

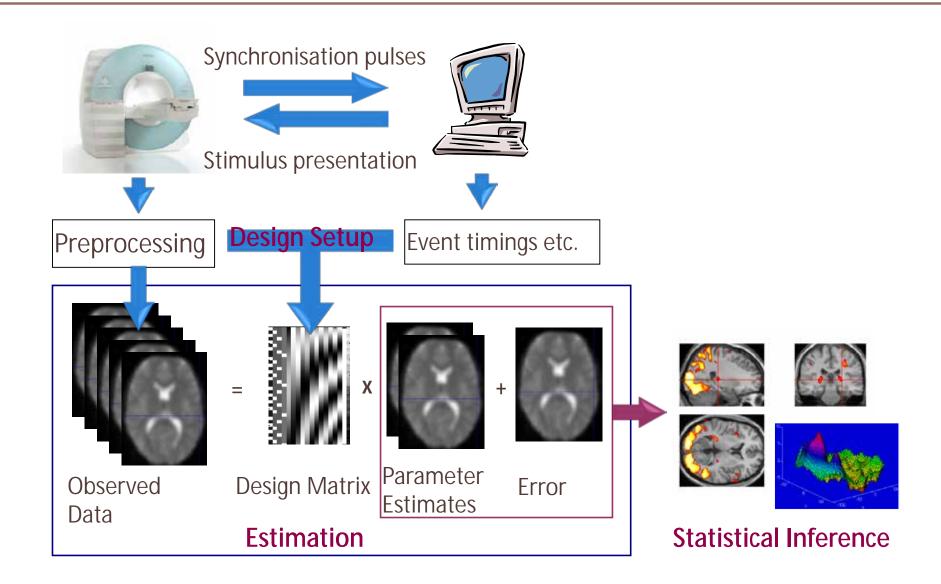
# Single subject analysis using GLM

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With thanks to Russell Thompson, Rik Henson, Matthew Brett and the authors of the HBF

# A functional experiment



# General Linear Model – Theory

#### GLM

- models observed data (dependent variable) Y
- as a linear combination (parameter estimate β) of
- regressors/predictor variables/explanatory variables (EV) (independent variables) X

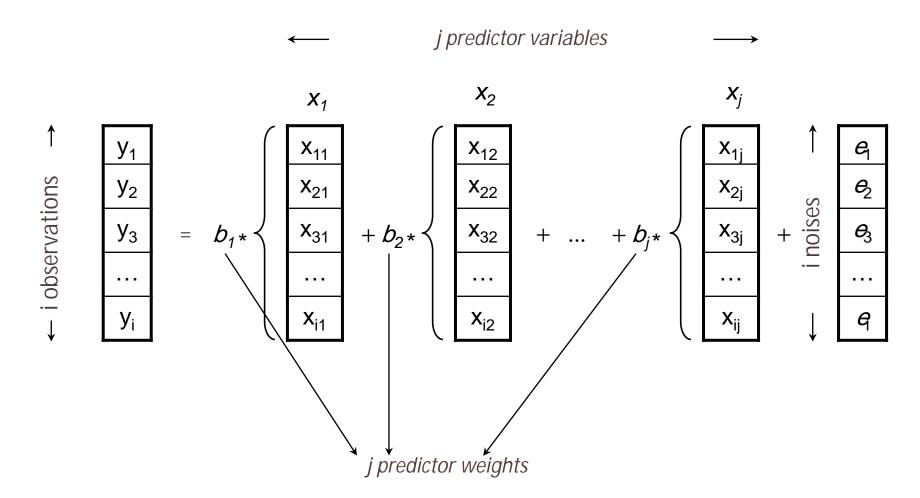
$$Y = X\beta + \epsilon$$

- AN(C)OVA, t-test, (multiple) regression, LDA, CCA are also GLMs.
- Relationship between a dependent variable and one or more independent variables

# **General Linear Model – Theory**

#### • GLM

• For *i* observations modelled using *j* predictor variables:

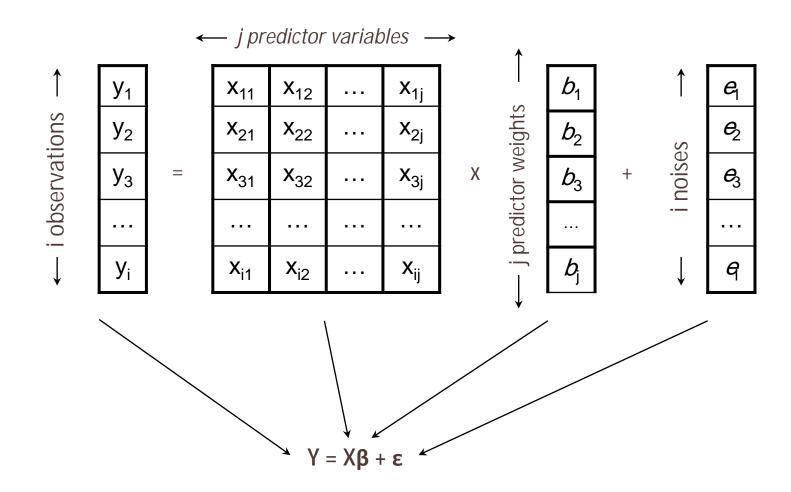




# General Linear Model – Theory

#### • GLM

• For *i* observations modelled using *j* predictor variables:



- Mass univariate approach:
  - Model  $X_{1-i,1-i}$  estimated for each voxel independently (multiple tests)
  - For each voxel:
    - Y<sub>1-i</sub>: timeseries of i observations at a single voxel
    - $\mathbf{B}_{1-j}$  for each of the j predictors



• Series of  $\beta_{1-j}$  images (beta0001-beta000j)



#### Model:

- Contains all known source of variance:
  - Controlled factors (e.g. stimuli)<sup>1</sup>
  - All nuisance variables<sup>1</sup>
- Assumption about noise (ε)
  - High-pass filter
  - Temporal autocorrelation
  - Spikes (aa)
  - Movement parameters (SPM)
  - PhysIO Toolbox
  - Imaging Wiki/PhysNoise
  - GLMDenoise (aa)
  - FIX (FSL)

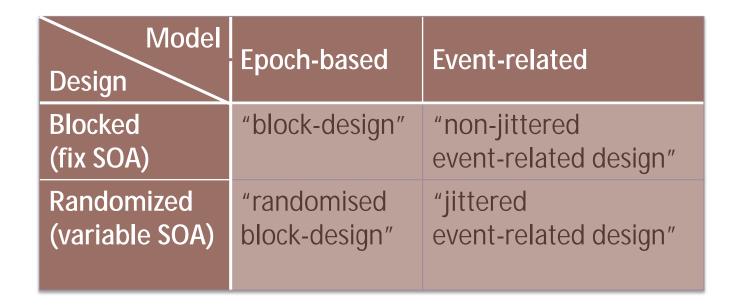


### Model vs. Design:

- Model
  - Event-related (duration = 0)
  - Epoch-based (duration > 0)
    - Can be modelled with events.
      - To model HRF along the epoch (e.g. FIR)
      - But:  $\hat{\beta} pR_{event} \sim \hat{\beta} pR_{epoch} / nEvent^1$
- Design
  - Blocked (fix SOA)
  - Randomized (variable SOA) jittering
    - Lower predictability (à subject is more engaged)
    - Higher estimability (B samples from various phases of the HRF)



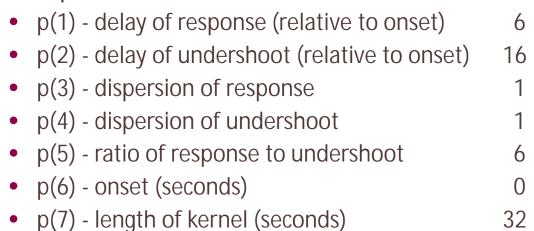
Model vs. Design:

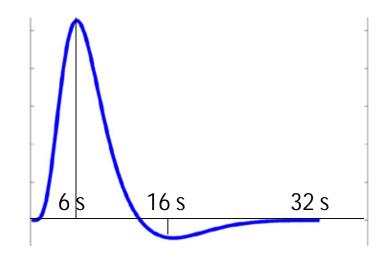




### BOLD response – Kernel:

- stereotyped pattern of response (based on primary sensory areas)
- Canonical Haemodynamic Response Function (HRF) – spm\_hrf(TR,p)
  - Double-gamma function
  - uses 7 parameters

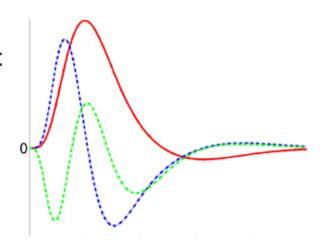


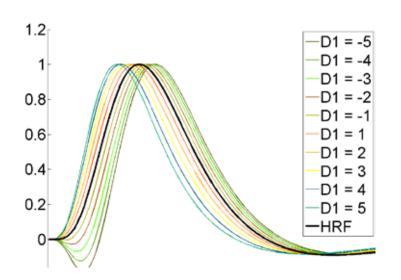


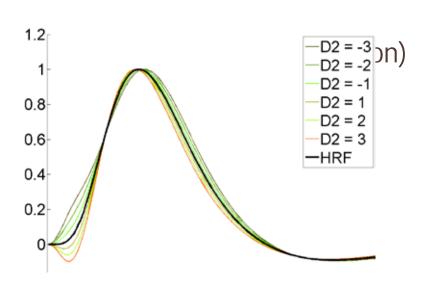


### HRF

Derivatives (to "adjust" HRF¹):



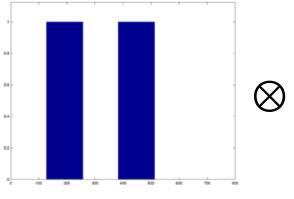


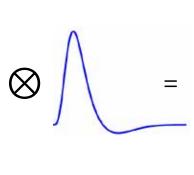


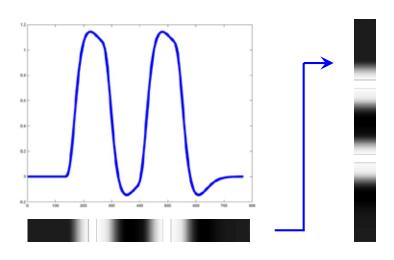


• BOLD response - Convolution:

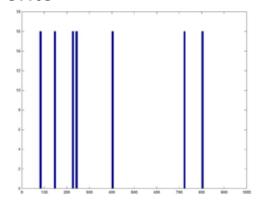


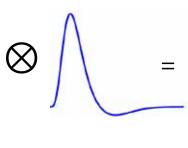


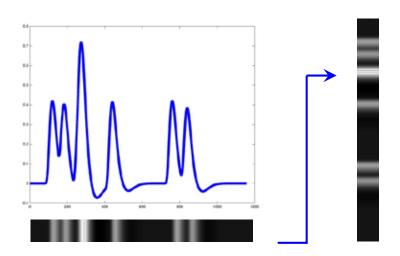




### Events





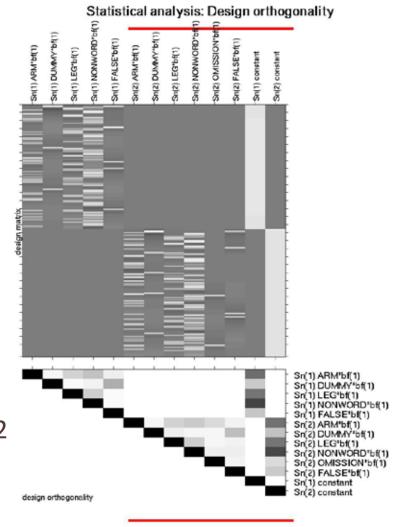




- Non-orthogonality
  - Pairwise correlation (SPM)
  - Rank deficiency (more general)
    - If any column of X is a linear combination of any others



