

Today

- Posters
- General poster feedback
- WWTBAFA



If you have not yet presented your poster
(and would like to) please make yourself
known.

Too much text

- If there is too much text, people will not read the content, or they will disengage.
- The text should be there to anchor the spoken content.
- Posters are not meant to be ‘read’, they are meant as visual aids for the spoken content.
- However, to some extent they should be explanatory, or at least interesting in their own right. A difficult balance.....

Colors are fine, but use them effectively.

Use visualisations effectively

- Some concepts may require a visual aid to explain them.
- Hand gestures are fine, but better with reference to figures.....
- Include a brief figure caption and talk the audience through the figures.

Naturalistic Stimulation Reveals The Tonotopic Structure of Human Auditory Cortex

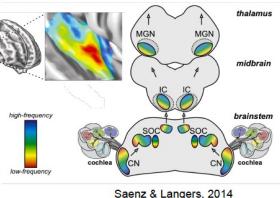
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1. Centre for Integrative Neuroscience and Neurodynamics, University of Reading

2. Spinoza Centre for Neuroimaging, Vrije Universiteit Amsterdam

Background

Auditory sensations are organised by sound frequency (tonotopically).



However, the detailed tonotopic organisation within the cortex is unclear.

Here, we applied a novel modeling procedure to a high powered dataset to elucidate the modes of organisation in auditory cortex.

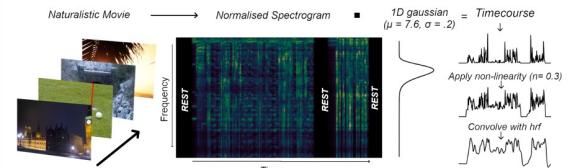
Participants and Stimuli

174 participants from human connectome project movie-watching dataset.

Participants viewed four 15 minute movies, consisting of Hollywood or Independent movie clips.

Data collected at 7 Tesla, sampling rate of 1 second.

CSS Model



Modeled responses as the overlap of spectrogram and a 1D Gaussian, parameterised by preferred frequency (μ) and size (σ).

Additional n parameter to quantify spectral nonlinearity.

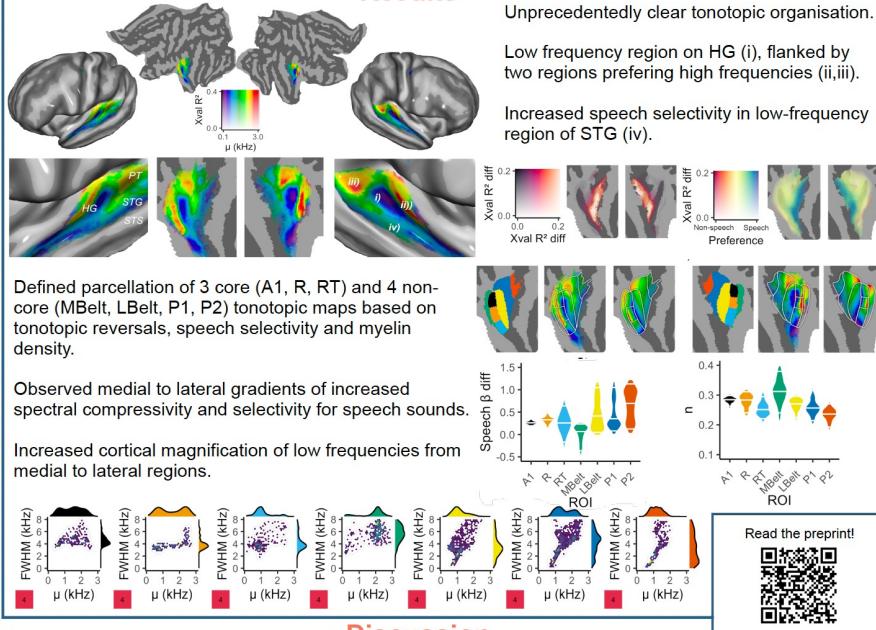
Performance tested via leave one movie out cross-validation.

Results

Unprecedentedly clear tonotopic organisation.

Low frequency region on HG (i), flanked by two regions preferring high frequencies (ii,iii).

Increased speech selectivity in low-frequency region of STG (iv).



Discussion

Model of auditory cortical organisation that goes beyond A1/ RT, consistent with 'working model' proposed by Moerel et al., 2014.

