

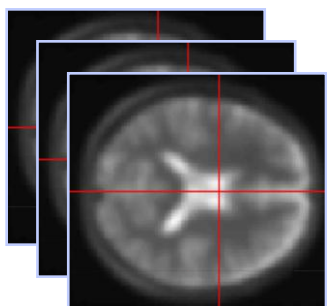
Group Analyses

Guillaume Flandin

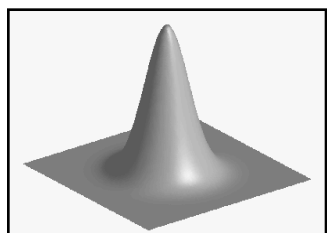
Wellcome Trust Centre for Neuroimaging
University College London

With many thanks to W. Penny, S. Kiebel, T. Nichols, R. Henson, J.-B. Poline, F. Kherif

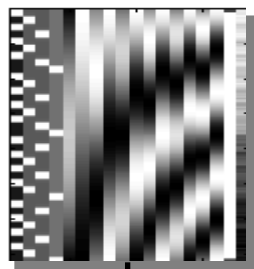
Image time-series



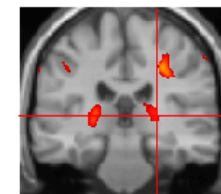
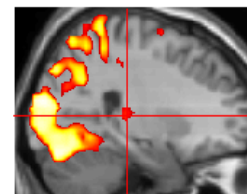
Spatial filter



