

Statistical inferences in fMRI

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Overview

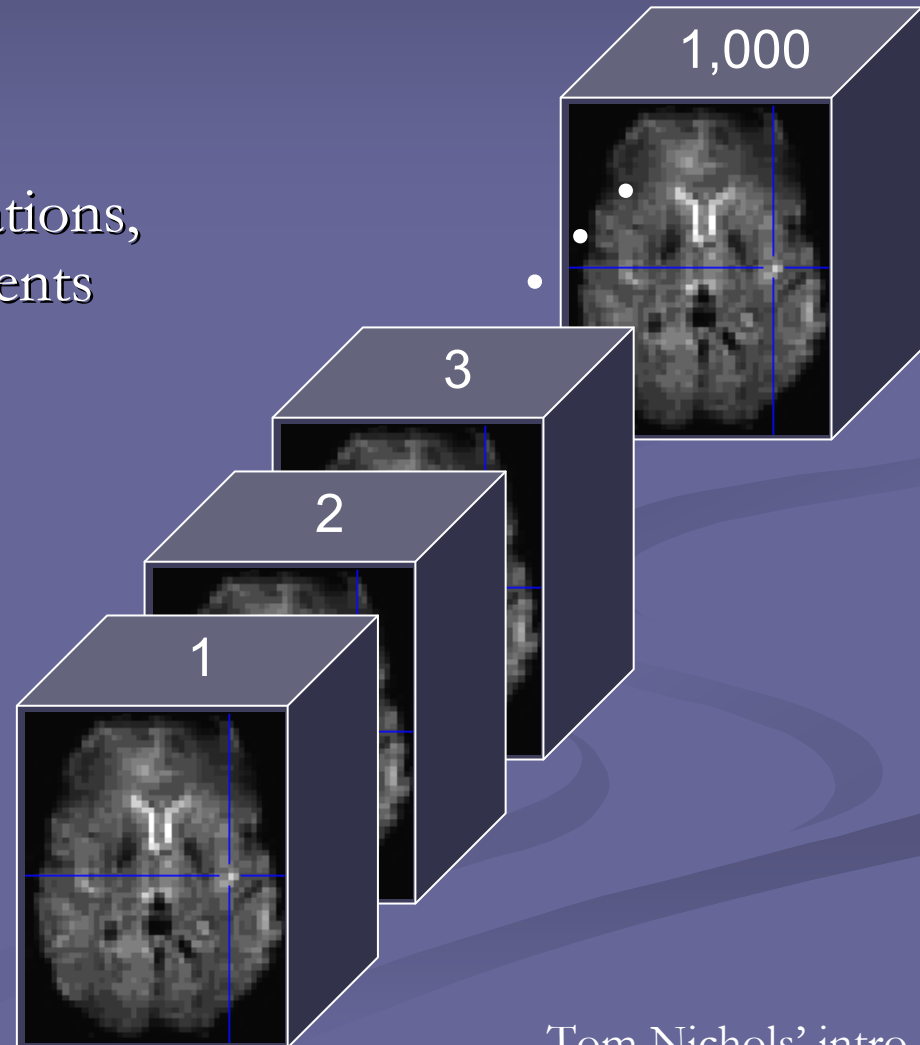
- Multiple comparisons correction procedures
- Levels of inferences (set, cluster, voxel)
- Circularity issues

Multiple comparison correction

Avoiding false positives

What Problem?

- 4-Dimensional Data
 - 1,000 multivariate observations, each with $> 100,000$ elements
 - 100,000 time series, each with 1,000 observations
- Massively Univariate Approach
 - 100,000 hypothesis tests
- Massive MCP!



Tom Nichols' intro

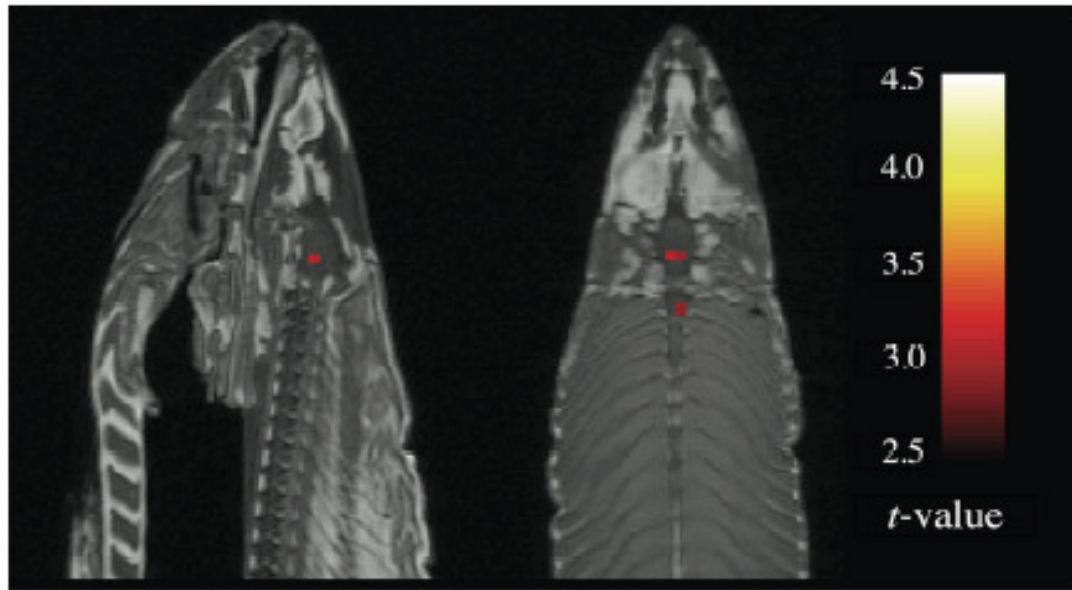
What Problem?

