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School of Medicine
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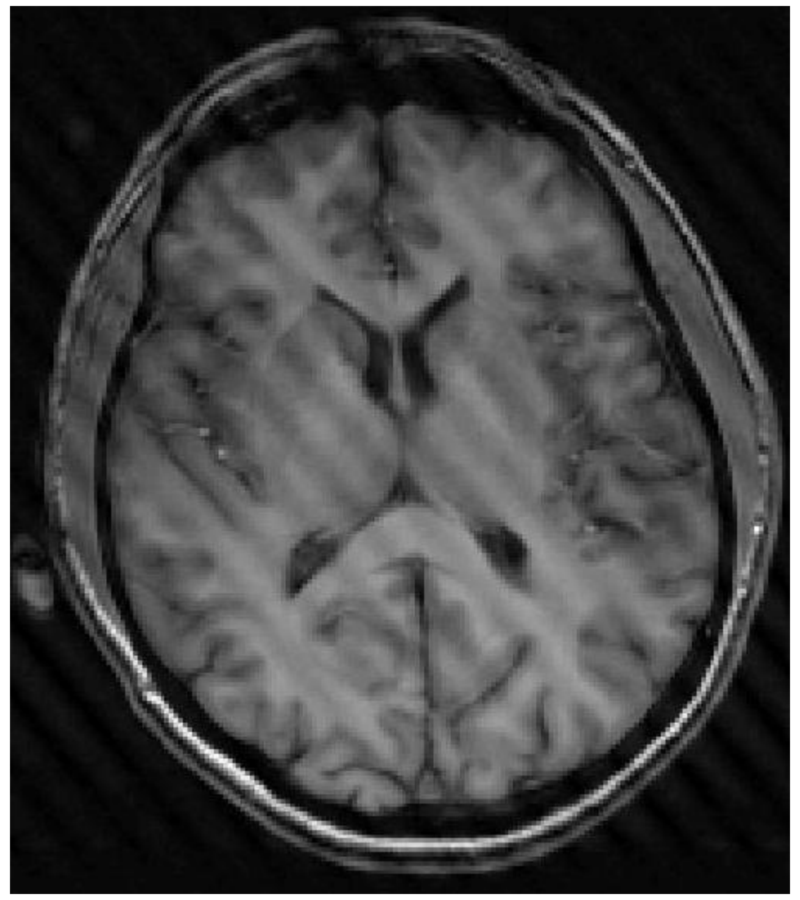
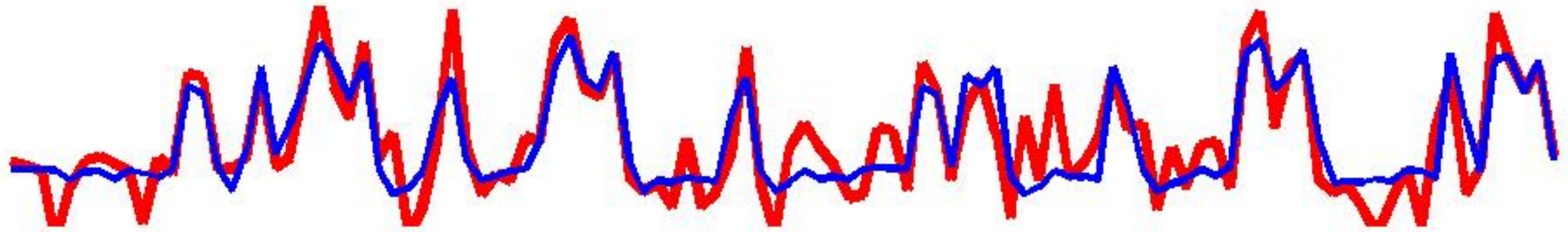
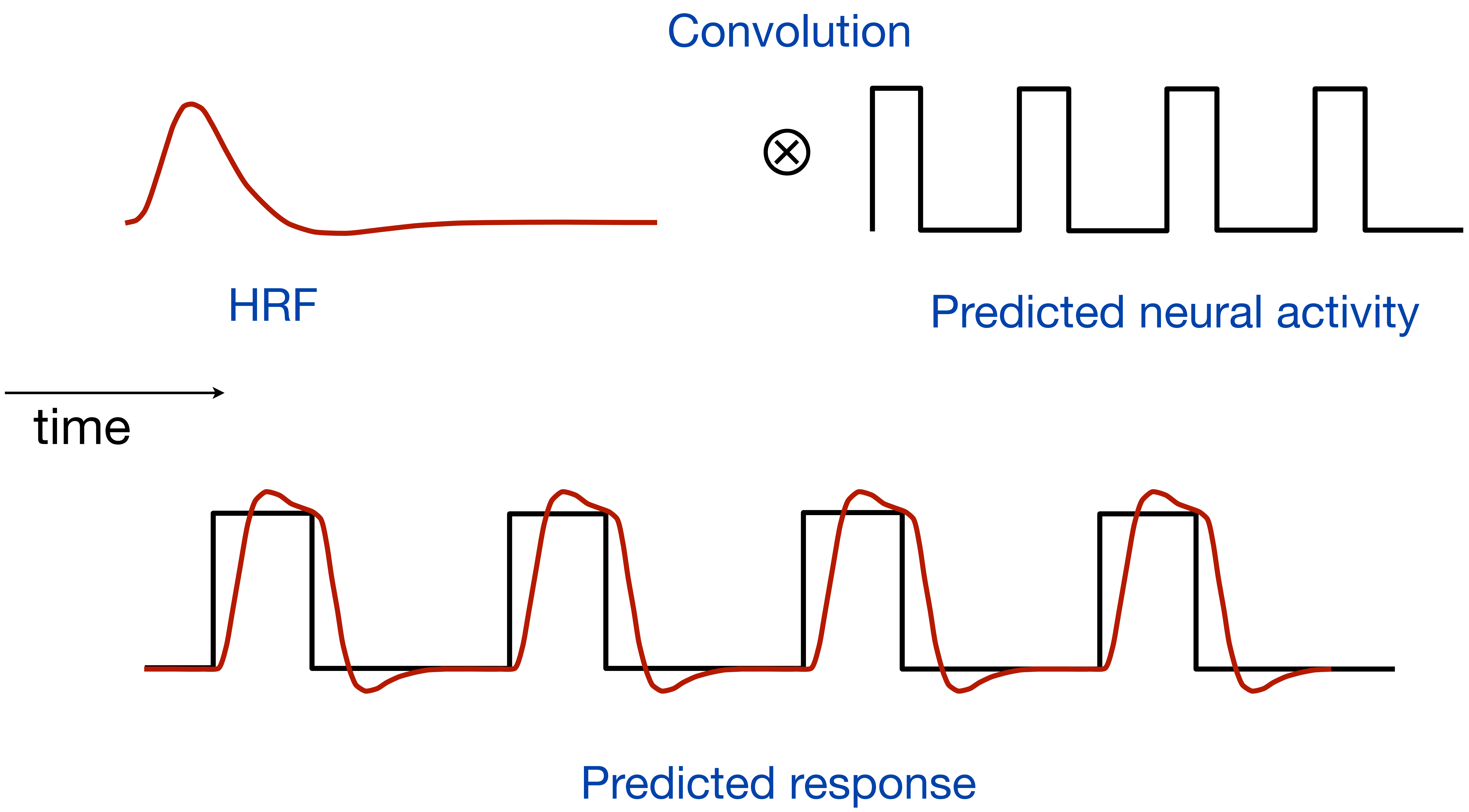
FMRI single subject analysis

- Overview
- Setting up a GLM model
- Contrasts and statistics



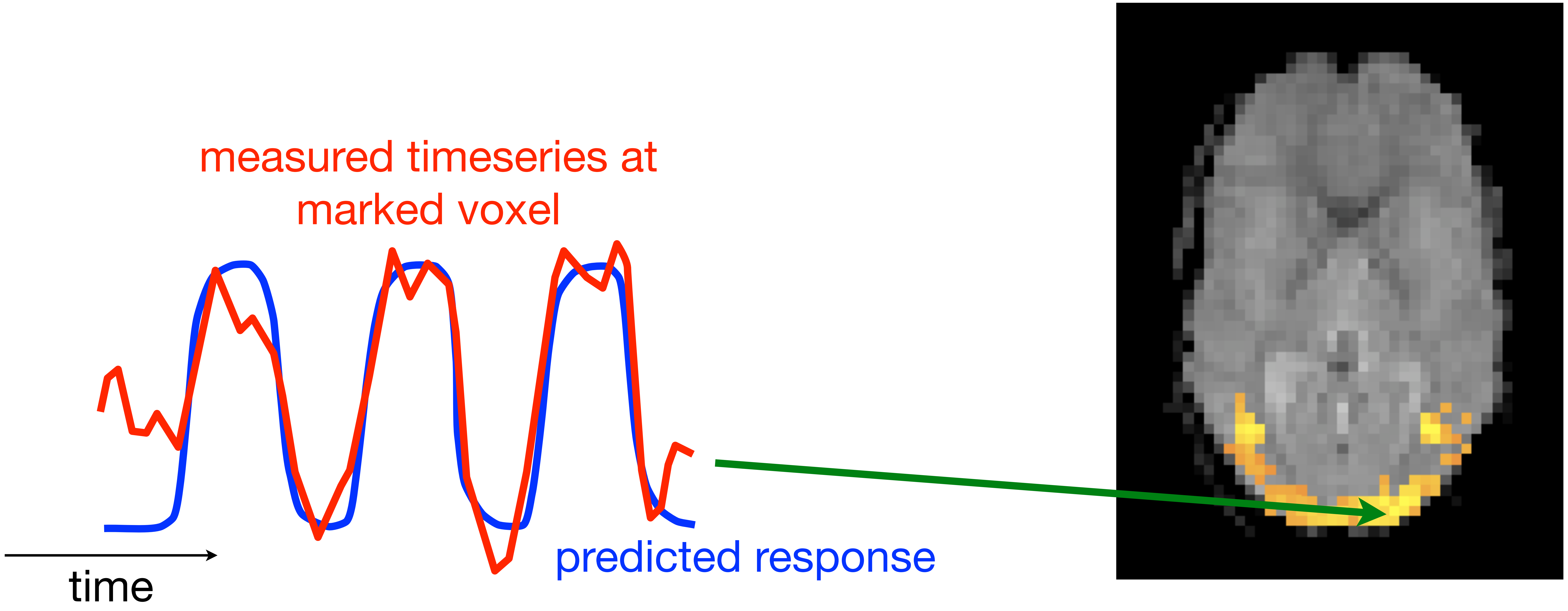


Model


Convolution
HRF
⊗
Predicted neural activity
time
Predicted response

Fit model to data

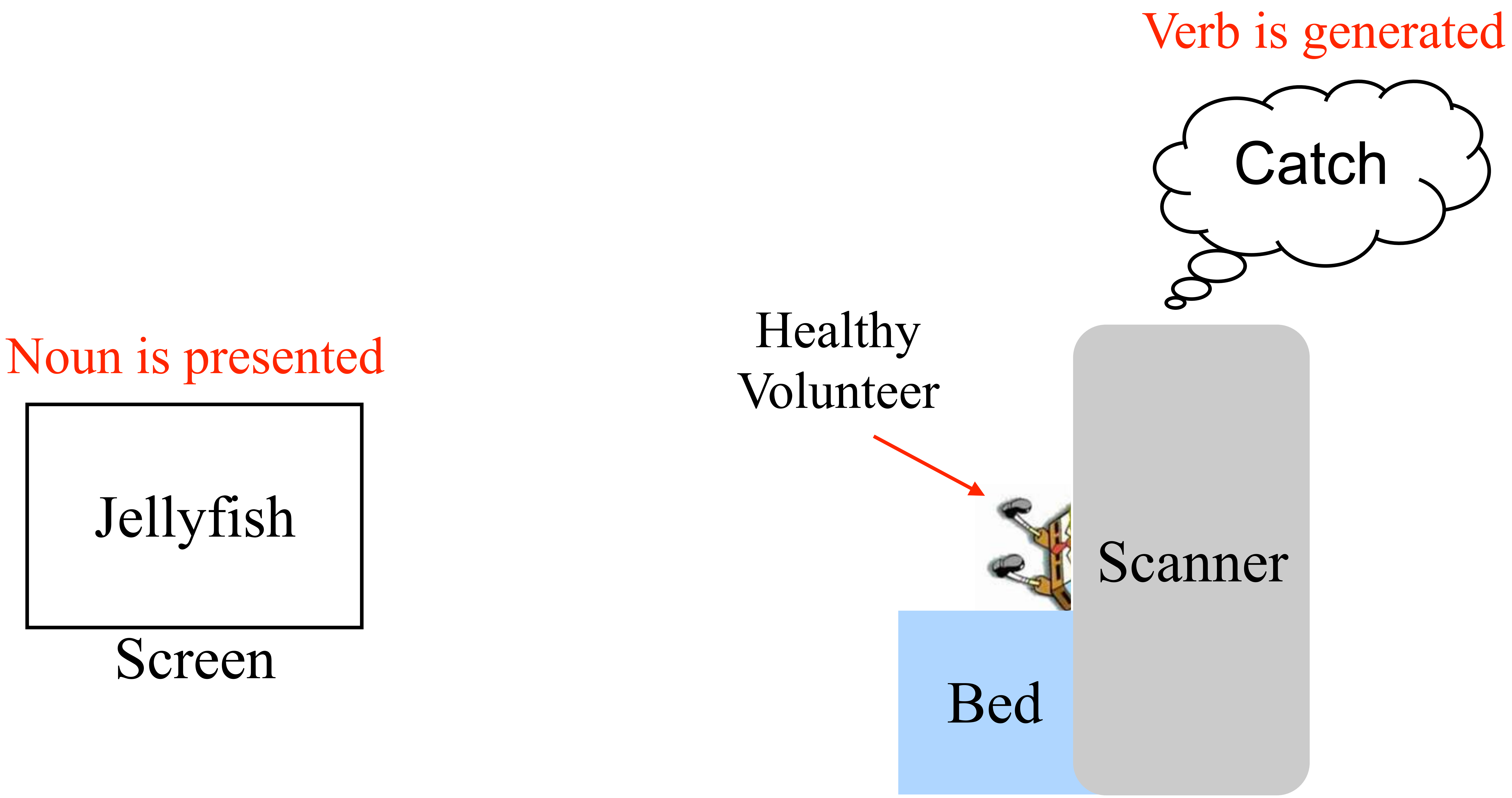
- Look for voxels that have a BOLD timeseries similar to the model