We reveal medial to lateral gradients of increased compressivity and category selectivity, supporting hierarchical models of speech perception that propose a sequence of spectral - articulatory - semantic representations running medially to laterally from HG- STG - STS.



nhedger1@gmail.com



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1	\$ 500

Second level analyses

(Slides, worksheet,
notebook) INCOMING

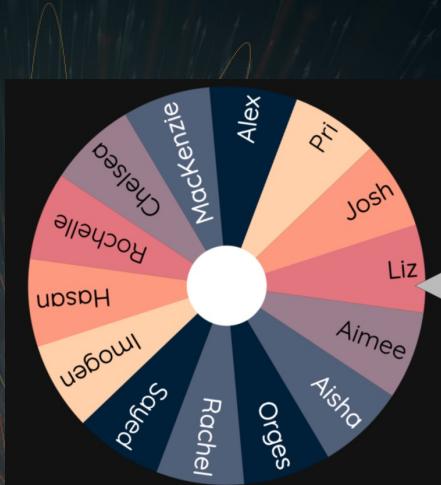
GLM

(Slides, worksheet, colab
notebook)

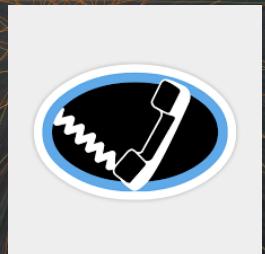
Preprocessing

(slides, worksheet)

Random selection of
answerers



BUT
You can **phone a friend**.
(nominate someone else
to answer the question)



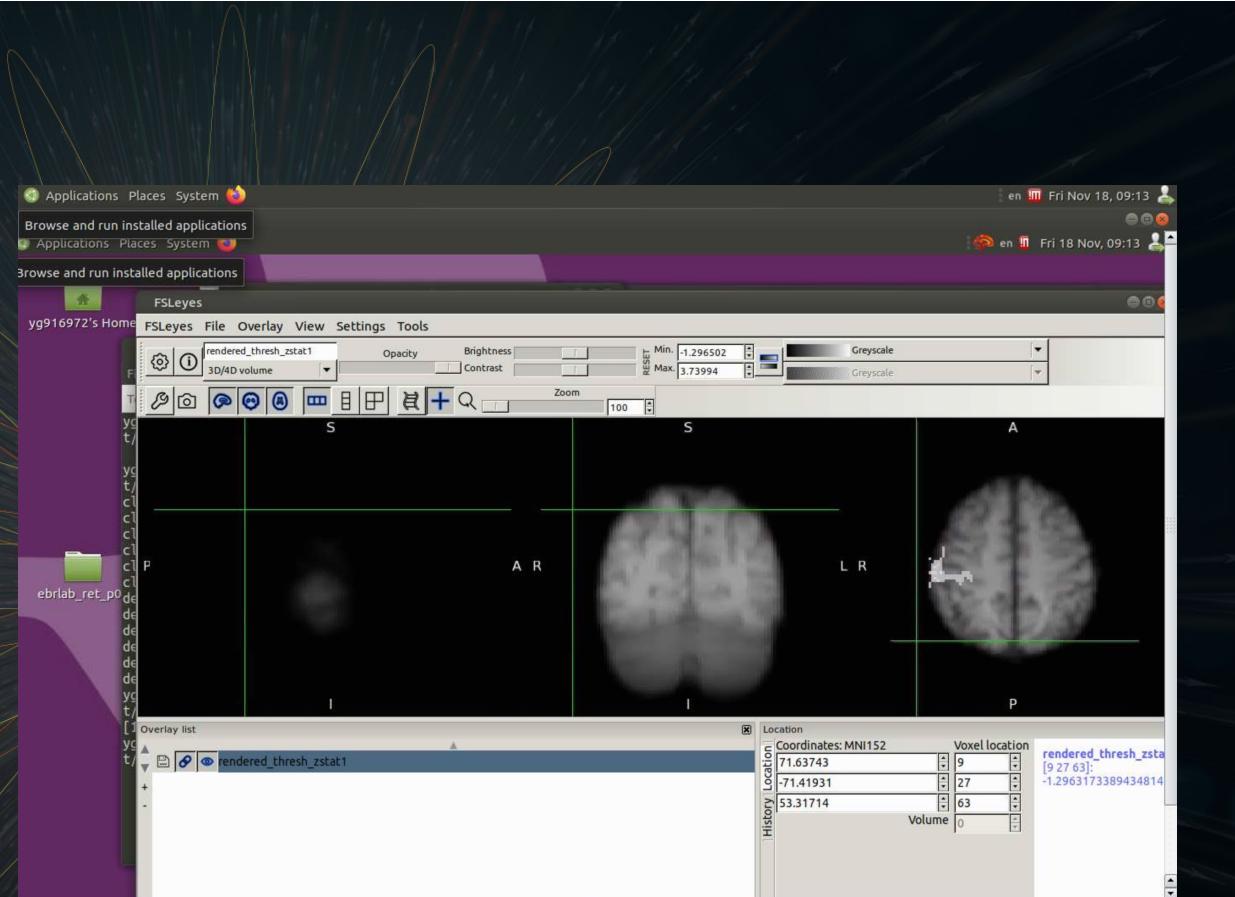
OR

Ask the audience.



Some questions will be practical “SHOW ME HOW” questions. You will have to show me how to do something on the VM.

These may or may not be useful for the assignment.....





Pre-processing



\$ 500

Which of these stages of preprocessing comes first?