- Typical brain ~ 130000 voxels
- @ $p = .05$, it is expected = 6500 false positives!
- @ a more conservative value like $p = .001$ we still expect 130 false positives.
- Using extend threshold k without correction is not enough as it, by chance, can cluster as well.

What Problem?

- Bennet et al., 2009
- Task: take a decision about emotions on pictures
- Design: blocks of 12 sec activation/rest
- Analysis: standard data processing with SPM
- Subject: a dead salmon!

What Problem?



A t -contrast was used to test for regions with significant BOLD signal change during the photo condition compared to rest. The parameters for this comparison were $t(131) > 3.15$, $p(\text{uncorrected}) < 0.001$, 3 voxel extent threshold.

- The cluster was 81mm^3 ! – after multiple comparison corrections all false activations were removed.

Solutions for MCP

- Height Threshold
- Familywise Error Rate (FWER)
 - Chance of *any* false positives; Controlled by Bonferroni & Random Field Methods
- False Discovery Rate (FDR)
 - Proportion of false positives *among* rejected tests
- Bayes Statistics

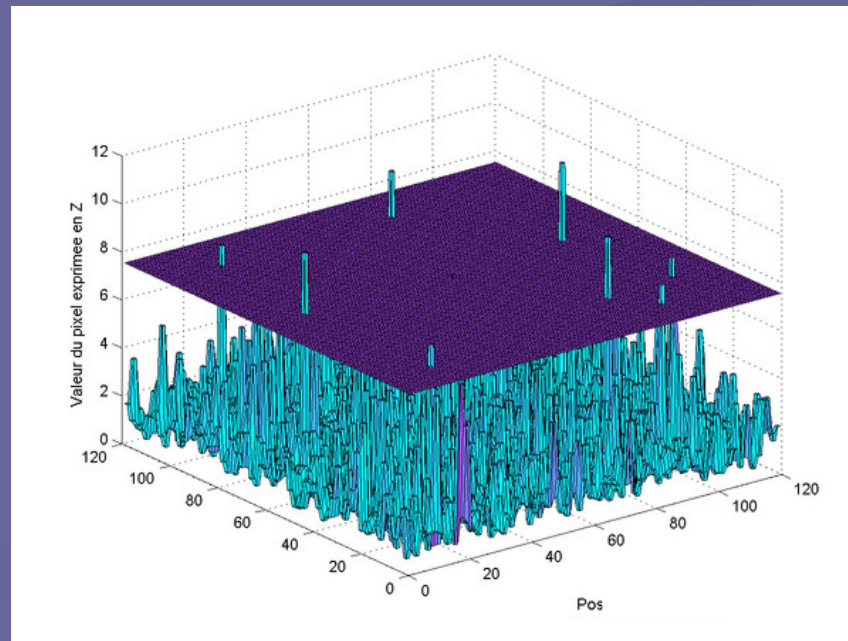
From single univariate to massive univariate

Univariate stat	Functional neuroimaging
1 observed data	Many voxels
1 statistical value	Family of statistical values
Type 1 error rate (chance to be wrong rejecting H_0)	Family-wise error rate
Null hypothesis	Family-wise null hypothesis