Example Experiment

Silent word generation

Silent word generation



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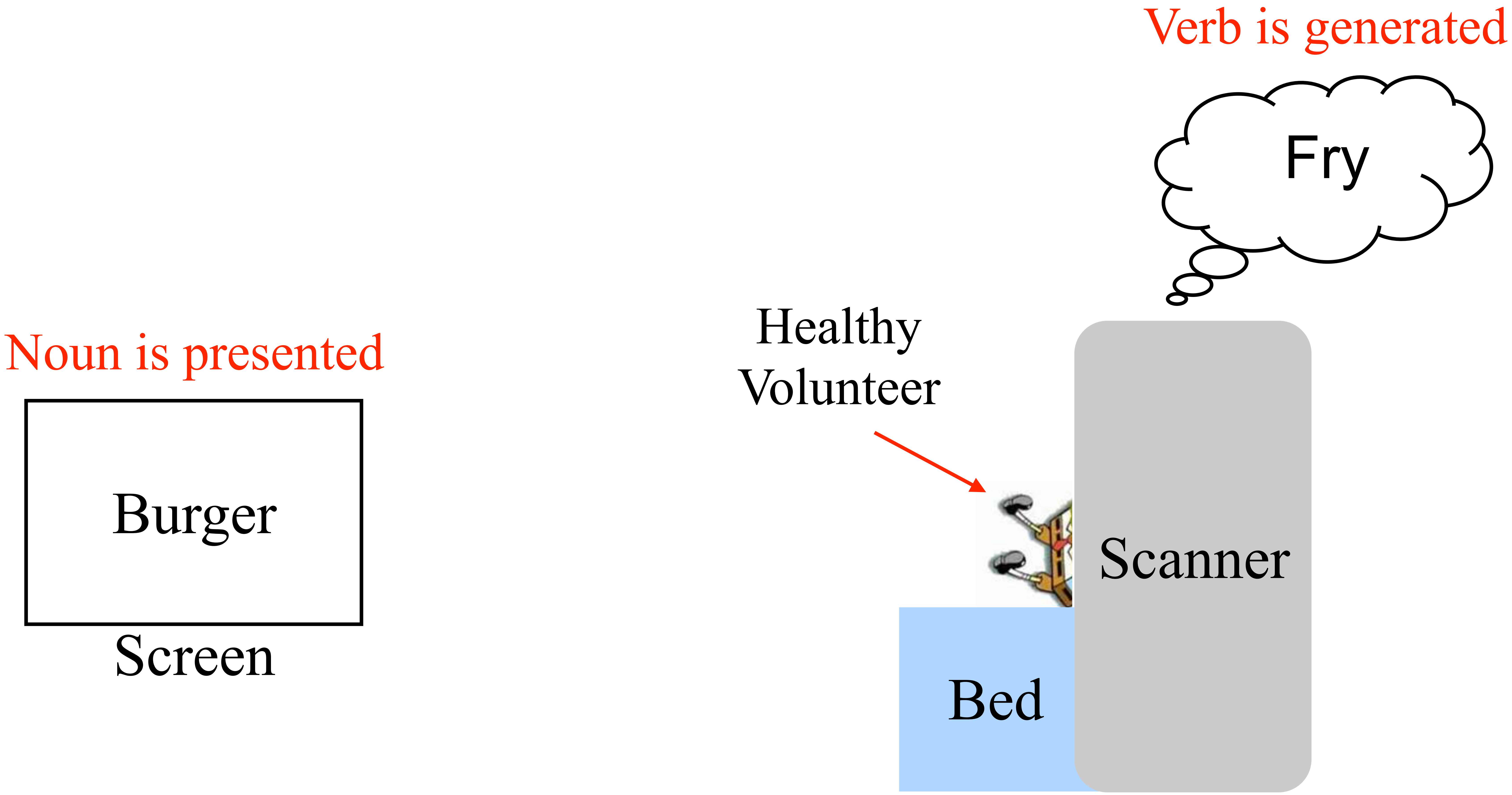
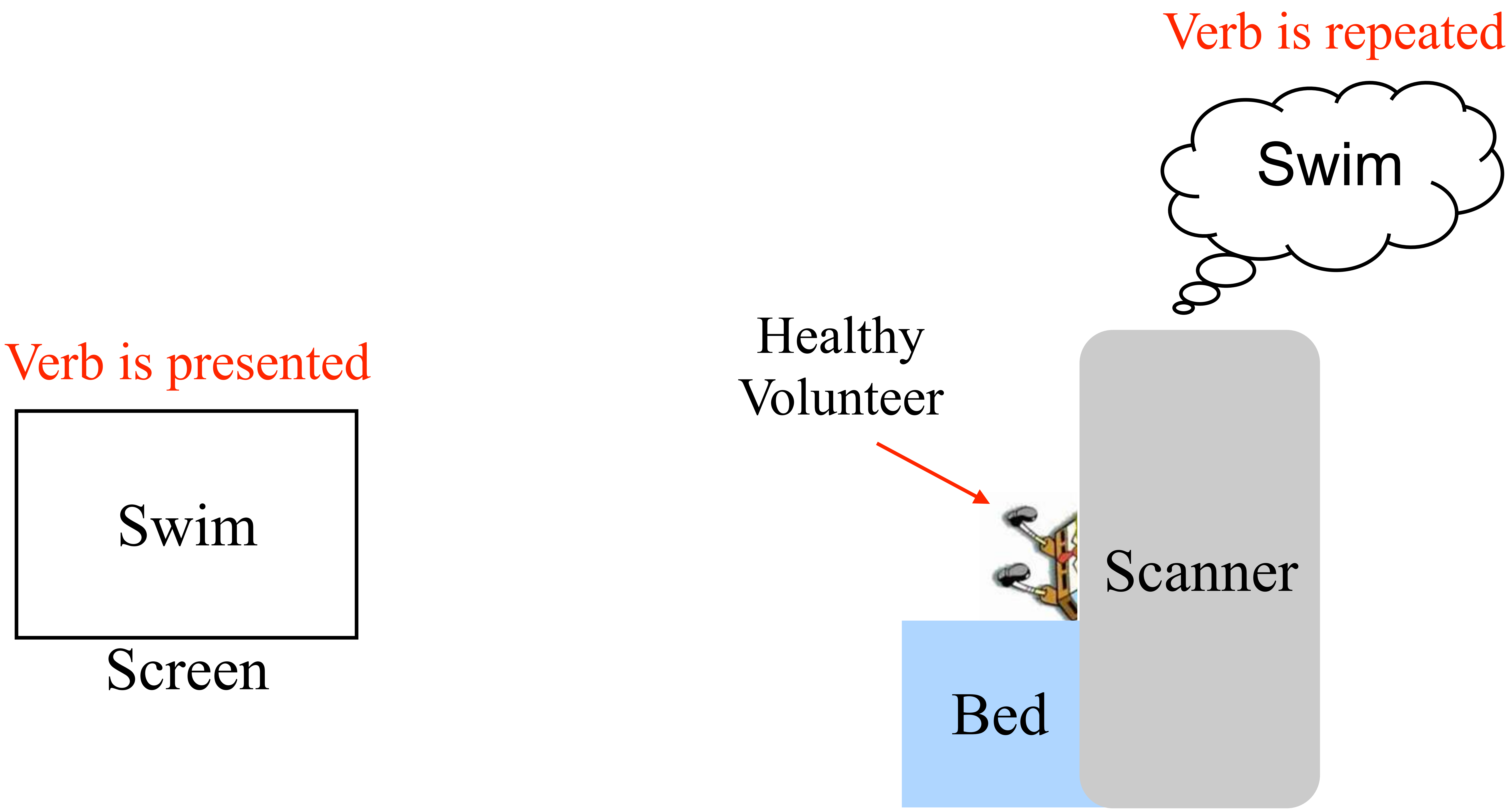
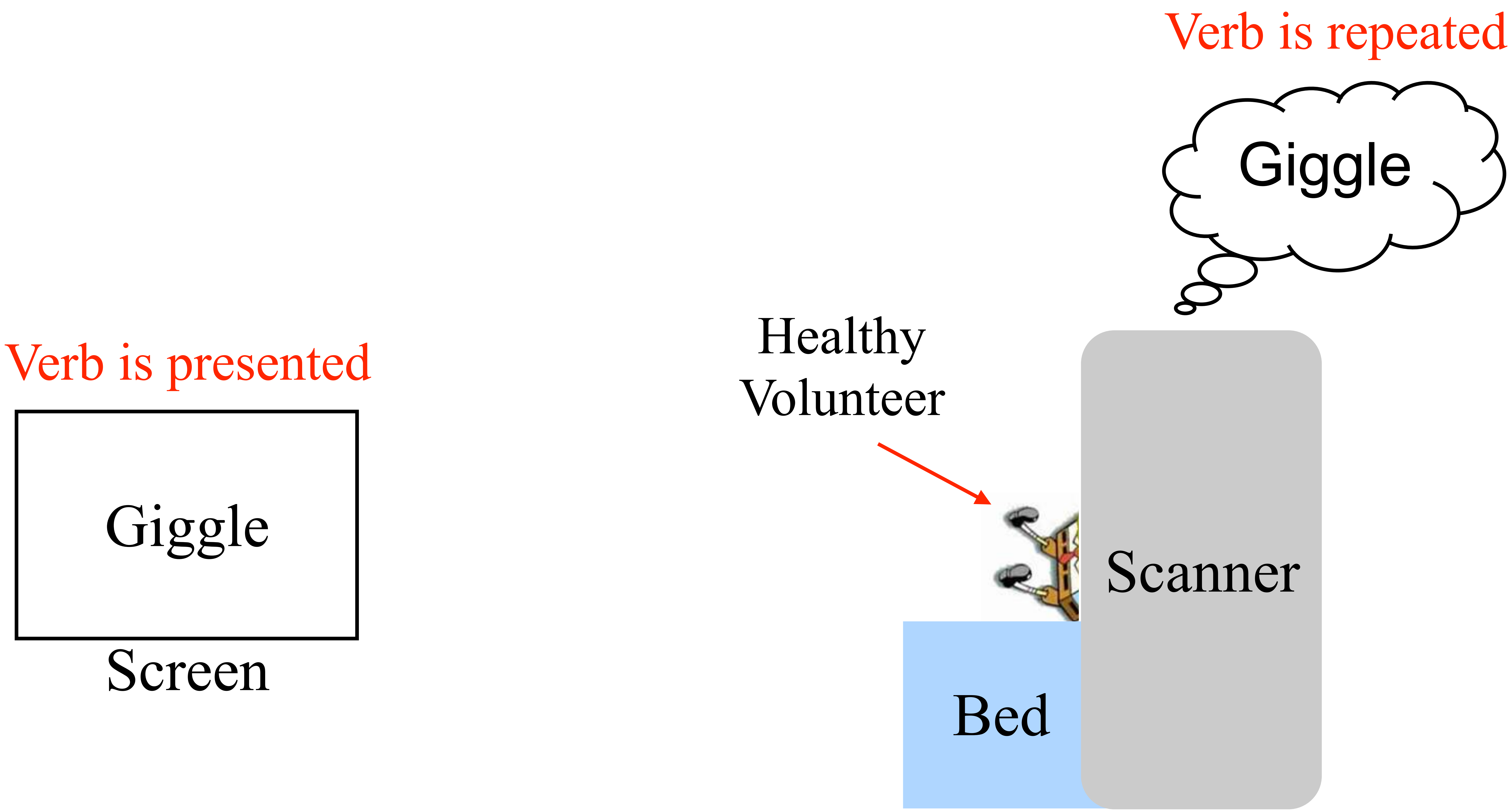
Silent word generation



