Statistical analysis of fMRI data

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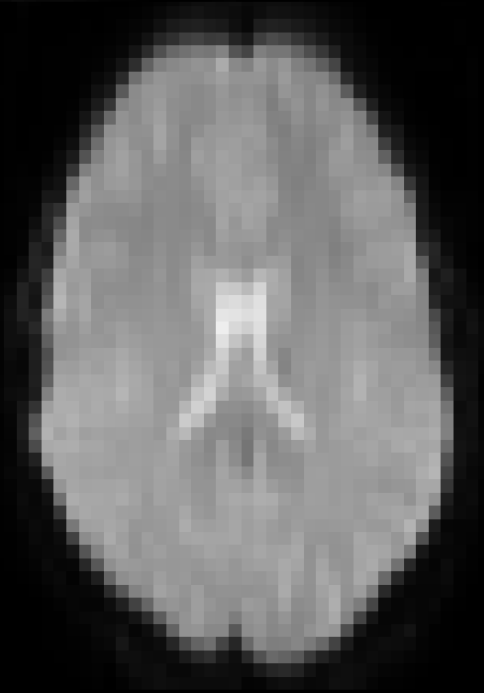
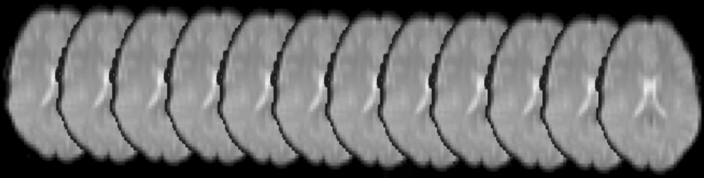
What is fMRI?