Height Threshold

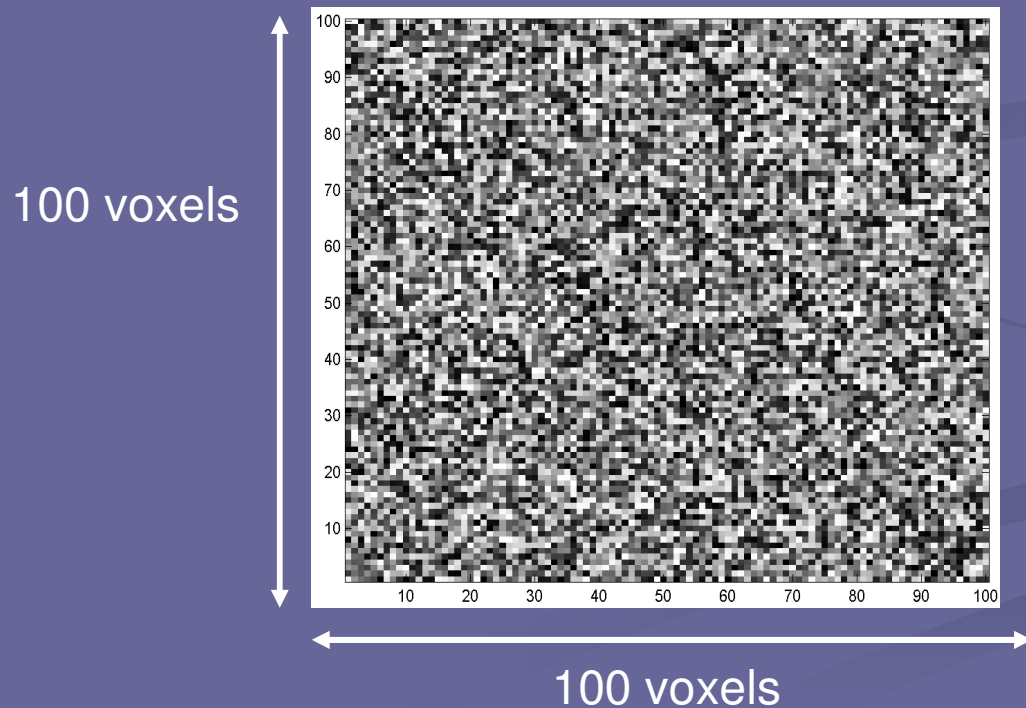
- Choose locations where a test statistic Z (T, F, ...) is large to threshold the image of Z at a height z
- The problem is how to choose this threshold z to exclude false positives with a high probability (e.g. 0.95)?

To control for family wise error on must take into account the nb of tests



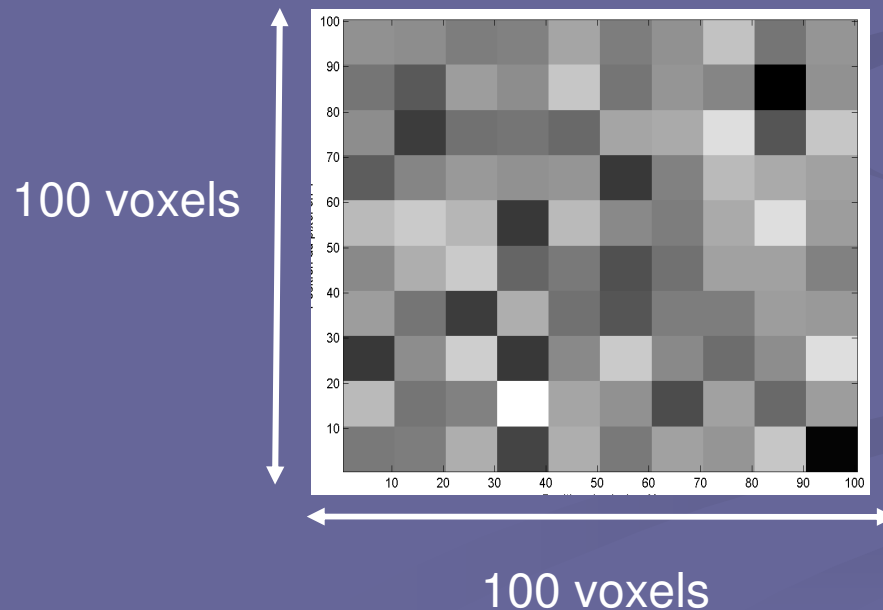
Bonferroni

- 10000 Z-scores ; $\alpha = 5\%$
- α corrected = .000005 ; z-score = 4.42



Bonferroni

- 10000 Z-scores ; $\alpha = 5\%$
- 2D homogeneous smoothing – 100 independent observations
- $\alpha \text{ corrected} = .0005$; $z\text{-score} = 3.29$