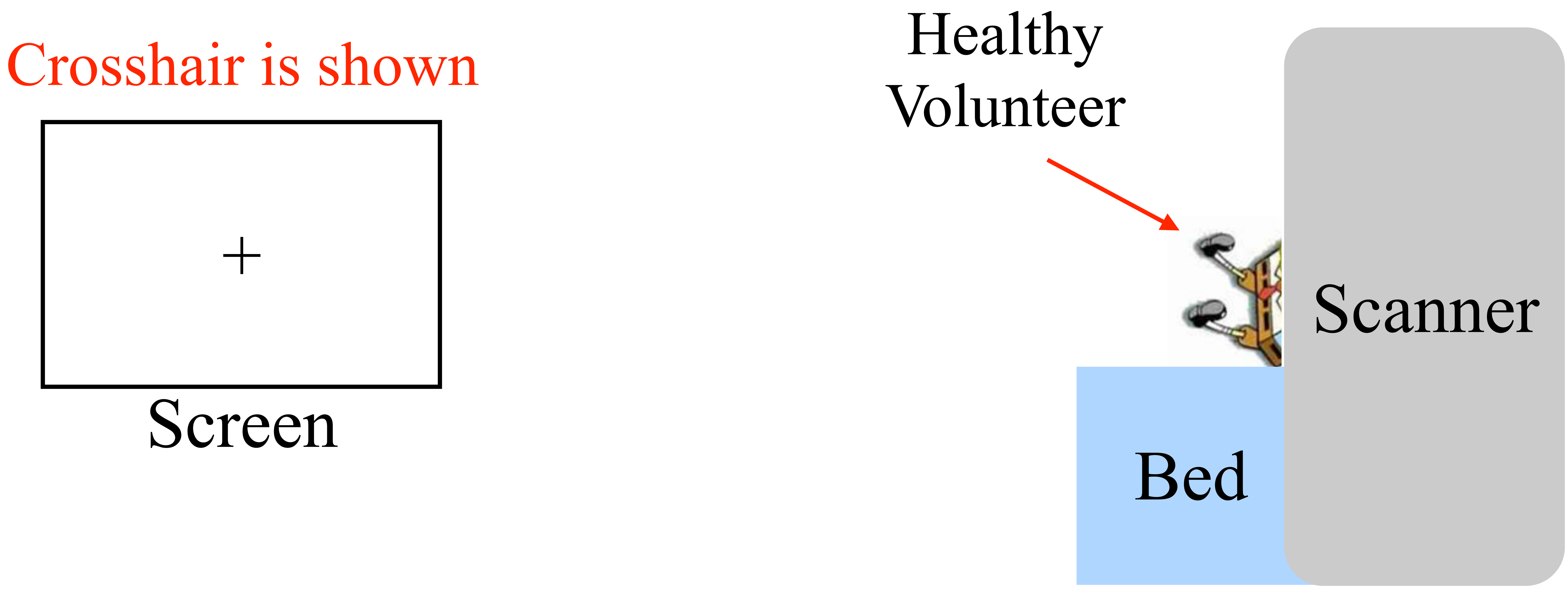
Control: silent word shadow



Control: silent word shadow

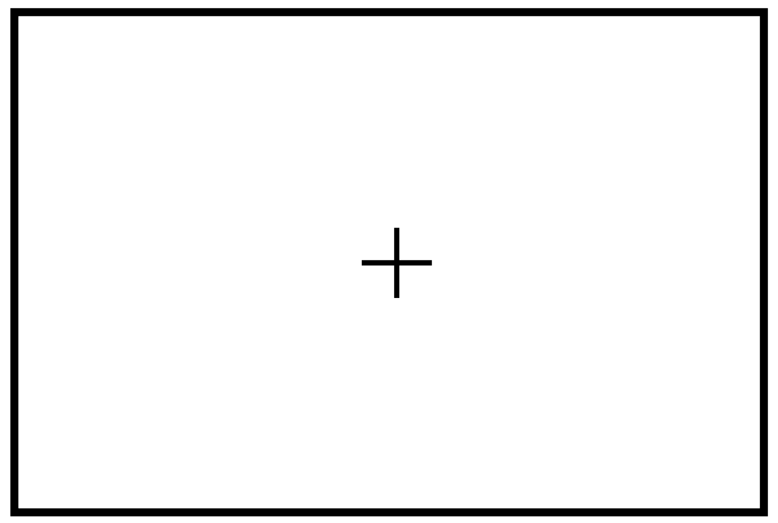


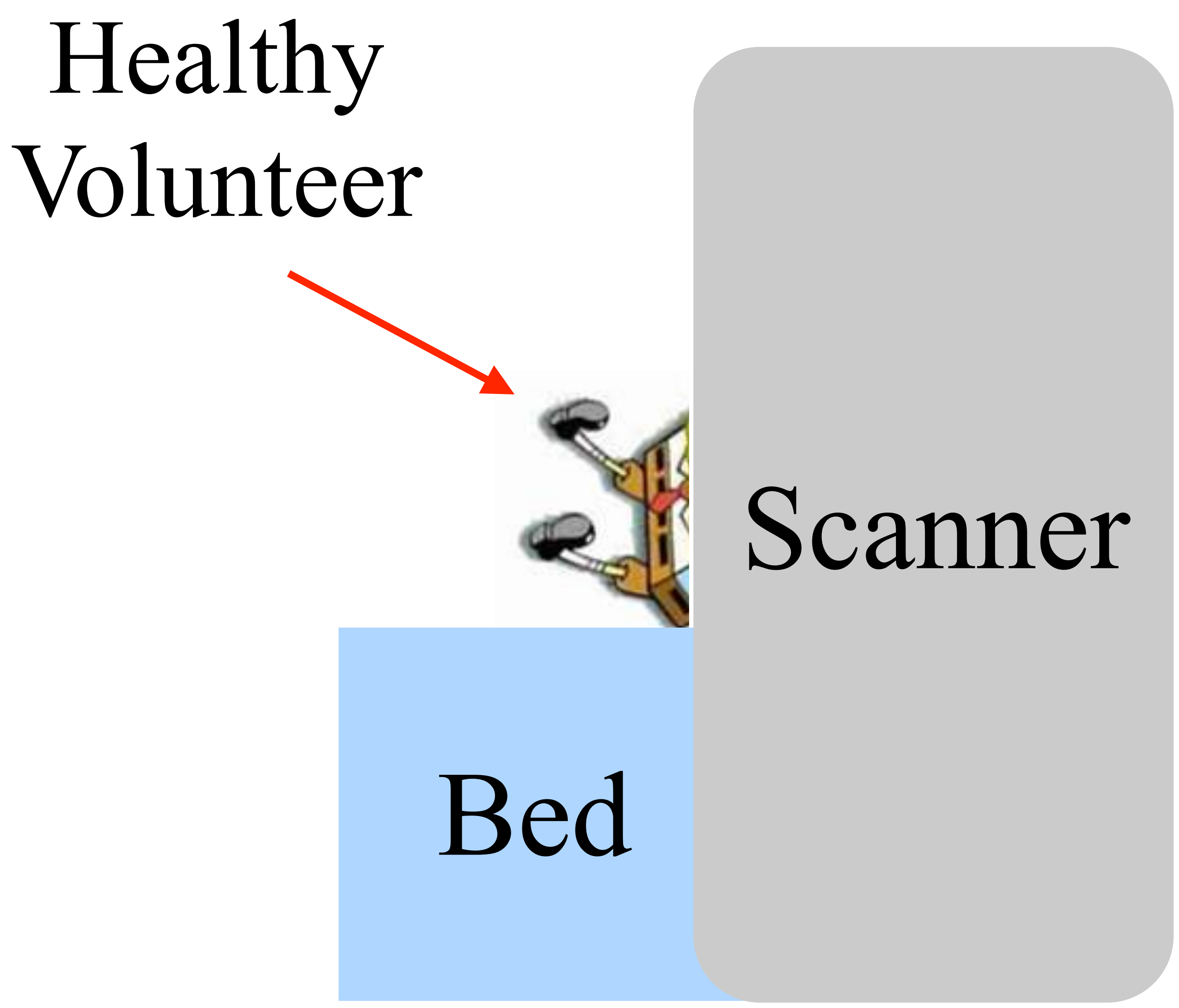
Baseline: crosshair



The full experiment

- Three types of events
  - 1st type: Word Generation
  - 2nd type: Word Shadowing
  - 3rd type: Null event
- 6 sec ISI, random order
- 24 events of each type


Screen



How to analyze the data?

1. Set up regressors

   What do we know the brain should be doing during the experiment?

   = *Explanatory variables, Design Matrix, Model*

2. Fit the regressors to the data

   Combine the regressors in a way that is most similar to the observed data

   = *Parameter Estimates (PE), Betas, Effect Sizes*

3. Set up contrasts to compare conditions

   Compare conditions by doing simple arithmetic

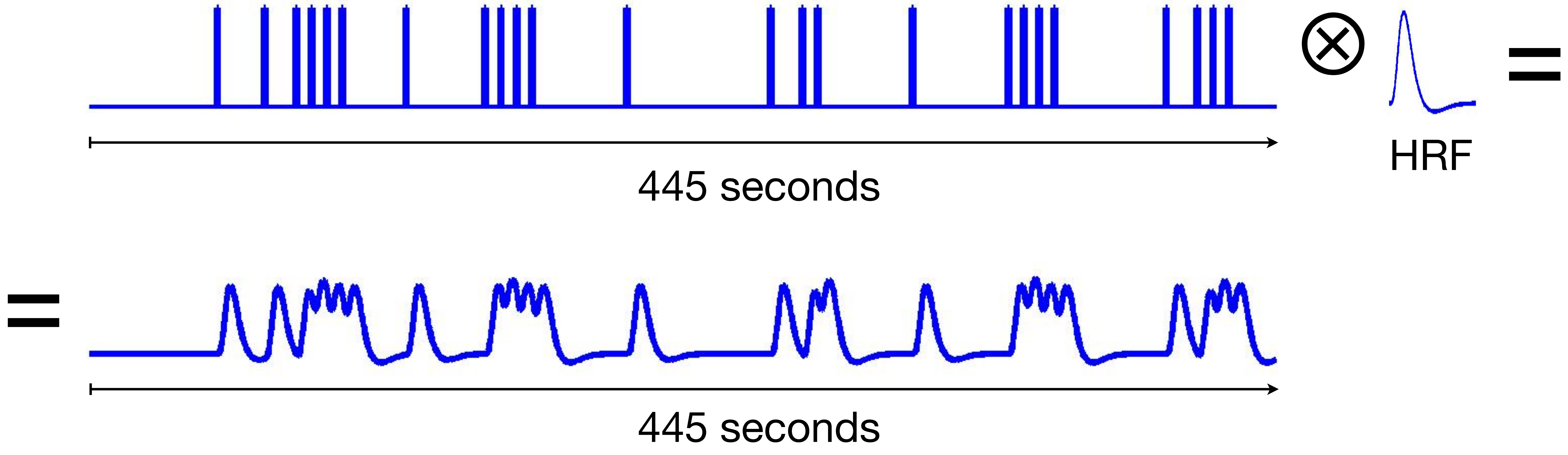
   = *Contrast of Parameter Estimates (COPE)*

4. Perform statistical inference

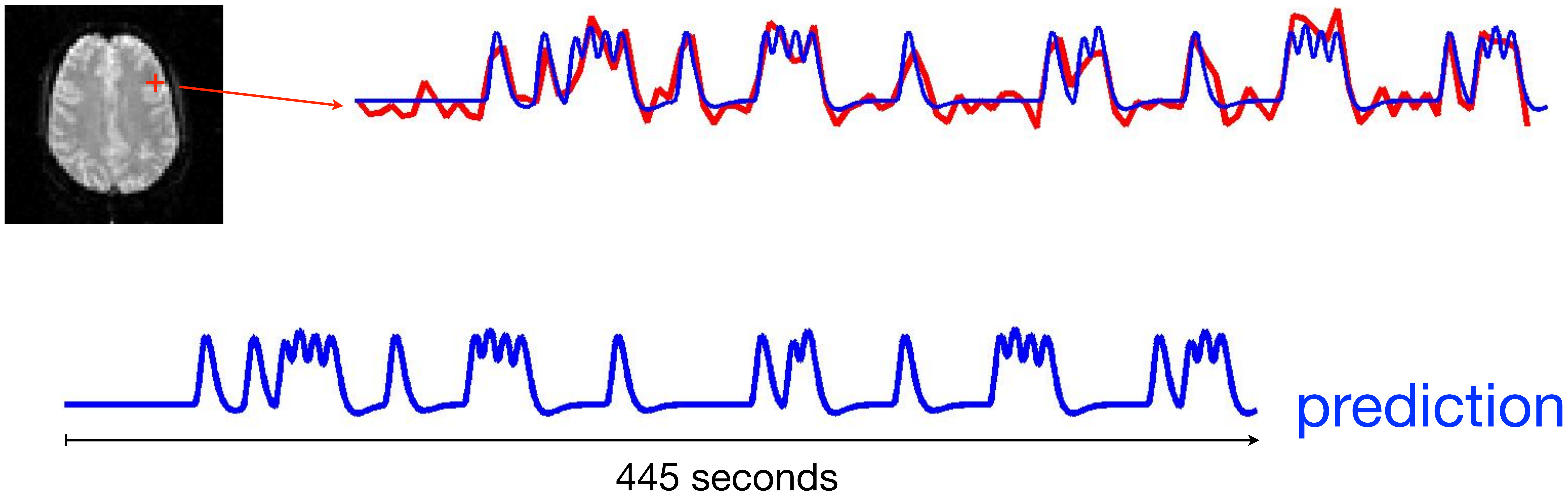
   Often t-test to see if COPE is bigger than zero

