Methods & Models for fMRI Analysis 2019

TUTORIAL

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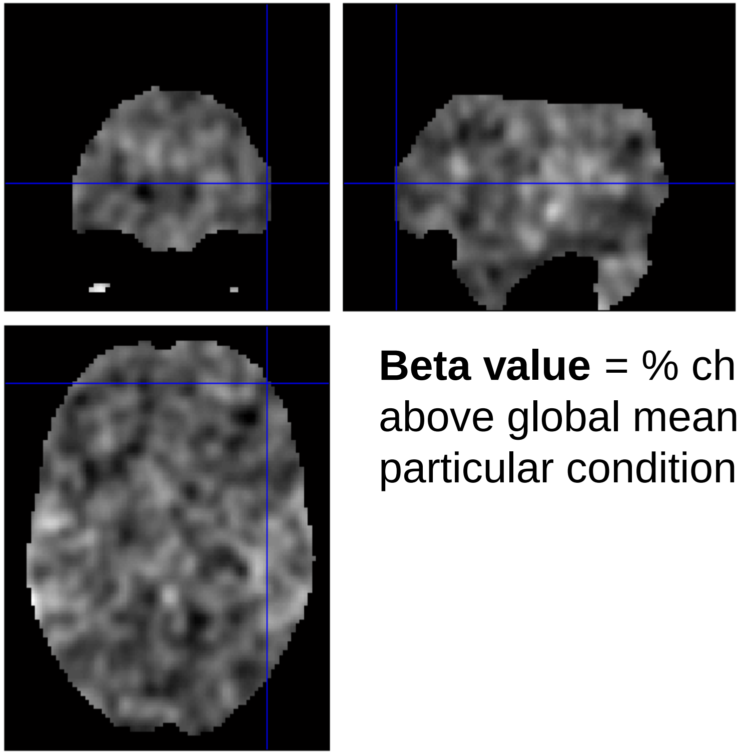
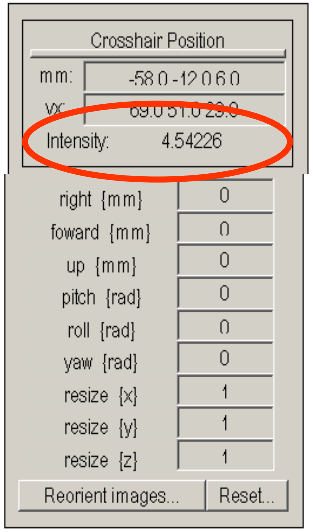
Swiss Federal Institute of Technology Zurich

Translational Neuromodeling Unit



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



Crosshair Position

mm: -58.0 -12.0 6.0

vx: 69.0 51.0 29.0

Intensity: 4.54226

right {mm}	0
foward {mm}	0
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roll {rad}	0
yaw {rad}	0
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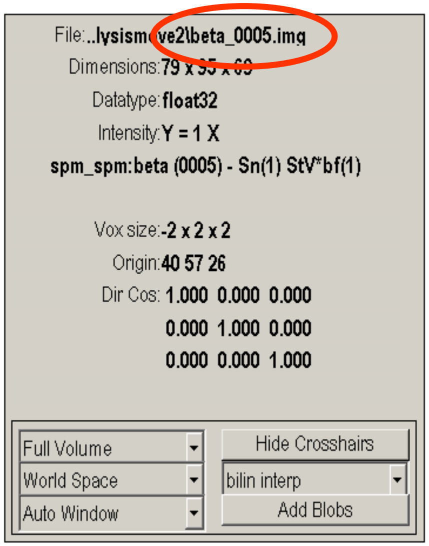
resize {y}	1
resize {z}	1



File:..lysismove2\beta_0005.img

Dimensions: 79 x 95 x 69

Datatype: float32

Intensity: Y = 1 X

spm_spm:beta (0005) - Sn(1) StV*bf(1)

Vox size: -2 x 2 x 2

Origin: 40 57 26

Dir Cos: 1.000 0.000 0.000
0.000 1.000 0.000
0.000 0.000 1.000

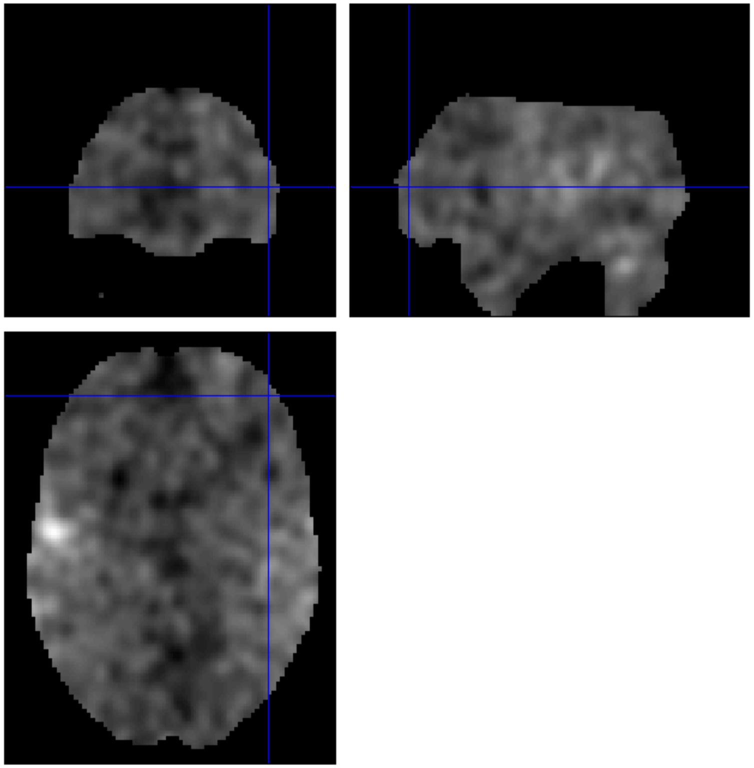
Full Volume

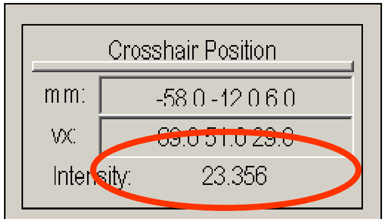
World Space

Auto Window

bilin interp

t



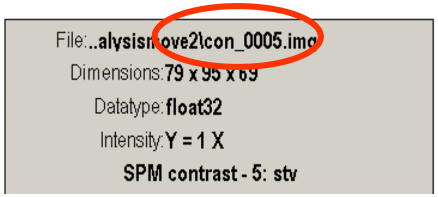


Crosshair Position

mm: -58.0 -12.0 6.0

vx: 69.0 51.0 29.0

Intensity: 23.356



File:..alysismove2\con_0005.img

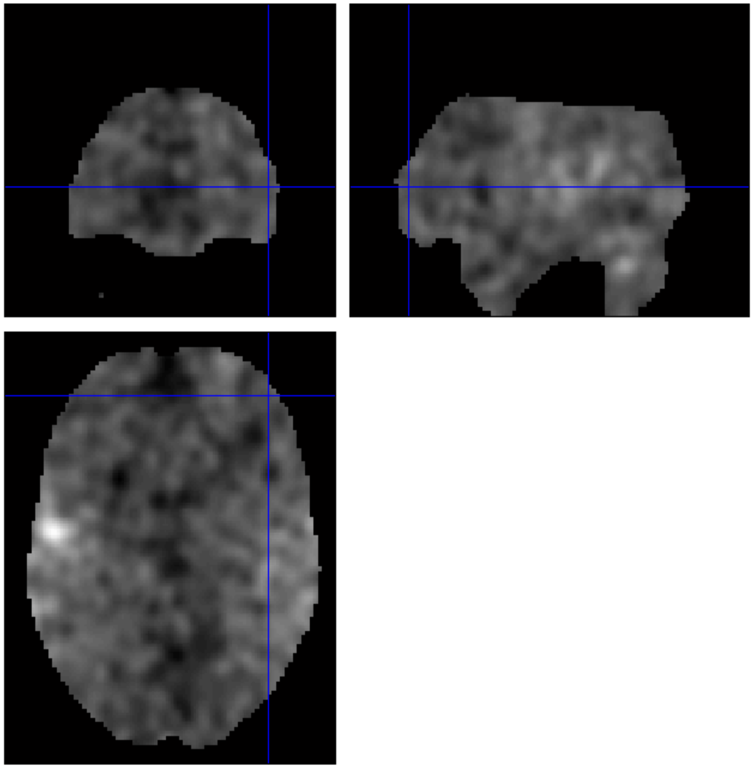
Dimensions: 79 x 95 x 69

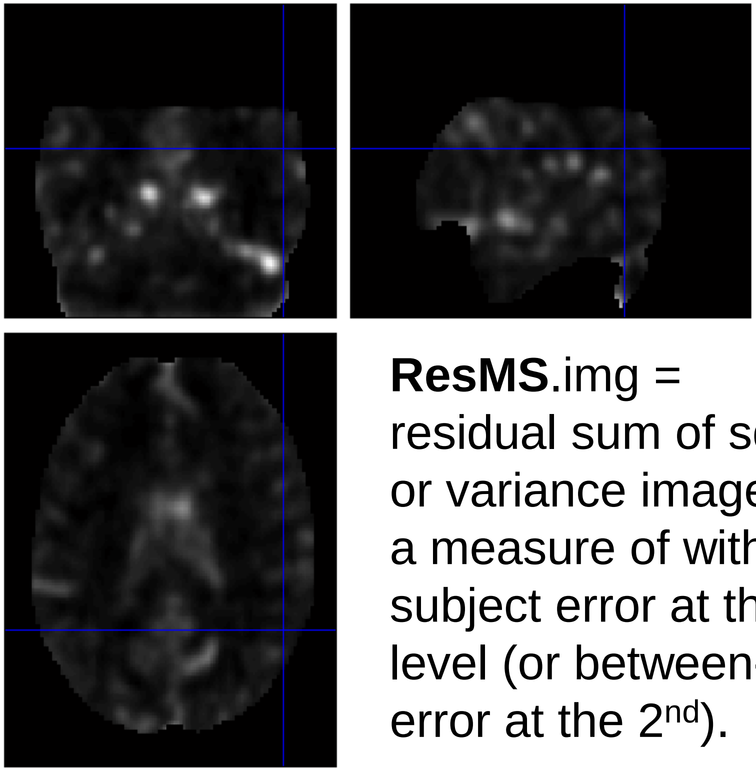
Datatype: float32

Intensity: Y = 1 X

SPM contrast - 5: stv

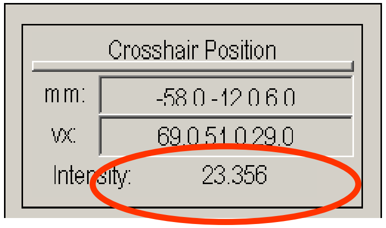
Con. value = summation of all relevant betas.