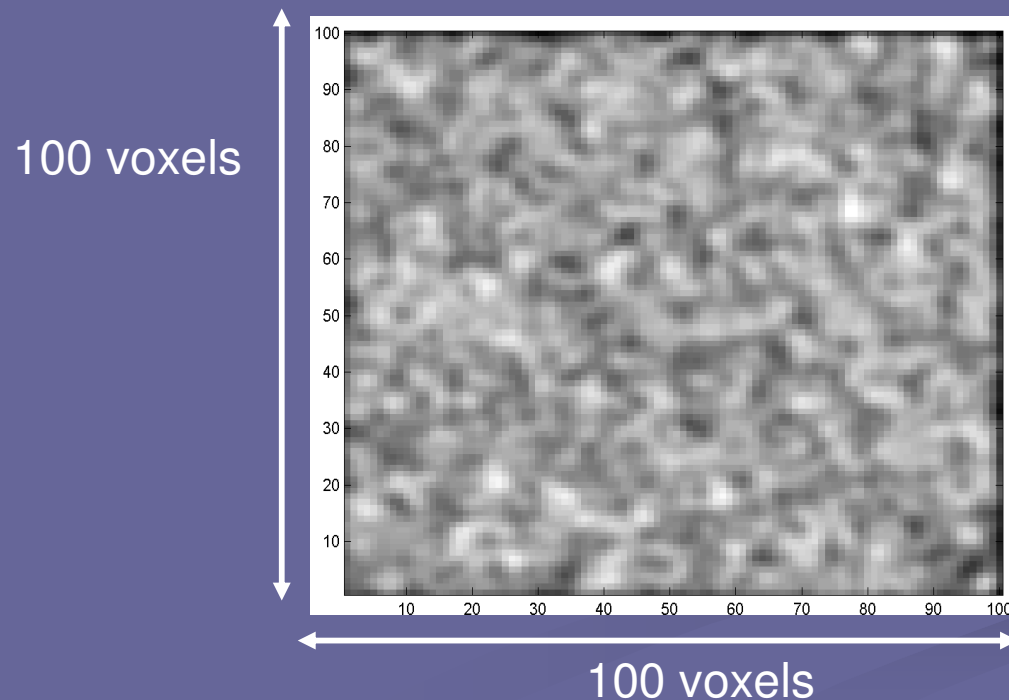


Solutions for MCP

- An important feature of neuroimaging data is that we have a family of stat values that has topological features (Bonferroni for instance consider tests as independent)
- Why considering data as a smooth lattice? (Chumbley et al., 2009 NeuroImage 44)
 - fMRI/PET are projection methods of data points onto the whole space – MEEG forms continuous functions in time and are smooth by the scalp (space)
 - Neural activity propagate locally through intrinsic/lateral connections and is distributed via extrinsic connections / Hemodynamic correlates are initiated by diffusing signals (e.g. NO)

Random Field Theory

- 10000 Z-scores ; $\alpha = 5\%$
- Gaussian kernel smoothing –
- How many independent observations ?

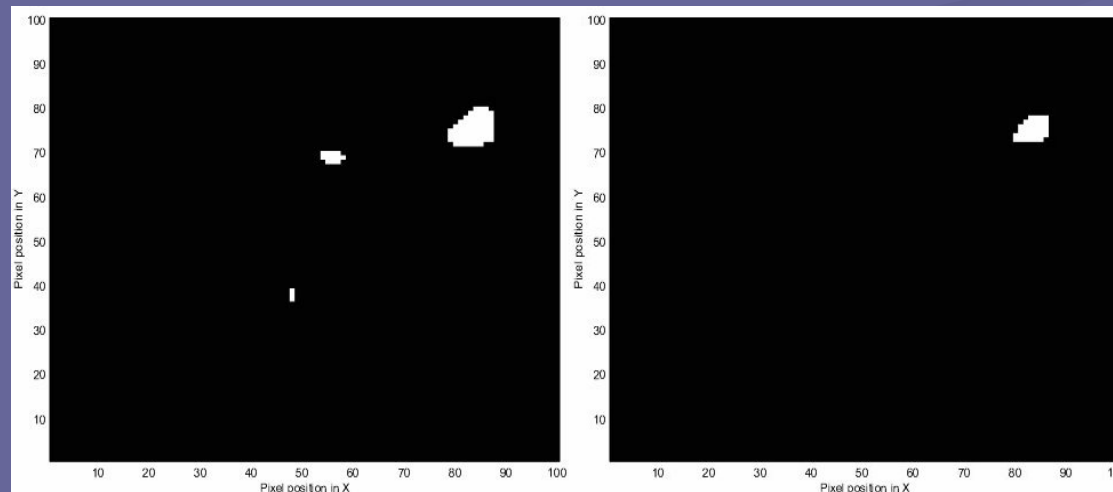


Random Field Theory

- RFT relies on theoretical results for smooth statistical maps (hence the need for smoothing), allowing to find a threshold in a set of data where it's not easy to find the number of independent variables. Uses the expected Euler characteristic (EC density)
- 1 Estimation of the smoothness = number of resel (resolution element) = $f(\text{nb voxels}, \text{FWHM})$
- 2 expected Euler characteristic = number of clusters above the threshold
- 3 Calculation of the threshold

Random Field Theory

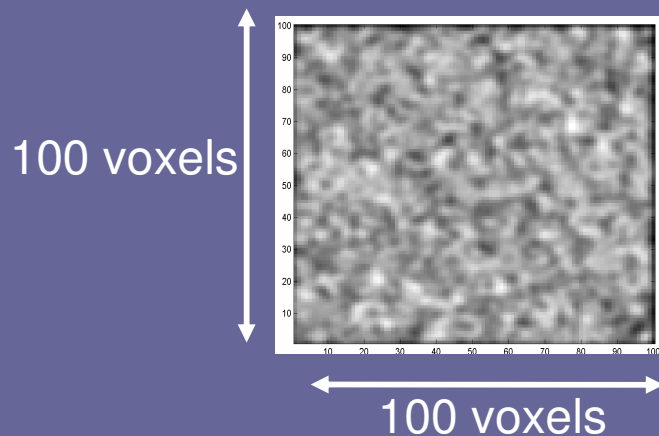
- The Euler characteristic can be seen as the number of blobs in an image after thresholding (p value that you select in SPM)
- At high threshold, $EC = 0$ or 1 per resel: $E[EC] \approx p^{\text{FWE}}$