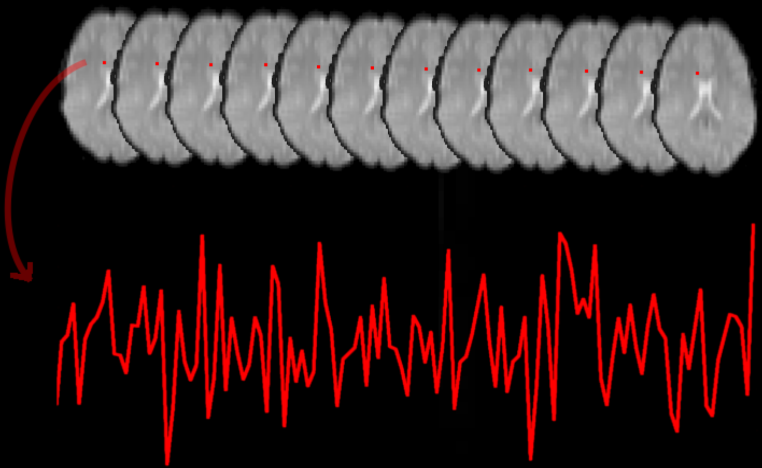
fMRI experiment design

The General Linear Model

Group inference







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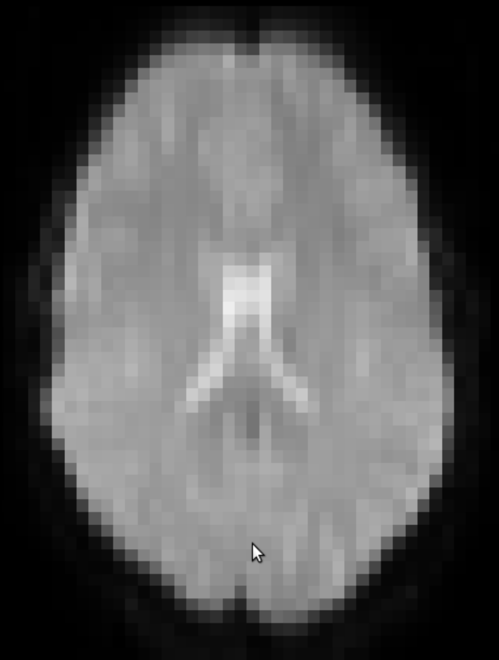
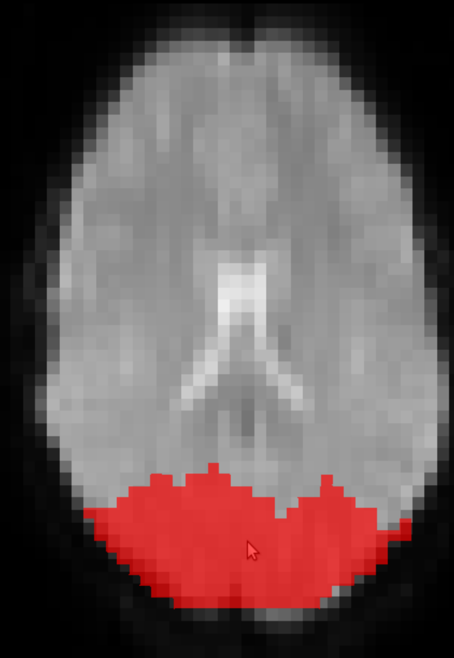
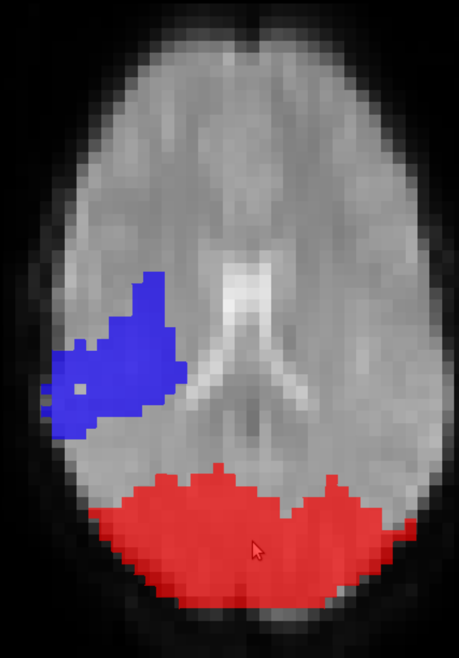
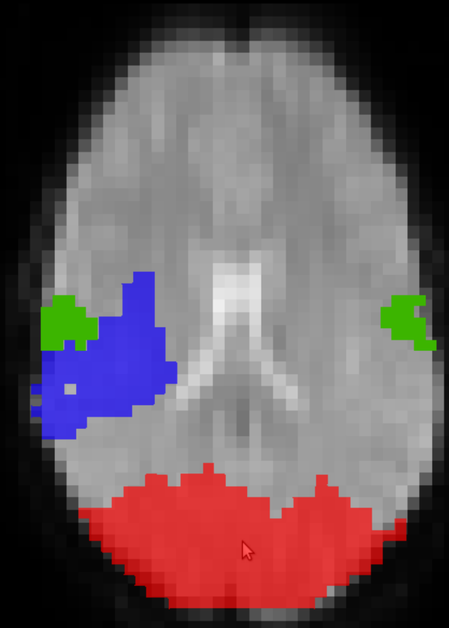
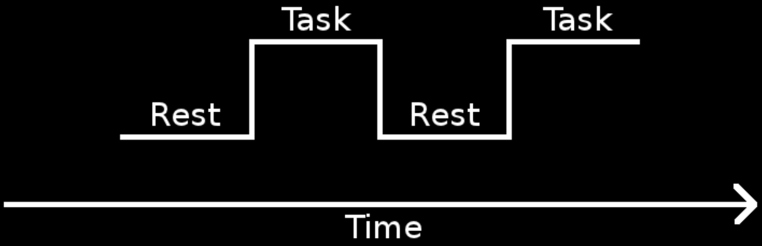
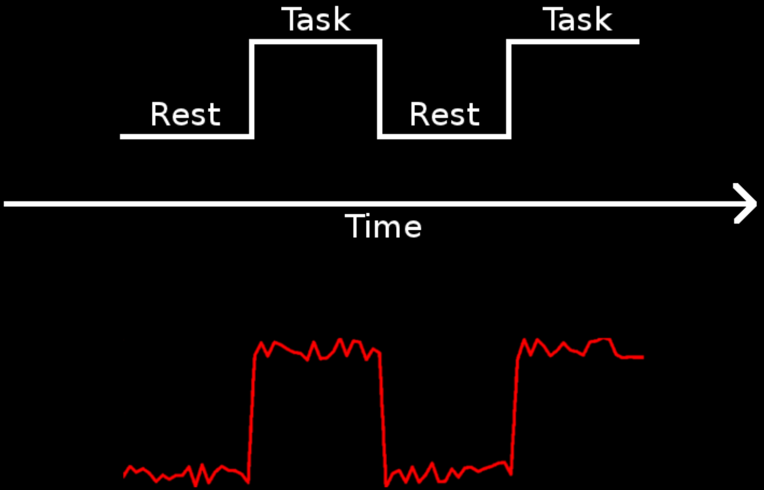