Defining regressors

Predicted response to word generation

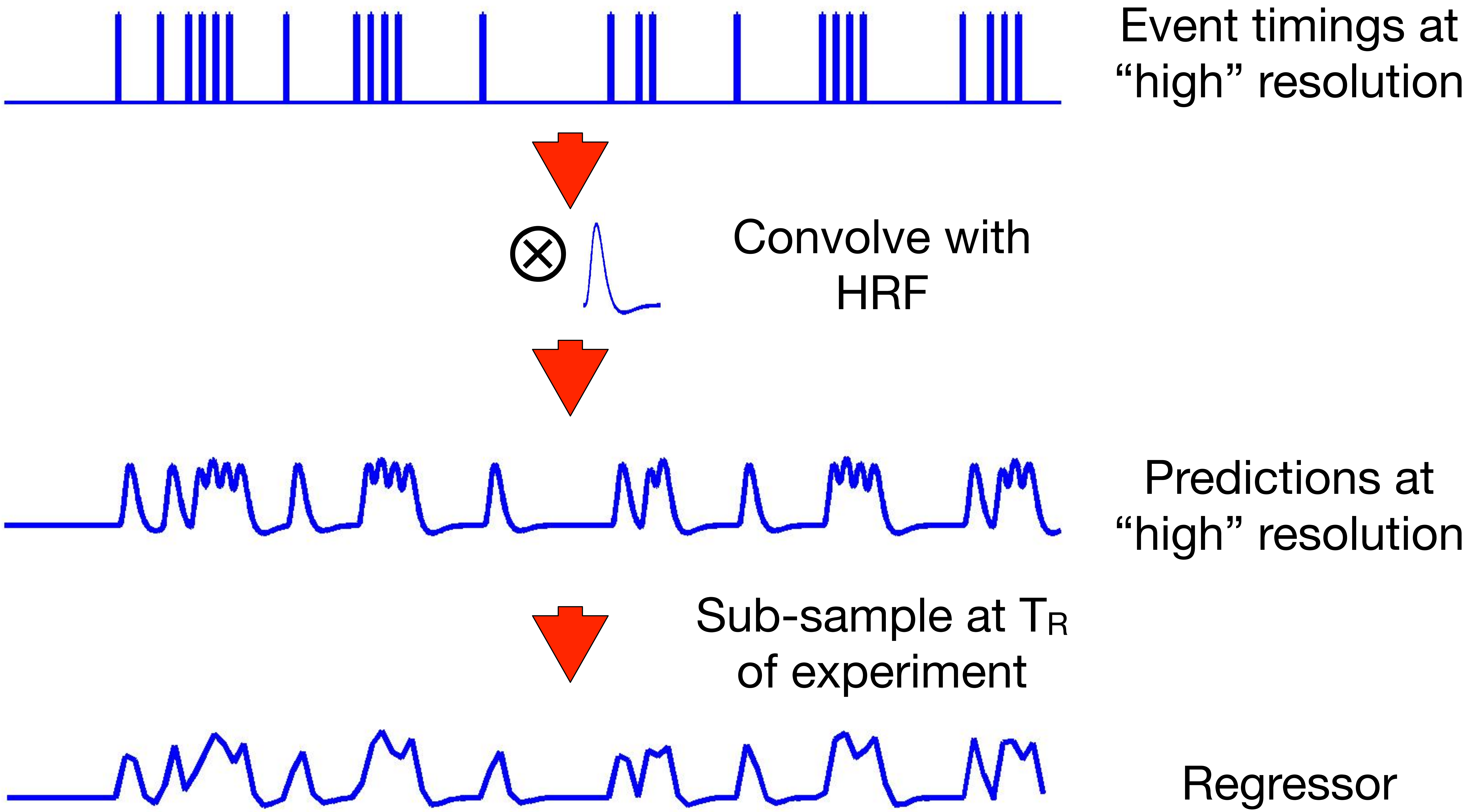


Voxel-wise analysis



Looking for voxels interested in during word generation

Subsampling to TR



What about baseline?

- Set up separate regressors for each condition of interest
  - Word generation
  - Word shadowing

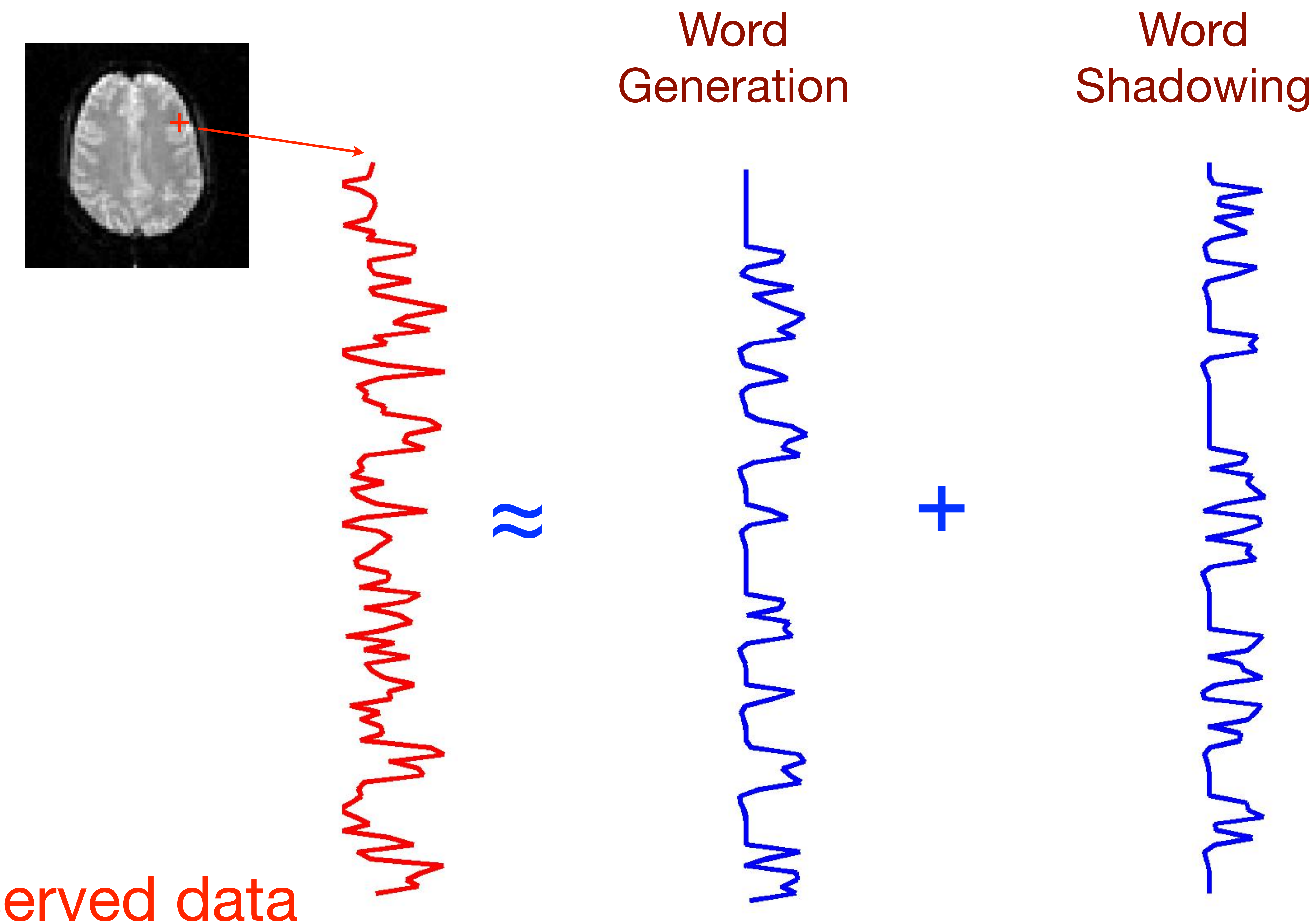
- The mean BOLD value is uninteresting in an FMRI session

- There are two equivalent options:

  1. Remove the mean from the data and don't model it (FSL 1st level; i.e. a regressor for the baseline is not included)

  2. Model the mean (FSL group & SPM 1st level + group)

Your new friend: the GLM



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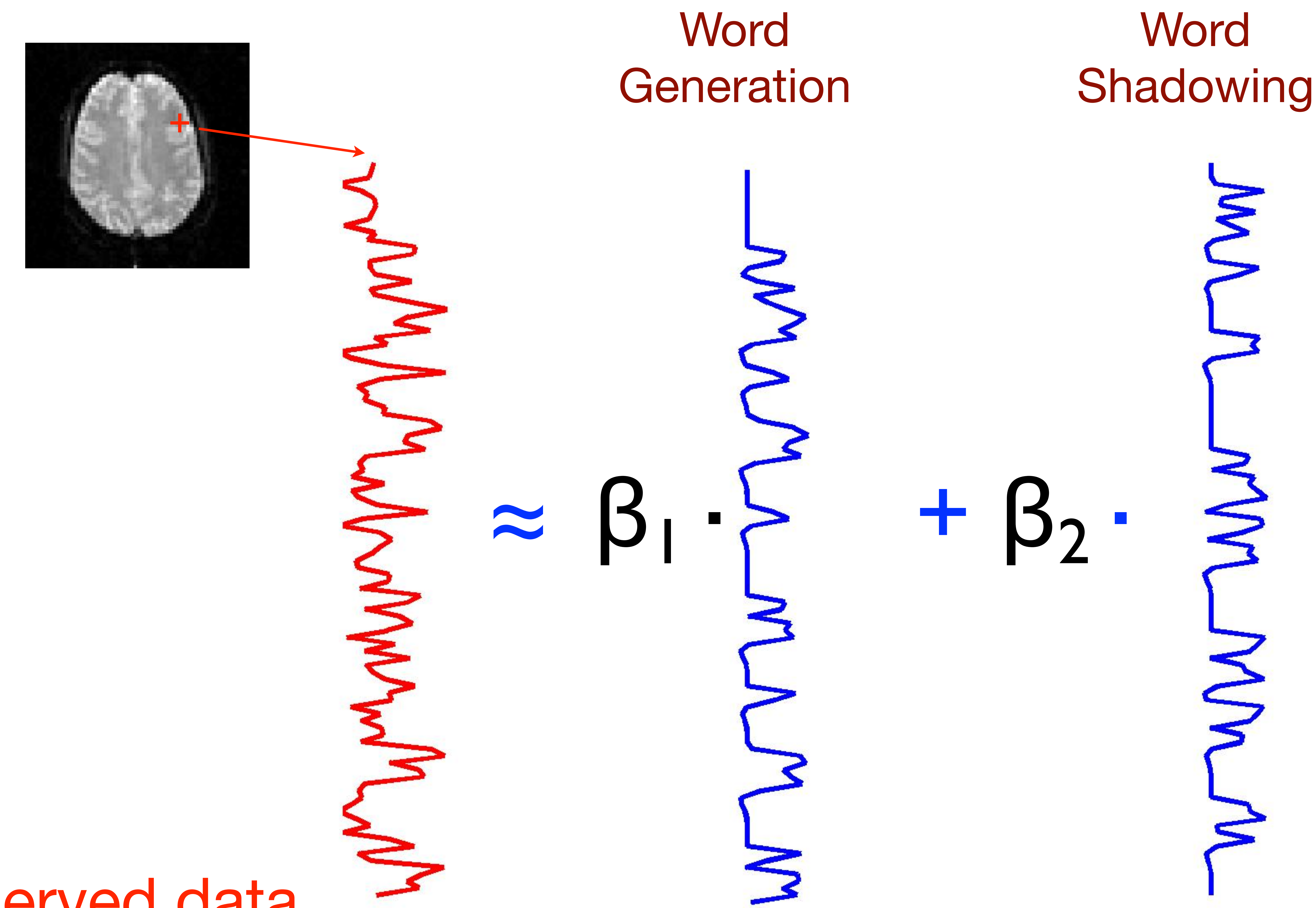
Parameter Estimates