$E[EC] = R \cdot (4 \log_e 2) \cdot (2\pi)^{-2/3} \cdot Z_t \cdot e^{-1/2 Z_t^2}$ for a 2D image, more complicated in 3D

Random Field Theory

- For 100 resels, the equation gives $E[EC] = 0.049$ for a threshold Z of 3.8, i.e. the probability of getting one or more blobs where Z is greater than 3.8 is 0.049



α	number of resels in the image	Bonferroni		RFT
		threshold	score Z	score Z
0.05	100	$\frac{0.05}{100}$	3.3	
				3.8

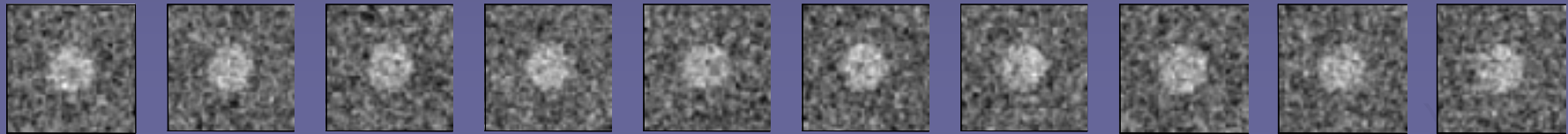
- If the resel size is much larger than the voxel size then $E[EC]$ only depends on the nb of resels otherwise it also depends on the volume, surface and diameter of the search area (i.e. shape and volume matter)

False discovery Rate

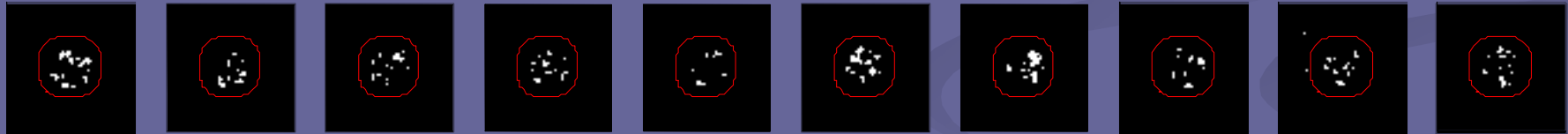
- Whereas family wise approach corrects for any false positive, the FDR approach aim at correcting among positive results only.
1. Run an analysis with $\alpha = x\%$
 2. Sort the resulting positive data
 3. Threshold to remove the false positives