Design matrix



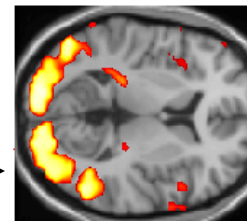
Statistical Parametric Map



Realignment

Smoothing

General Linear Model

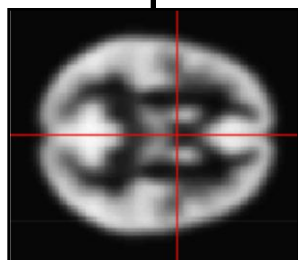


Normalisation

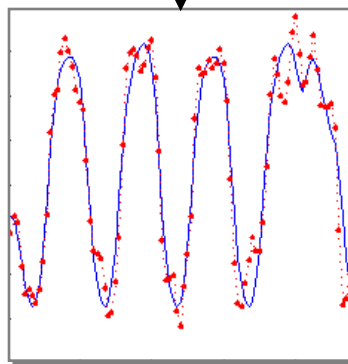
Statistical Inference

RFT

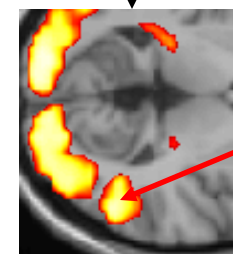
Anatomical reference



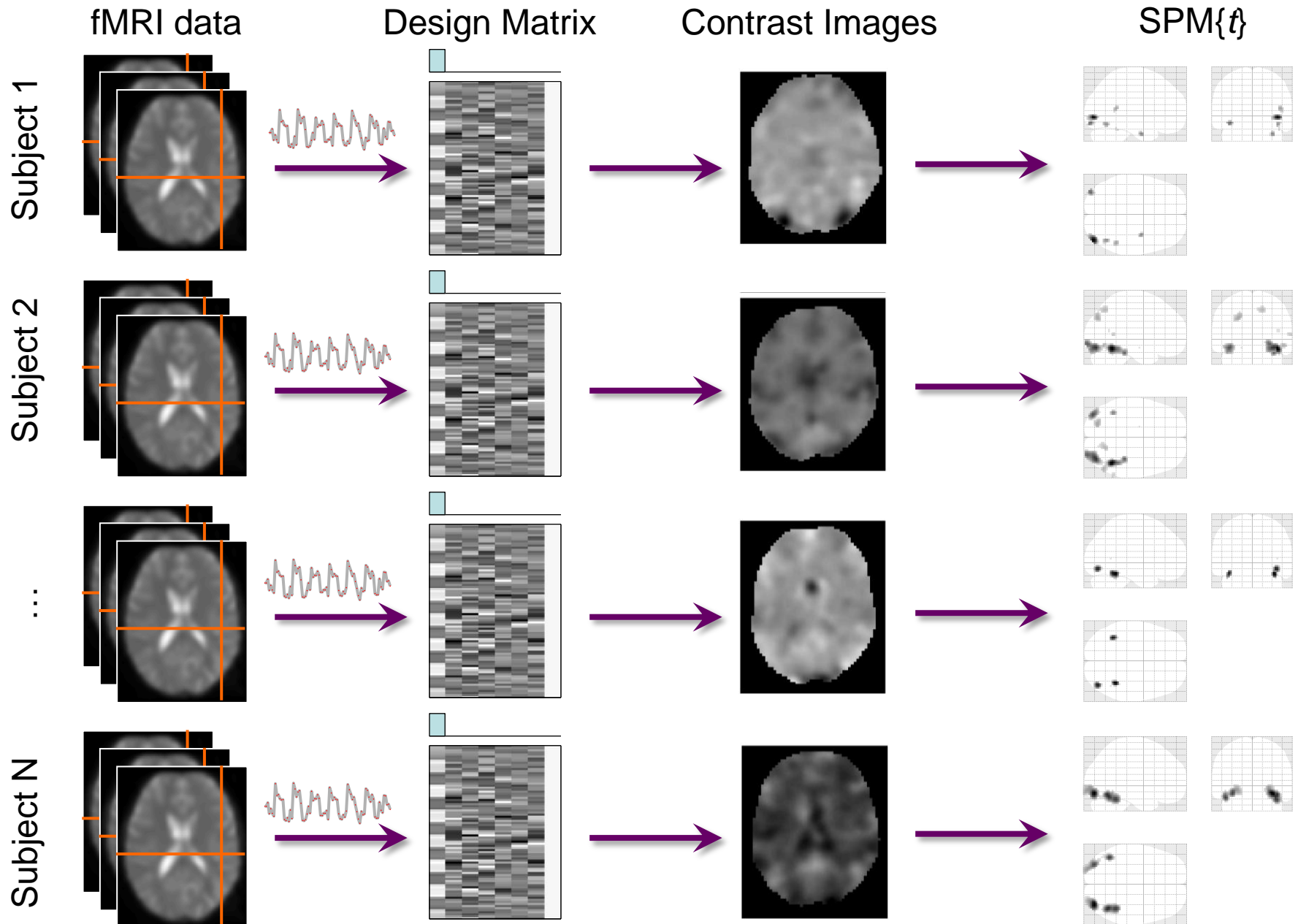
Parameter estimates



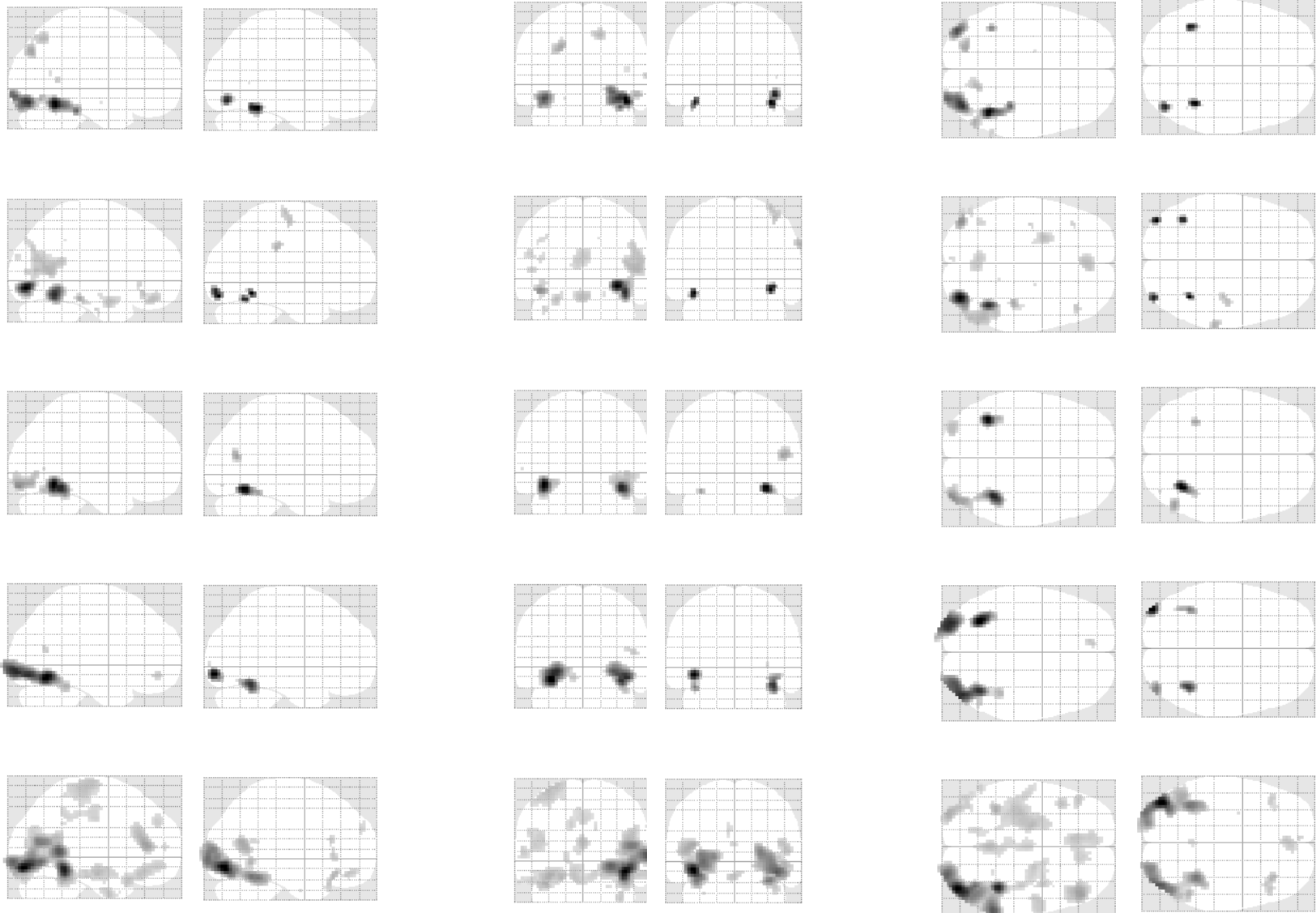
$p < 0.05$



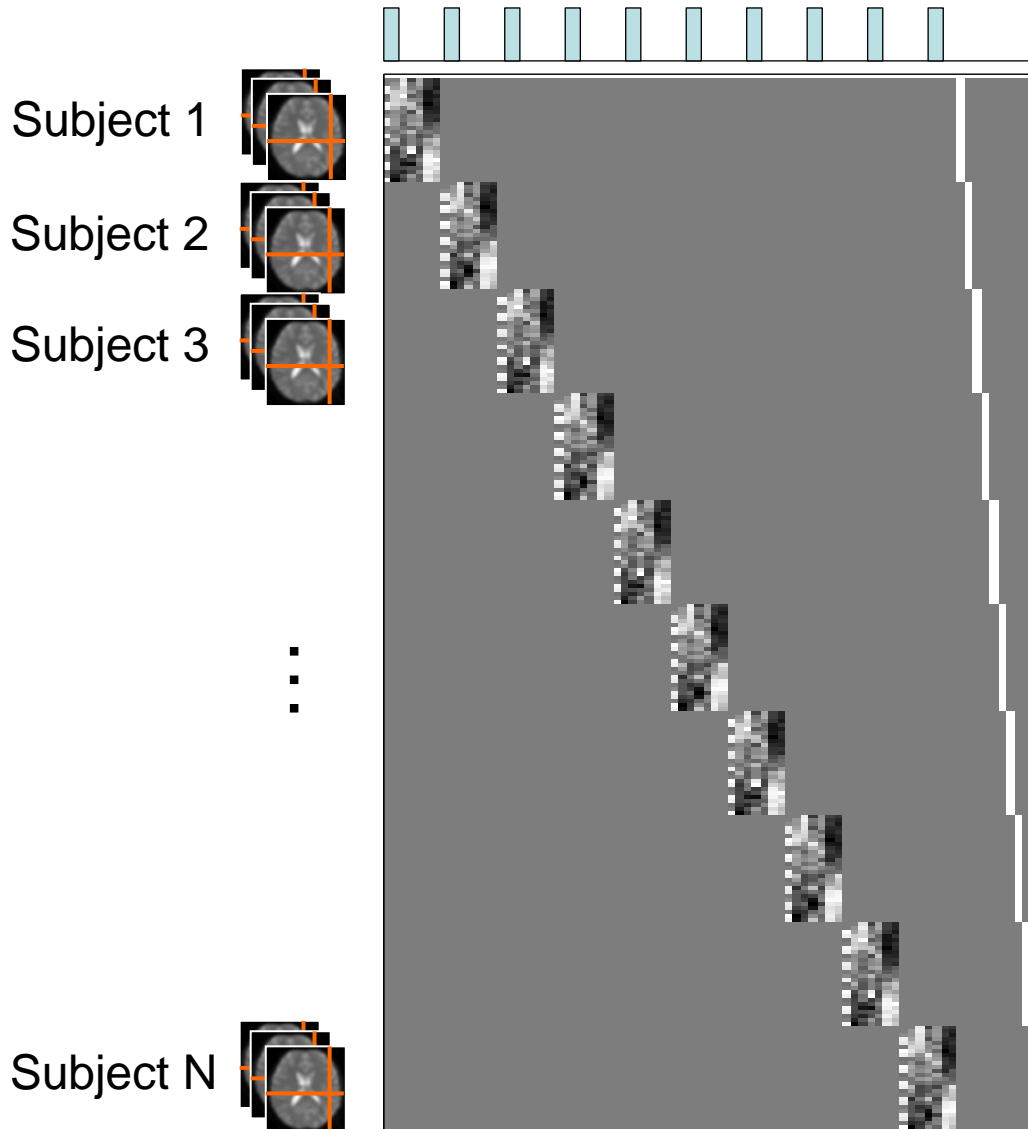
GLM: repeat over subjects



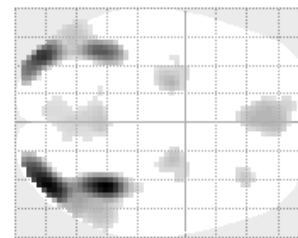
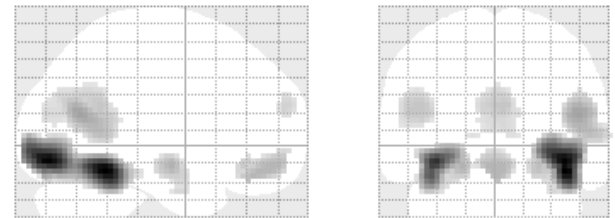
First level analyses ($p < 0.05$ FWE):



Fixed effects analysis (FFX)



Modelling all subjects at once

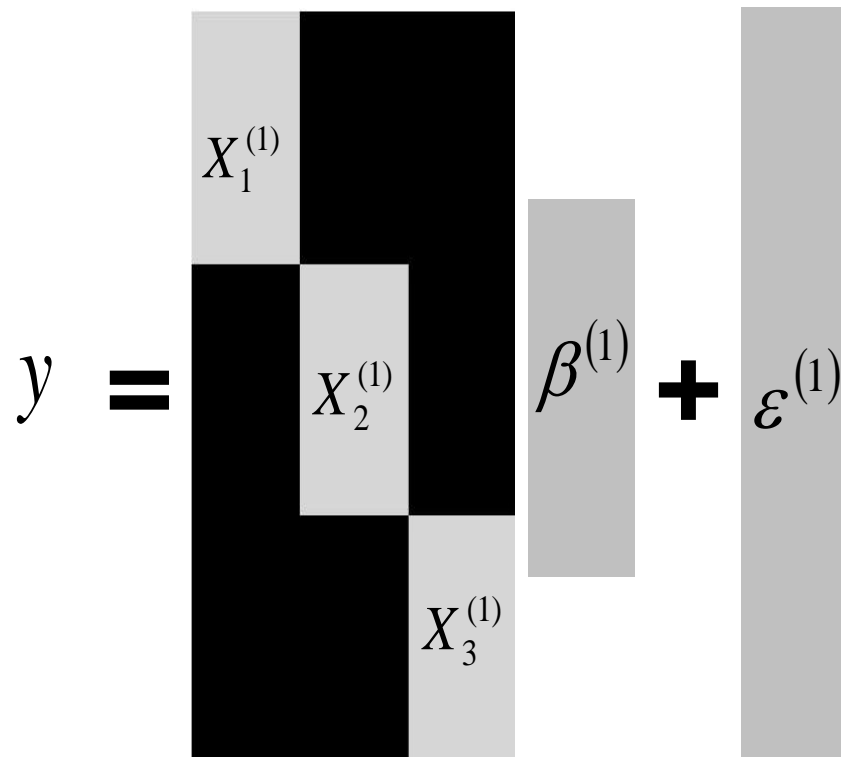


variance over subjects at each voxel

Fixed effects analysis (FFX)

$$y = X^{(1)} \beta^{(1)} + \varepsilon^{(1)}$$

Modelling all subjects at once



The diagram illustrates the equation $y = X^{(1)} \beta^{(1)} + \varepsilon^{(1)}$ using a grid of colored squares. The variable y is represented by a single black square. The equals sign is followed by a large black square representing the design matrix $X^{(1)}$. Within this matrix, three specific elements are highlighted with white squares and labeled: $X_1^{(1)}$ in the top-left, $X_2^{(1)}$ in the middle-right, and $X_3^{(1)}$ in the bottom-right. To the right of the design matrix is a gray vertical bar representing the parameter vector $\beta^{(1)}$. This is followed by a plus sign and another gray vertical bar representing the error term $\varepsilon^{(1)}$.