$\hat{\sigma}_i^2$

ResMS.img = 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).

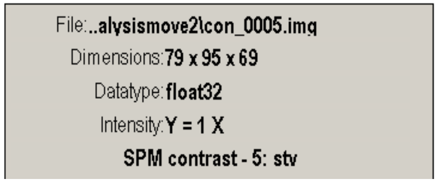


Crosshair Position

mm: -58.0 -12.0 6.0

vx: 69.0 51.0 29.0

Intensity: 23.356



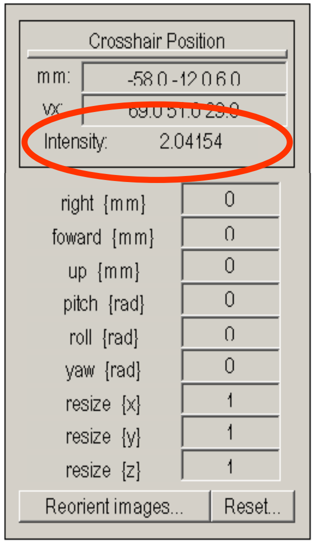
File: ..alysismove2\con_0005.img

Dimensions: 79 x 95 x 69

Datatype: float32

Intensity: Y = 1 X

SPM contrast - 5: stv



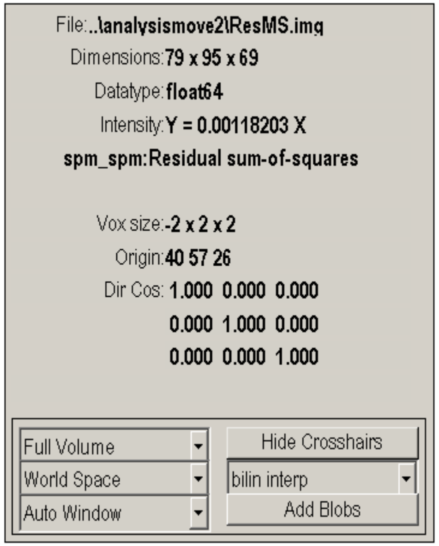
Crosshair Position

mm: -58.0 -12.0 6.0

vx: 69.0 51.0 29.0

Intensity: 2.04154

right {mm}	0
foward {mm}	0
up {mm}	0
pitch {rad}	0
roll {rad}	0
yaw {rad}	0
resize {x}	1
resize {y}	1
resize {z}	1



File: ..\analysismove2\ResMS.img

Dimensions: 79 x 95 x 69

Datatype: float64

Intensity: Y = 0.00118203 X

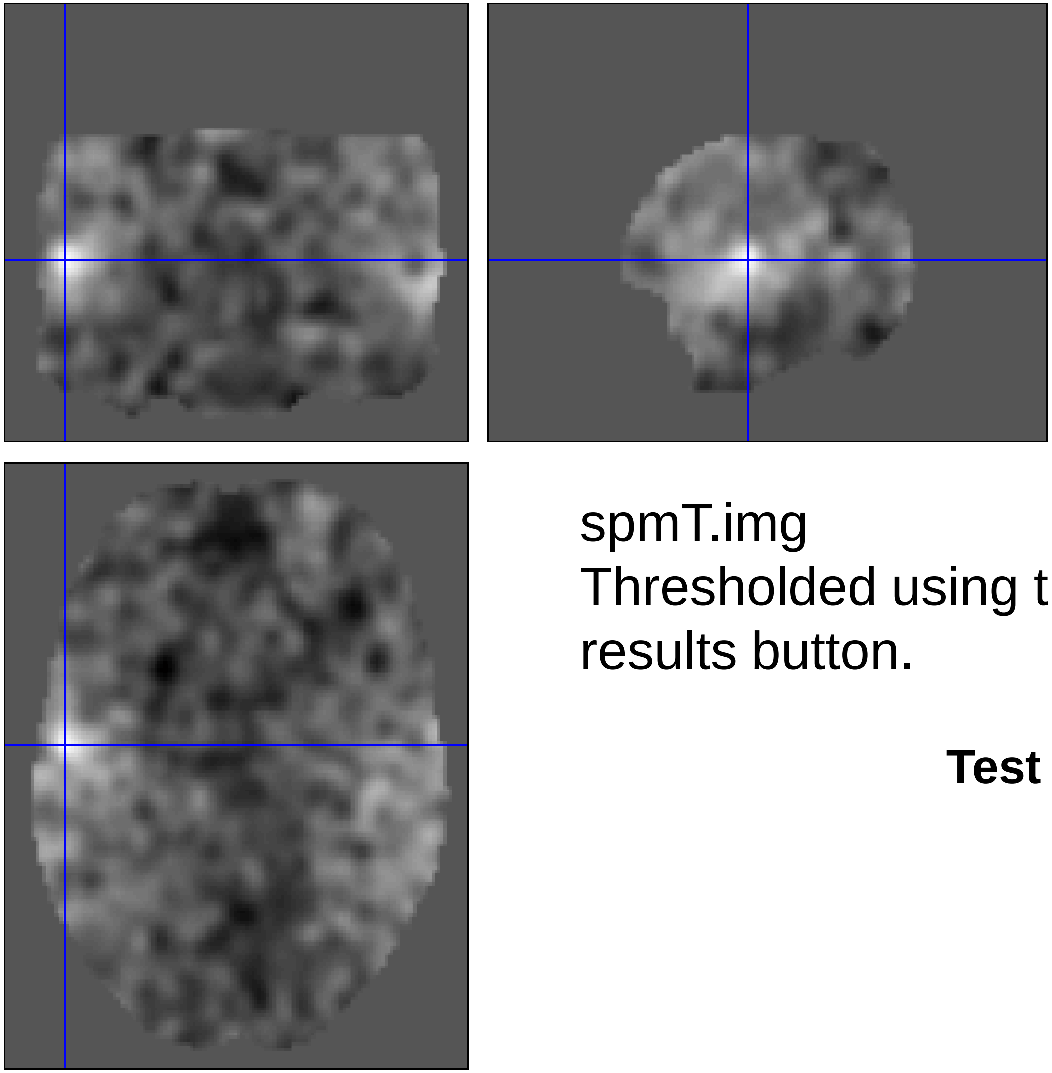
spm_spm:Residual sum-of-squares

Vox size: -2 x 2 x 2

Origin: 40 57 26

Dir Cos: 1.000 0.000 0.000
0.000 1.000 0.000
0.000 0.000 1.000

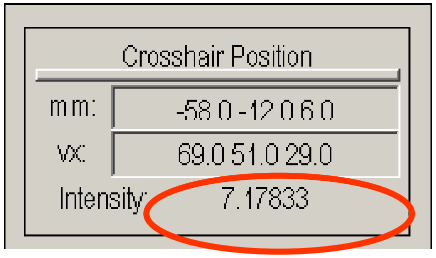
Con. value is combined with ResMS value at that voxel to produce a T statistic or spm.T.img.



spmT.img
Thresholded using the
results button.

Test statistic:

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

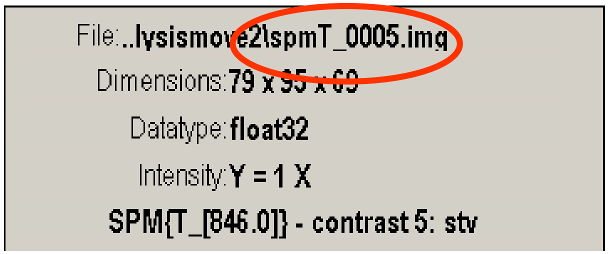


Crosshair Position

mm: -58.0 -12.0 6.0

vx: 69.0 51.0 29.0

Intensity: 7.17833



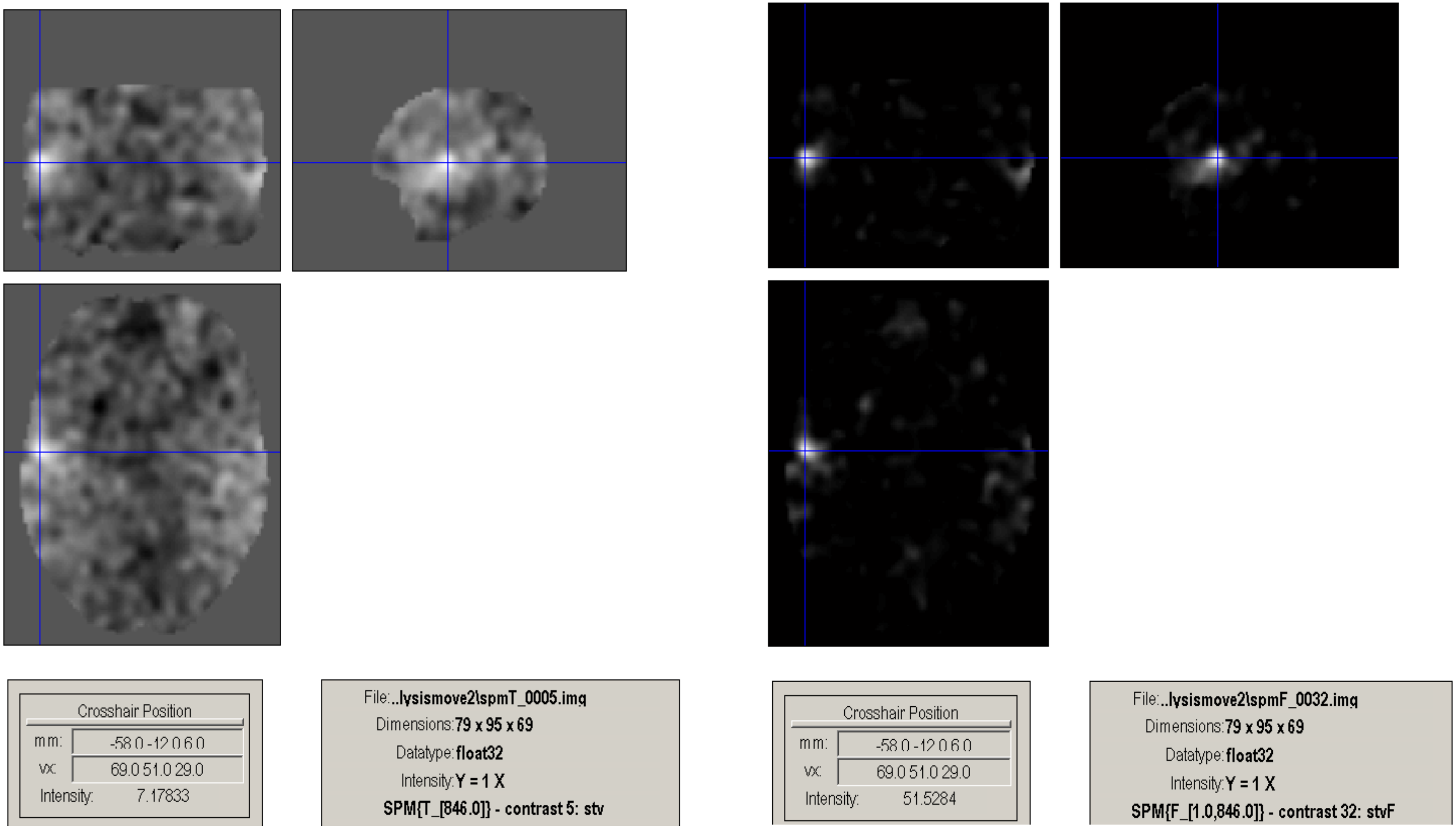
File:..lysismove2\spmT_0005.img

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: 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