- Some parameters cannot be estimated uniquely (e.g. in case of EV1 and EV2)
  - ◆ efficiency for EV1, EV2 and EV1+EV2
  - Good efficiency for EV1-EV2

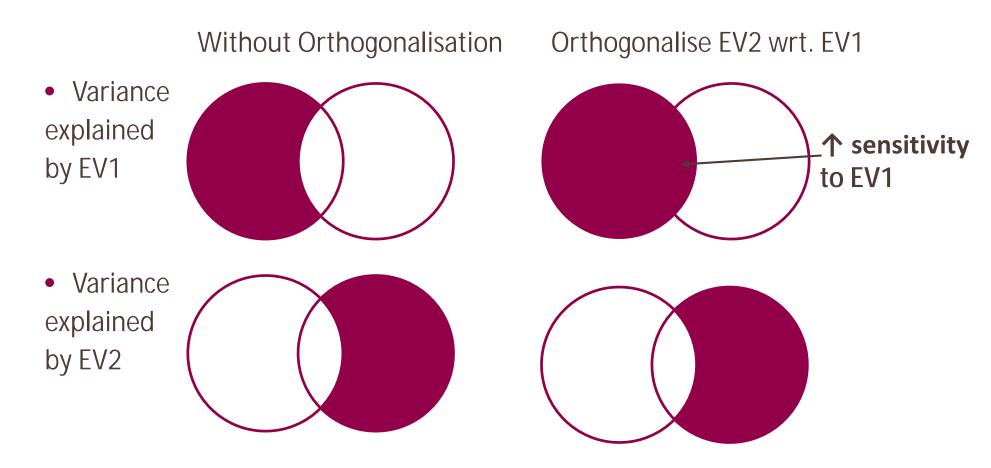


Measure: abs. value of cosine of angle between columns of design matrix Scale: black - colinear (cos=+1/-1)

white - orthogonal (cos=0) gray - not orthogonal or colinear

### Orthogonalisation

Assigning shared explained variance



# General Linear Model – SPM input

- Regressor = predictor variables/explanatory variables One ß for each regressor
  - Condition ⊗ HRF
    - Name
    - Onset
    - Duration
    - Modulation
  - Covariate: it will not be convolved with HRF
- aa\_user\_fmri.m
  - aas\_addevent(aap, 'aamod\_firstlevel\_model', mriname, sessname, onsets, durations, modulation)
  - aas\_addcovariate(aap, 'aamod\_firstlevel\_model', mriname, sessname, covarName, covarVector, HRF, interest)



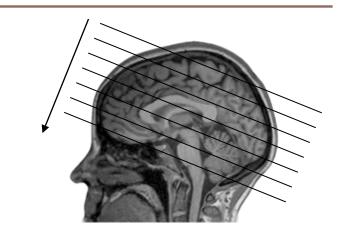
# General Linear Model – SPM input

- Modulation: effect with many level (or continuous)
  - Parametric modulation
    - Stimulus strength
    - Response accuracy
  - Temporal modulation = Parametric modulation using onset as parameter
    - Habituation
    - Learning
  - Polynomial Expansion: higher-order effects
  - Disadvantages
    - Correlated regressors à Orthogonalisation
      - < SPM12: always on (left to right)<sup>1</sup>
      - SPM12: switchable
    - Difficult to set up interactions between factors



# General Linear Model – SPM input

- "Microtiming" ~ Slicetiming<sup>1</sup>
  - Microtime resolution: time bins within one TR
    - Highest temporal precision = TR / MicRes
    - Divided equally for the whole TR
  - Microtime onset: first time bin



• <sup>2</sup>Sparse EPI: e.g. TR = 3s, TA = 2s, 20 slices

Slicetiming																<u></u>
Microtiming										·		·				

• Use middle slice (#10) as reference:

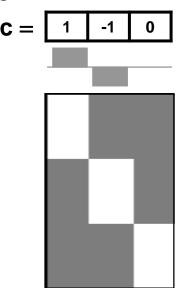
Slicetiming		Microtiming <sup>2</sup>							
Slice order	20:-1:1	Microtime resolution	30						
Reference slice	10	Micortime onset	10						



# General Linear Model – SPM output

- beta\_XXXX  $\widehat{\beta}$  (XXXX: for each EV)
- brain mask (voxels included in the analysis)<sup>1</sup> mask
- ResMS  $-\hat{\epsilon}$  (mean squared)
  - Heterogeneity may indicate unexplained variance in the data
- RPV RESELs Per Voxel (local smoothness)
  - RPV =  $FWHM_{in \ voxel}^{-3}$
  - $\leq$  0.037 (RESEL  $\geq$  3 voxel) to ensure the minimum smoothness for GRFT<sup>2</sup>

- Specific hypotheses to be tested using t or F statistics
  - How each predictor (column of the design matrix) plays a role
  - E.g. condition 1 > condition 2 à contrast [1 -1 0]



- aa\_user\_fmri.m
  - aas\_addcontrast(aap, 'aamod\_firstlevel\_contrasts', mriname, format, vector, conname,contype)



#### F contrast:

- Model comparison: How much variance is explained by the model including the conditions of interest (e.g. movement parameters)?
- Non-directional
- Can contain more rows (OR)

[1 0 0; % EV1 > baseline OR 0 1 0] % EV2 > baseline How much variance is explained by EV1 and FV2? Should we include them in the model?1

- SPM output:
  - ess\*.img (Extra Sum of Squares)
  - spmF\*.img (F-map à p)

#### T contrast:

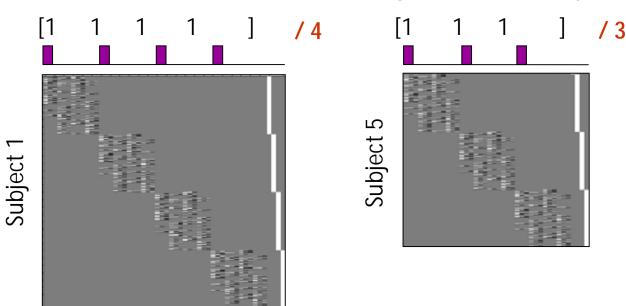
- Hypothesis test: How do the conditions of interest relate to each other and/or to the baseline?
- Directional
- Can contain only one row

- SPM output:
  - con\*.img (Contrast)
  - spmT\*.img (T-map à p)



#### T contrast:

- The contrast vector sums to 0, 1 or -1
- Positive weights sum to 1
- Negative weights sum to -1
- Scaling issue
  - T-stat does not depend on scaling (of both the regressors and the contrast).
  - Contrast<sup>1</sup> depend on scaling<sup>2</sup> à consistency across subjects!





#### T contrast:

Examples<sup>1</sup>:

: condition 1 > unmodelled/implicit baseline • [1 0 0]

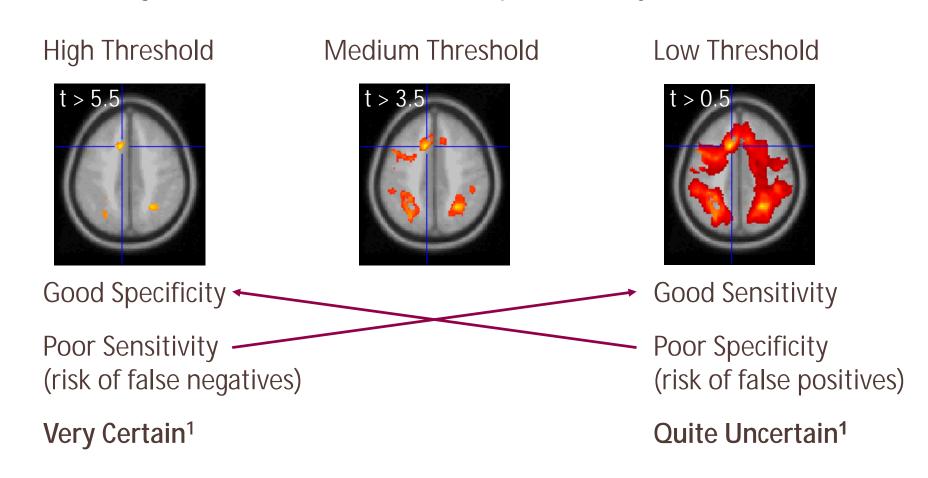
: condition 1 > sum of conditions 2 and 3 • [2 -1 -1]