False discovery Rate

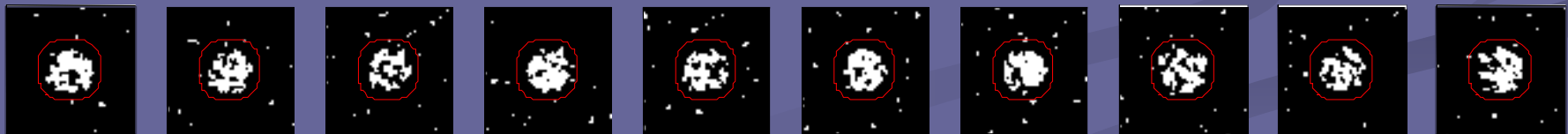
Signal+Noise



FEW correction



FDR correction

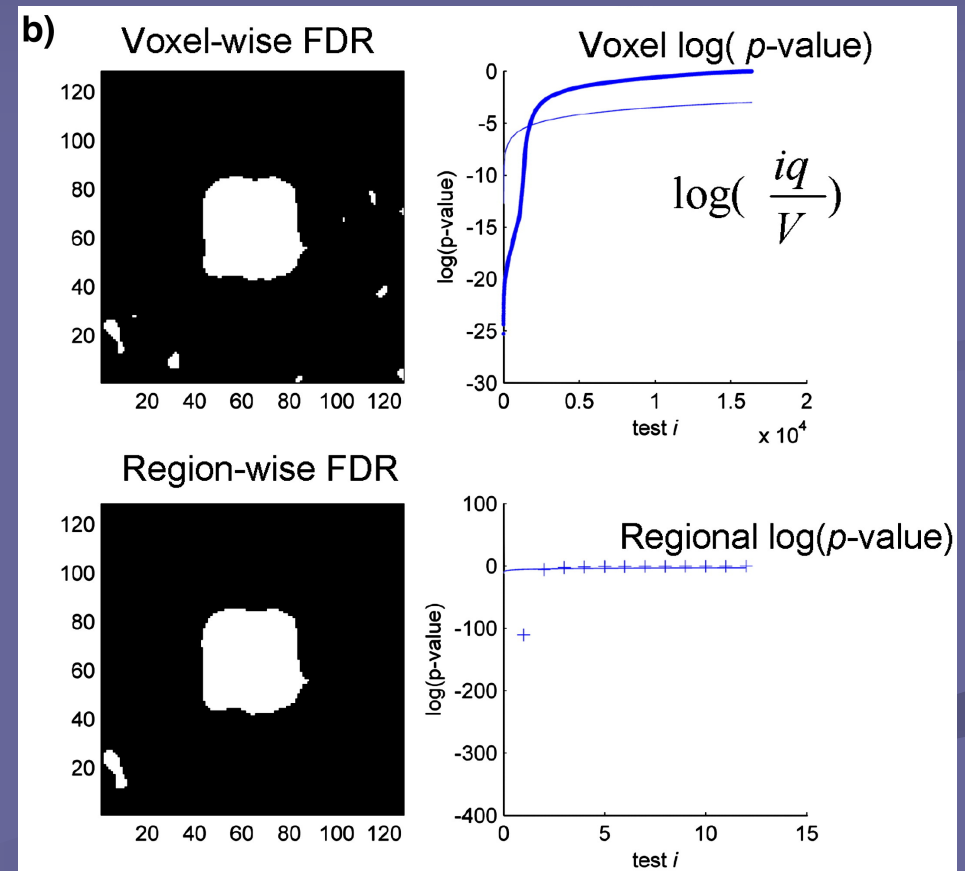


False discovery Rate

takes the spatial structure into account

Under H_0 the nb of voxels per cluster is known \rightarrow uncorrected p value for clusters \rightarrow apply FDR on the clusters (volume-wise correction)

Assumes that the volume of each cluster is independent of the number of clusters



Levels of inference

Voxel, cluster and set

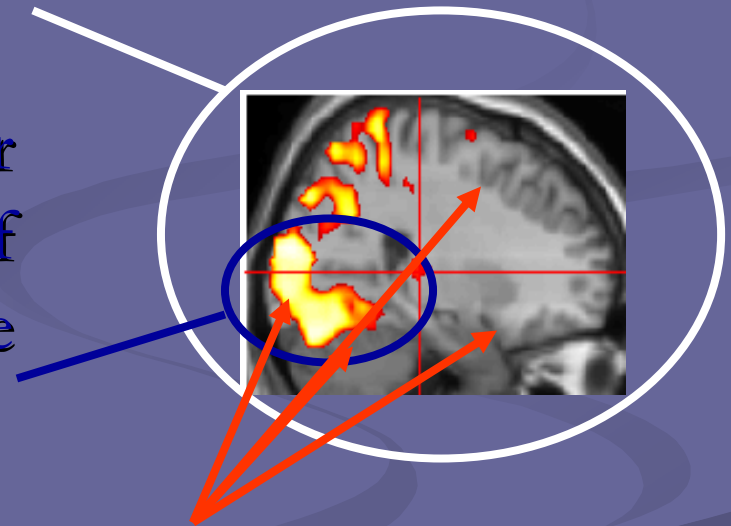
Levels of inference

- 3 levels of inference can be considered:
 - Voxel level (prob associated at each voxel)
 - Cluster level (prob associated to a set of voxels)
 - Set level (prob associated to a set of clusters)

- The 3 levels are nested and based on a single probability of obtaining c or more clusters (set level) with k or more voxels (cluster level) above a threshold u (voxel level):
 $P_w(u, k, c)$

Levels of inference

- Set level: we can reject H_0 for an omnibus test, i.e. there are some significant clusters of activation in the brain.
- Cluster level: we can reject H_0 for an area of a size k , i.e. a cluster of 'activated' voxels is likely to be true for a given spatial extend.
- Voxel level: we can reject H_0 at each voxel, i.e. a voxel is 'activated' if exceeding a given threshold



Levels of inference

- Each level of inference is valid, but the inferences are different – e.g. a set might be enough to check that subjects activated regions selected a priori for a connectivity analysis – clusters might be good enough if hypotheses are about the use of different brain areas between groups
- Both voxel and cluster levels need to address the multiple comparison problem. If the activated region is predicted in advance, the use of corrected p values is unnecessary and inappropriately conservative – a correction for the number of predicted regions (Bonferroni) is enough