A: Conversion

B: Registration

C: Slice-timing correction

D: Motion correction



\$ 1000

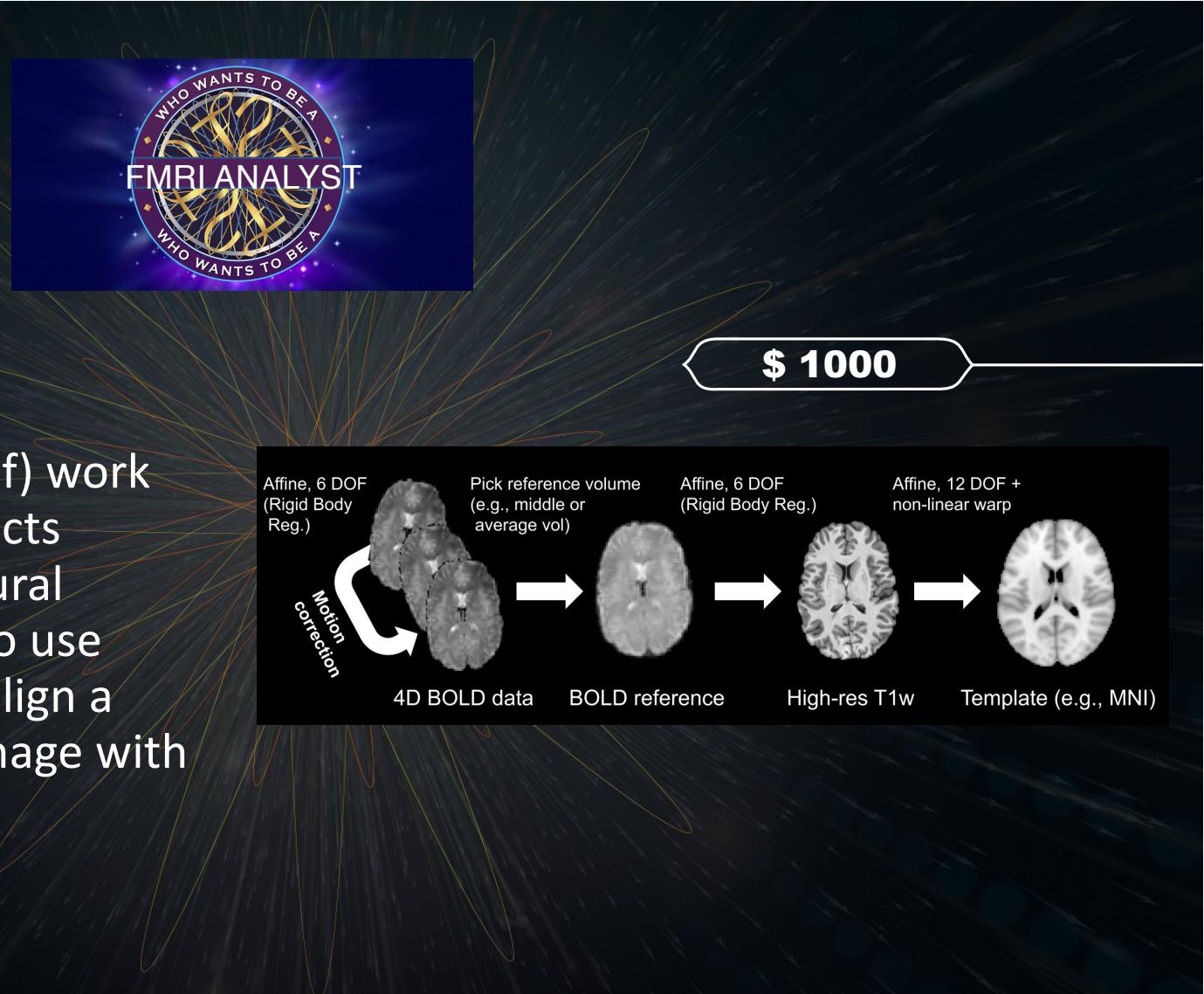
CONVERSION. Before we do anything else we need to convert our files to nifti format.

A:

fMRI software packages tend to only recognize files in nifti format.

Therefore, we are prevented from doing anything else until we have done conversion.

- Why do rigid-body transformations (6 dof) work for registering a subjects functional and structural image, but we need to use more parameters to align a subject's structural image with a 'standard' brain?



