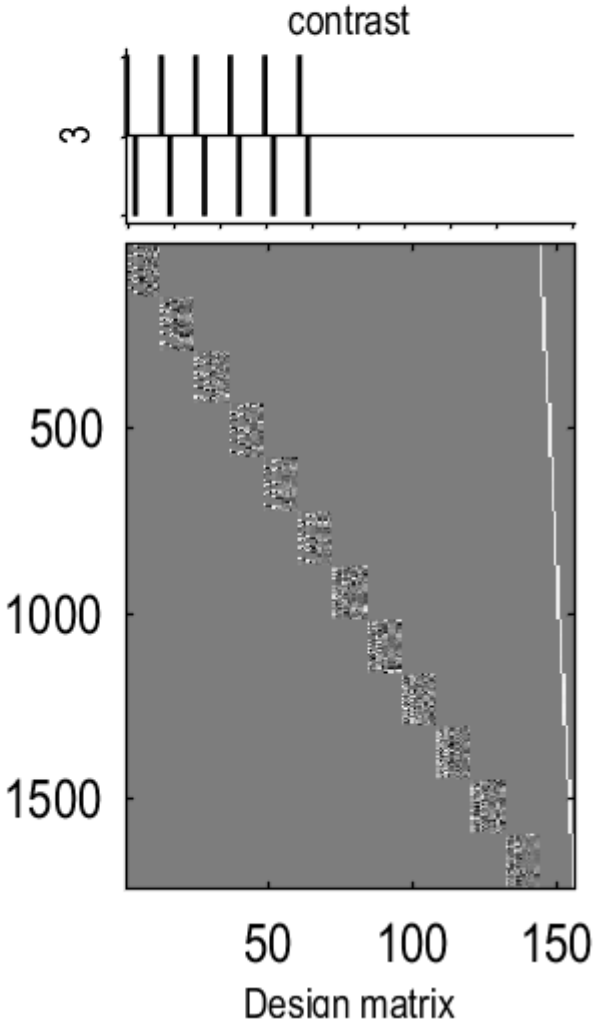
Left vs Right Arrow: block







SPM{T$_{1536}$}



SPMresults:.\Data2017\Group\FFX\Arrow_ffx

Height threshold T = 3.095547 {p<0.001 (unc.)}

Extent threshold k = 127 voxels

p<0.05 FWE at cluster-level, with CDT:p<0.001

One-sample t-test:

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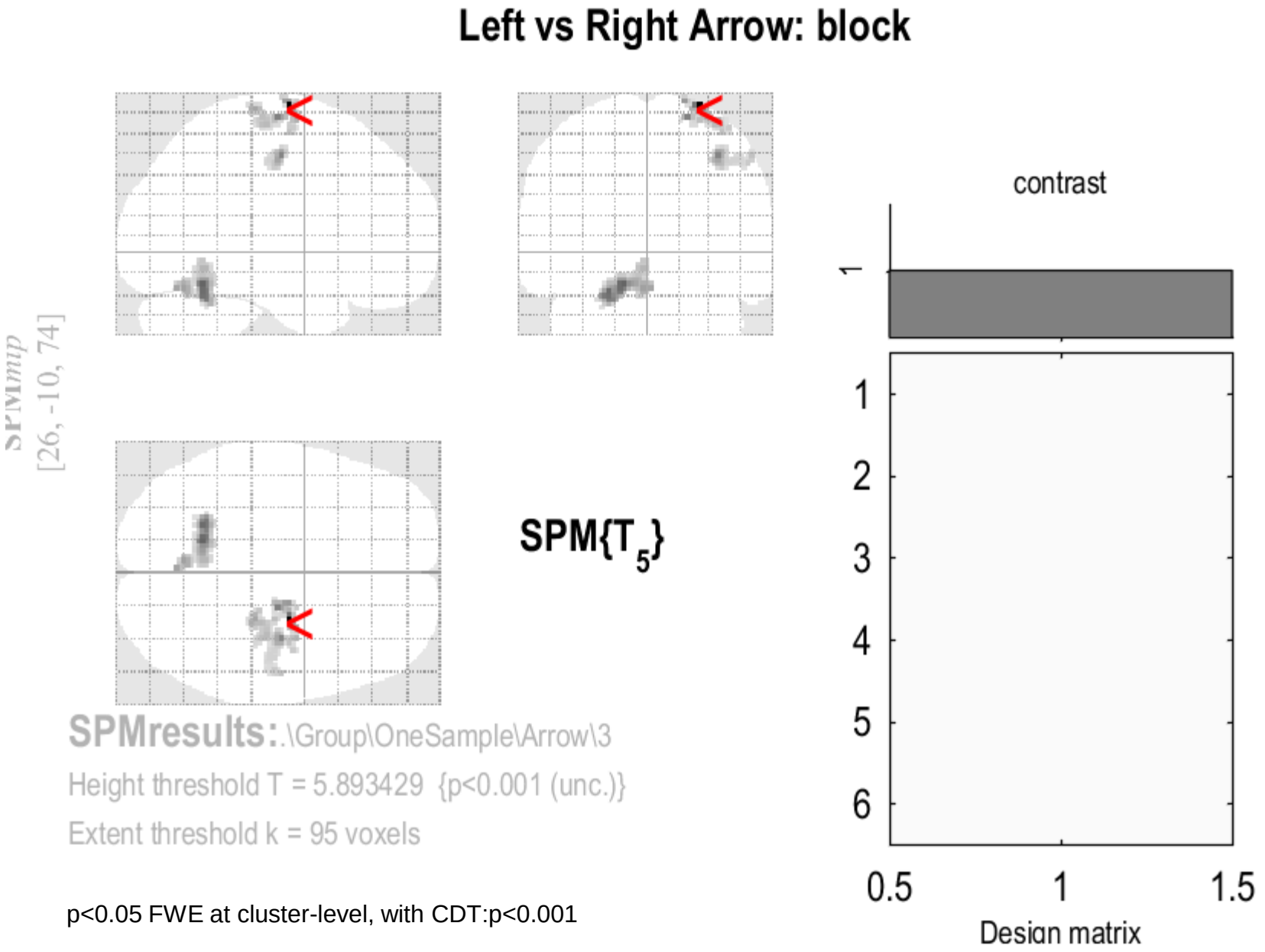
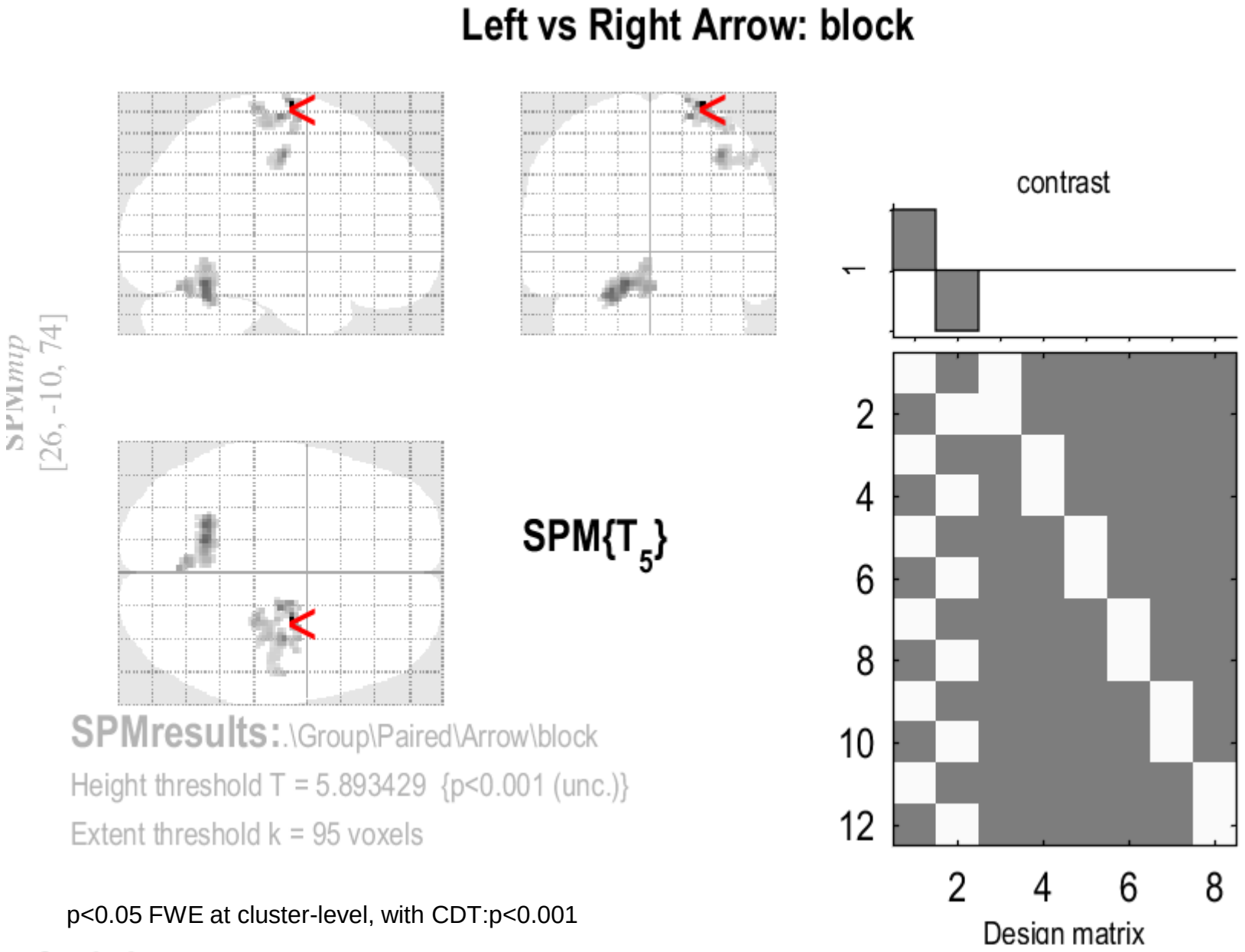