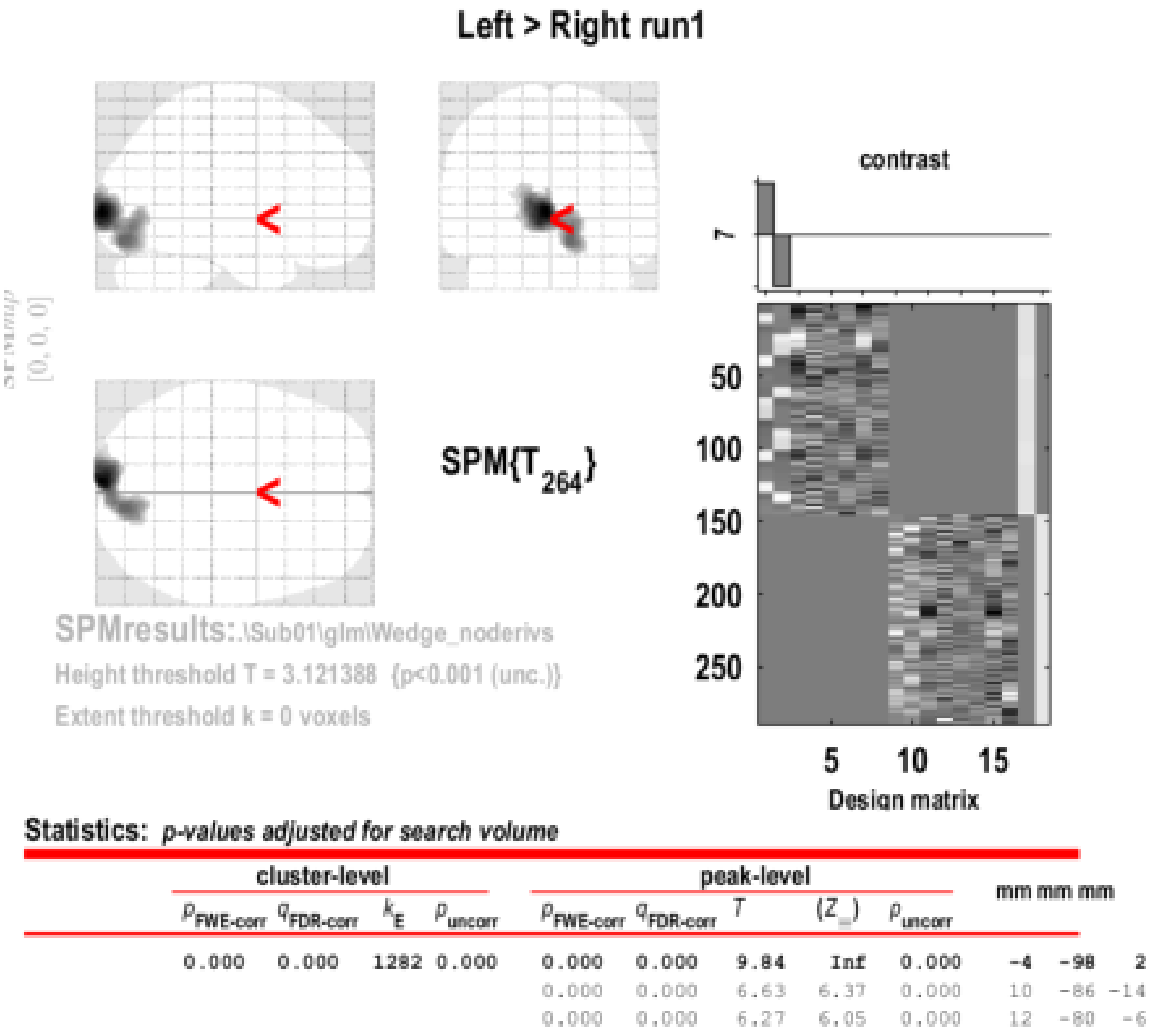
Dimensions: 79 x 95 x 69

Datatype: float32

Intensity: Y = 1 X

SPM{F_[1.0,846.0]} - contrast 32: stvF

spmT.img and corresponding spmF.img



Left > Right run1

SPM{T_{264}}

SPMresults: .\Sub01\glm\Wedge_noderivs

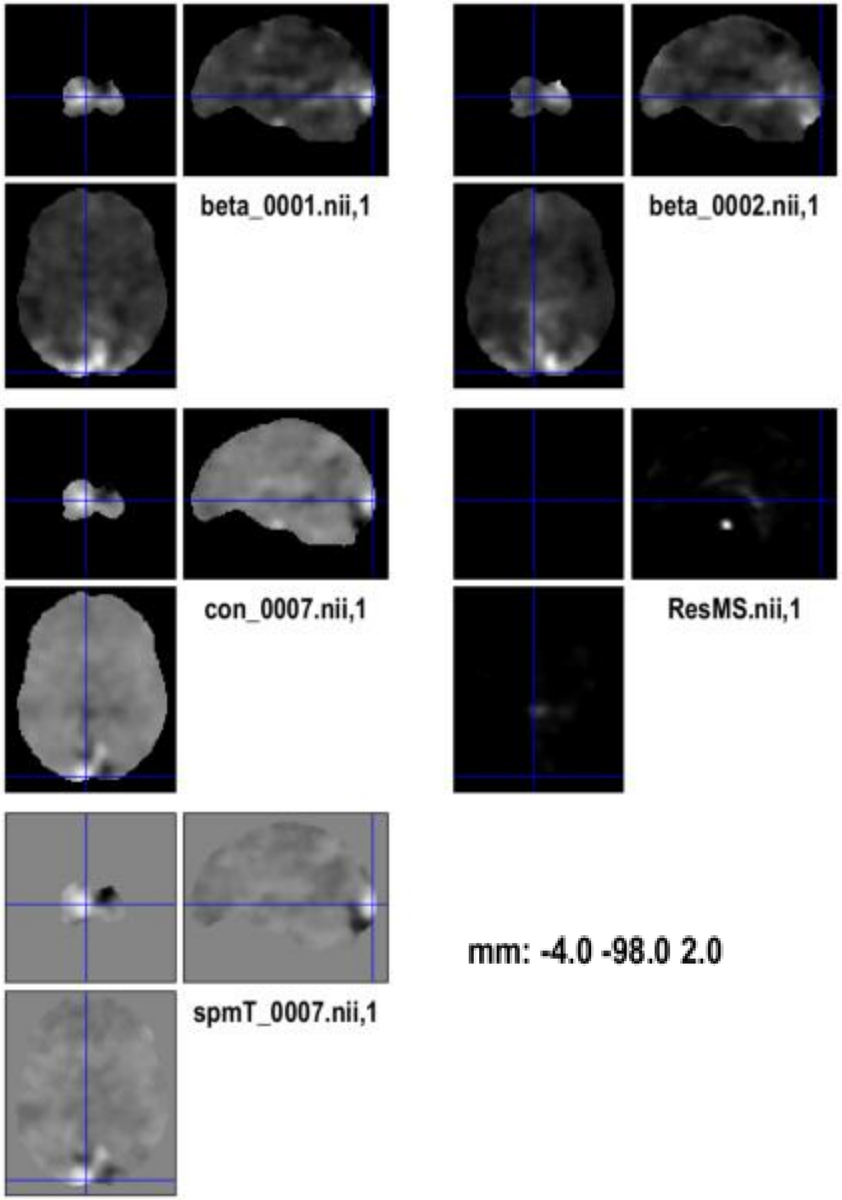
Height threshold T = 3.121388 {p<0.001 (unc.)}