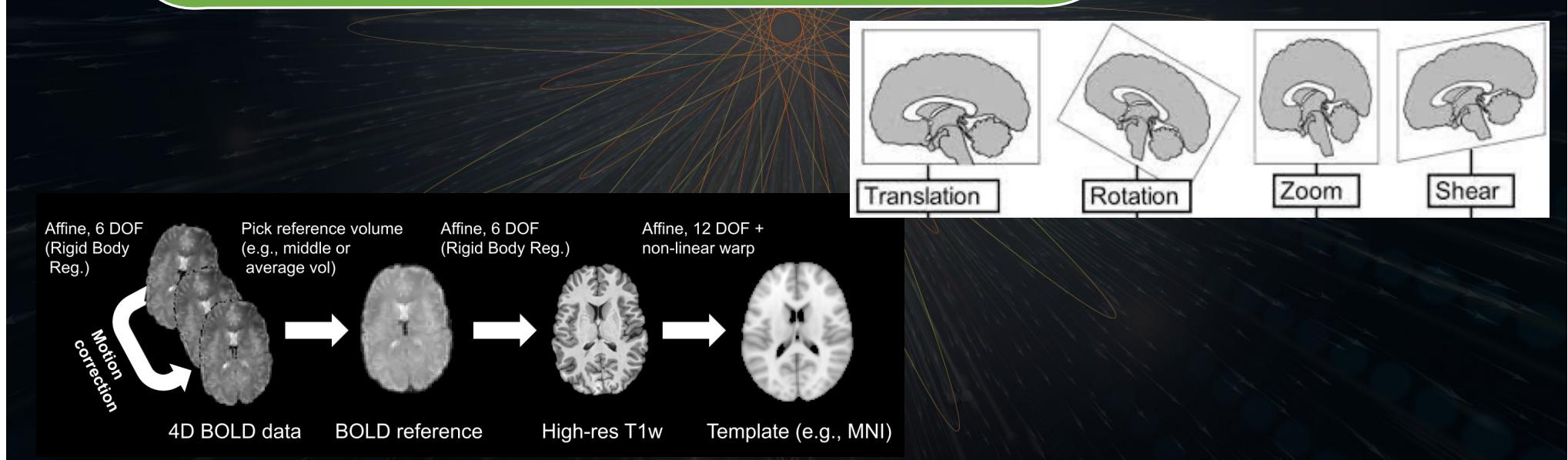
A functional image and structural image are images of the same brain. Hence, this can be treated as a 'rigid body problem'.

A:

However, any given subject's brain is going to be different size and shape from the MNI brain.

Thus we need extra parameters that scale and stretch the brain to overcome these anatomical differences (zooms and shears).

\$ 1000



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\$ 2000

What is the point of normalization?

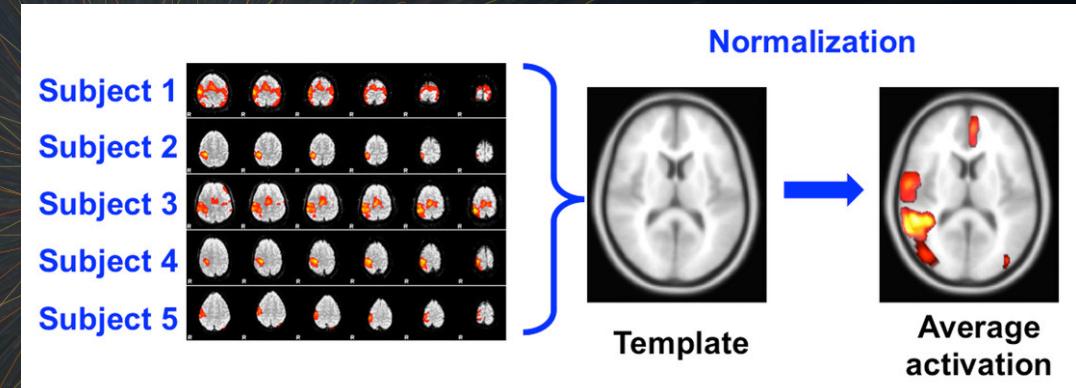
A: Ahead of group analysis, we want to make sure that each voxel at each location (X,Y,Z) is in roughly the same location in the brain.

Since individual brains are slightly different sizes and shapes, we need to warp them to a standard space.

Secondly, many ‘atlases’ are defined in standard space – allowing us to relate activations to anatomical regions



\$ 2000



DEMO

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 - 2 · \$ 1,000**
 - 1 · \$ 500**



\$ 3000

I want to:

Perform **motion correction** on a volume using the **command line**.

I want to **output the estimated motion parameters**.

I want to use **mutual information** as a **cost function**.