- ✓ Simple model
- ✓ Lots of degrees of freedom
- ✗ Large amount of data
- ✗ Assumes common variance over subjects at each voxel

Fixed effects

$$y = X^{(1)}\beta^{(1)} + \varepsilon^{(1)}$$



□ Only one source of random variation (over sessions):

➤ measurement error

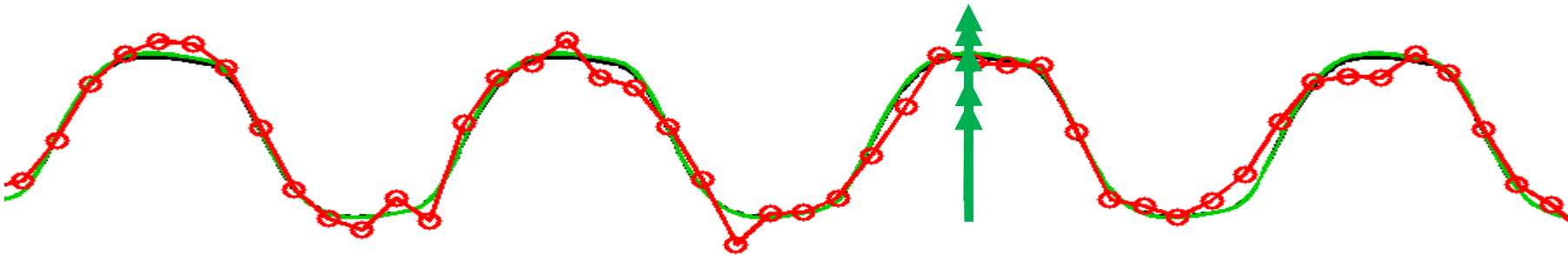
Within-subject Variance

□ True response magnitude is *fixed*.

Random effects

$$y = X^{(1)} \beta^{(1)} + \varepsilon^{(1)}$$

$$\beta^{(1)} = X^{(2)} \beta^{(2)} + \varepsilon^{(2)}$$



□ Two sources of random variation:

➤ measurement errors

➤ response magnitude (over subjects)

Within-subject Variance

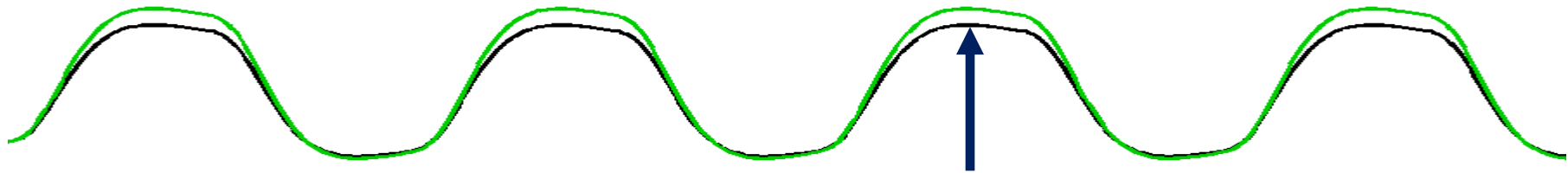
Between-subject Variance

□ Response magnitude is *random*

➤ each subject/session has random magnitude

Random effects

$$y = X^{(1)}\beta^{(1)} + \varepsilon^{(1)}$$
$$\beta^{(1)} = X^{(2)}\beta^{(2)} + \varepsilon^{(2)}$$



□ Two sources of random variation:

➤ measurement errors

➤ response magnitude (over subjects)

Within-subject Variance

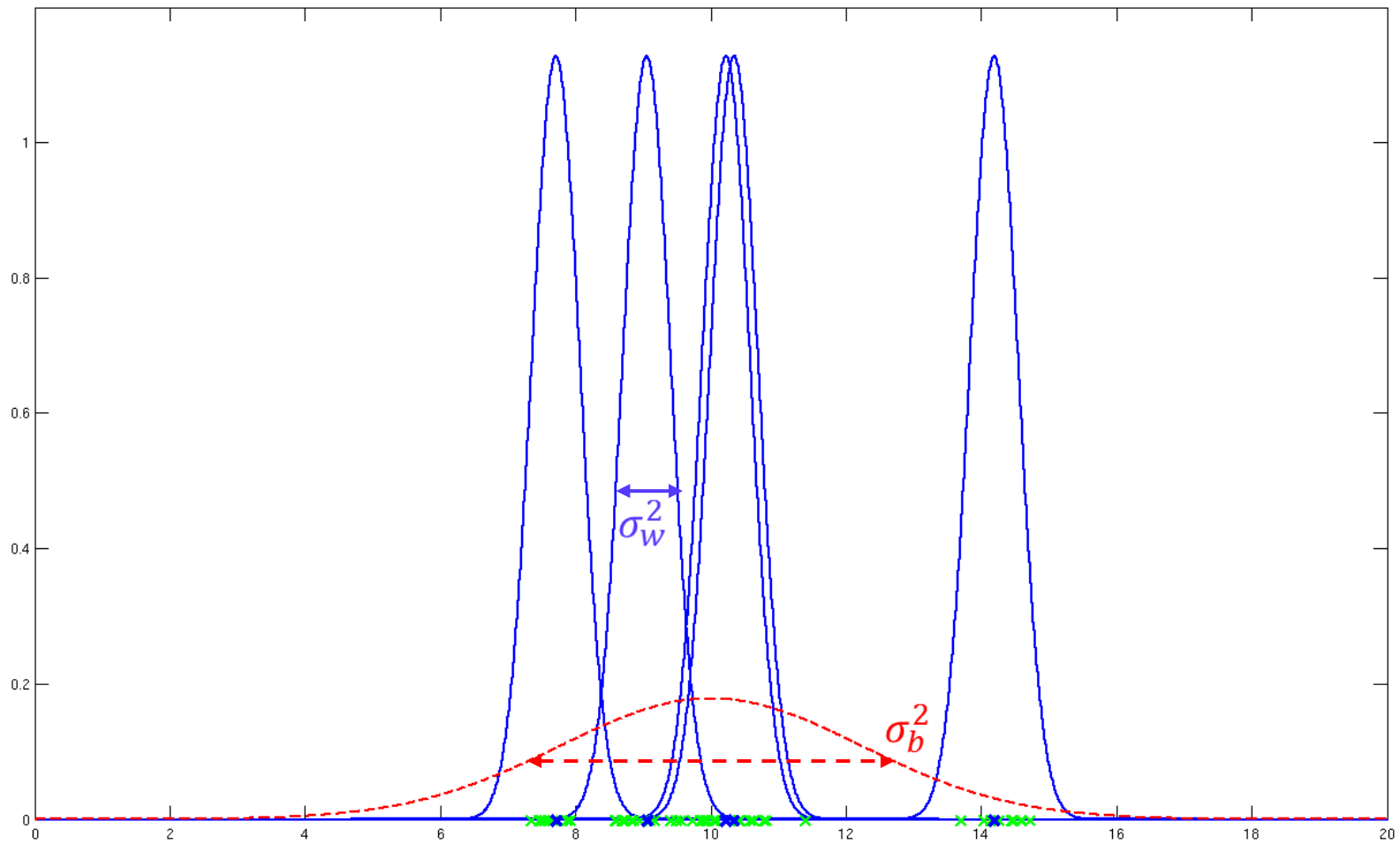
Between-subject Variance

□ Response magnitude is *random*

➤ each subject/session has random magnitude

➤ but population mean magnitude is *fixed*.