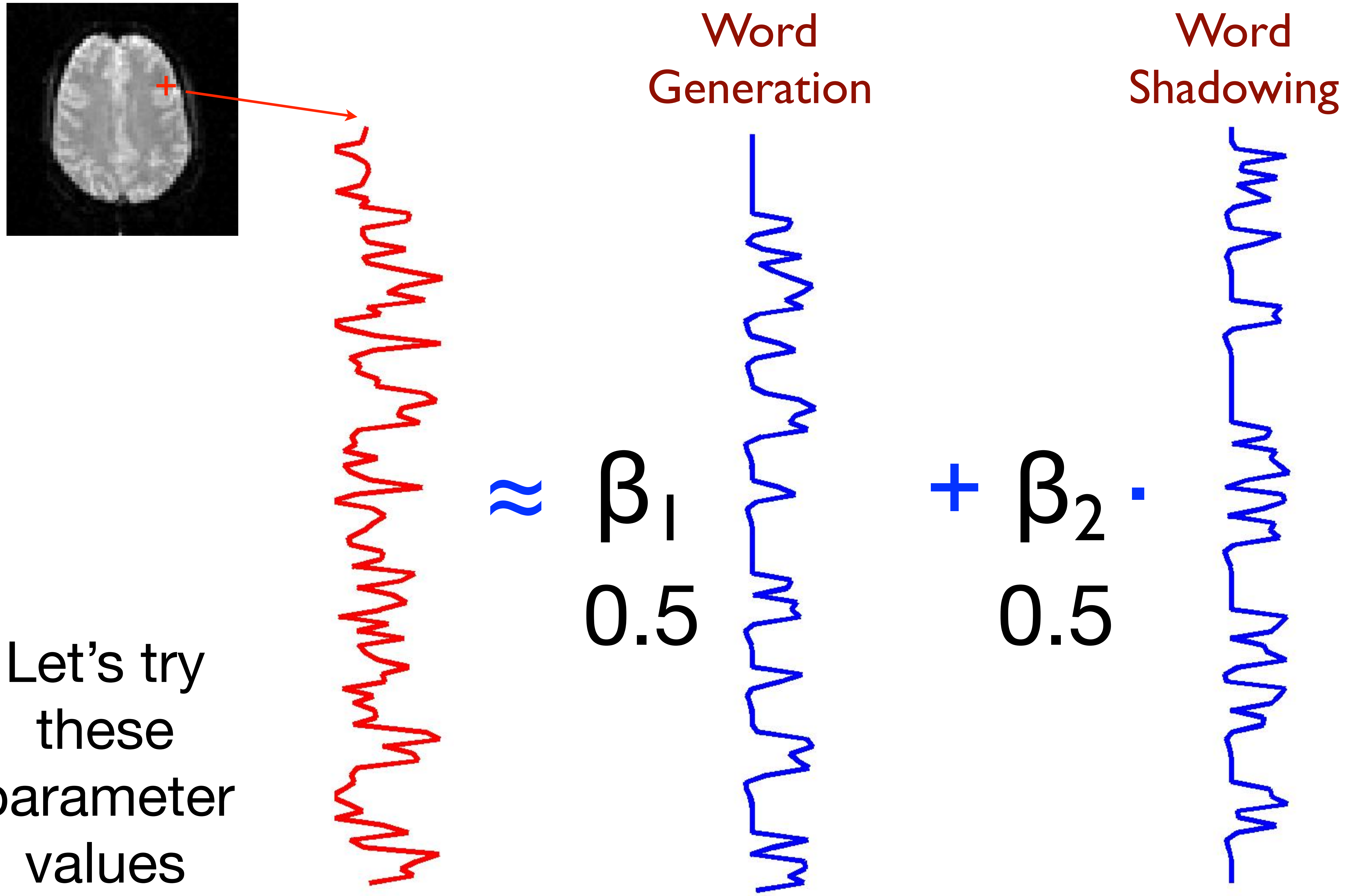


Observed data

Predicted responses
= EVs = regressors

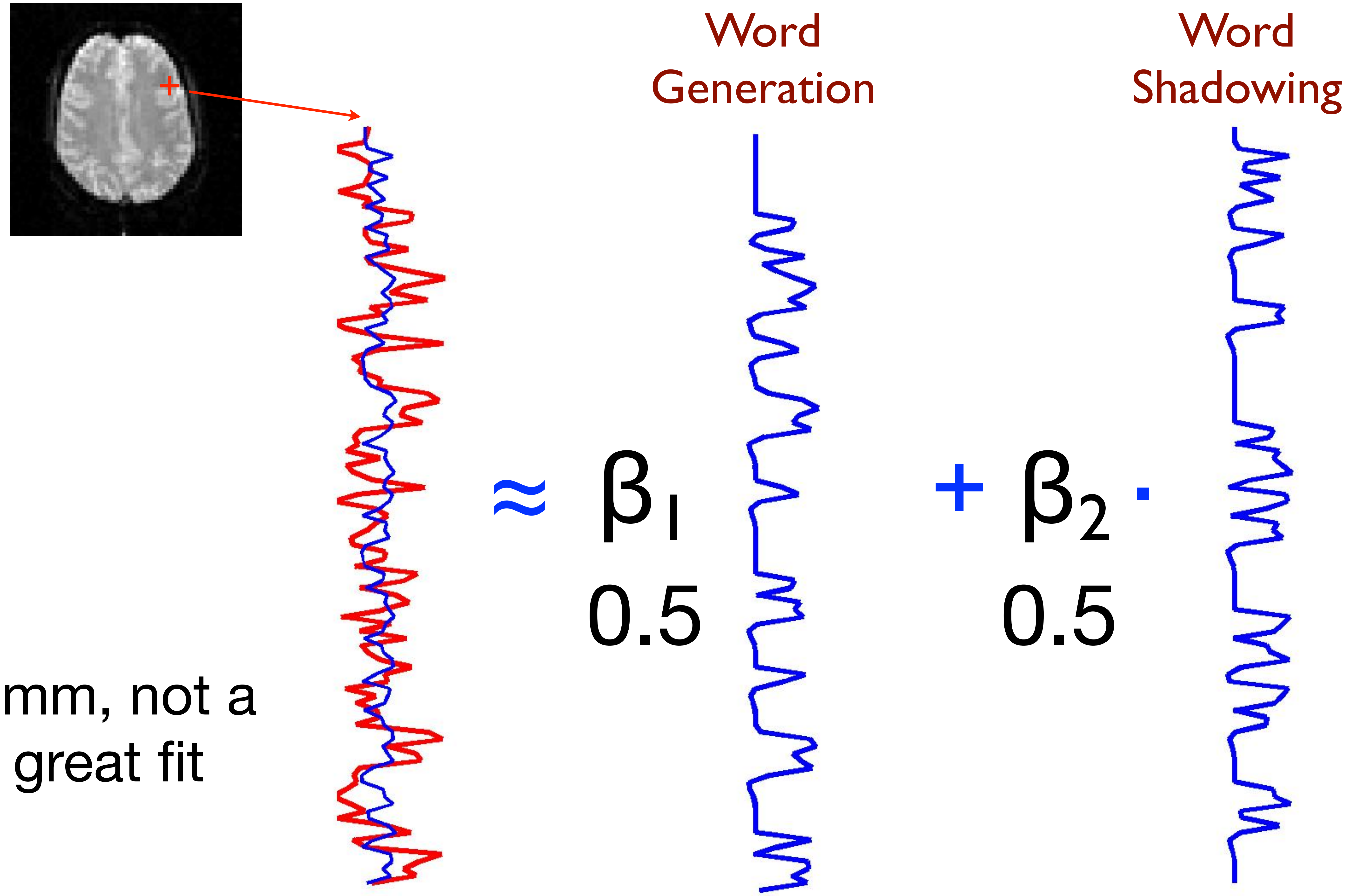
Estimation: finding a good fit

The estimation entails finding the parameter values such that the linear combination “best” fits the data