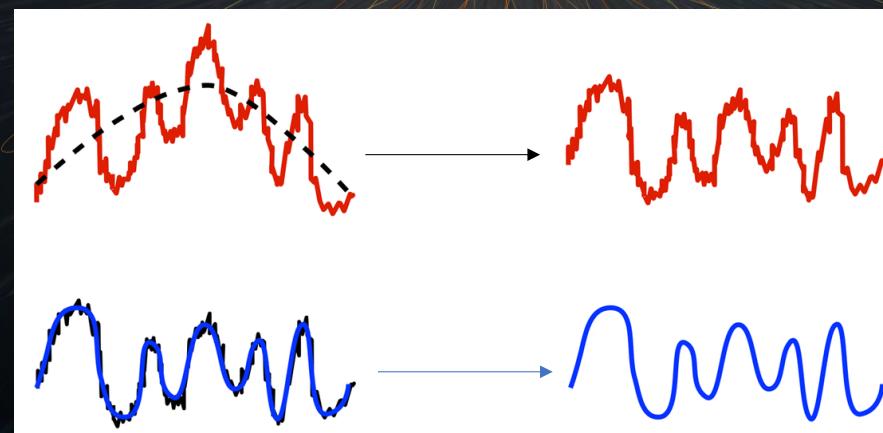
SHOW ME HOW

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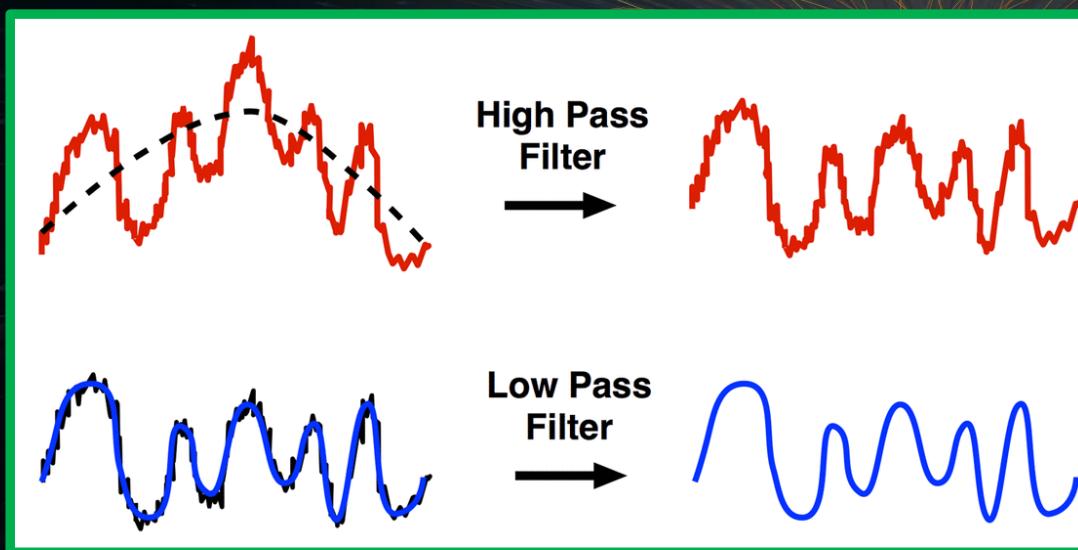
\$ 5000

What operation has been performed on each of these timecourses?