Random effects



Probability model underlying random effects analysis

Fixed vs random effects

With **Fixed Effects Analysis (FFX)** we compare the group effect to the *within-subject variability*. It is not an inference about the population from which the subjects were drawn.

With **Random Effects Analysis (RFX)** we compare the group effect to the *between-subject variability*. It is an inference about the population from which the subjects were drawn. If you had a new subject from that population, you could be confident they would also show the effect.

Fixed vs random effects

- ❑ Fixed isn't "wrong", just usually isn't of interest.

- ❑ Summary:

 - **Fixed effects inference:**

 - "I can see this effect in this cohort"*

 - **Random effects inference:**

 - "If I were to sample a new cohort from the same population I would get the same result"*

Terminology

Hierarchical linear models:

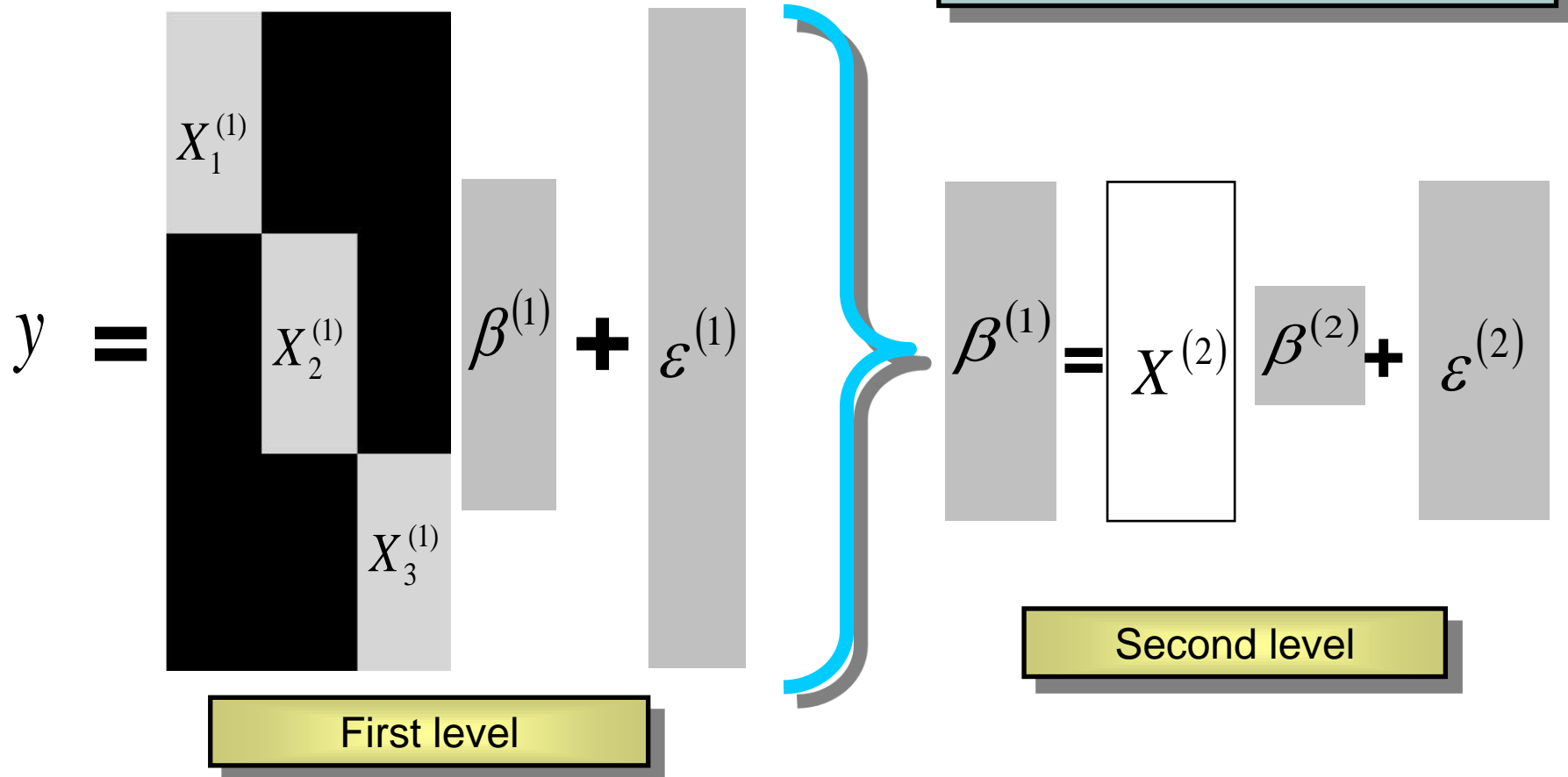
- Random effects models
- Mixed effects models
- Nested models
- Variance components models

... all the same

... all alluding to multiple sources of variation
(in contrast to fixed effects)

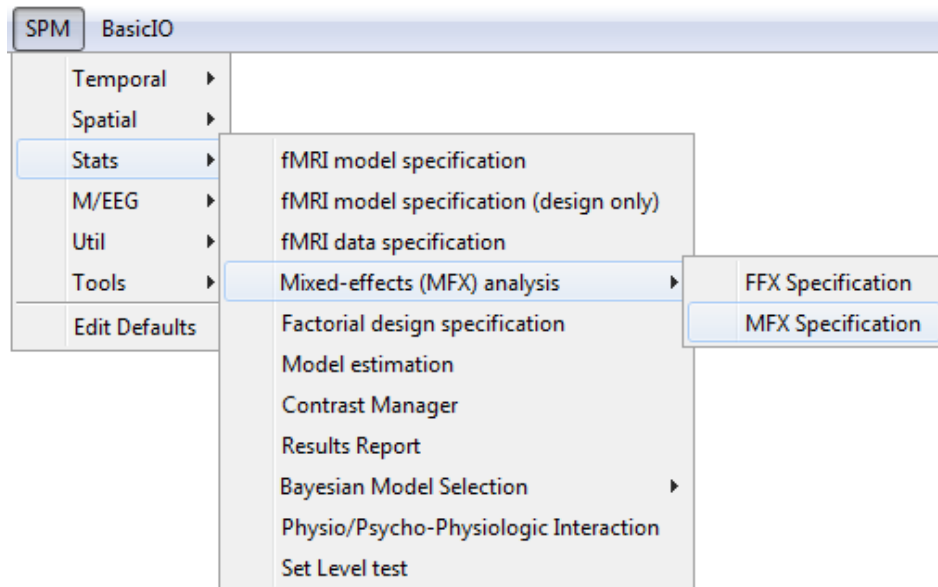
Hierarchical models

Example: Two level model



Hierarchical models

- Restricted Maximum Likelihood (ReML)
- Parametric Empirical Bayes
- Expectation-Maximisation Algorithm



`spm_mfx.m`

But:

- Many two level models are just too big to compute.
- And even if, it takes a long time!
- Any approximation?

First level

Second level

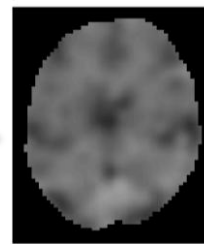
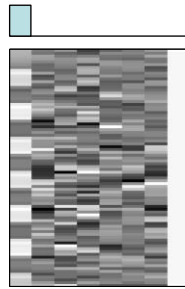
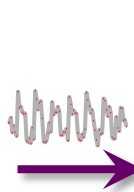
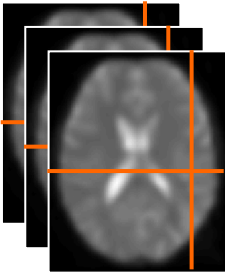
fMRI data

Design Matrix

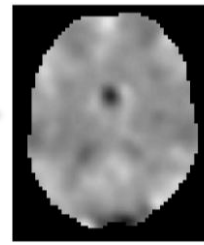
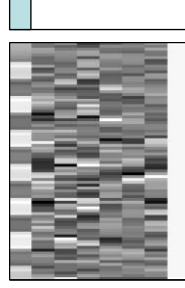
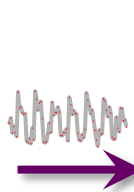
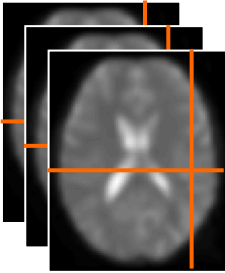
Contrast Images