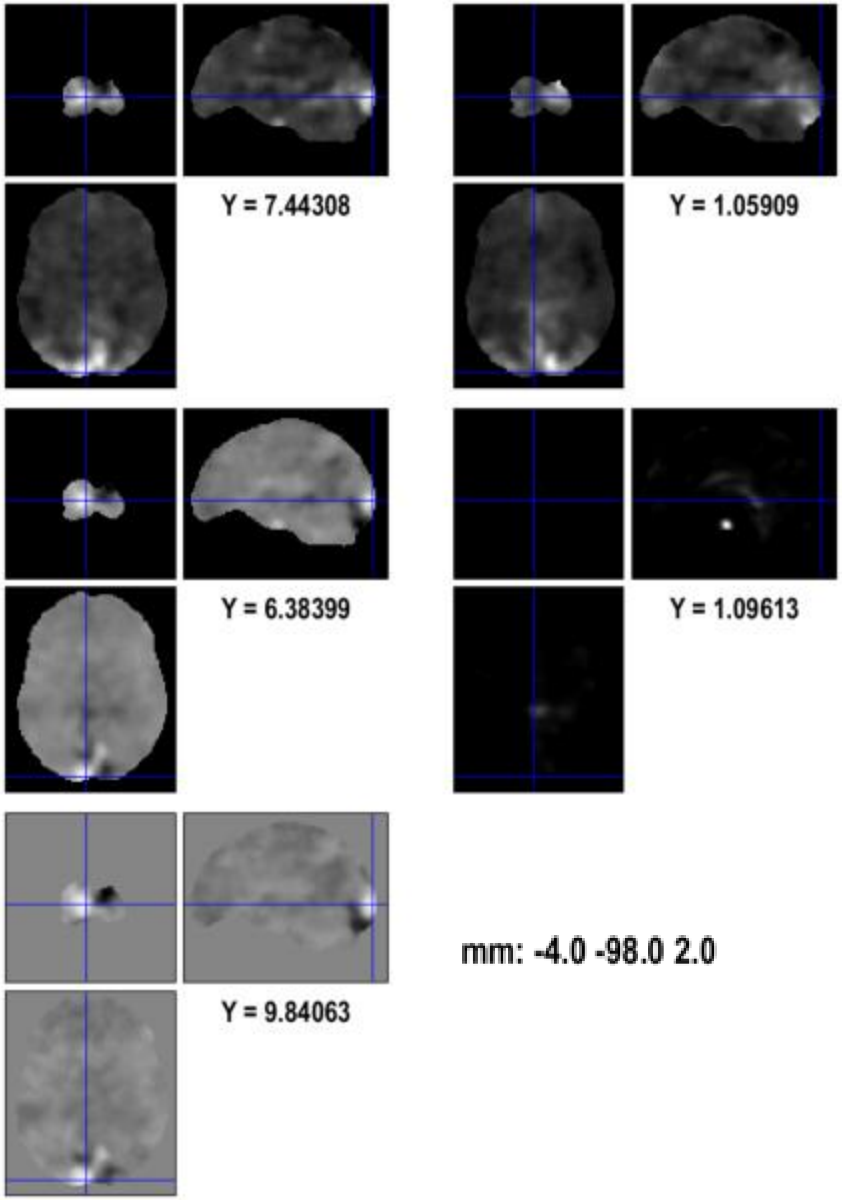
Extent threshold k = 0 voxels

Statistics: *p-values adjusted for search volume*

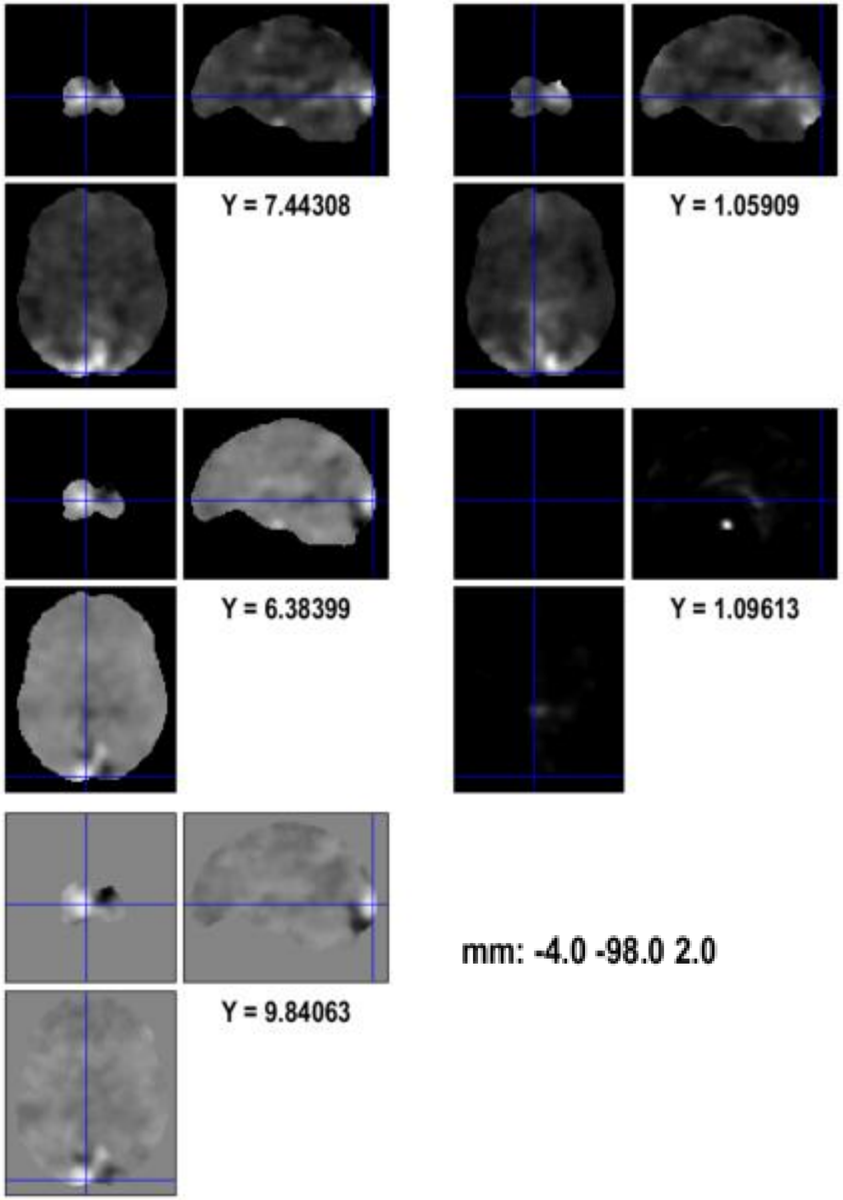
cluster-level				peak-level					mm mm mm		
$p_{FWE\text{-}corr}$	$q_{FDR\text{-}corr}$	k_E	p_{uncorr}	$p_{FWE\text{-}corr}$	$q_{FDR\text{-}corr}$	T	$(Z_{\equiv})$	p_{uncorr}			
0.000	0.000	1282	0.000	0.000	0.000	9.84	Inf	0.000	-4	-98	2
				0.000	0.000	6.63	6.37	0.000	10	-86	-14
				0.000	0.000	6.27	6.05	0.000	12	-80	-6

spm_contrasts.m → Compute SPM{t} image line 213





spm_contrasts.m → Compute SPM{t} image line 213



c = contrast weights
c=[1 -1 zeros(1,16)]

ResMS_intensity = 1.09613
con_image_intensity = 6.38399

Vc=c*SPM.xX.Bcov*c'
SE = sqrt(Vc*ResMS_intensity)
con_image_intensity/SE

So, which images?

- **beta images** contain information about the size of the effect of interest.
- Information about the error variance is held in the **ResMS.img**.
- beta images are linearly combined to produce relevant **con.img.**
- The design matrix, contrast, constant and ResMS.img are subjected to matrix multiplication to produce an estimate of the st.dev. associated with each voxel in the con.img.
- The **spmT.img** are derived from this and are thresholded in the results step.

Worth to check:

Review Design
- Matrix
- Orthogonality

Explore Design:
- Sessions

mask.nii

Correlation among regressors:

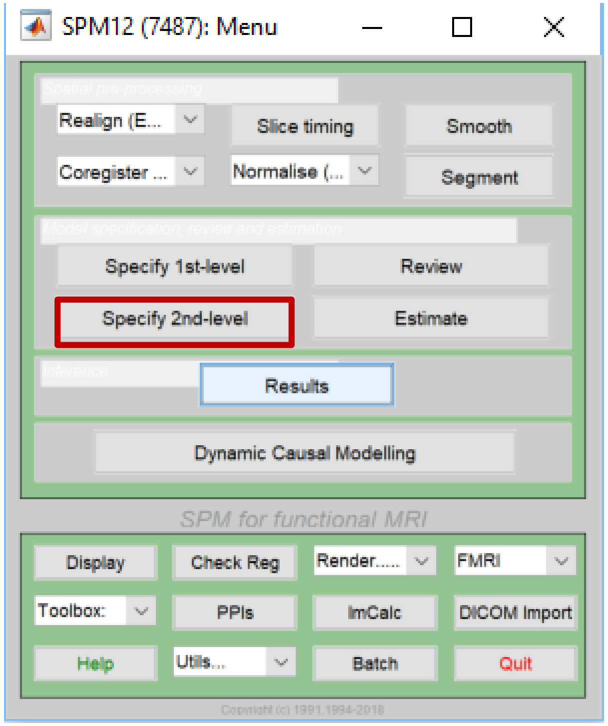
```
%% SPM.xX.xKXs.X: matrix of trials and betas (columns) in each trial
%%  R=corrcoef(X) calculates a matrix R of correlation coefficients
corr_pre=corrcoef(SPM.xX.X);
figure; imagesc(corr_pre, [-1 1]);colorbar
%% after whitening:
corr=corrcoef(SPM.xX.xKXs.X);
figure; imagesc(corr, [-1 1]);colorbar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

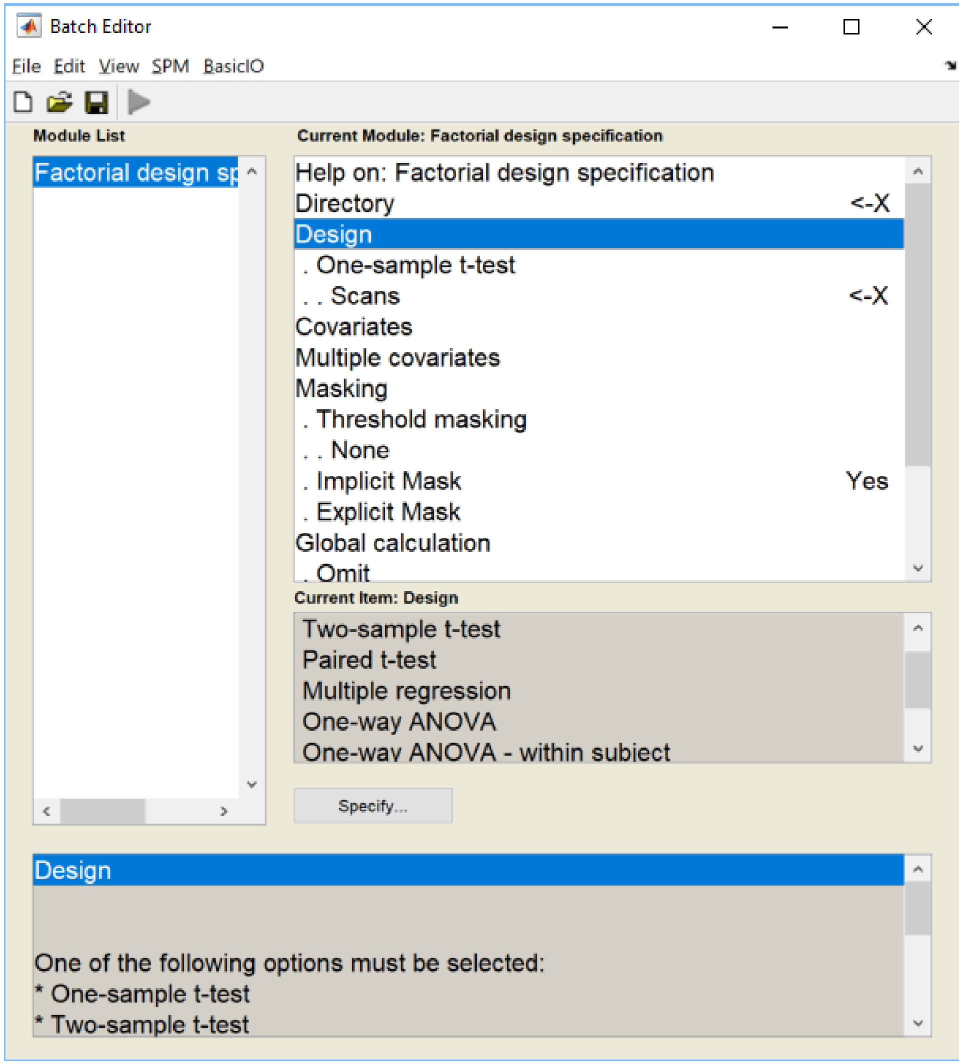
SPM interface: factorial design specification

Options:

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

SPM interface: factorial design specification





Current Module: Factorial design specification

Help on: Factorial design specification
Directory <-X
Design
. One-sample t-test
. . Scans <-X
Covariates
Multiple covariates
Masking
. Threshold masking
. . None
. Implicit Mask Yes
. Explicit Mask
Global calculation
. Omit

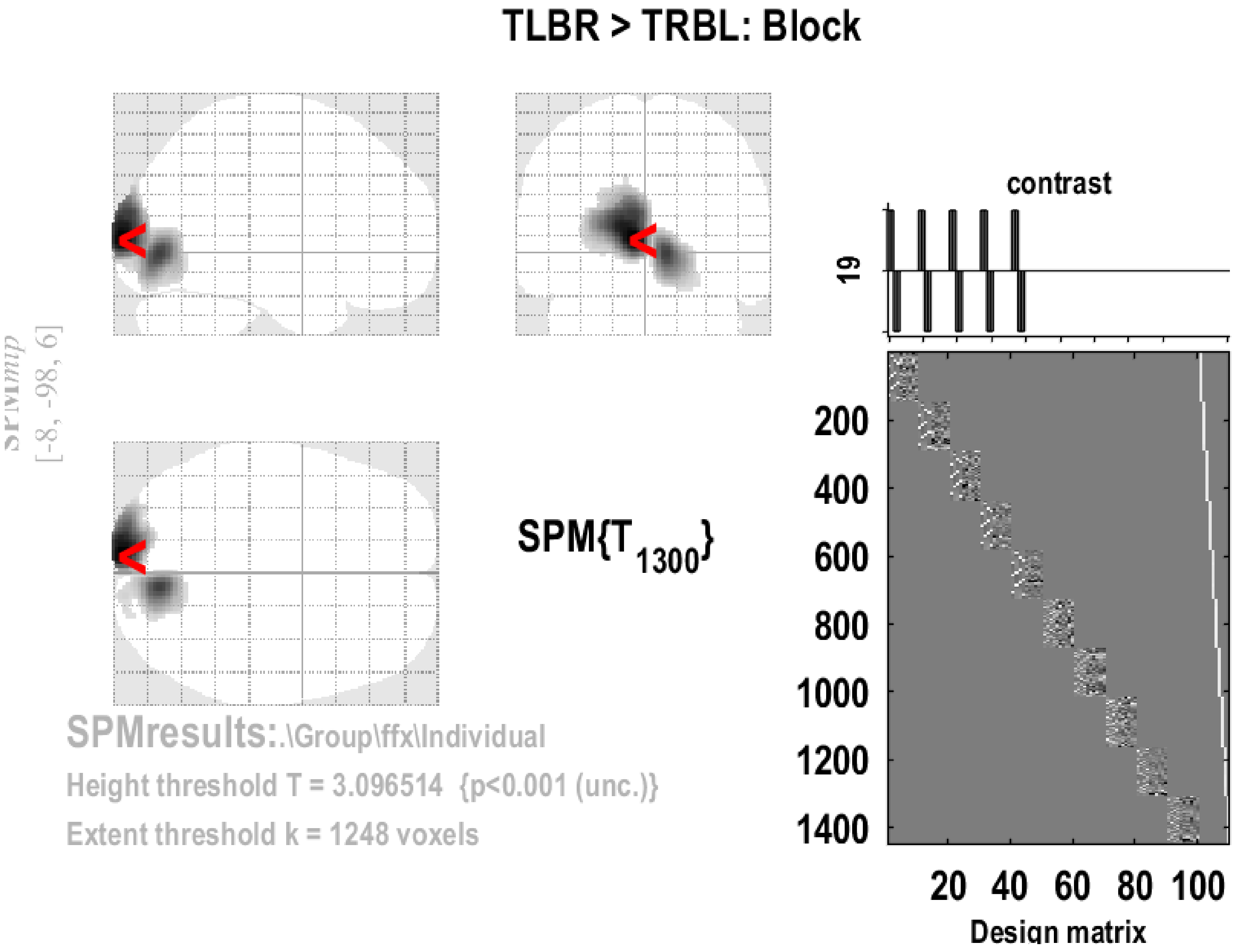
Current Item: Design

Two-sample t-test
Paired t-test
Multiple regression
One-way ANOVA
One-way ANOVA - within subject

Design