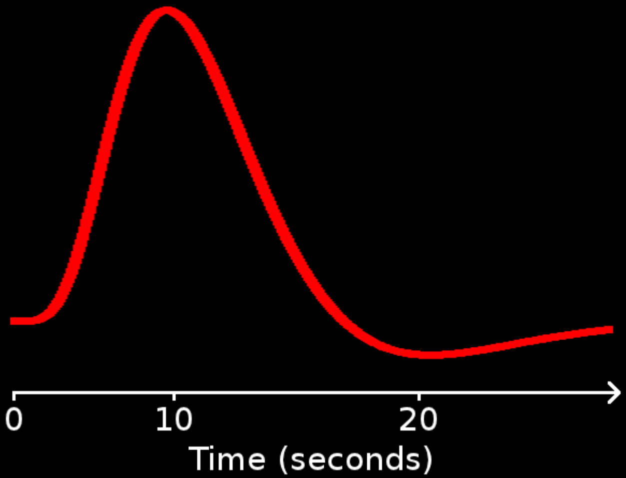


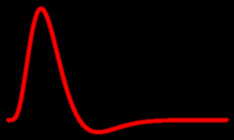


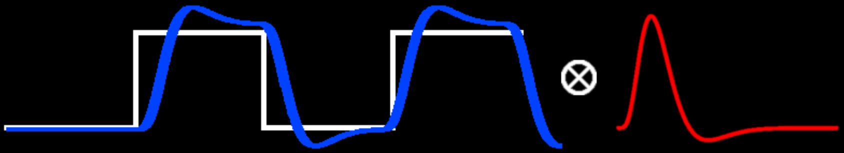



Task
Task
Rest
Rest
Time


Task
Task
Rest
Rest
Time


0
10
20
Time (seconds)





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GLM (seriously simplified)

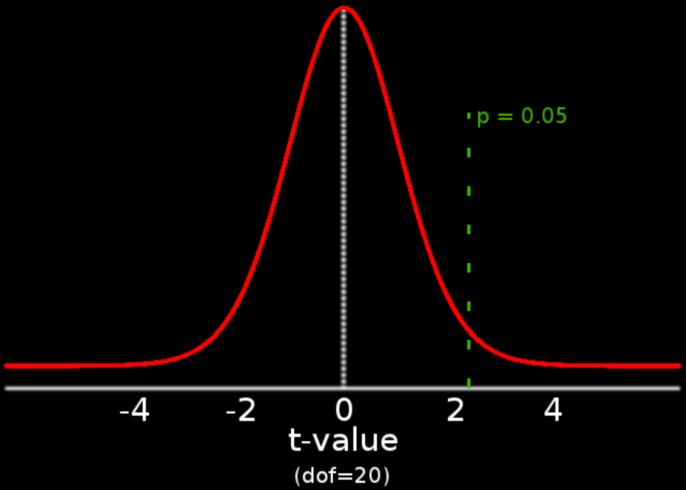
For a voxel	$v = (x, y, z) \in \mathbb{R}^3$
with an observed time course	$Y(v) = \{Y_1(v), Y_2(v), ..., Y_n(v)\}$
and expected time course (based upon the experiment design)	$X = \{X_1, X_2, ..., X_n\}$
Solve for $\beta(v)$:	$Y(v) = X\beta(v) + \epsilon(v)$

- $\beta(v)$ is the parameter estimate, which fits $Y(v)$ to X.
- $\epsilon(v)$ is the error at each time point.

$$t(v) \approx \frac{\beta(v)}{\epsilon(v)}$$

Dividing the parameter estimate $\beta(v)$ by its error $\epsilon(v)$ gives us a t value, which we can use to answer the question:

Was voxel v activated by our experimental task?


p = 0.05
-4
-2
0
2
4
t-value
(dof=20)

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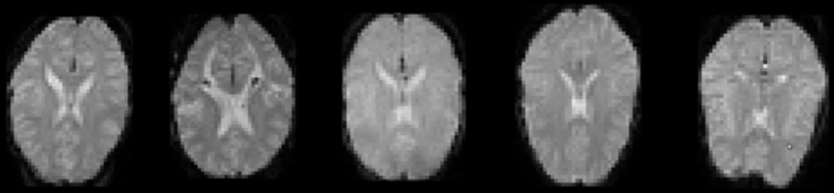