One-sample t-test @ second level

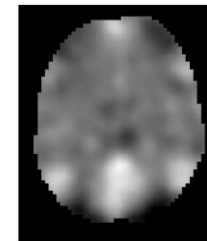
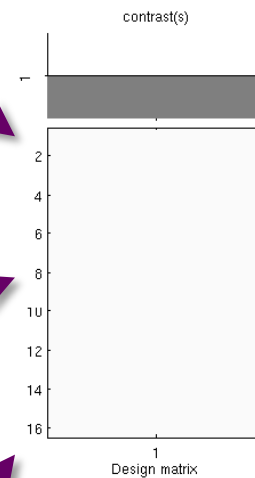
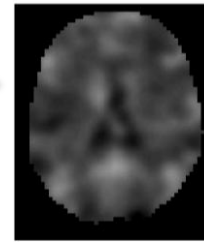
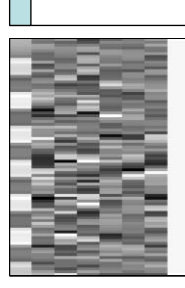
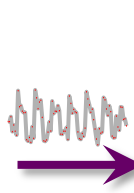
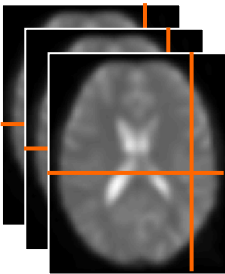
Subject 1



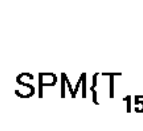
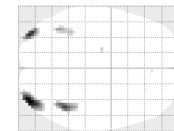
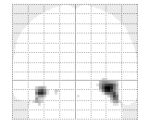
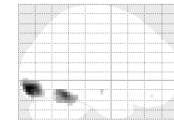
...



Subject N



$$t = \frac{c^T \hat{\beta}}{\sqrt{\text{Var}(c^T \hat{\beta})}}$$



SPM{T}_{15}

Generalisability, Random Effects & Population Inference. Holmes & Friston, NeuroImage, 1998.

Assumptions

- ❑ The summary statistics approach is exact if for each session/subject:
 - Within-subjects variances the same
 - First level design the same (e.g. number of trials)
- ❑ Other cases: summary statistics approach is robust against typical violations.

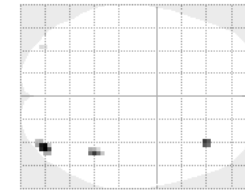
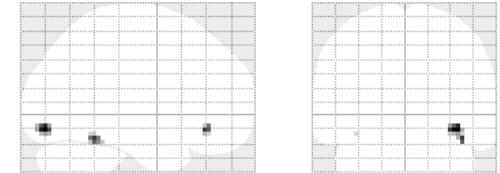
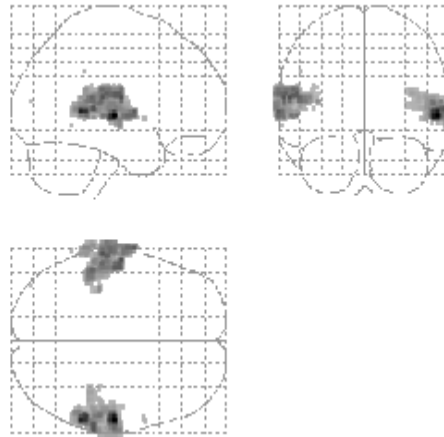
Mixed-effects and fMRI studies. Friston et al., NeuroImage, 2005.

Statistical Parametric Mapping: The Analysis of Functional Brain Images. Elsevier, 2007.

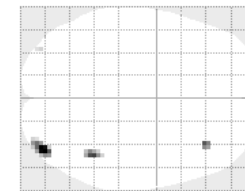
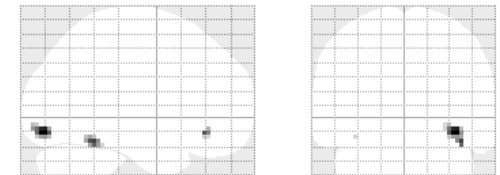
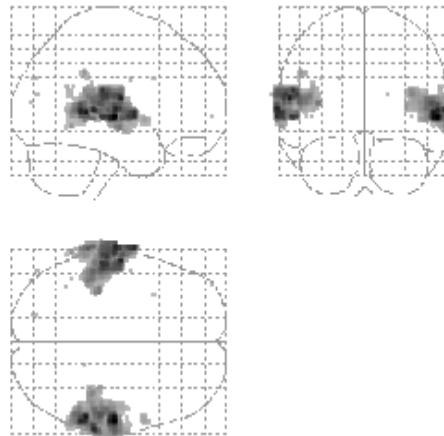
Simple group fMRI modeling and inference. Mumford & Nichols. NeuroImage, 2009.

Robustness

Summary
statistics



Hierarchical
Model



Listening to words

Viewing faces

ANOVA & non-sphericity

❑ One effect per subject:

- Summary statistics approach
- One-sample t-test at the second level

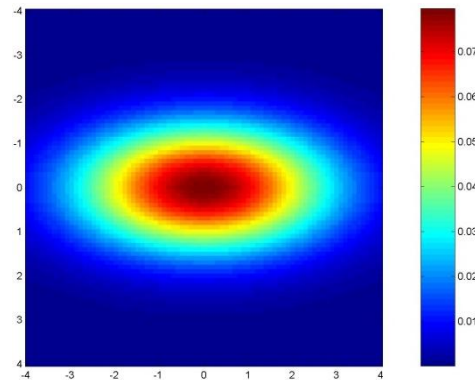
❑ More than one effect per subject or multiple groups:

- Non-sphericity modelling
- Covariance components and ReML

GLM assumes Gaussian “spherical” (i.i.d.) errors

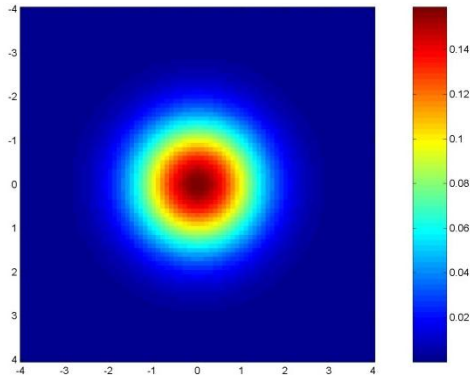
sphericity = iid:
error covariance is
scalar multiple of
identity matrix:
 $\text{Cov}(e) = \sigma^2 \mathbf{I}$

Examples for non-sphericity:

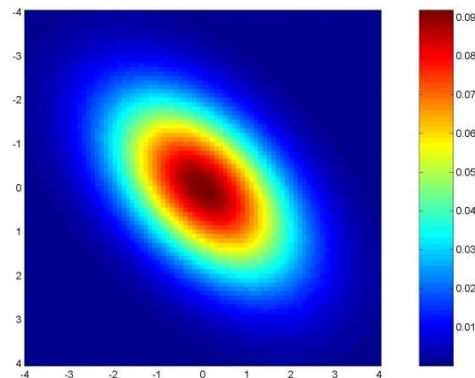


$$\text{Cov}(e) = \begin{bmatrix} 4 & 0 \\ 0 & 1 \end{bmatrix}$$

non-identically
distributed



$$\text{Cov}(e) = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}$$



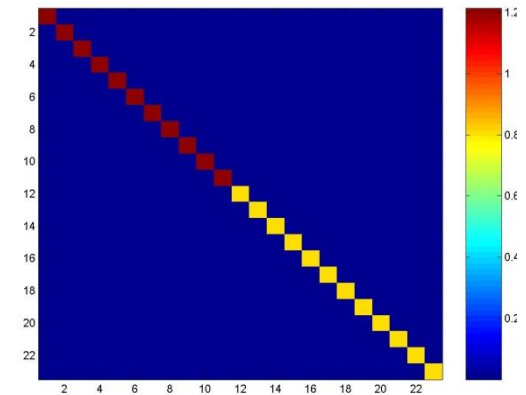
$$\text{Cov}(e) = \begin{bmatrix} 2 & 1 \\ 1 & 2 \end{bmatrix}$$

non-independent

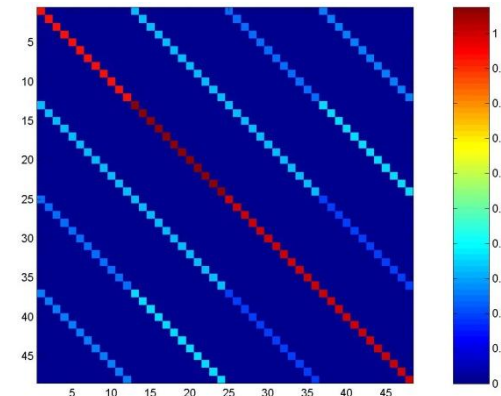
2nd level: Non-sphericity

Errors are independent
but not identical
(e.g. different groups (patients, controls))

Error covariance matrix



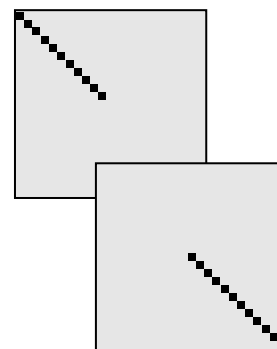
Errors are not independent
and not identical
(e.g. repeated measures for each subject
(multiple basis functions, multiple
conditions, etc.))