• [1 -0.5 -0.5] : condition 1 > average of conditions 2 and 3

• [-3 -1 1 3] : linear increase over 4 conditions



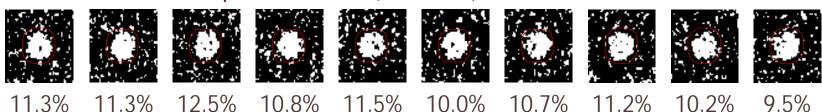
- How much is enough?
  - Converting a continuous statistical value (p) to a binary decision à cut-off





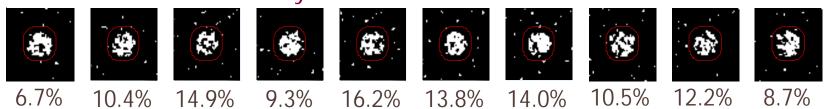
- How to make certainty comparable?
- Multiple comparison
  - Testing 100,000 random voxels at  $p = 0.05 \ge 5000$  "significant" by chance (false positives, or "type I" errors)<sup>1</sup>
- FamilyWise Error Rate (FWER):
  - Chance of any false positive in the "family" (any similar measurement)
- False Discovery Rate (FDR):
  - Chance/Proportion of false positives in the rejected tests (i.e. suprathreshold results)
  - To enable in SPM:
    - global defaults
    - defaults.stats.topoFDR = 0;

### Control of Per Comparison Rate (i.e.none) at 10%



Percentage of Null Pixels that are False Positives

### Control of False Discovery Rate at 10%



Percentage of Activated Pixels that are False Positives

### Control of Familywise Error Rate at 10%





















Occurrence of Familywise Error

**FWE** 

#### FWE

- Bonferroni correction:  $p_{(corrected)} = p_{(uncorrected)}/n_{comparisons}$ 
  - Overly conservative in fMRI due to spatial dependence:
  - Nearby voxels are correlated: smoothness
    - Smoother data = More voxels in correlation à fewer indep. elements



- Gaussian Random Field Theory (GRFT) default in SPM
  - Estimate the true number of independent/RESolution Elements (RESEL) using GRFT à RPV.img: RESEL Per Voxel (local smoothness)
  - Corrects for the number of RESELs à Less conservative than Bonferroni



- aa default
  - aamod\_firstlevel\_threshold.xml
- aa\_user\_fmri.m / aap\_parameters.mat
  - aap.tasksettings.aamod\_firstlevel\_threshold.threshold.correction = 'none';
  - aap.tasksettings.aamod\_firstlevel\_threshold.threshold.p = 0.001;
  - aap.tasksettings.aamod\_firstlevel\_threshold.threshold.extent = 0;