One of the following options must be selected:
* One-sample t-test
* Two-sample t-test

FFX:



TLBR > TRBL: Block

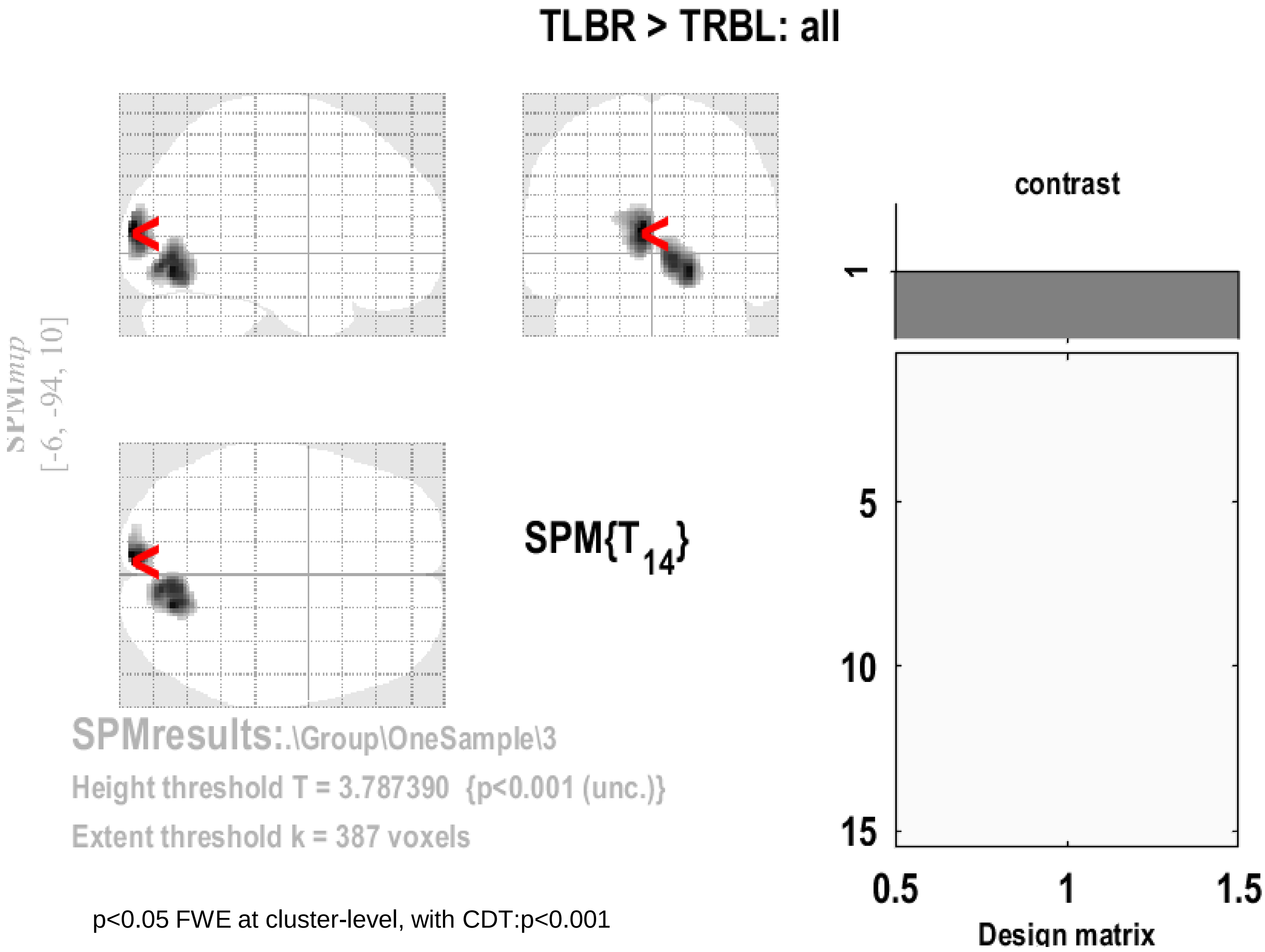
SPMresults:.\Group\ffx\Individual

Height threshold T = 3.096514 {p<0.001 (unc.)}

Extent threshold k = 1248 voxels

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

One-sample t-test:



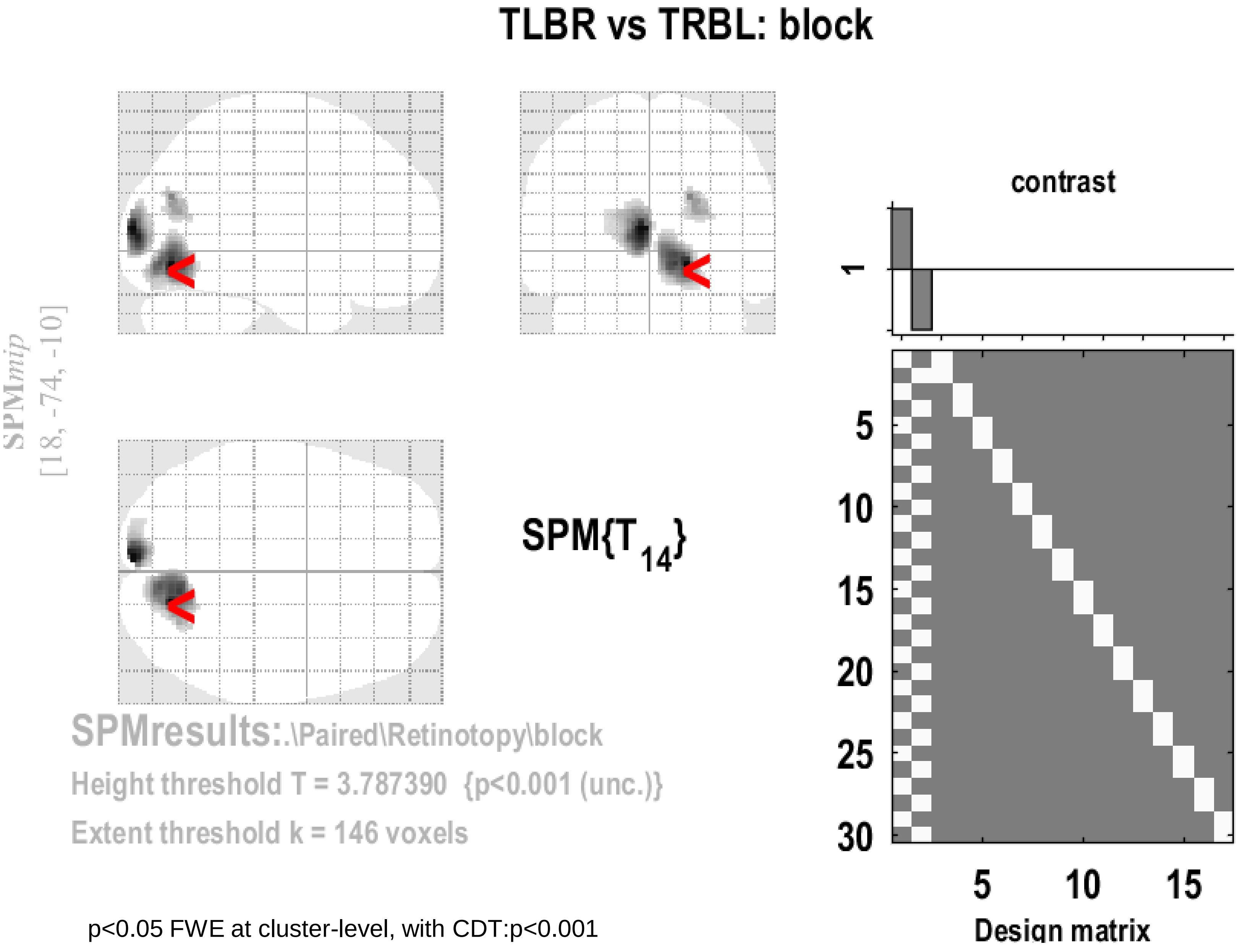
SPMresults:.\Group\OneSample\3

Height threshold T = 3.787390 {p<0.001 (unc.)}

Extent threshold k = 387 voxels

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

Paired t-test:



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

wANOVA:

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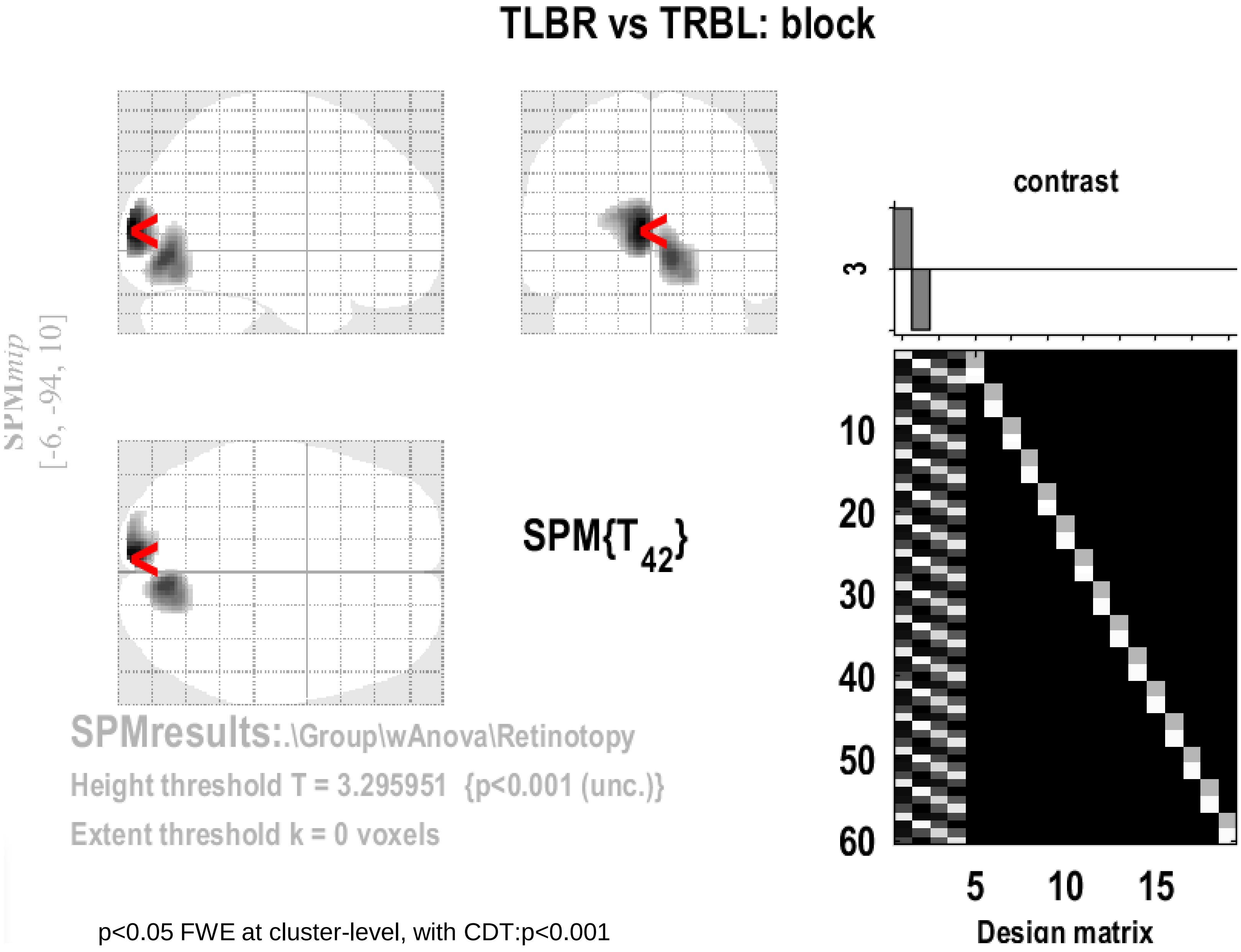


TLBR vs TRBL: block

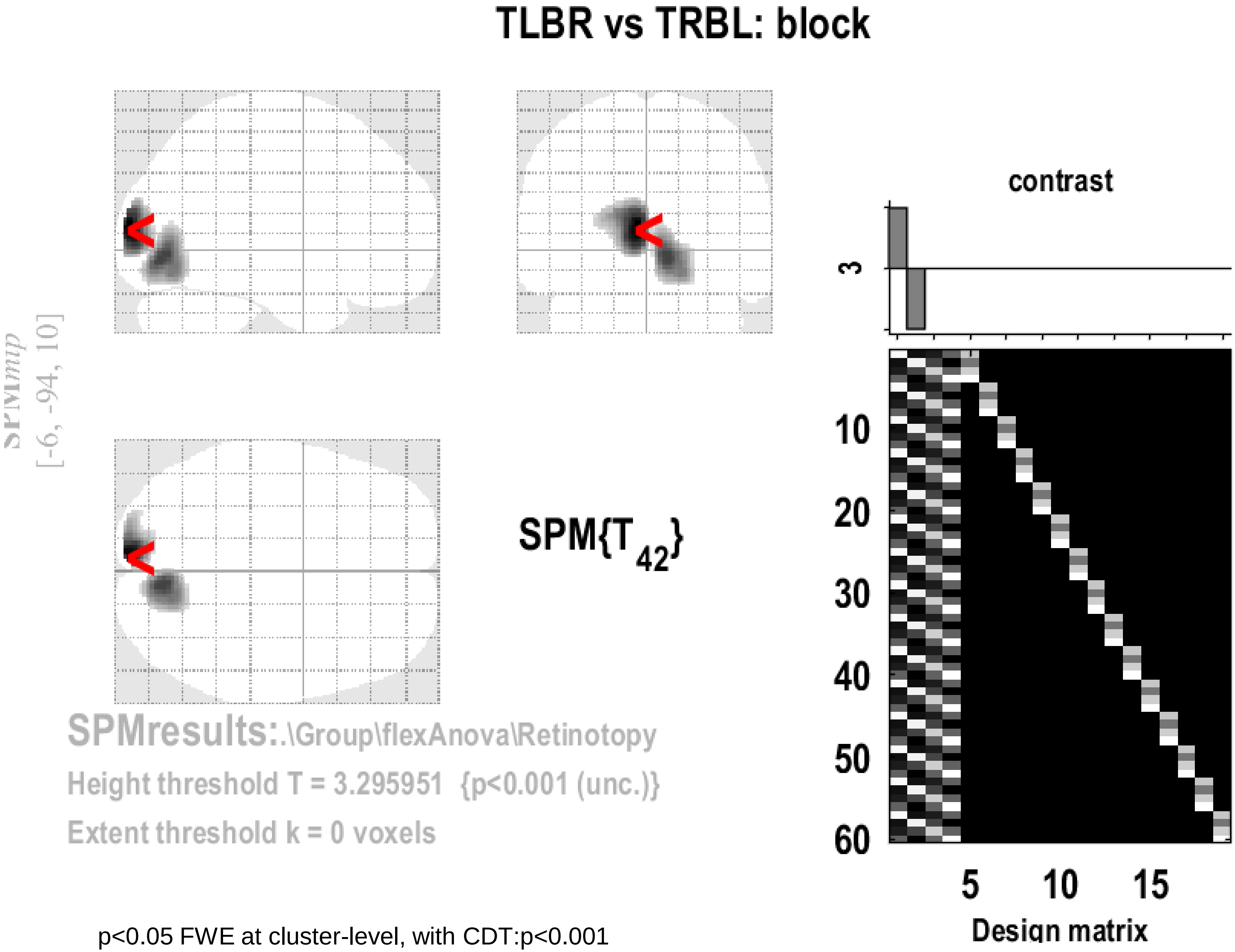
SPMresults:.\Group\wAnova\Retinotopy

Height threshold T = 3.295951 {p<0.001 (unc.)}

Extent threshold k = 0 voxels

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

flexANOVA:



TLBR vs TRBL: block

SPMresults:.\Group\flexAnova\Retinotopy