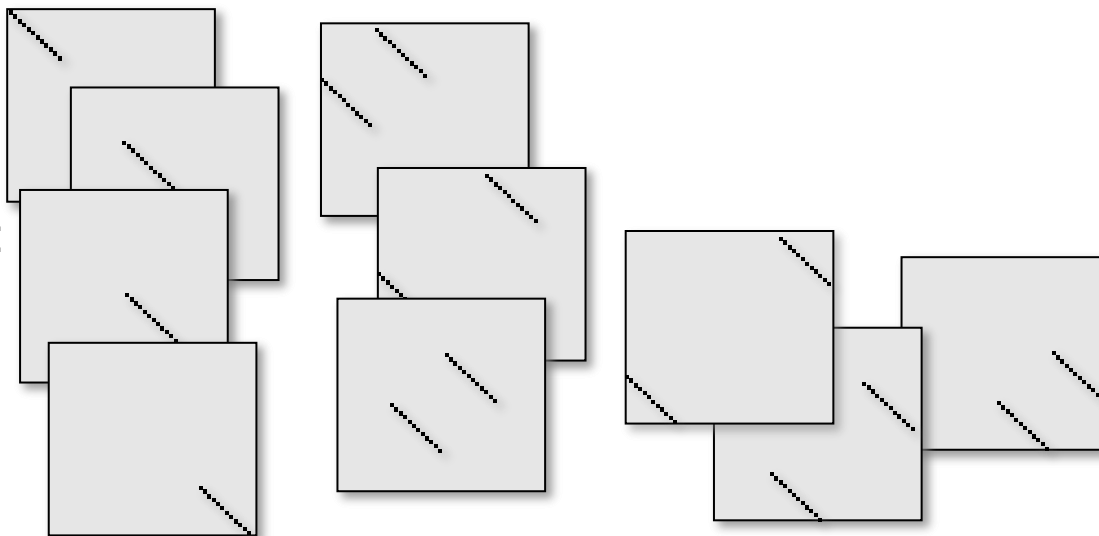
2nd level: Variance components

$$\text{Cov}(\varepsilon) = \sum_k \lambda_k Q_k$$

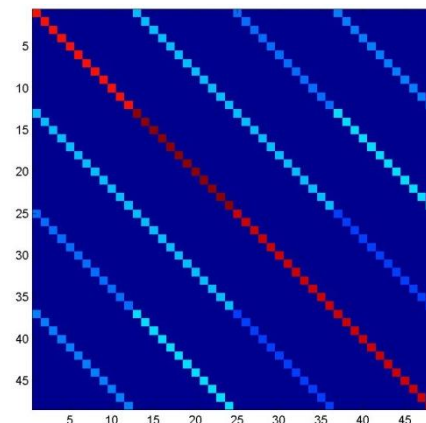
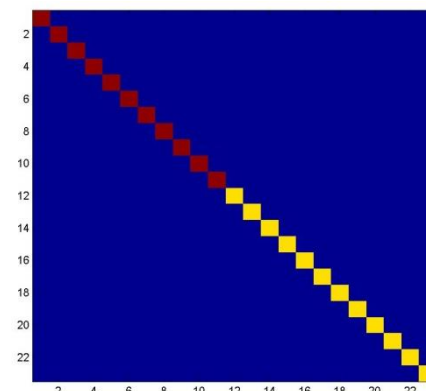
Q_k 's:



Q_k 's:



Error covariance matrix



Example 1: between-subjects ANOVA

□ Stimuli:

- Auditory presentation (SOA = 4 sec)
- 250 scans per subject, block design
- 2 conditions
 - Words, e.g. “book”
 - Words spoken backwards, e.g. “koob”

□ Subjects:

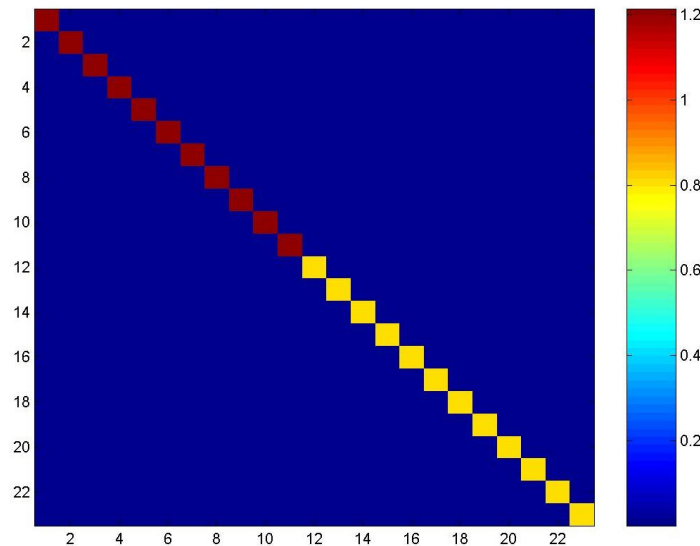
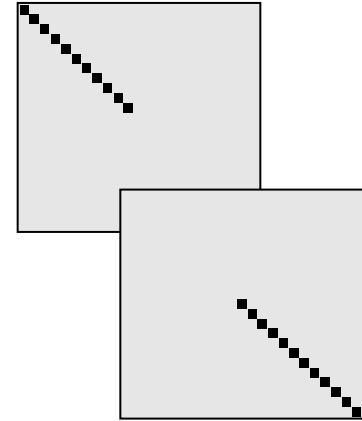
- 12 controls
- 11 blind people

Example 1: Covariance components

□ Two-sample t-test:

- Errors are independent but not identical.
- 2 covariance components

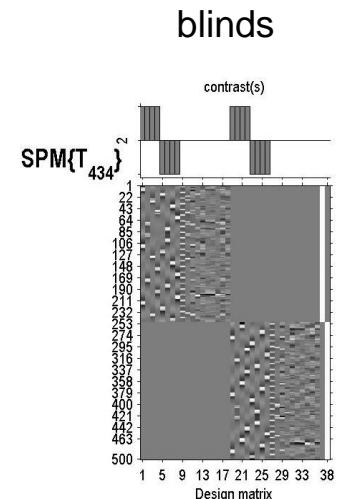
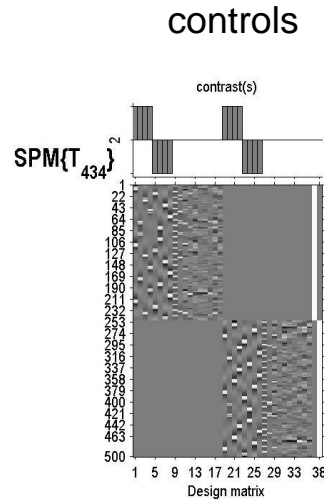
Q_k 's:



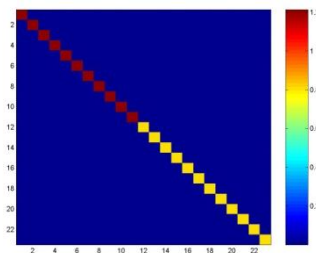
Error covariance matrix

Example 1: Group differences

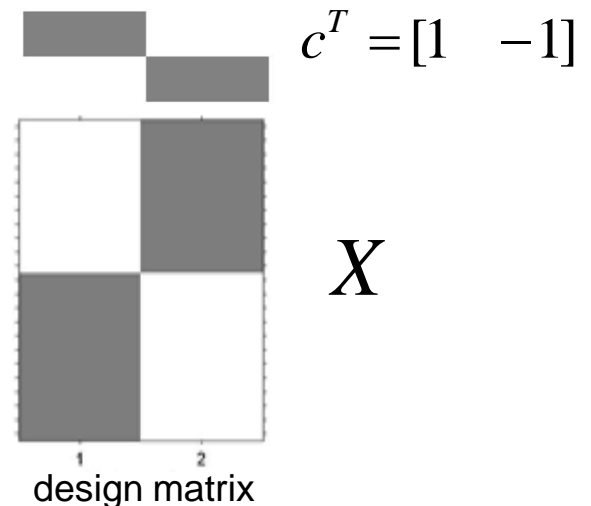
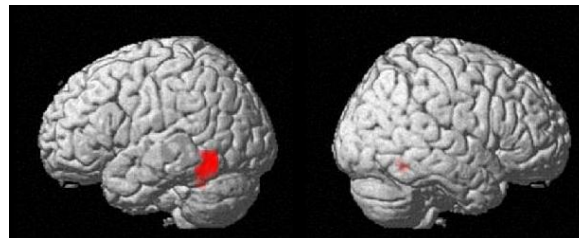
First Level