Levels of inference

Statistics: *p-values adjusted for search volume*

set-level		cluster-level				peak-level					mm mm mm		
D	C	D _{FWE-corr}	q _{FDR-corr}	k _E	D _{uncorr}	D _{FWE-corr}	q _{FDR-corr}	T	(Z _≡)	D _{uncorr}			
0.226	21	0.000	0.000	508	0.000	0.070	0.101	7.94	4.90	0.000	-8	54	-4
						0.184	0.101	7.09	4.63	0.000	8	40	-8
						0.704	0.309	5.71	4.10	0.000	-4	38	-6
		0.001	0.000	227	0.000	0.146	0.101	7.30	4.70	0.000	-40	-78	34
						0.959	0.364	5.00	3.78	0.000	-48	-66	24
						0.999	0.588	4.43	3.49	0.000	-44	-66	38
		0.000	0.000	273	0.000	0.187	0.101	7.08	4.62	0.000	-24	36	46
		0.000	0.000	498	0.000	0.198	0.101	7.03	4.61	0.000	-6	-50	30
						0.865	0.332	5.35	3.94	0.000	-6	-62	24
						0.910	0.358	5.21	3.88	0.000	-20	-50	28
		0.021	0.005	133	0.001	0.773	0.309	5.57	4.04	0.000	2	60	16
		0.852	0.256	25	0.110	0.818	0.326	5.46	3.99	0.000	-32	-22	22
		0.995	0.487	10	0.301	0.868	0.332	5.34	3.93	0.000	2	10	-8
		0.422	0.099	49	0.031	0.930	0.358	5.14	3.84	0.000	50	-70	36
		0.957	0.346	17	0.181	0.947	0.358	5.06	3.81	0.000	-2	-26	42
		0.590	0.134	39	0.051	0.964	0.364	4.97	3.76	0.000	12	-56	18
		0.913	0.294	21	0.140	0.989	0.475	4.74	3.65	0.000	-30	-50	8
		0.437	0.099	48	0.033	0.998	0.572	4.51	3.53	0.000	26	34	40
						1.000	0.781	4.07	3.29	0.001	20	38	34
		0.985	0.419	13	0.240	0.999	0.588	4.43	3.49	0.000	-16	64	10
		1.000	0.704	5	0.470	1.000	0.777	4.13	3.33	0.000	-36	-48	-2
		1.000	0.772	2	0.663	1.000	0.777	4.12	3.32	0.000	-12	62	20
		1.000	0.772	3	0.584	1.000	0.781	4.08	3.29	0.000	-30	-26	54
		1.000	0.772	1	0.772	1.000	0.936	3.87	3.17	0.001	44	-78	30

table shows 3 local maxima more than 8.0mm apart

Height threshold: $t = 3.73$, $p = 0.001$ (1.000)
 Extent threshold: $k = 0$ voxels, $p = 1.000$ (1.000)
 Expected voxels per cluster, $\langle k \rangle = 10.115$
 Expected number of clusters, $\langle c \rangle = 17.44$
 FWEp: 8.202, FDRp: Inf, FWEc: 133, FDRc: 133

Degrees of freedom = [1.0, 15.0]
 FWHM = 10.8 10.6 10.0 mm mm mm; 5.4 5.3 5.0 (voxels)
 Volume: 1265568 = 158196 voxels = 1018.0 resels
 Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 142.91 voxels)
 Page 1

RFT (Gaussian Random Fields)
 -> Prob of cluster
 -> Prob of voxel

Using $p=.001$ this creates an excursion set
 Prob clusters of that size
 Prob peak that height
 → after FDR correction

Uncorrected (bad)

Circularity issues in fMRI

Definition

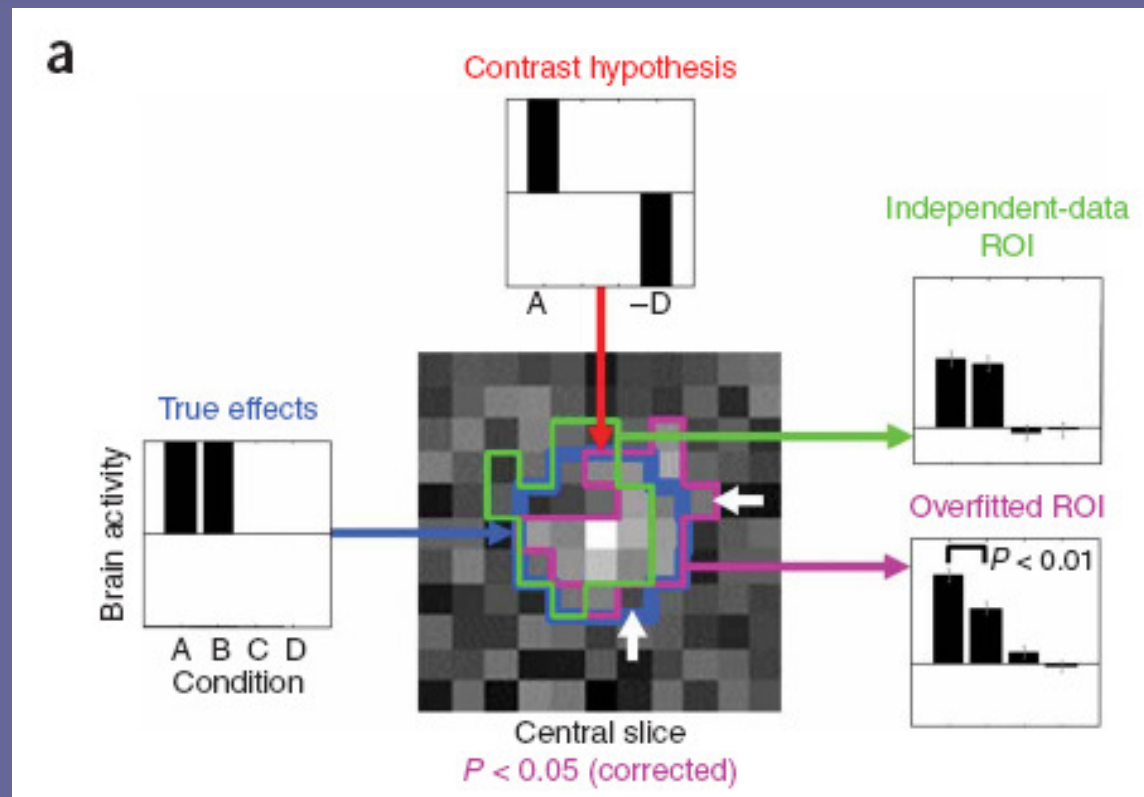
- Refers to the problem of selecting data for analysis
- How data (areas usually) are selected, analysed and sorted is key to avoid circularity
- Put forward by Vul et al. 2009, *Perspectives on Psychological Science*. 4
- Better explained in Kriegeskorte et al., 2009 *Nat. Neuroscience* 12