Height threshold T = 3.295951 {p<0.001 (unc.)}

Extent threshold k = 0 voxels

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

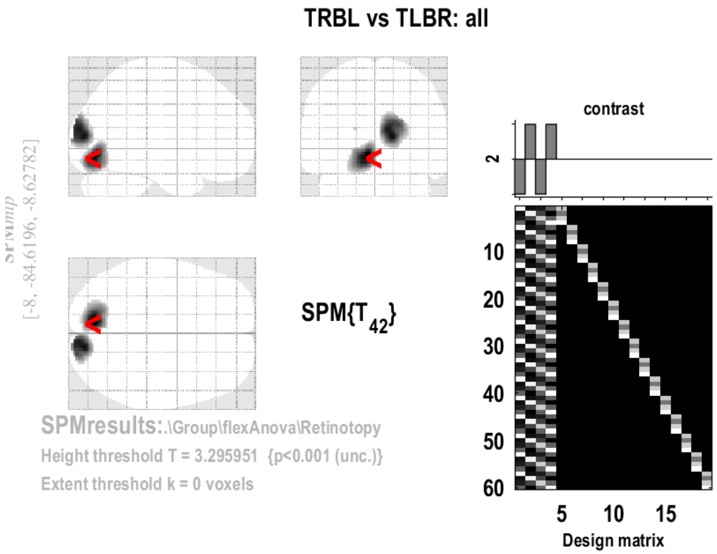
Importance of sphericity specification:

Compare one-way within-subject ANOVA using:

- correct sphericity specification vs.
- wrong sphericity specification

Sphericity specification:

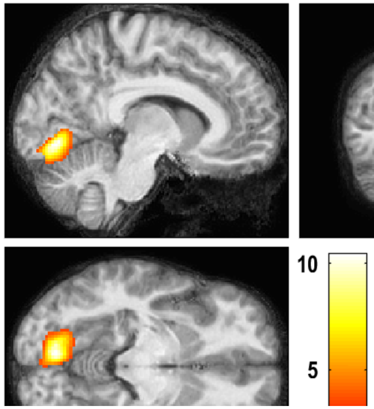
correct sphericity specification

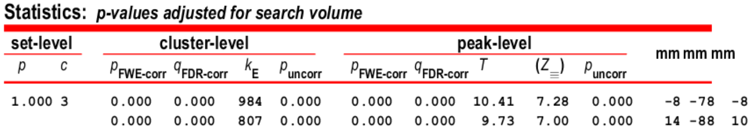


SPMresults:.\Group\flexAnova\Retinotopy

Height threshold T = 3.295951 {p<0.001 (unc.)}

Extent threshold k = 0 voxels

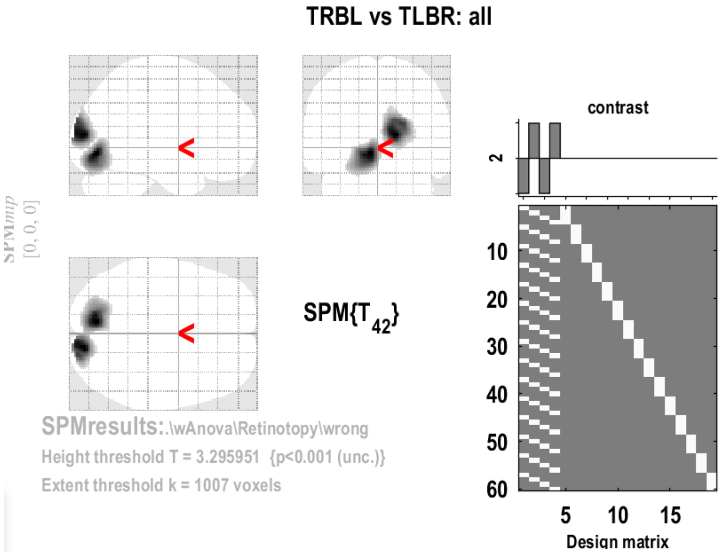




Statistics: *p-values adjusted for search volume*

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	$(Z_\equiv)$	p_{uncorr}	
1.000	3	0.000	0.000	984	0.000	0.000	0.000	10.41	7.28	0.000	-8 -78 -8
		0.000	0.000	807	0.000	0.000	0.000	9.73	7.00	0.000	14 -88 10

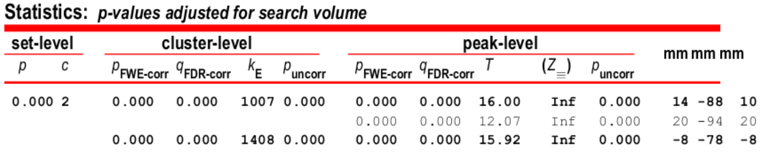
wrong sphericity specification



SPMresults:.\wAnova\Retinotopy\wrong