Second Level



$$Cov(\varepsilon)$$



Example 2: within-subjects ANOVA

□ Stimuli:

- Auditory presentation (SOA = 4 sec)
- 250 scans per subject, block design

➤ Words:

Motion	Sound	Visual	Action
“jump”	“click”	“pink”	“turn”

□ Subjects:

- 12 controls

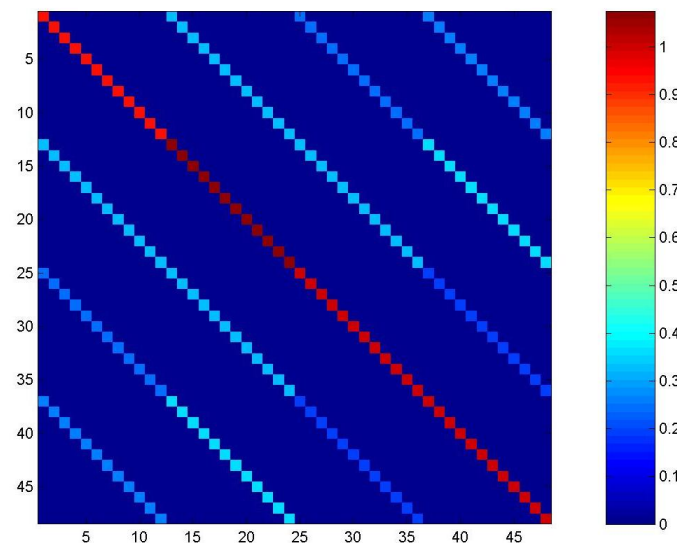
□ Question:

- What regions are generally affected by the semantic content of the words?

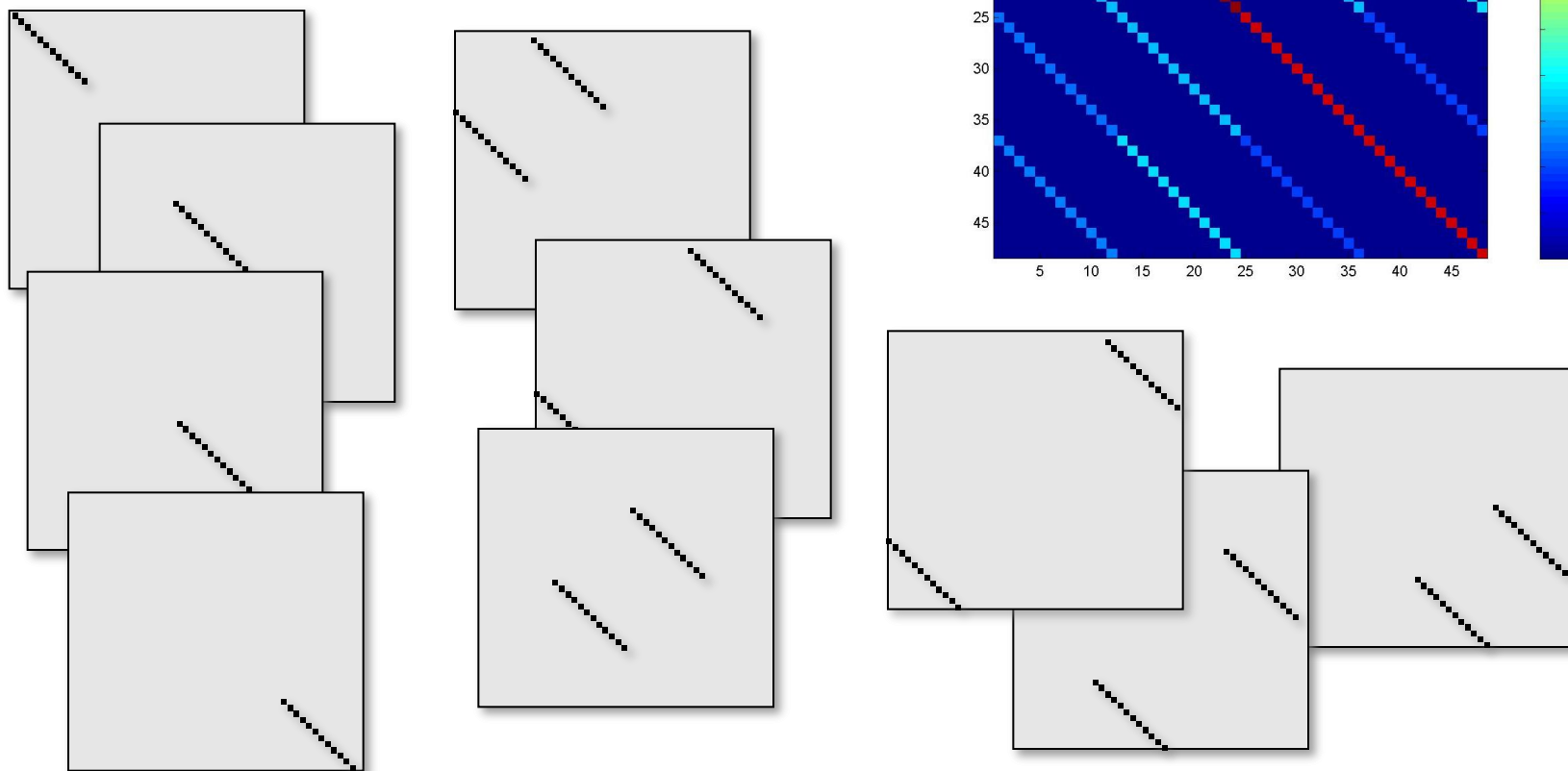
Example 2: Covariance components

- Errors are not independent and not identical

Error covariance matrix



Q_k 's:



Example 2: Repeated measures ANOVA

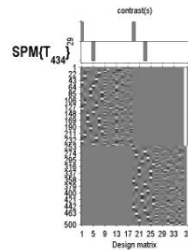
Motion

Sound

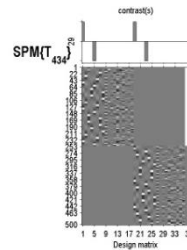
Visual

Action

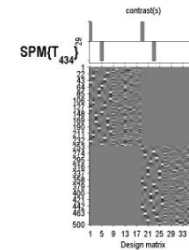
First
Level



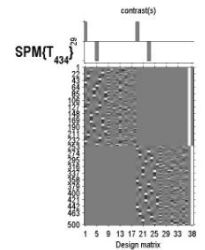
?



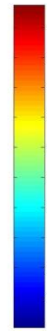
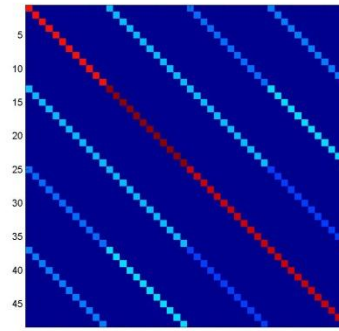
?