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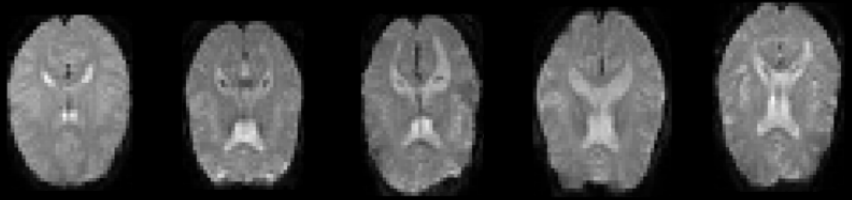
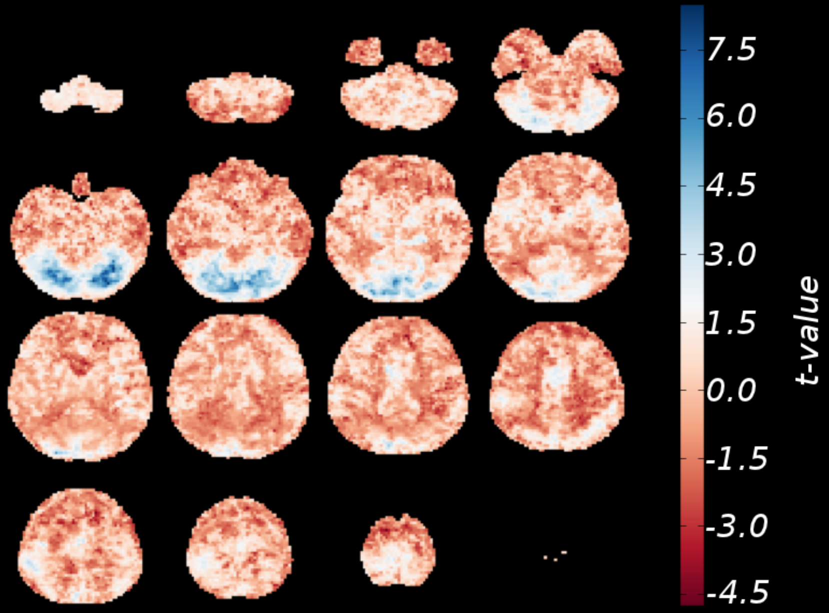


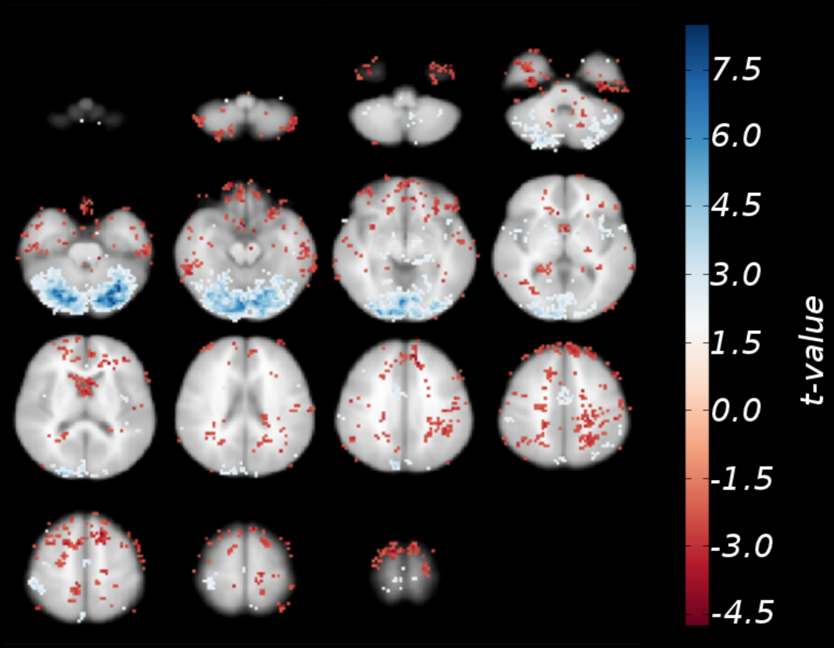
?

Two sample t-test

$$t(x, y) = \frac{\bar{x} - \bar{y}}{S_{xy}\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

$$s_{xy} = \sqrt{\frac{(n_1 - 1)S_x^2 + (n_2 - 1)S_y^2}{n_1 + n_2 - 2}}$$


7.5
6.0
4.5
3.0
1.5
0.0
-1.5
-3.0
-4.5
t-value



7.5
6.0
4.5
3.0
1.5
0.0
-1.5
-3.0
-4.5
t-value

- **Null hypothesis**: There is no difference between the two groups at voxel X.
- If a single test at a voxel has a t value with 5% likelihood of occurrence, we can reject the null hypothesis with 95% confidence.
- But that means if we perform many tests, we will incorrectly reject the null hypothesis in 5% of those tests: **false positives**.
- We need to correct for multiple comparisons.