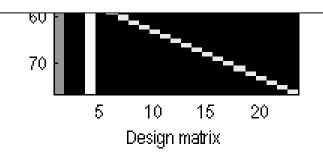
### Levels of inference

- Peak
- Cluster
- Set

#### SPMresults: ANOVA

Height threshold T = 4.802783 {p<0.05 (FWE)}

Extent threshold k = 0 voxels

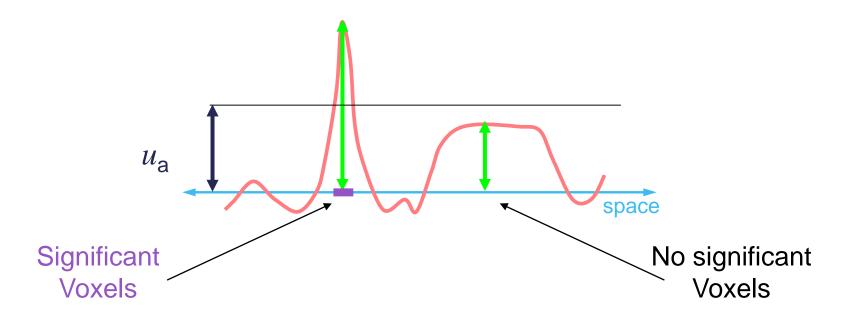


#### Statistics: p-values adjusted for search volume

set-level cluster-level						mm mm mm							
р	С	p <sub>FIME-corr</sub>	р FWE-com <sup>g</sup> FDR-com k		рипсоп	p <sub>FIME-com</sub>	а́ FDR-com	Ţ	(Z_)	рипсоп	111111 111111 111111		
0.000	5	0.000	0.000	1292	0.000	0.000	0.000	8.99	7.00	0.000	36 -22	62	
						0.000	0.000	8.90	5.95	0.000	40 -18	55	
		0.000	0.004	321	0.001	0.000	0.000	7.63	6.26	0.000	-18 -50	-26	
		0.003	0.085	84	0.068	0.002	0.062	5.84	5.12	0.000	-58 -18	18	
		0.003	0.085	97	0.052	0.007	0.185	5.45	4.84	0.000	-56 6	10	
						0.012	0.271	5.28	4.72	0.000	-44 -4	ł 8	
		0.035	0.703	4	0.703	0.041	0.810	4.87	4.42	0.000	-60 -22	40	

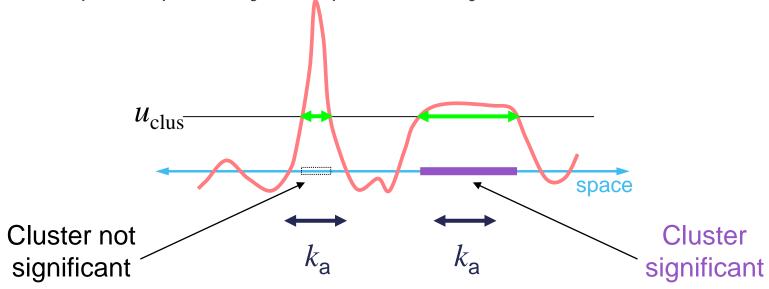
#### Levels of inference

- Peak-level (voxel-level) inference
  - Probability p of that or higher peak voxel intensity (i.e. T/F-value)
  - Retains voxels above the threshold ( $p \le u_a$ )
  - Best spatial specificity: interpretable for each voxel



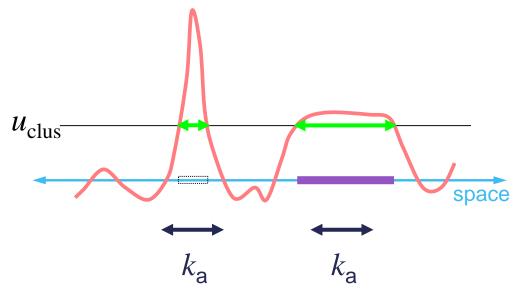
#### Levels of inference

- Cluster-level inference (default in FSL)
  - Probability p of that or larger number of neighbouring significant voxels
  - Two thresholds
    - Define significant voxels by "cluster-forming" threshold ( $p \le u_{clus}$ )
    - Retains only large clusters  $(p \le P(k_a))$
  - Worse spatial specificity: interpretable only for the whole cluster



#### Levels of inference

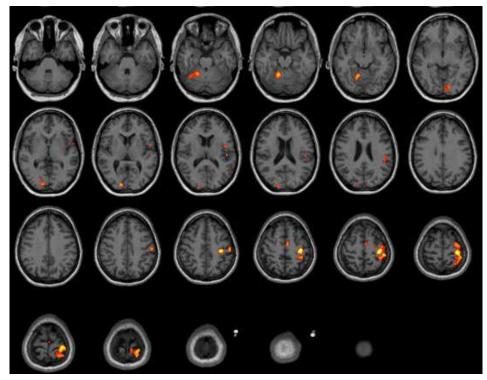
- Set-level inference
  - Probability *p* of that or larger number of significant clusters
  - Worst spatial specificity: interpretable only globally