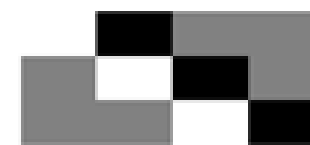
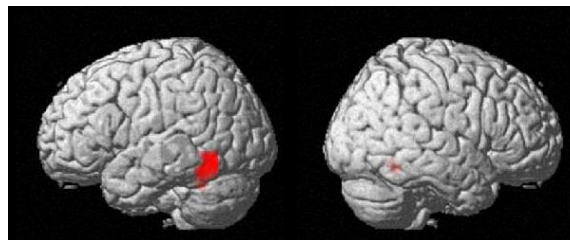
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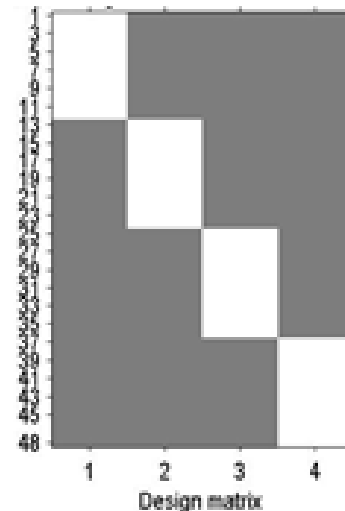
Second
Level



$Cov(\varepsilon)$

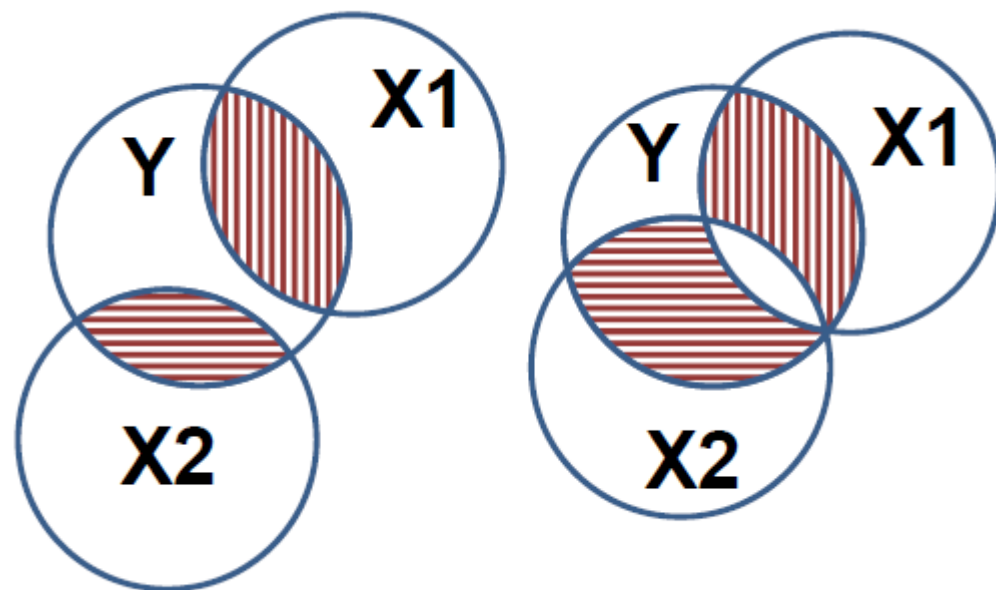
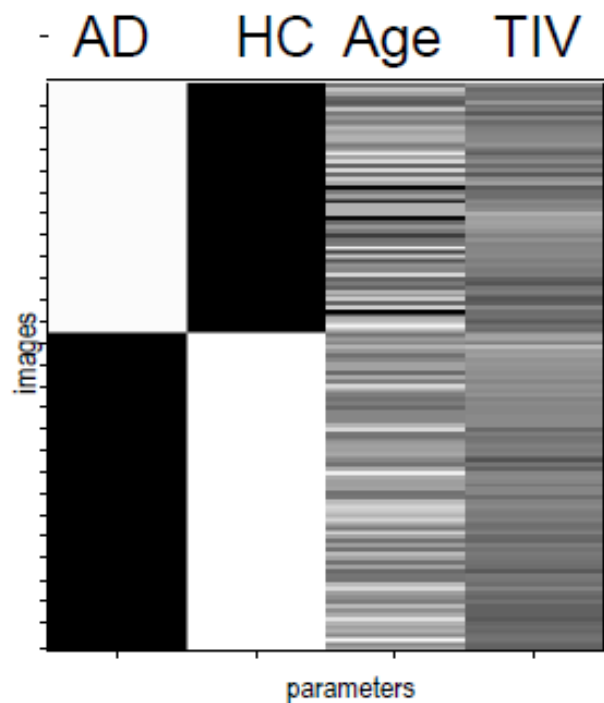


$$c^T = \begin{pmatrix} 1 & -1 & 0 & 0 \\ 0 & 1 & -1 & 0 \\ 0 & 0 & 1 & -1 \end{pmatrix}$$



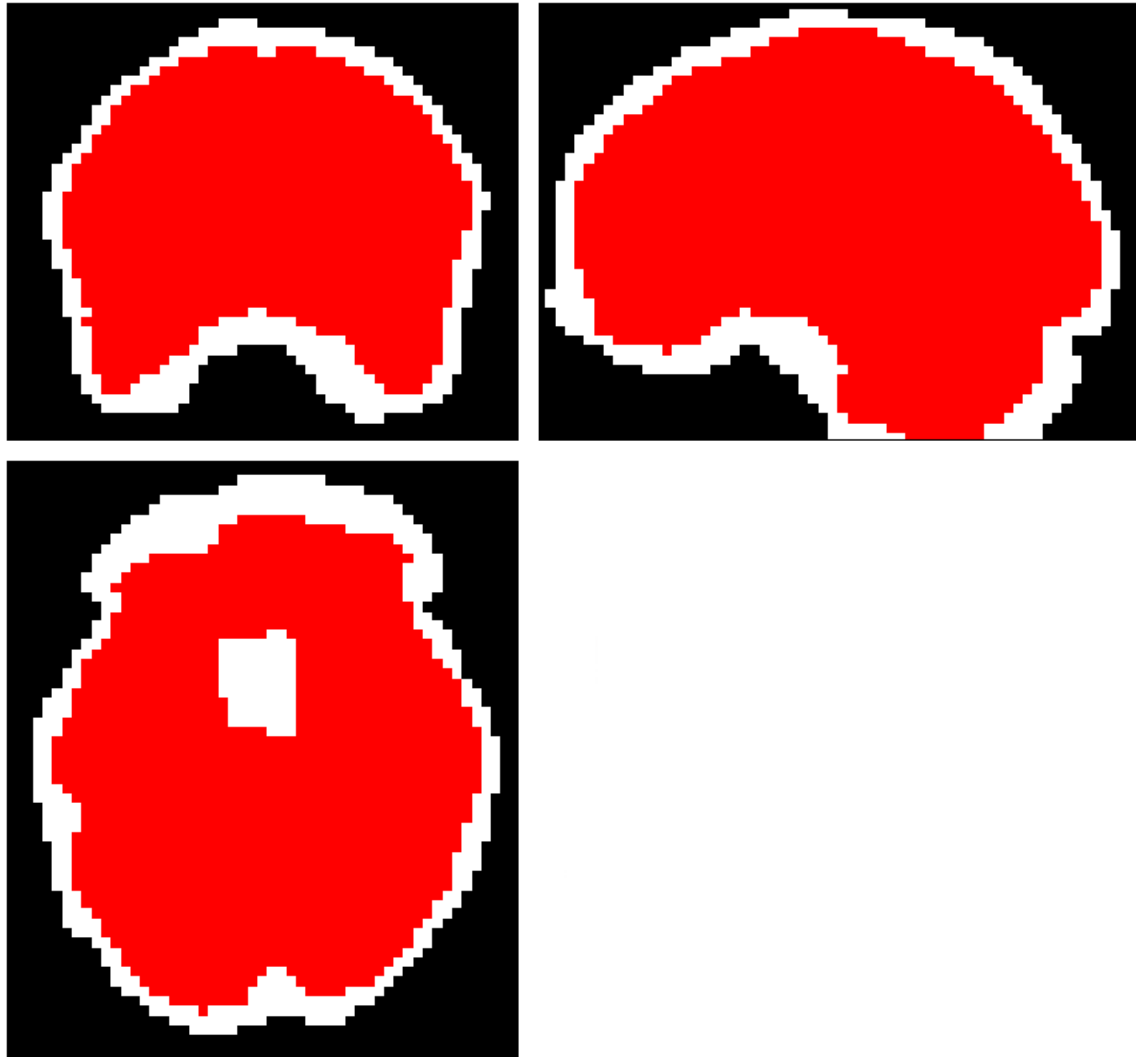
X

ANCOVA model



Mean centering continuous covariates for a group fMRI analysis, by J. Mumford:
http://mumford.fmripower.org/mean_centering/

Analysis mask: logical AND



SPM interface: factorial design specification

□ Options:

- One-sample t-test
- Two-sample t-test
- Paired t-test
- Multiple regression
- One-way ANOVA
- One-way ANOVA – within subject
- Full factorial
- Flexible factorial

Summary

- ❑ Group Inference usually proceeds with **RFX analysis**, not FFX. Group effects are compared to between rather than within subject variability.
- ❑ **Hierarchical models** provide a gold-standard for RFX analysis but are computationally intensive.
- ❑ **Summary statistics** approach is a robust method for RFX group analysis.
- ❑ Can also use '**ANOVA**' or '**ANOVA within subject**' at second level for inference about multiple experimental conditions or multiple groups.

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