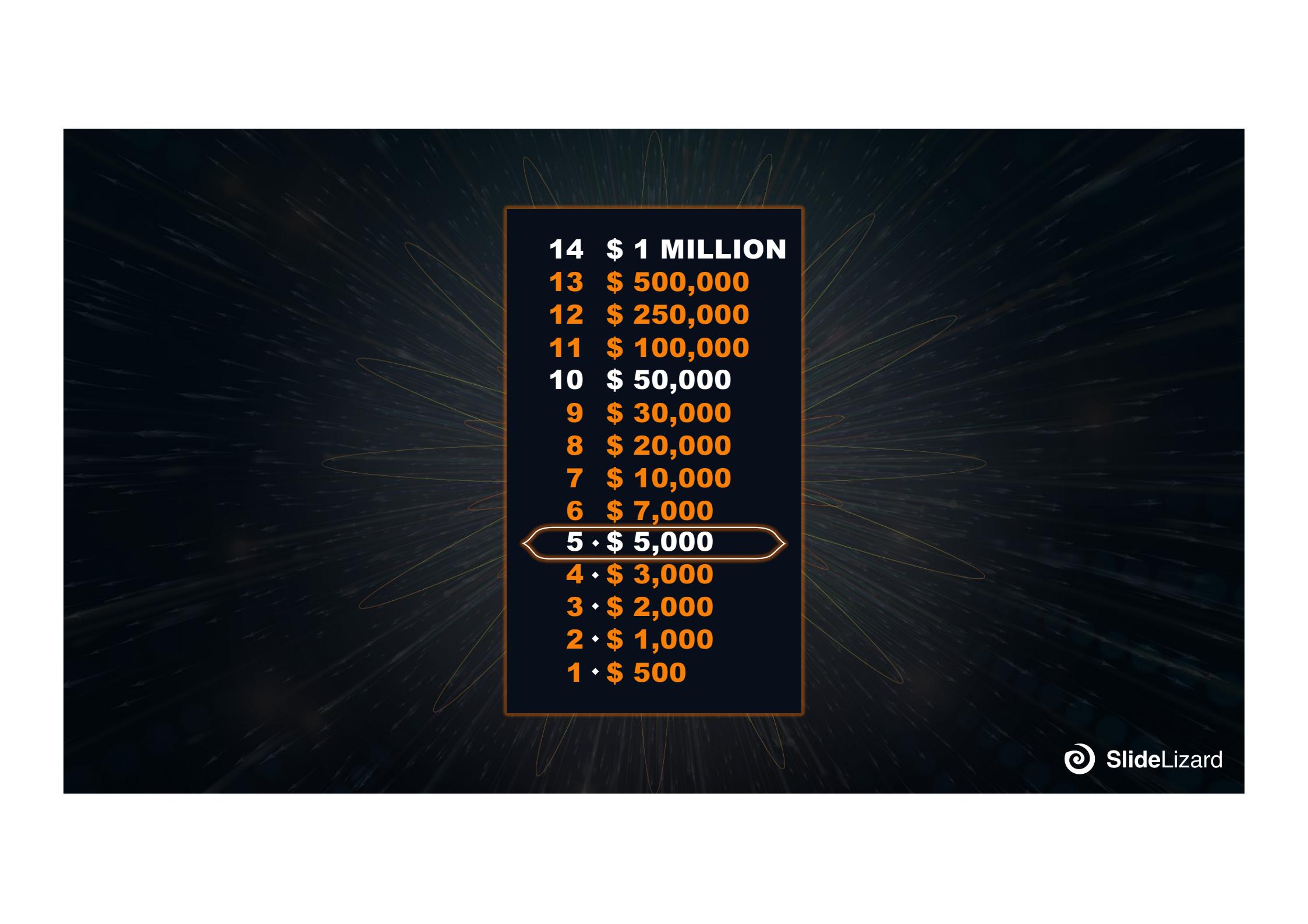


\$ 5000



High pass filtering: Removes low frequency components of the signal (drifts).

Low pass filtering: Removes high frequency parts of the signal (physical noise, cardiac/ respiratory noise.)

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GLM



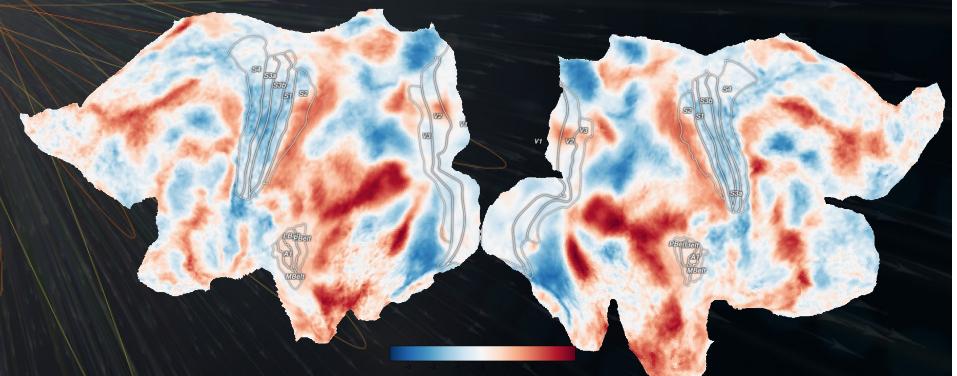
\$ 7000

In FSL/FEAT, what is a COPE? + Give an example of a cope we have estimated in previous weeks.



\$ 7000

β body – β scene



A COPE stands for a contrast of parameter estimates.

A classic example would be an image of the difference between two β .

For instance, in the colab notebook we looked at the difference between body and scene betas.

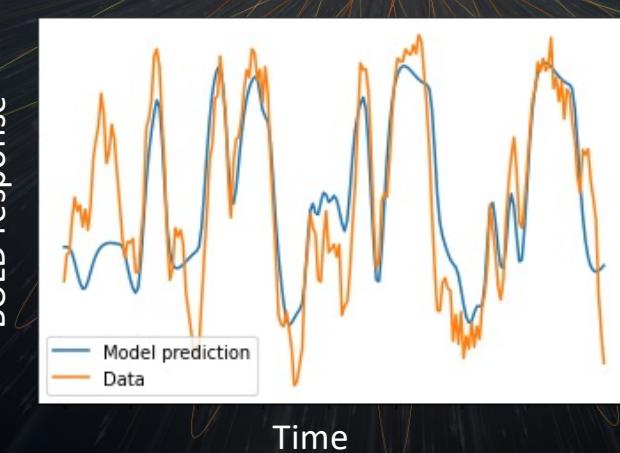


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\$ 10,000

How might I summarize the error of this model in one number?

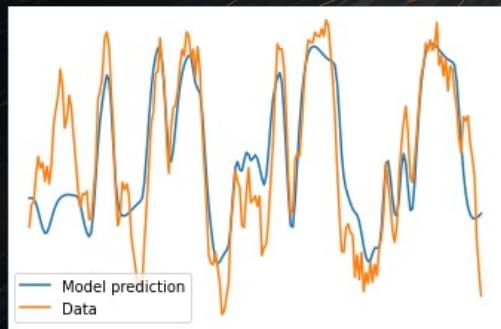




\$ 10,000

A. We may calculate the sum of squared errors

$$\sum_{i=1}^N (\hat{y}_i - y_i)^2$$



1. At each time point, take the difference between the model predictions and the data
2. Square these
3. Take the sum.



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\$ 20,000

Here it seems that faces have more influence on the signal than houses. What parameter of the GLM is this reflected in?





A: β reflects the weight we estimate for each regressor in our X (design matrix).