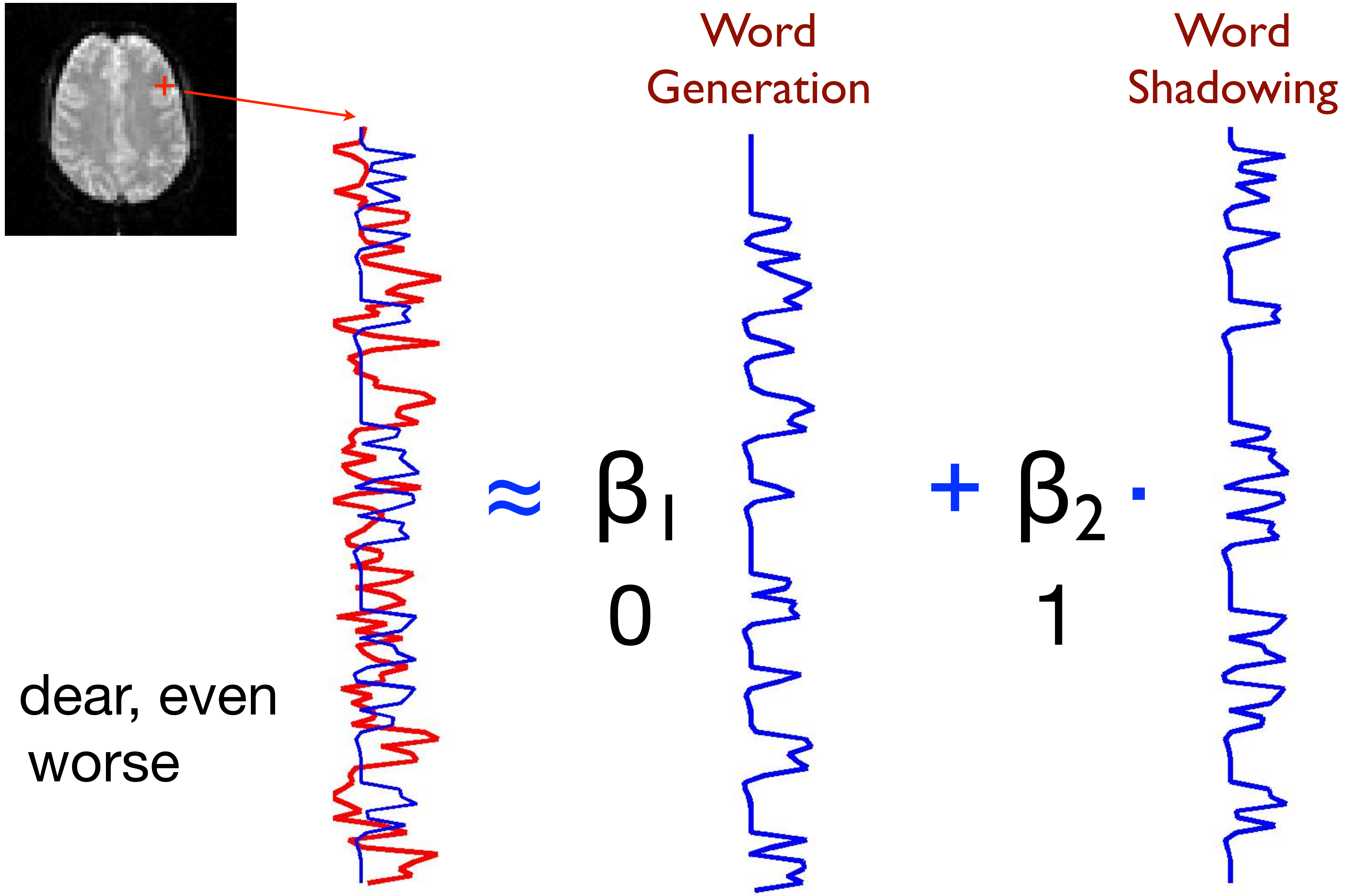
Let’s try these parameter values

Estimation: finding a good fit



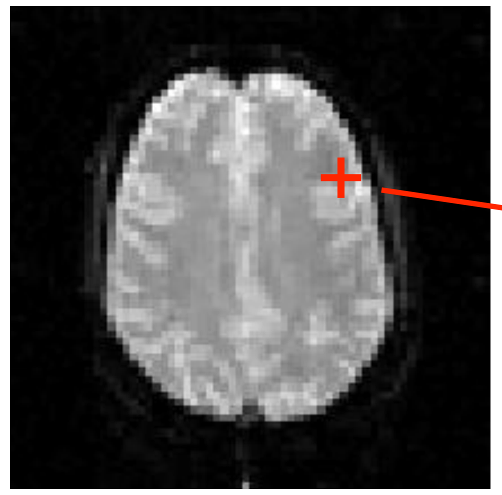
Hmm, not a great fit

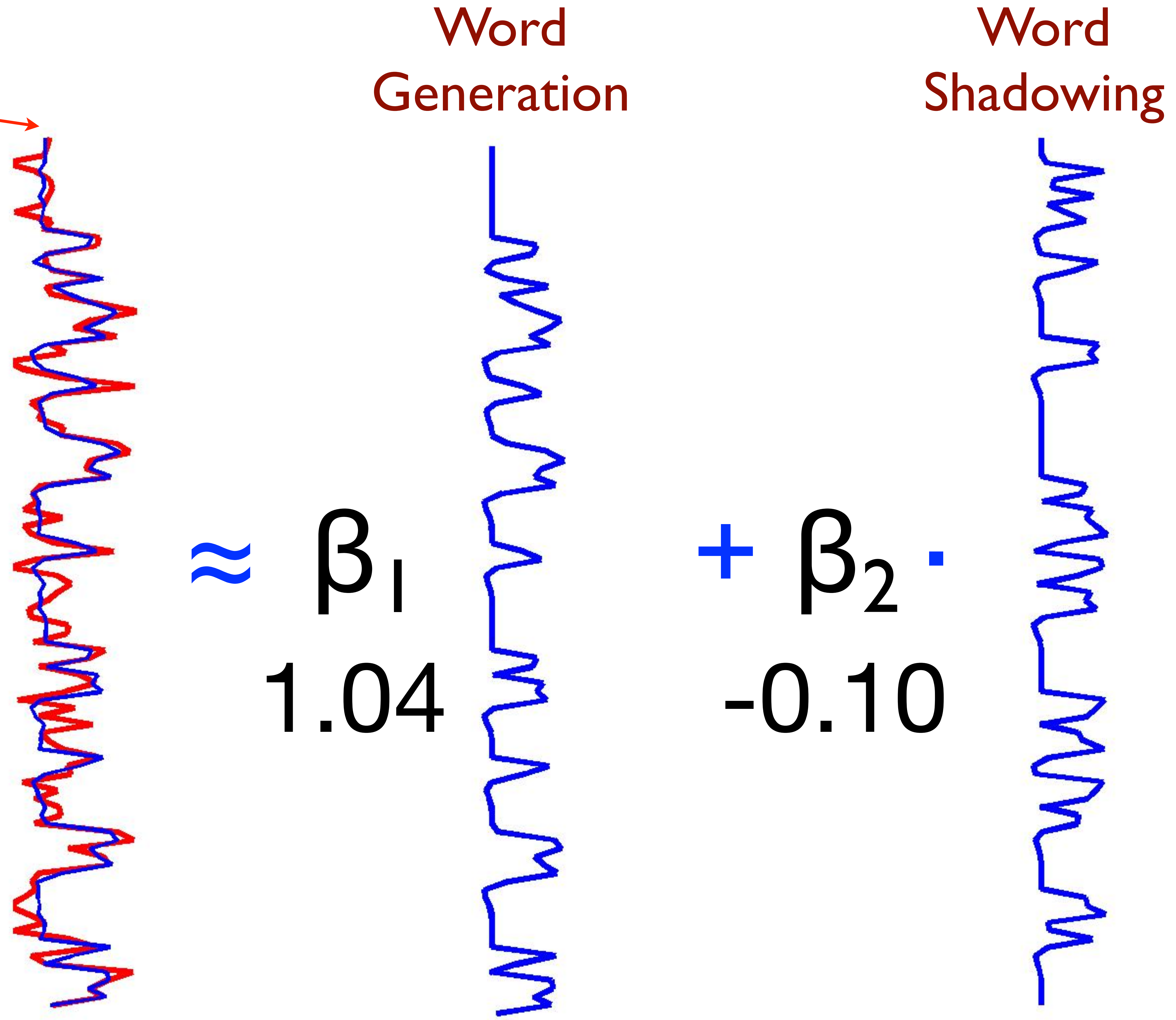
Estimation: finding a good fit



Oh dear, even worse

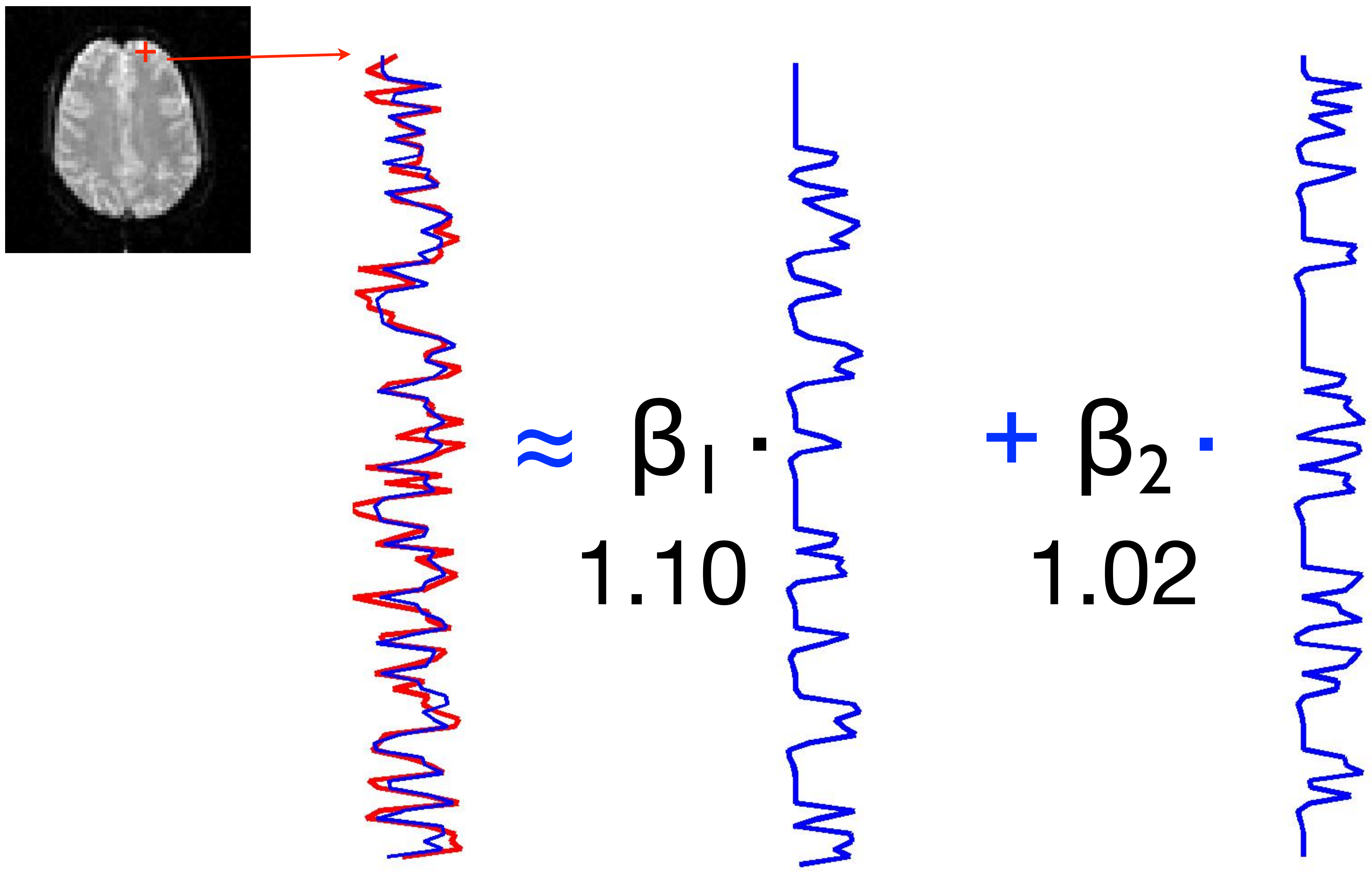
Estimation: finding a good fit



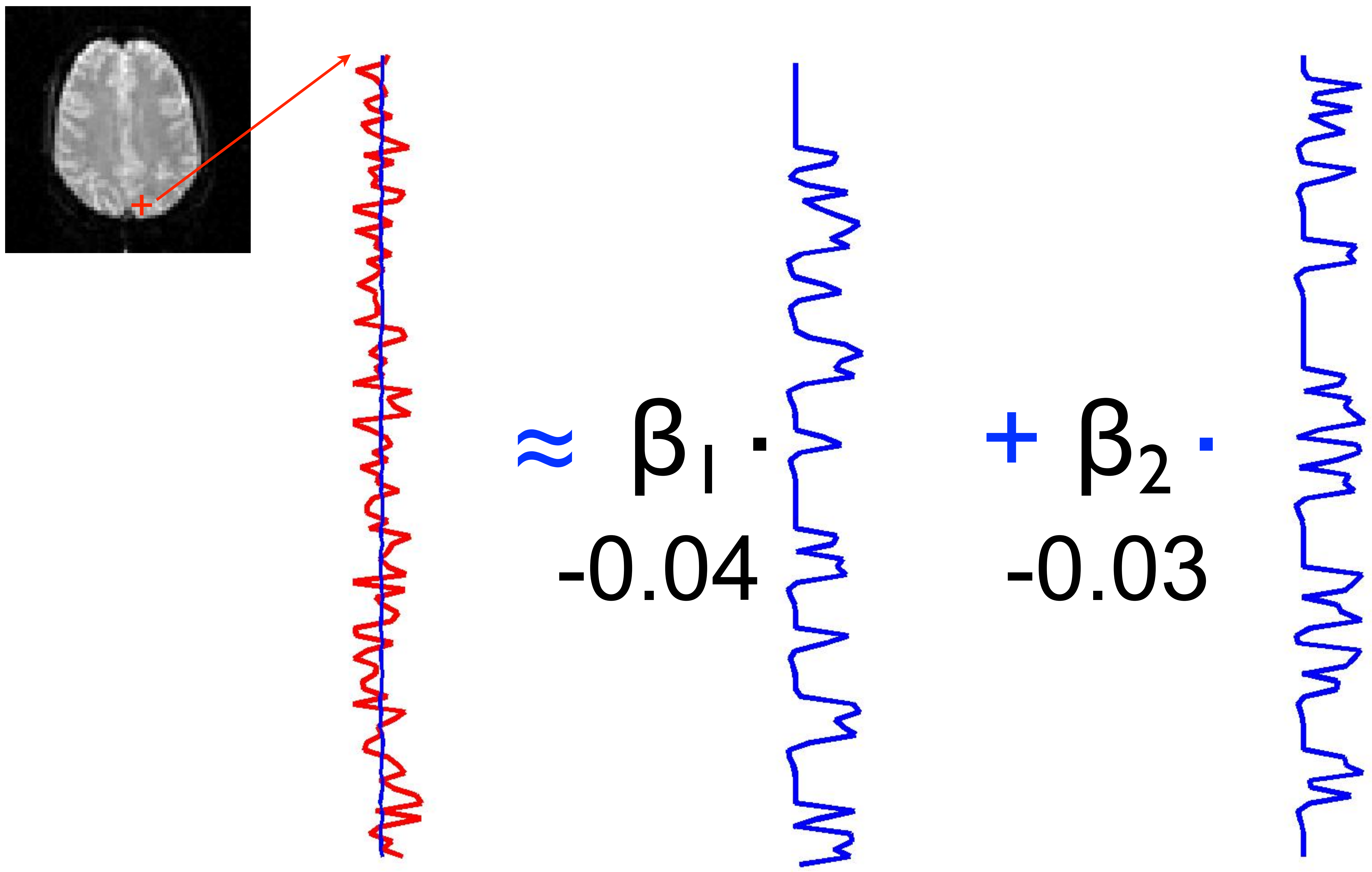


But that looks good

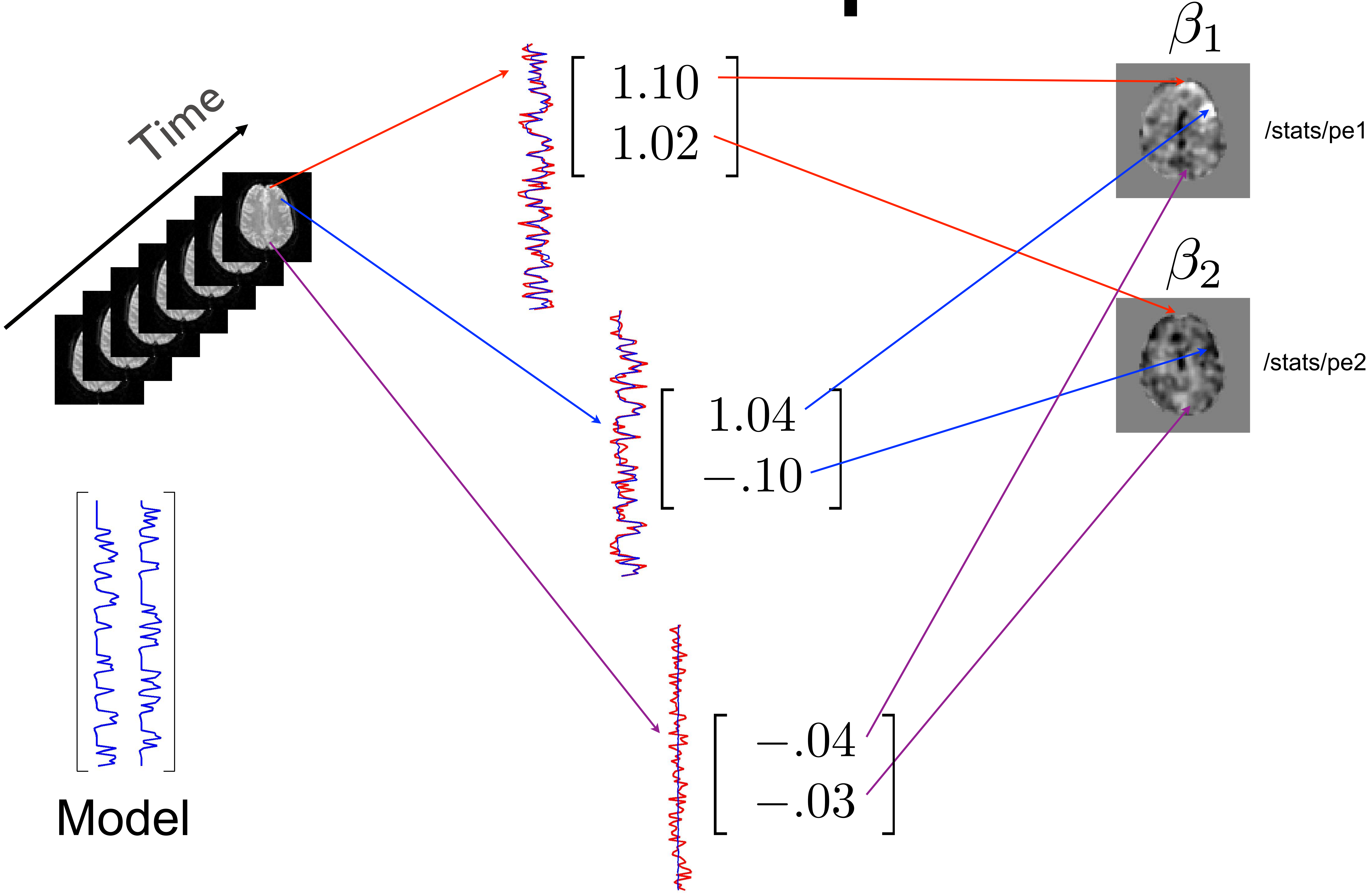
Estimate PEs separately for each voxel



Estimate PEs separately for each voxel

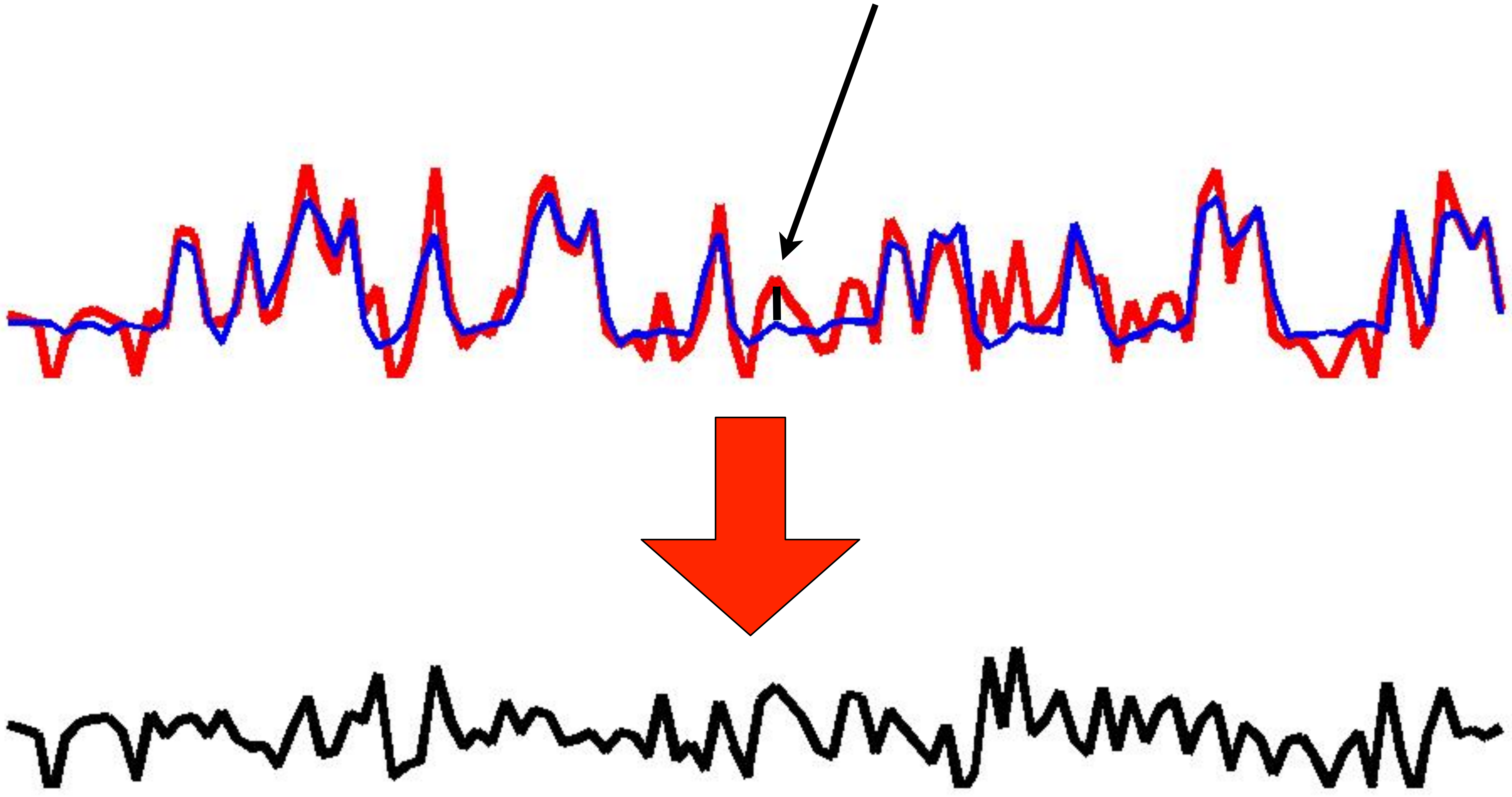


Beta maps


Time
$\begin{bmatrix} 1.10 \\ 1.02 \end{bmatrix}$
$\begin{bmatrix} 1.04 \\ -.10 \end{bmatrix}$
$\begin{bmatrix} -.04 \\ -.03 \end{bmatrix}$
β_1
/stats/pe1
β_2
/stats/pe2
Model