Circularity

- Double dipping pblm: “data are first analyzed to select a subset and then the subset is reanalyzed to obtain the results. In this context, assumptions and hypotheses determine the selection criterion and selection can, in turn, distort the results.”
- Take a gp of subjects and measures RTs, then take 2 subgroups from the same subjects and re-do some analysis?? → increases the diff.
- Take fMRI data and get activated areas, extract ROI and re-do some analyses??

Circularity

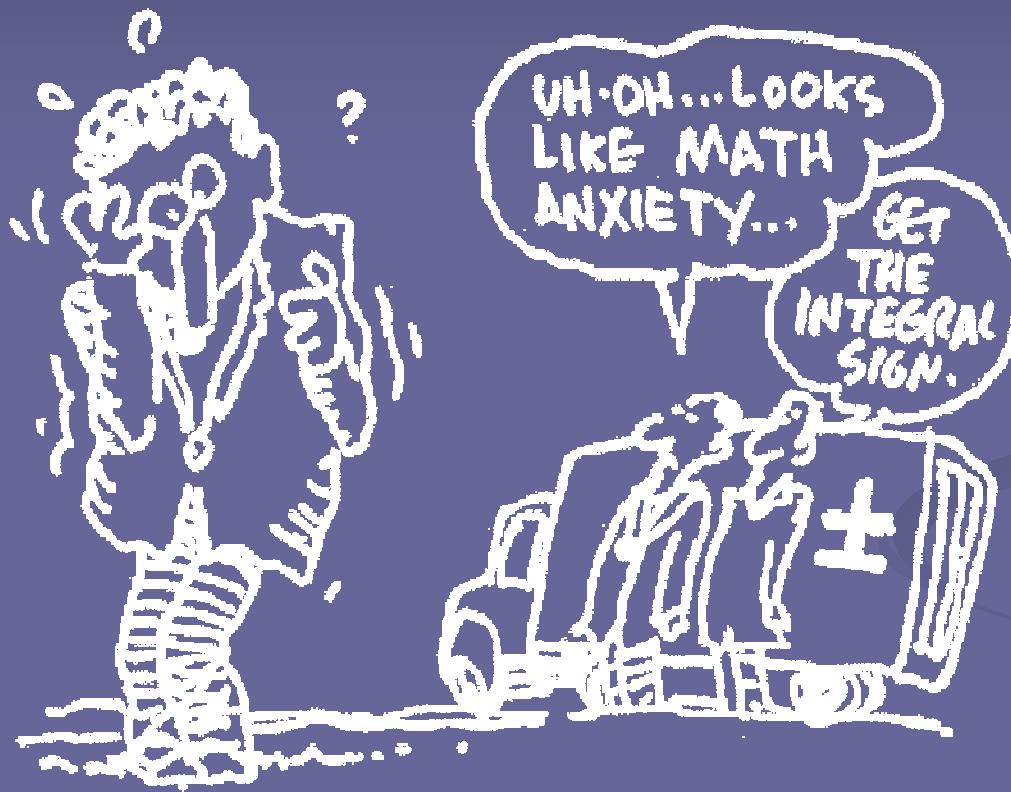
- Selection and tests must be independent – non independence create spurious effects



Circularity

- Independence of the selection and tests
 1. Anatomic ROI, analysis of fMRI
 2. SPM, minimal requirement is orthogonality of the contrasts (e.g. find regions using $A+B>0$ $C=[1 \ 1]$ and test A vs B $C=[1 \ -1]$) but if N_A and N_B are different there is still a bias when testing $A-B$ (across subjects independence is ensured by $C_{\text{selection}}^T (X^T X)^{-1} C_{\text{test}}$)
 3. Select using a subset of data, test with another one

Enough for today 😊



Thanks for your attention