Higher β = more weight = more influence = more importance.



I have two events during my functional run and I want to set up a GLM in FEAT.

Faces are presented at 10, 20 and 30 seconds for 1 second.

Houses are presented at 5, 15 and 25 seconds for 2 seconds

I want to make a 3-column format file the face and house regressor.

\$ 30,000

SHOW ME HOW

Faces.txt

Houses.txt



\$ 30,000

A: Let's make these now.

Faces.txt

Onset	Duration	Magnitude
10	1	1
20	1	1
30	1	1

Houses.txt

Onset	Duration	Magnitude
5	2	1
15	2	1
25	2	1

- 
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\$ 50,000

Here I open up `rendered_thresh_zstat1` (left v right hand movements) from the paired t test example we did on Friday.

I want to use `fsleyes` to see where this cluster of activation is located in the Juelich histological atlas.

SHOW ME HOW





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Higher level analyses.



\$ 100,000

What is the goal of higher-level analysis. How does it differ from first-level analysis?



\$ 100,000

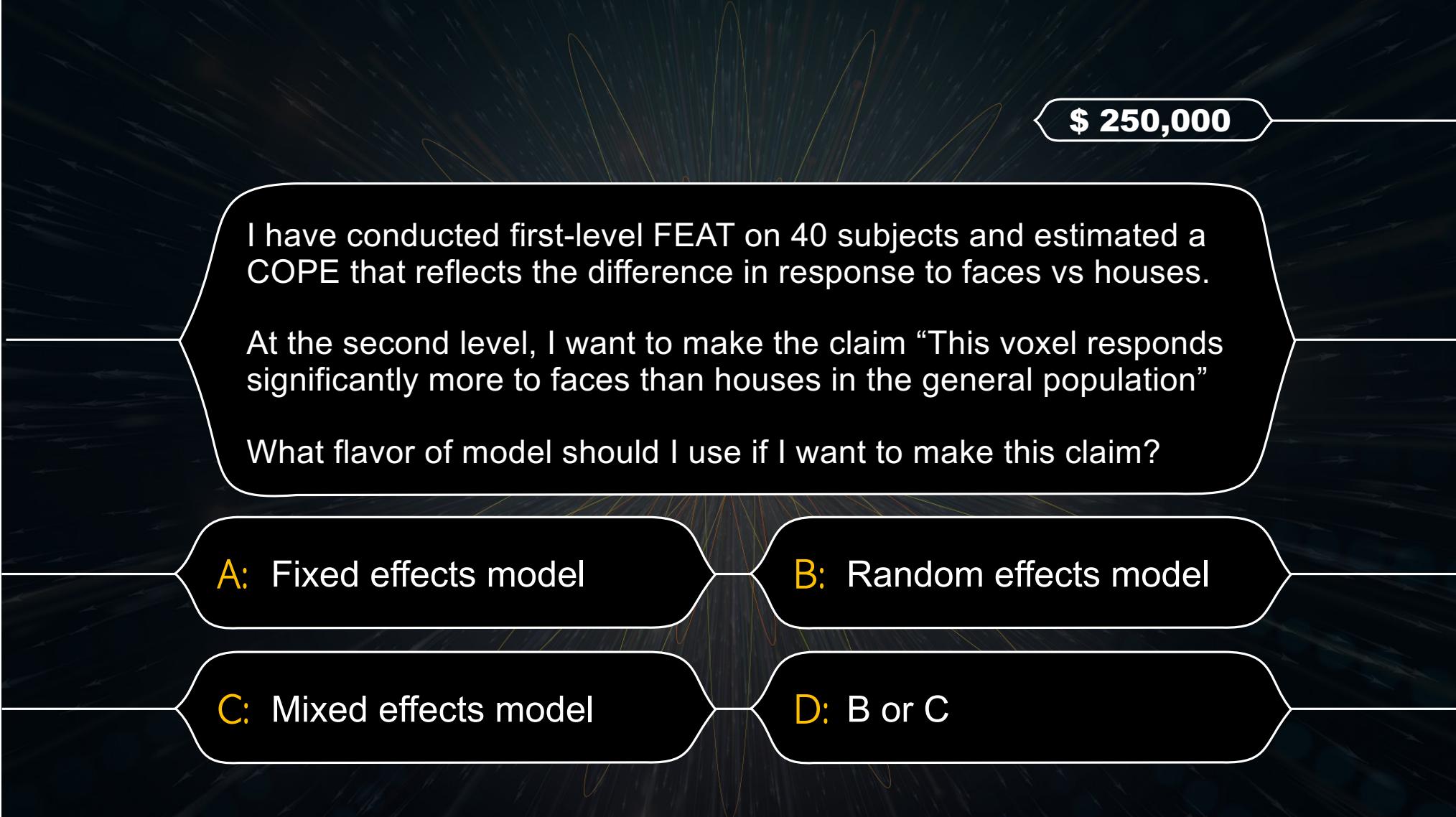
A Whereas first level-analysis typically involves estimating parameters from one run of functional data, higher level analysis typically involves combining data across runs, or combining data across participants to make inferences about the general population.