Residuals

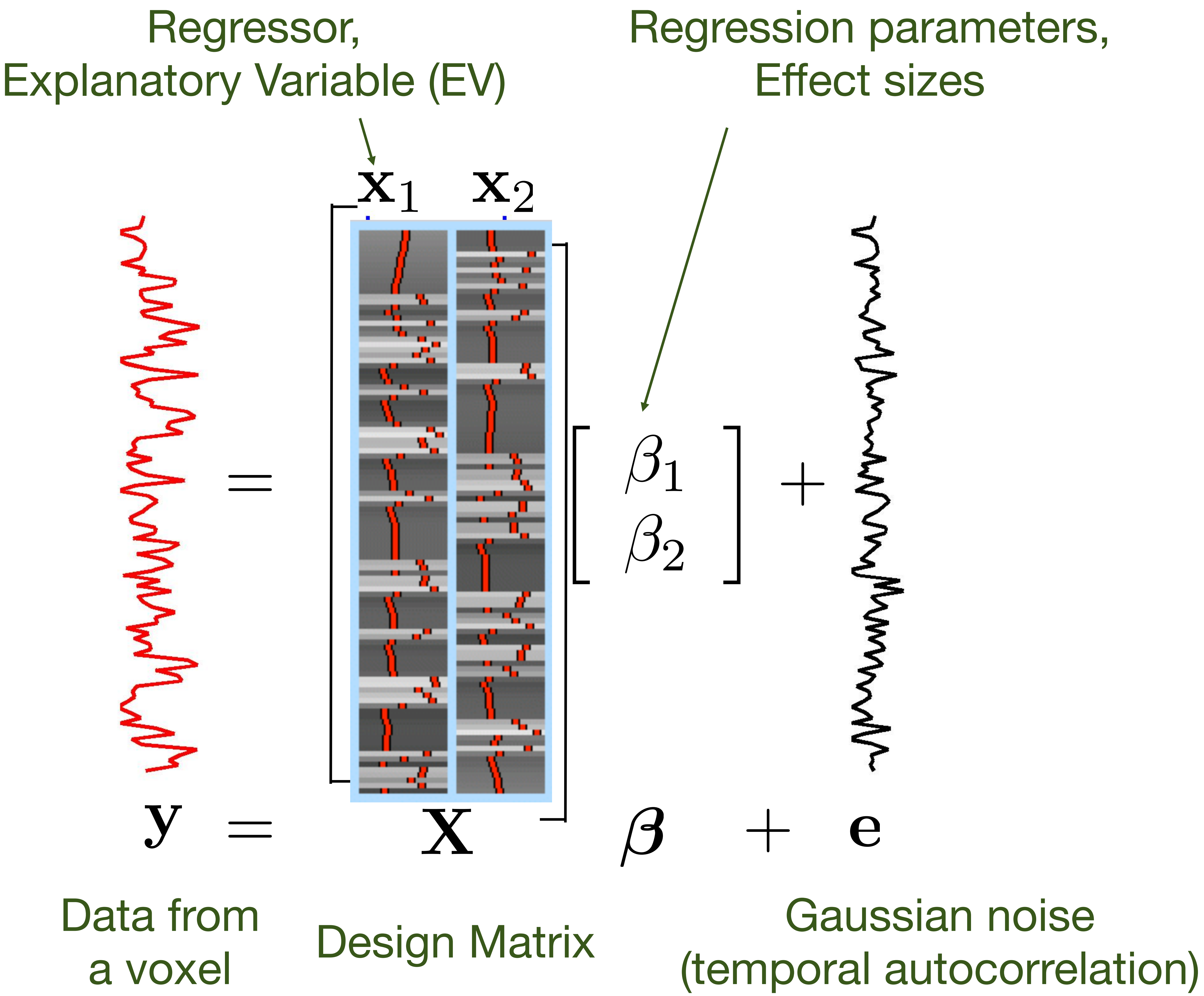
Difference between data and best fit: “Residual error”



Residual errors

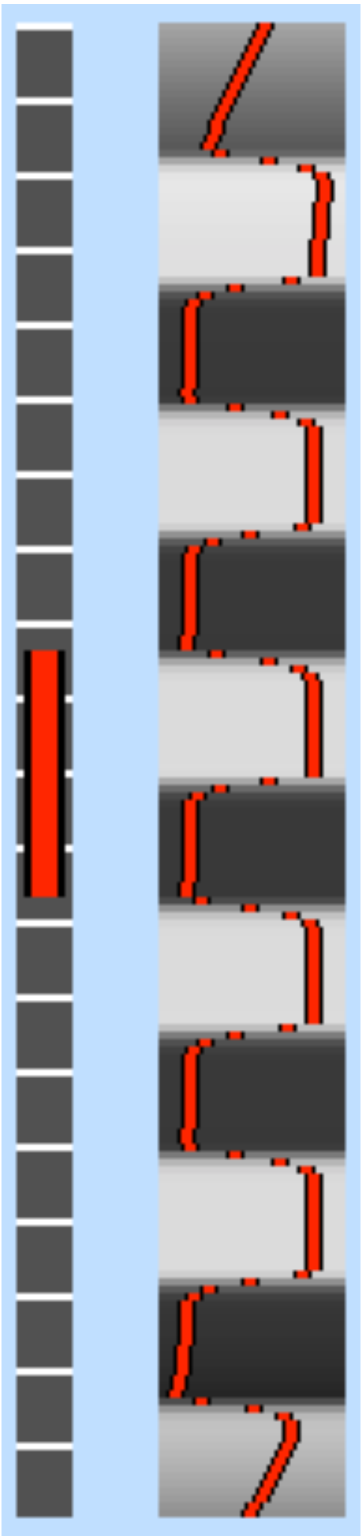
$\updownarrow \sigma$ Used to calculate t-statistic