Height threshold T = 3.295951 {p<0.001 (unc.)}

Extent threshold k = 1007 voxels



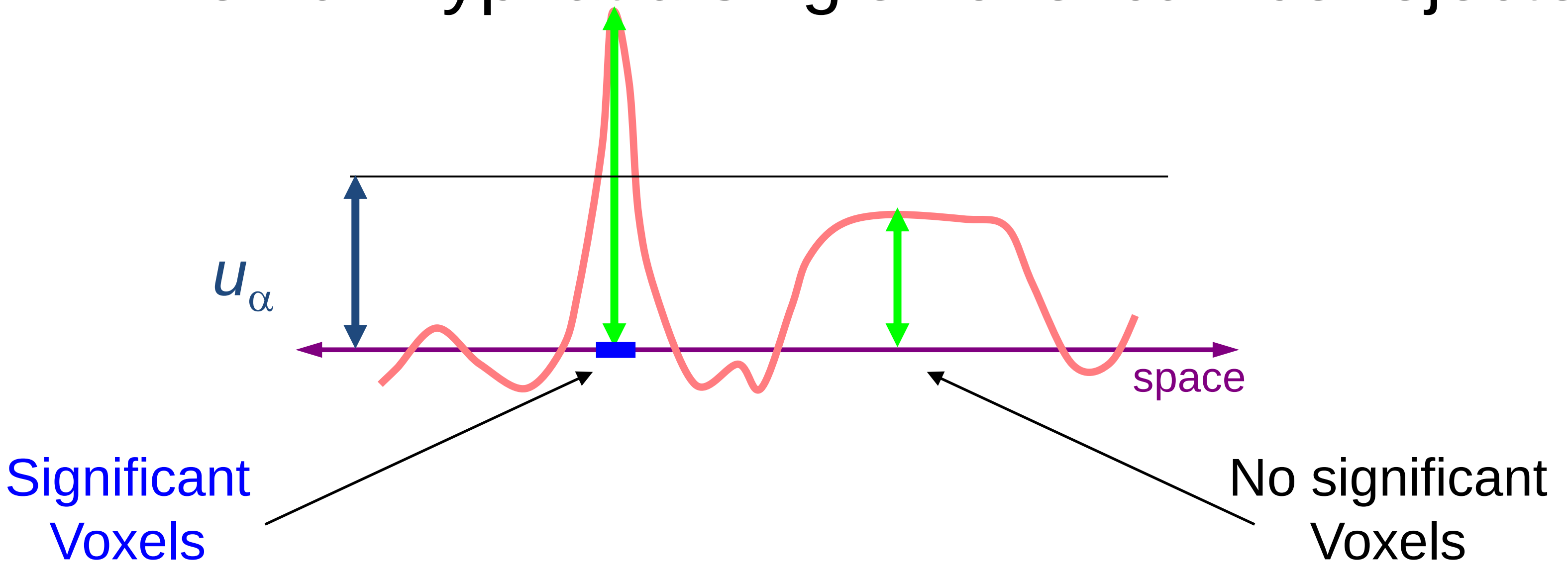
Statistics: *p-values adjusted for search volume*

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	$(Z_\equiv)$	p_{uncorr}	
0.000	2	0.000	0.000	1007	0.000	0.000	0.000	16.00	Inf	0.000	14 -88 10
						0.000	0.000	12.07	Inf	0.000	20 -94 20
		0.000	0.000	1408	0.000	0.000	0.000	15.92	Inf	0.000	-8 -78 -8

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

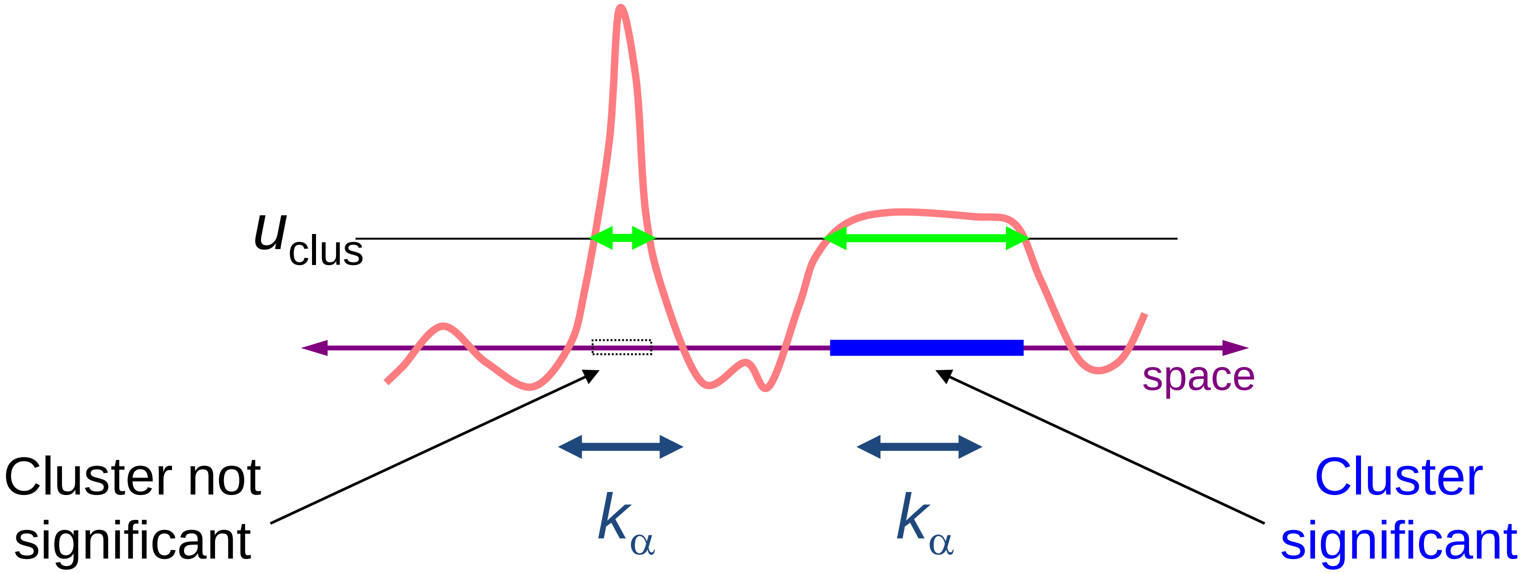
Voxel-level Inference

- 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

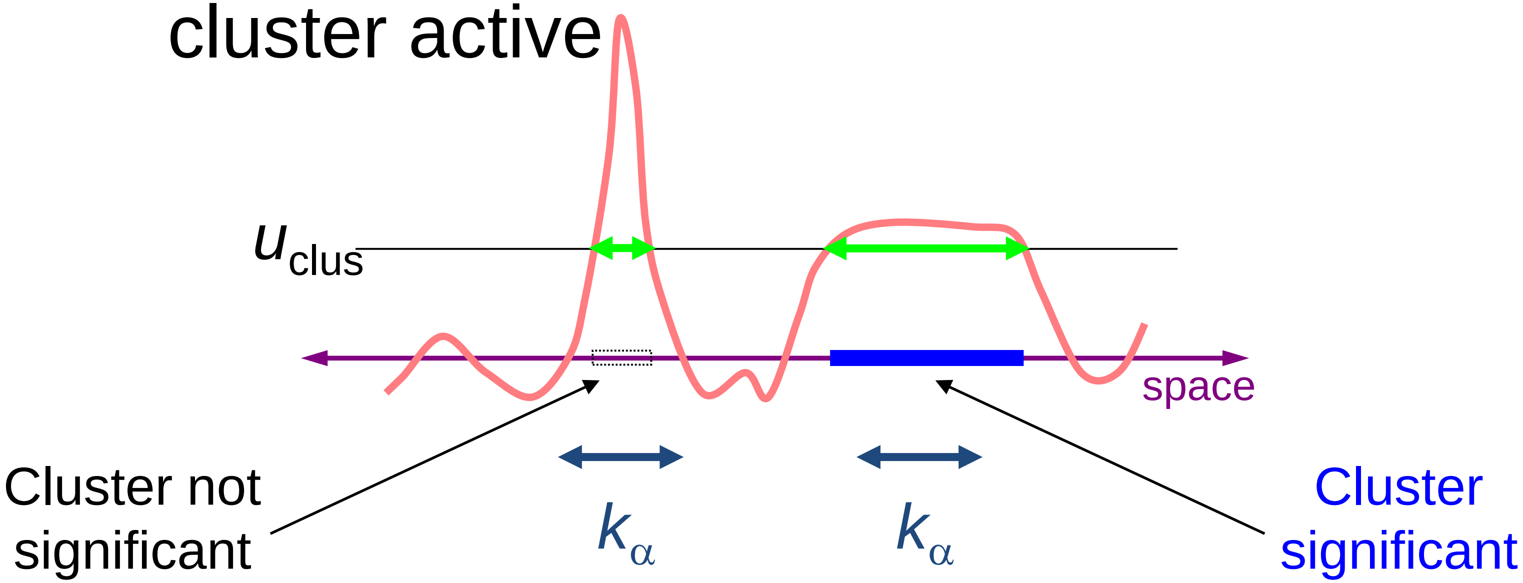


Cluster not significant

Cluster significant

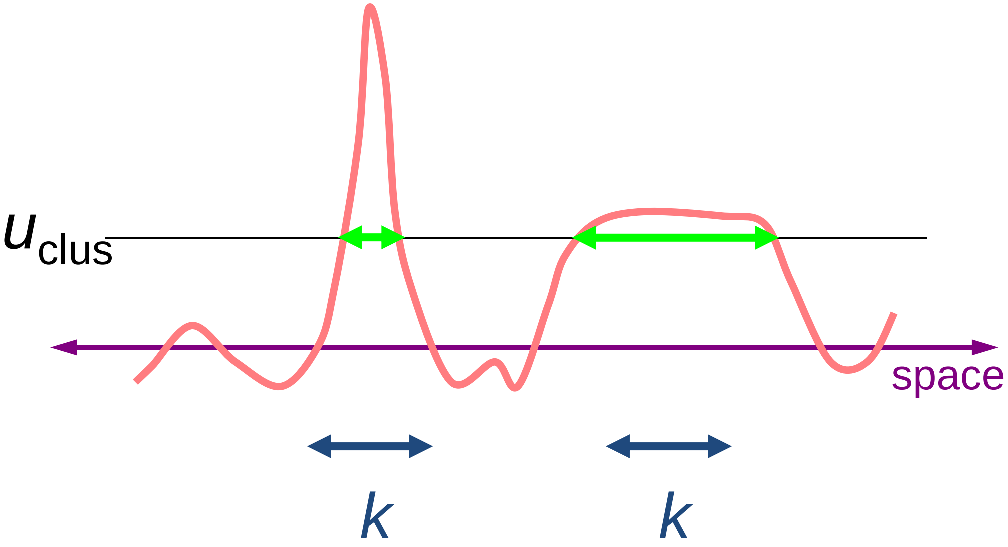
Cluster-level Inference

- 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



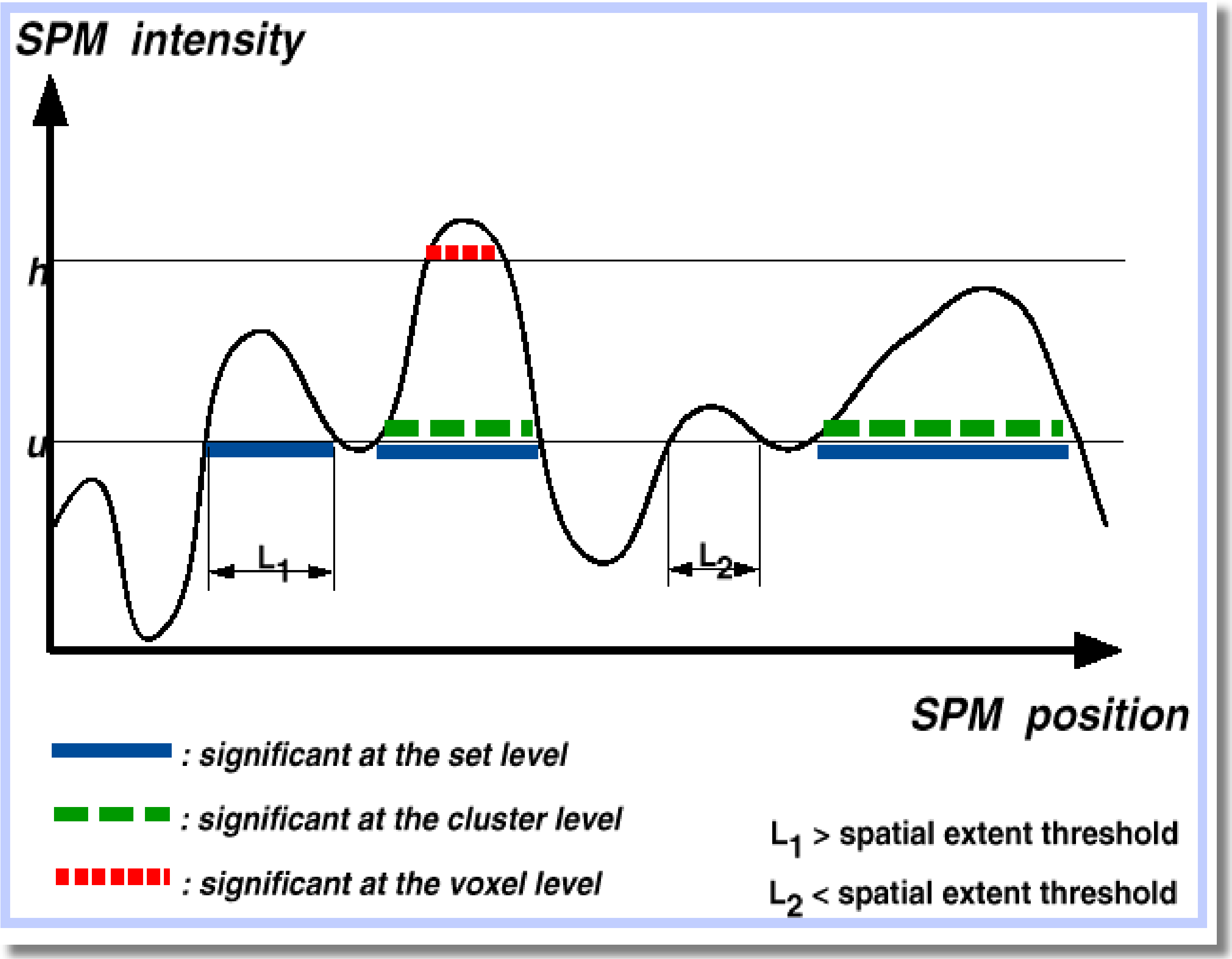
Set-level Inference

- 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…

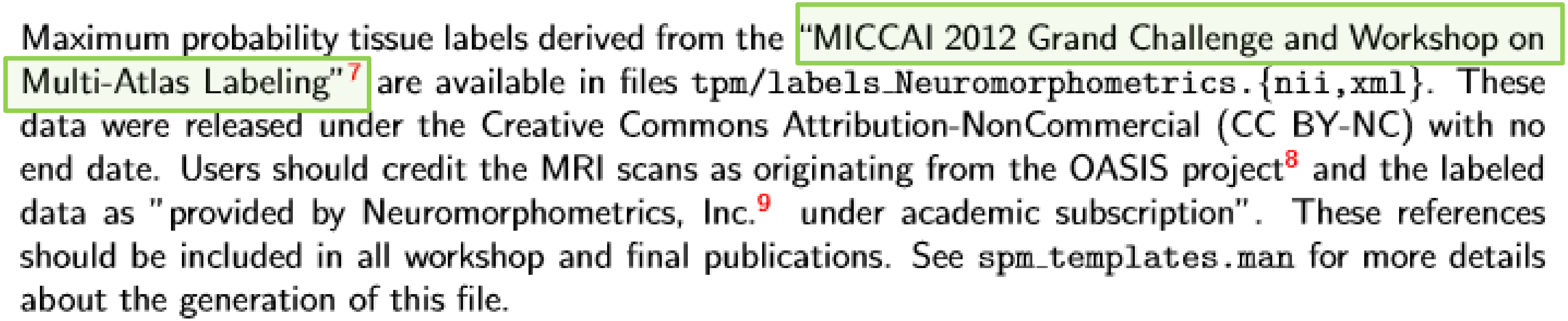
Cluster level…

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