At the first level, we want to explain each voxels response throughout the scan as some weighted combination of regressors – estimating β .

At the second level, we may want to explain the subject-level variation in the β , or determine if β is significantly different from 0, or significantly different between groups etc..



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\$ 250,000

I have conducted first-level FEAT on 40 subjects and estimated a COPE that reflects the difference in response to faces vs houses.

At the second level, I want to make the claim “This voxel responds significantly more to faces than houses in the general population”

What flavor of model should I use if I want to make this claim?

A: Fixed effects model

B: Random effects model

C: Mixed effects model

D: B or C

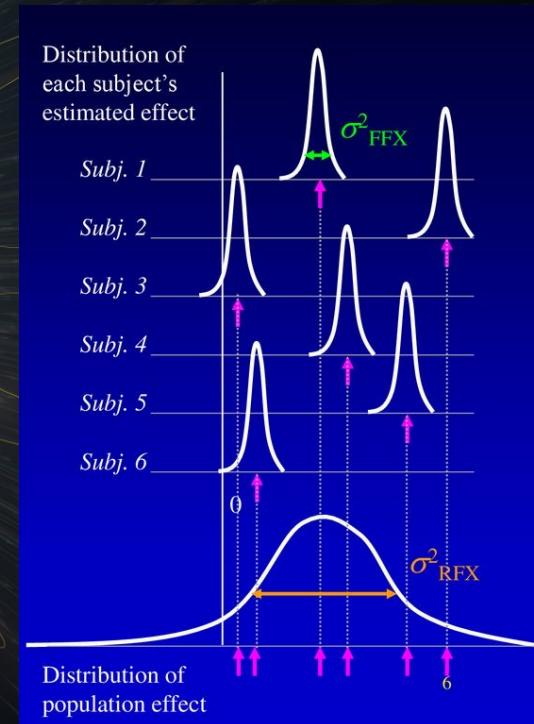
A: B & C.

Fixed effects models only take into account within-subject variation in estimating uncertainty of effects. Thus, all inferences are specific to the sample itself.

By contrast, random and mixed effects models take into account the between-subject variability

Hence, they allow us to make inferences about the population from which the sample is drawn.

\$ 250,000





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\$ 500,000

Here is a first level GLM equation and a group level GLM equation.

What is Y ?

What is Y^+ ?

First level

$$y = X\beta + \varepsilon$$

Group level

$$Y^+ = X^+ \beta^+ + \varepsilon^+$$



\$ 500,000

A: At the first level, Y is the timeseries data throughout the brain.

At the second level it is the β parameters (or copes) estimated from the first level.

Level 1 model for subject k

$$\begin{pmatrix} \text{timeseries} \\ \vdots \end{pmatrix} = \begin{pmatrix} \text{stimulus} \\ \vdots \end{pmatrix} \begin{pmatrix} \beta_{\text{faces}}^k \\ \beta_{\text{houses}}^k \end{pmatrix} + \begin{pmatrix} \text{error} \\ \vdots \end{pmatrix}$$

$H_0: \beta_{\text{faces}}^k - \beta_{\text{houses}}^k = 0$

$c\beta^k = [1 \ -1] \begin{pmatrix} \beta_{\text{faces}}^k \\ \beta_{\text{houses}}^k \end{pmatrix}$

Level 2 model for comparing group 1 to group 2

$$\begin{pmatrix} \text{timeseries} \\ \vdots \end{pmatrix} = \begin{pmatrix} \text{stimulus} \\ \vdots \end{pmatrix} \begin{pmatrix} \beta_{G1} \\ \beta_{G2} \end{pmatrix} + \begin{pmatrix} \text{error} \\ \vdots \end{pmatrix}$$

$H_0: \beta_{G1} - \beta_{G2} = 0$

$c\beta_G = [1 \ -1] \begin{pmatrix} \beta_{G1} \\ \beta_{G2} \end{pmatrix}$

$$y = X\beta + \varepsilon$$

$$Y^+ = X^+ \beta^+ + \varepsilon^+$$

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1 · \$ 500

\$ 1 MILLION

In FEAT I have estimated first level copes for 6 faces > 6 houses for 5 neurotypical and 5 schizophrenic subjects.

In the second level, I want to conduct an independent samples t test to see if I can detect a difference in this cope between the two groups. (neurotypical > schizophrenic).

Neurotypical P1 cope
Neurotypical P2 cope
Neurotypical P3 cope
Neurotypical P4 cope
Neurotypical P5 cope
schiz P1 cope
schizP2 cope
schiz P3 cope
schiz P4 cope
Schiz P5 cope

SHOW ME HOW

EV1	EV2
0	0
0	0
0	0
0	0
0	0
0	0
0	0
0	0
0	0
0	0
0	0
0	0

EVs Contrasts & F-tests

Contrasts 1 F-tests 0

Paste Title EV1 EV2

C1 0 0