p<0.05 FWE at cluster-level, with CDT:p<0.001

Paired t-test:

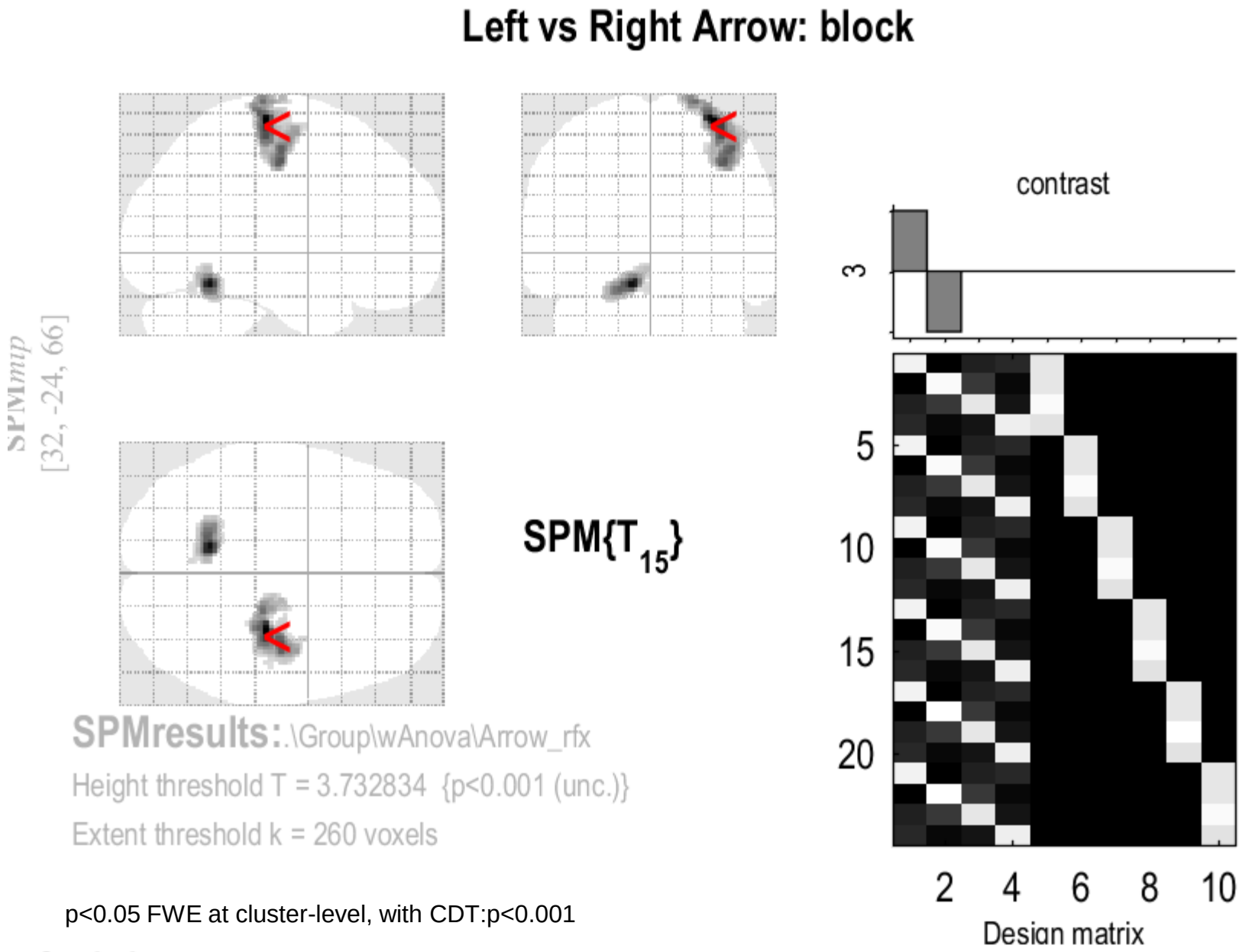
Translational Neuromodeling Unit



p<0.05 FWE at cluster-level, with CDT:p<0.001

wANOVA:

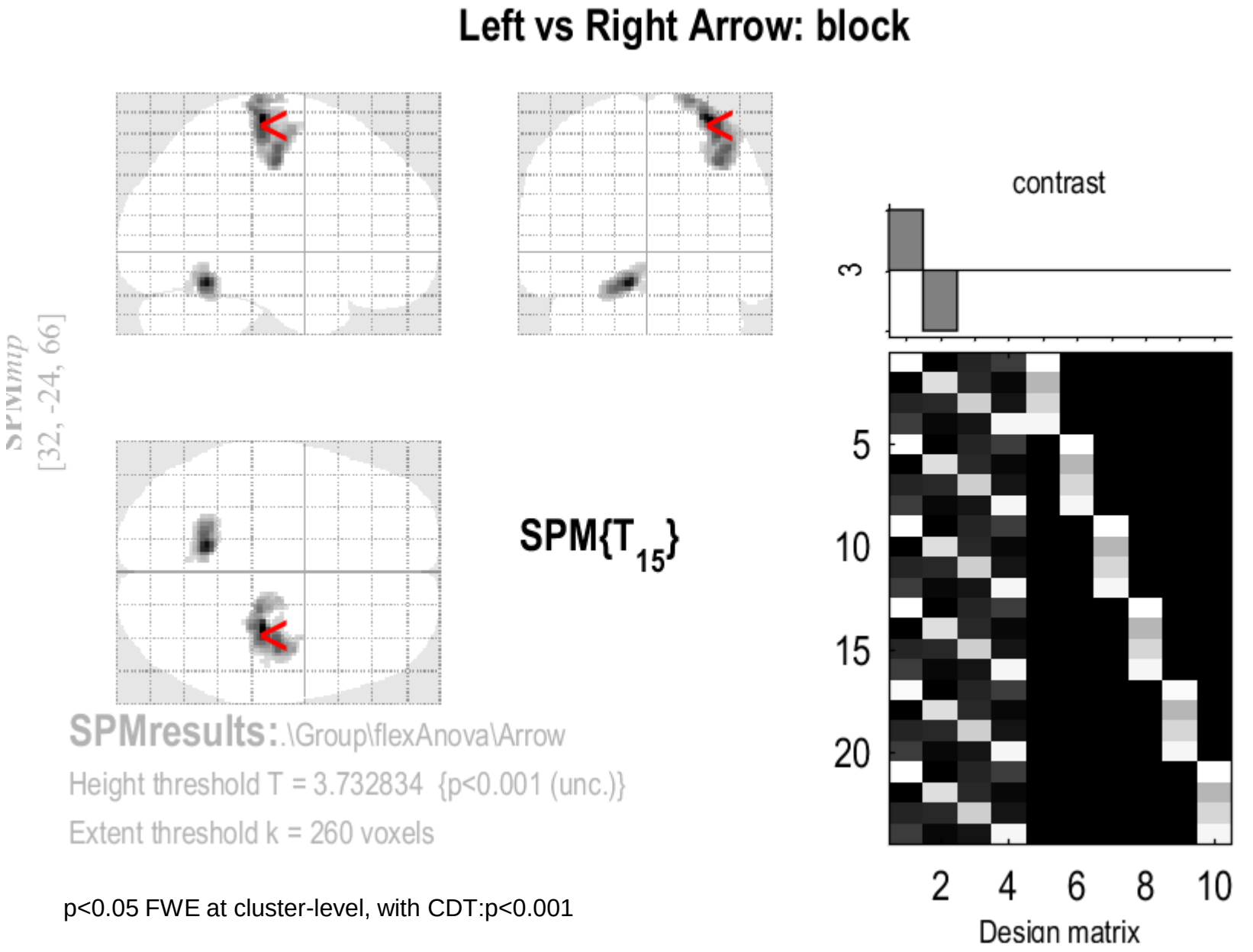
Translational Neuromodeling Unit



p<0.05 FWE at cluster-level, with CDT:p<0.001

flexANOVA:

Translational Neuromodeling Unit



p<0.05 FWE at cluster-level, with CDT:p<0.001

Sphericity specification:

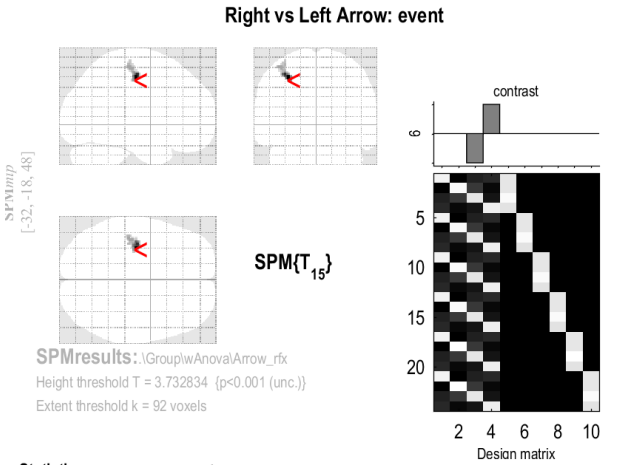
Compare one-way within-subject ANOVA using:

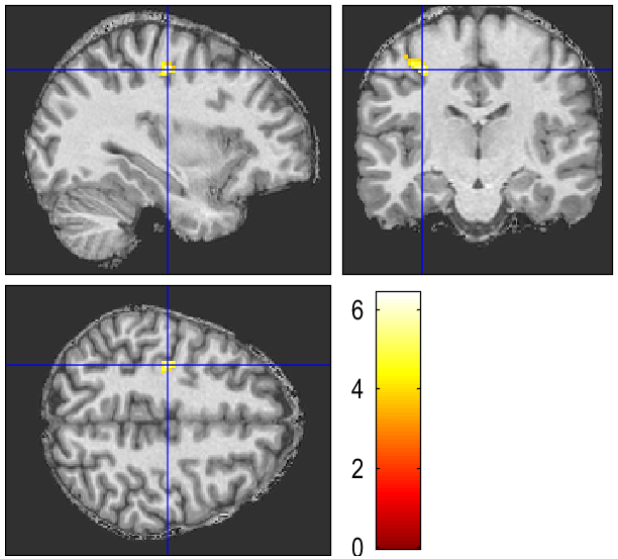
- correct sphericity specification vs.
- wrong sphericity specification

Sphericity specification:

Translational Neuromodeling Unit

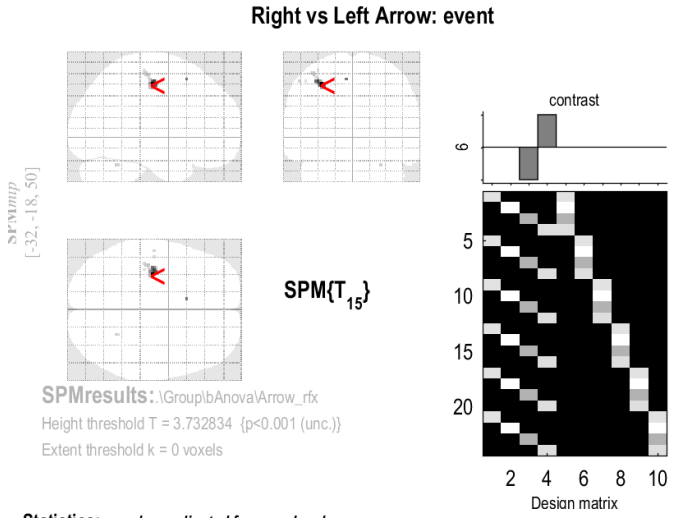
correct sphericity specification





p<0.05 FWE at cluster-level, with CDT:p<0.001

wrong sphericity specification



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	$(Z_{=})$	p_{uncorr}			
1.000	7	0.458	0.149	36	0.021	0.877	0.582	5.69	4.09	0.000	-32	-18	50
		1.000	0.702	1	0.702	1.000	0.778	4.66	3.61	0.000	-8	16	54
		1.000	0.702	5	0.356	1.000	0.984	4.01	3.25	0.001	-40	-22	58
		1.000	0.702	2	0.571	1.000	0.984	3.88	3.18	0.001	26	-54	-28
		1.000	0.702	1	0.702	1.000	0.984	3.87	3.17	0.001	-54	-16	52
		1.000	0.702	1	0.702	1.000	0.984	3.77	3.11	0.001	-48	-16	52
		1.000	0.702	1	0.702	1.000	0.984	3.75	3.10	0.001	-36	-26	62