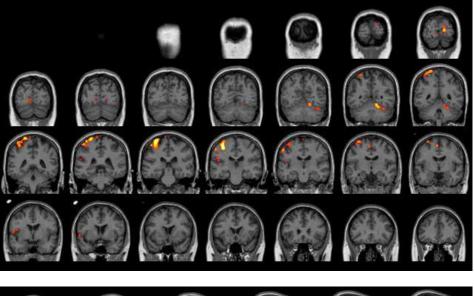


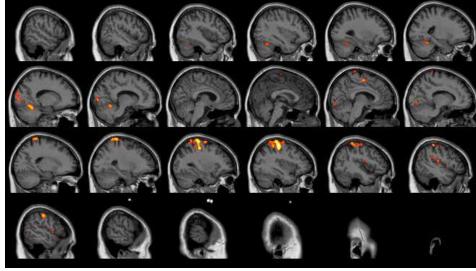
Only 1 significant cluster

### Visualisation

aamod\_firstlevel\_threshold

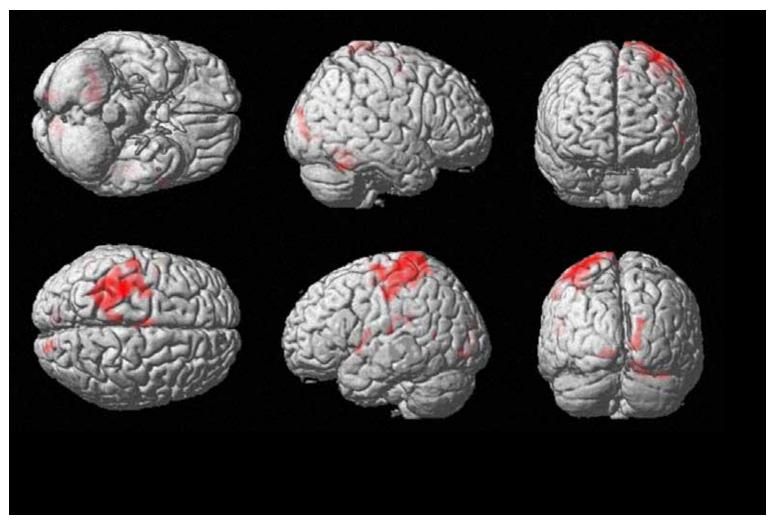






### Visualisation

aamod\_firstlevel\_threshold



#### **Visualisation**

- aamod\_firstlevel\_threshold\_register2FS
  - Launch a VNC session on a login-gpu01-03 machine
    - ssh login-gpu0X à remember the machine name (e.g. login-gpu01)
    - vncstart à remember the desktop number (50+account number; e.g. 51)
    - TurboVNC (e.g. login-gpu01:51)
  - FreeView
    - cdw
    - cd Material/4\_aa/AA\_fMRI/aamod\_firstlevel\_threshold\_register2FS\_00001/S1
    - vglrun freeview
    - View à Viewport Layout à 1 & 3 Horizontal
    - View à Viewport Layout à 3D
    - View à Show Slices (3D View): off



#### Visualisation

- aamod\_firstlevel\_threshold\_register2FS
  - Load volume (brain.mgz) and overlay (rthr\*.nii)
    - File à Load Volume à brain.mgz
    - File à Load Volume à ../stats/rthrT\_0001.nii à Color map: Heat
  - Load Surface (lh.\*) and overlay (rthr\*2FS\_lh.mgh)
    - File à Load Surface à Ih.pial
    - Curvature: binary
    - Overlay à Load generic... à ../stats/rthrT\_00012FS\_lh.mgh
    - Configure Overlay à Min = 3