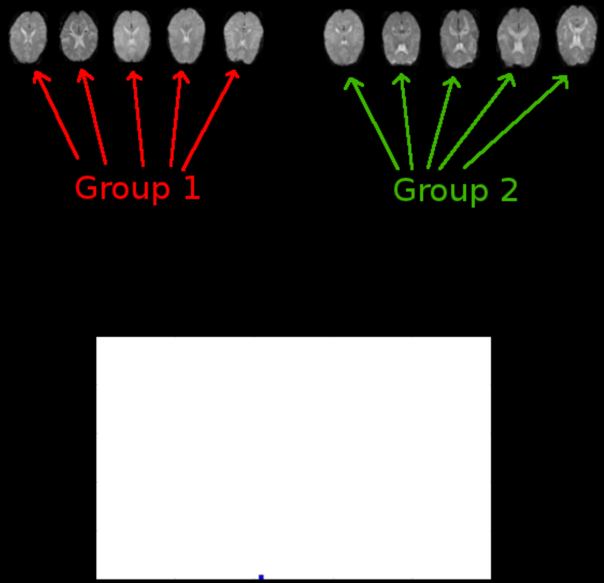
- Bonferroni correction
- False discovery rate
- Gaussian Random Field Theory
- **Random Permutation**
- **Cluster size thresholding**

Random permutation

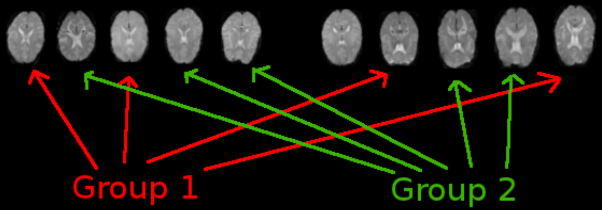
- *Parametric* statistical inferences makes assumptions about the data (e.g. comparing against an idealised, theoretical t-distribution).
- Why do this, when you can generate your own distribution from the data itself?
- Relabel your data set, and repeat the t-test for all possible relabellings (or for a random sample of them).

Random permutation

- For each relabelling of your groups, create a t image (results of a t test at every voxel).
- Save the maximum t value which occurs in this t image, and the t images for every relabelling. In this way, a *Maximal t distribution* is generated.
- Use the t value at the 95th percentile of this distribution to threshold your observed t image - all voxels with a t value greater than this threshold are significant.



Group 1
Group 2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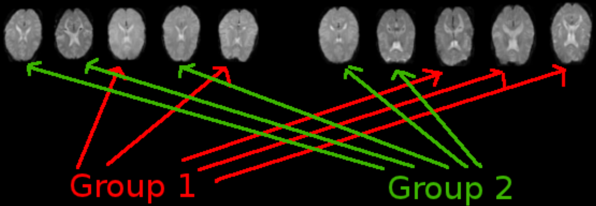
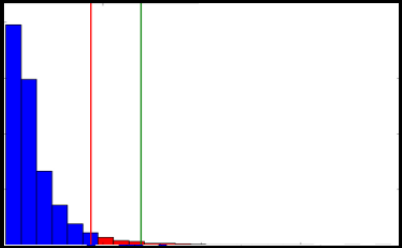
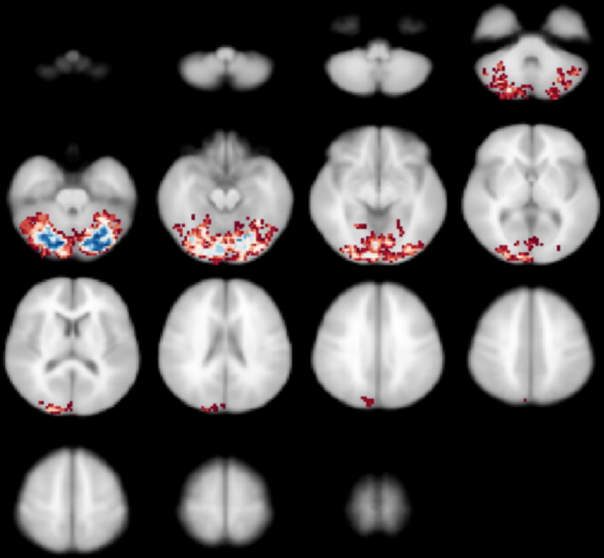

Group 1
Group 2



Cluster size thresholding

- If a voxel with a t-value of (say) 3.1 has a 5% likelihood, what is the likelihood that a cluster of 100 adjacent voxels all have t-values greater than (say) 2.3?
- Build a null-distribution of the likelihood of a cluster of size X occuring, using the random permutation techinque.
- Use the cluster size at the 95th percentile of the null distribution as your threshold - all clusters larger than this threshold are declared as significant.



The End

Questions?