The GLM framework

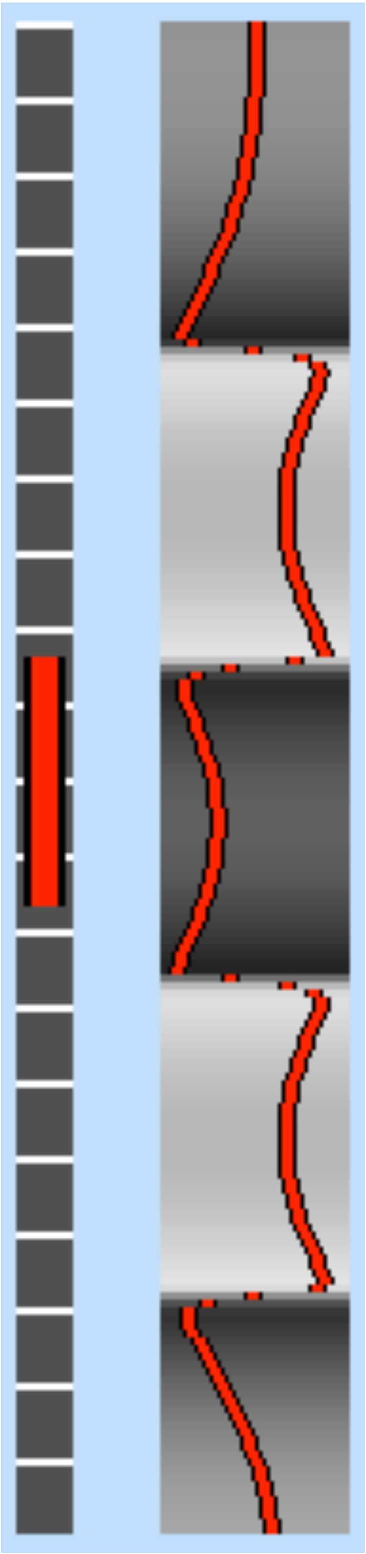


Choosing the high pass filter

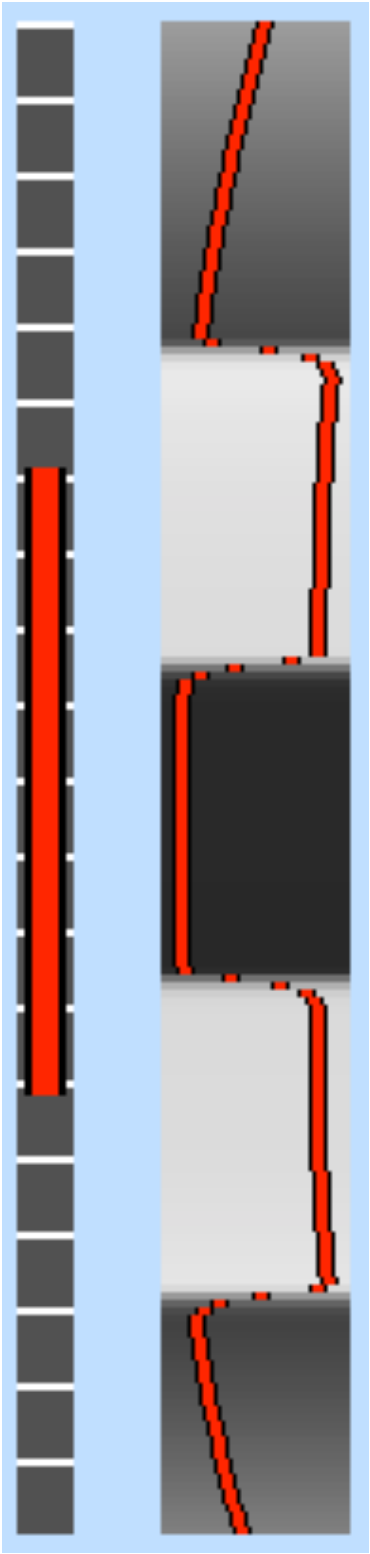
Cut-off=100s



Cut-off=100s

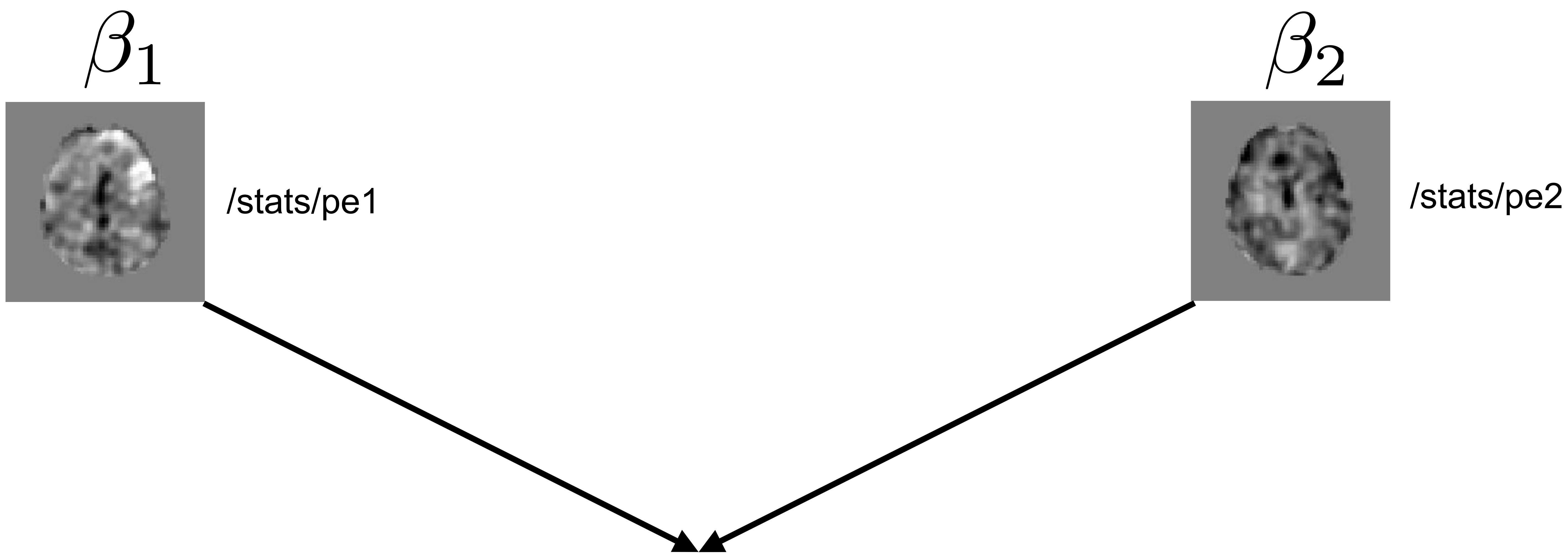


Cut-off=250s



Contrasts

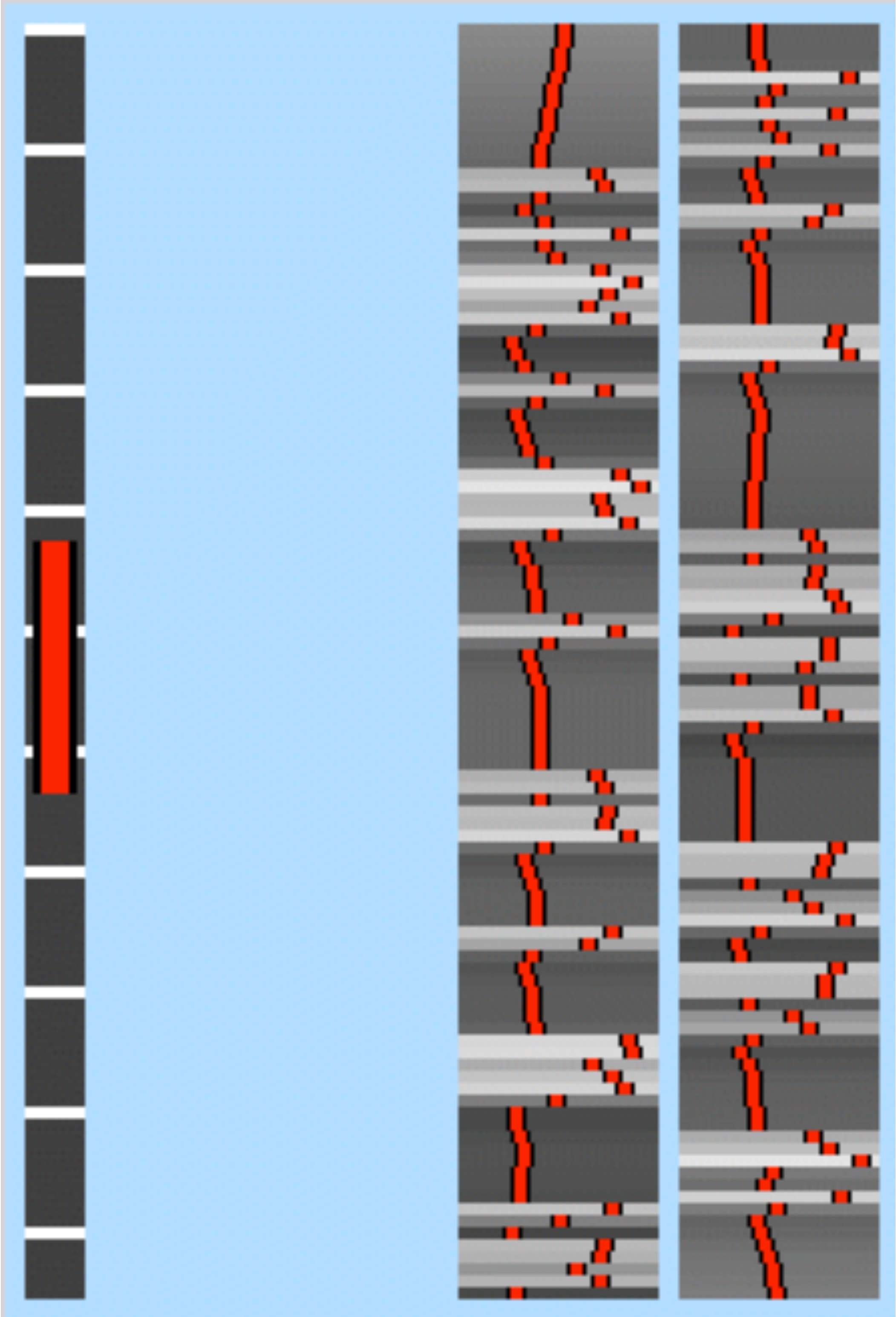
Research questions



Which areas of the brain are significantly activated during word generation compared to baseline?

Which areas of the brain are significantly more activated during word generation compared to word shadowing?

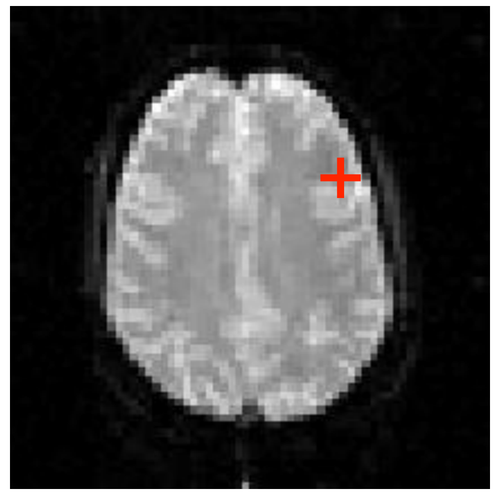
Possible contrasts



		Gen	Shad
C1	Generation	1	0
C2	Shadowing	0	1
C3	Mean	1	1
C4	Shad > Gen	-1	1
C5	Gen > Shad	1	-1

- [1 0] : EV1 vs baseline
- [0 1] : EV2 vs baseline
- [1 1] : Mean of EV1 and EV2
- [-1 1]: More activated in EV2 than EV1
- [1 -1]: More activated in EV1 than EV2

COPEs = simple arithmetic



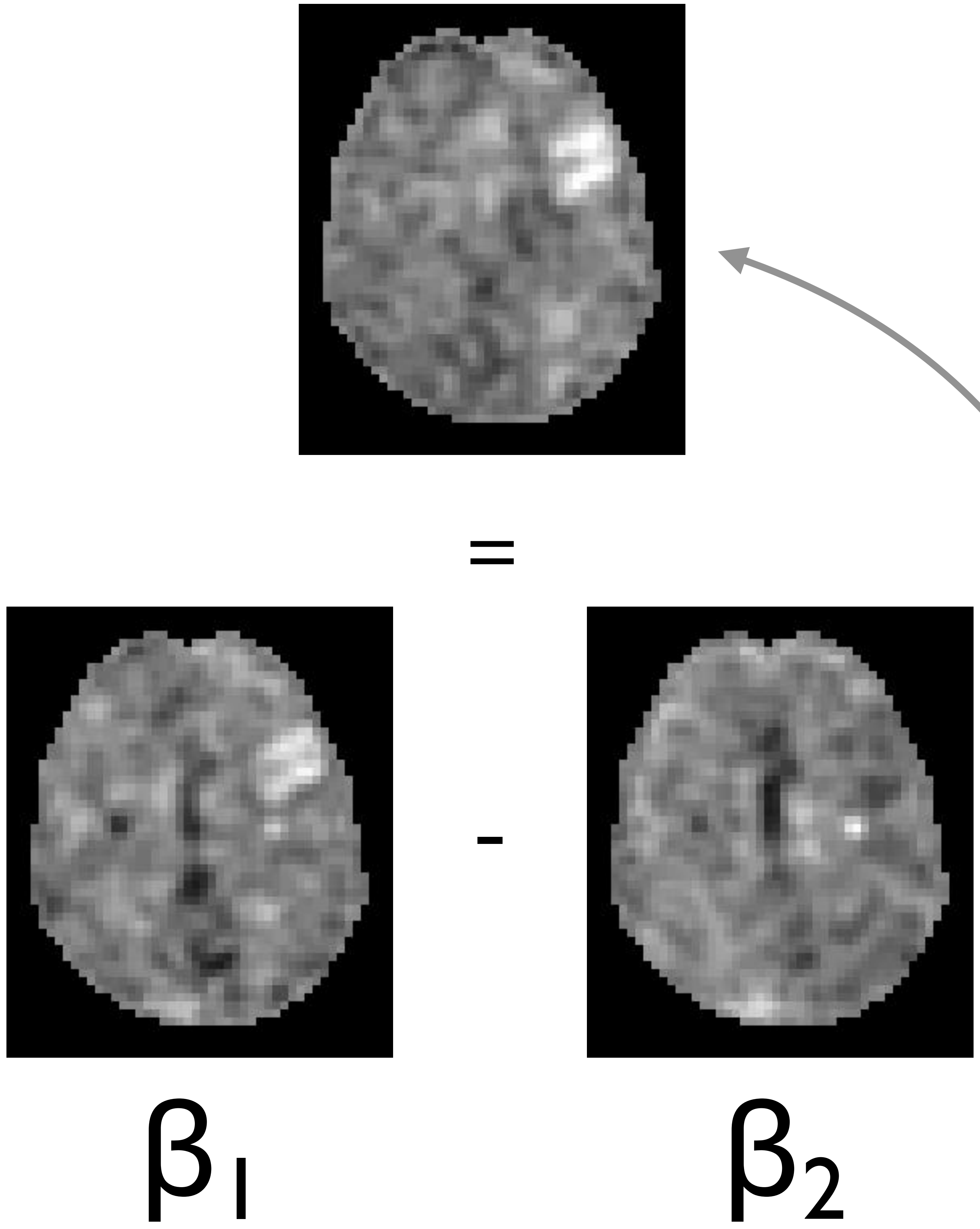
$\beta_1 = 1.04$

$\beta_2 = -0.10$

- [1 0] : 1 x 1.04 + 0 x -0.10 = 1.04
- [0 1] : 0 x 1.04 + 1 x -0.10 = -0.10
- [1 1] : 1 x 1.04 + 1 x -0.10 = 0.94
- [-1 1]: -1 x 1.04 + 1 x -0.10 = -1.14
- [1 -1]: 1 x 1.04 + -1 x -0.10 = 1.14

Use t-test to determine if COPE is significantly greater than zero

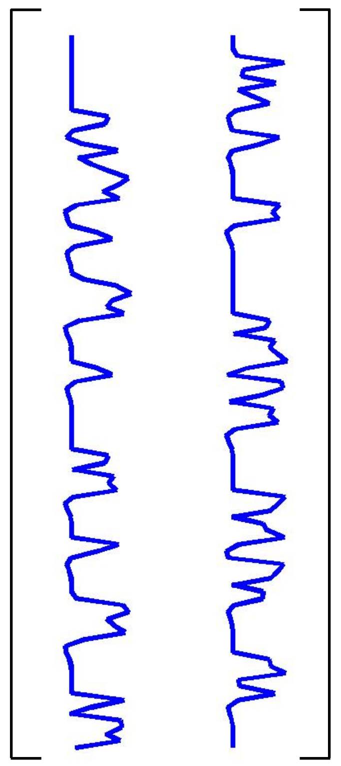
COPE images



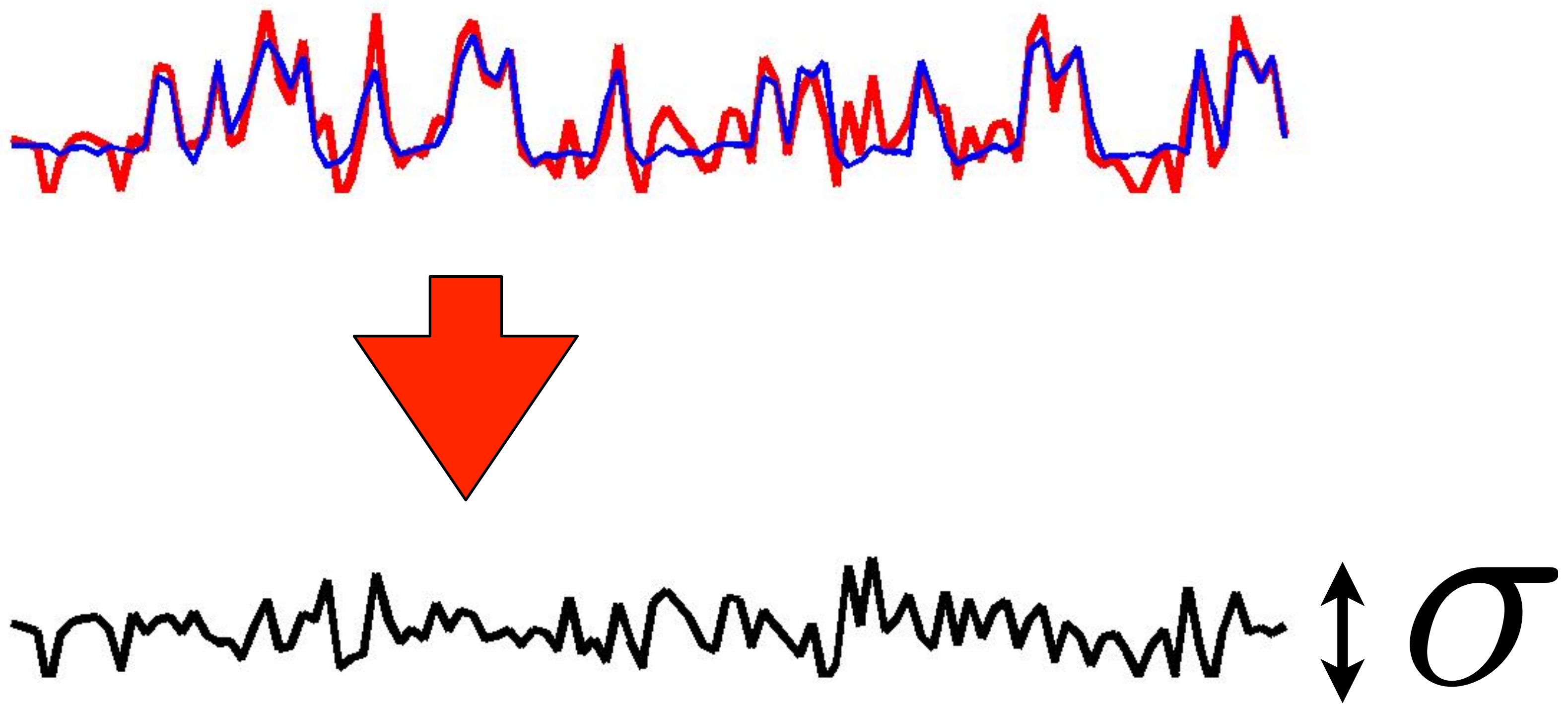
- [1 0] : 1 x 1.04 + 0 x -0.10 = 1.04
- [0 1] : 0 x 1.04 + 1 x -0.10 = -0.10
- [1 1] : 1 x 1.04 + 1 x -0.10 = 0.94
- [-1 1]: -1 x 1.04 + 1 x -0.10 = -1.14
- [1 -1]: 1 x 1.04 + -1 x -0.10 = 1.14

t-statistic

$$t = \frac{COPE}{std(COPE)}$$



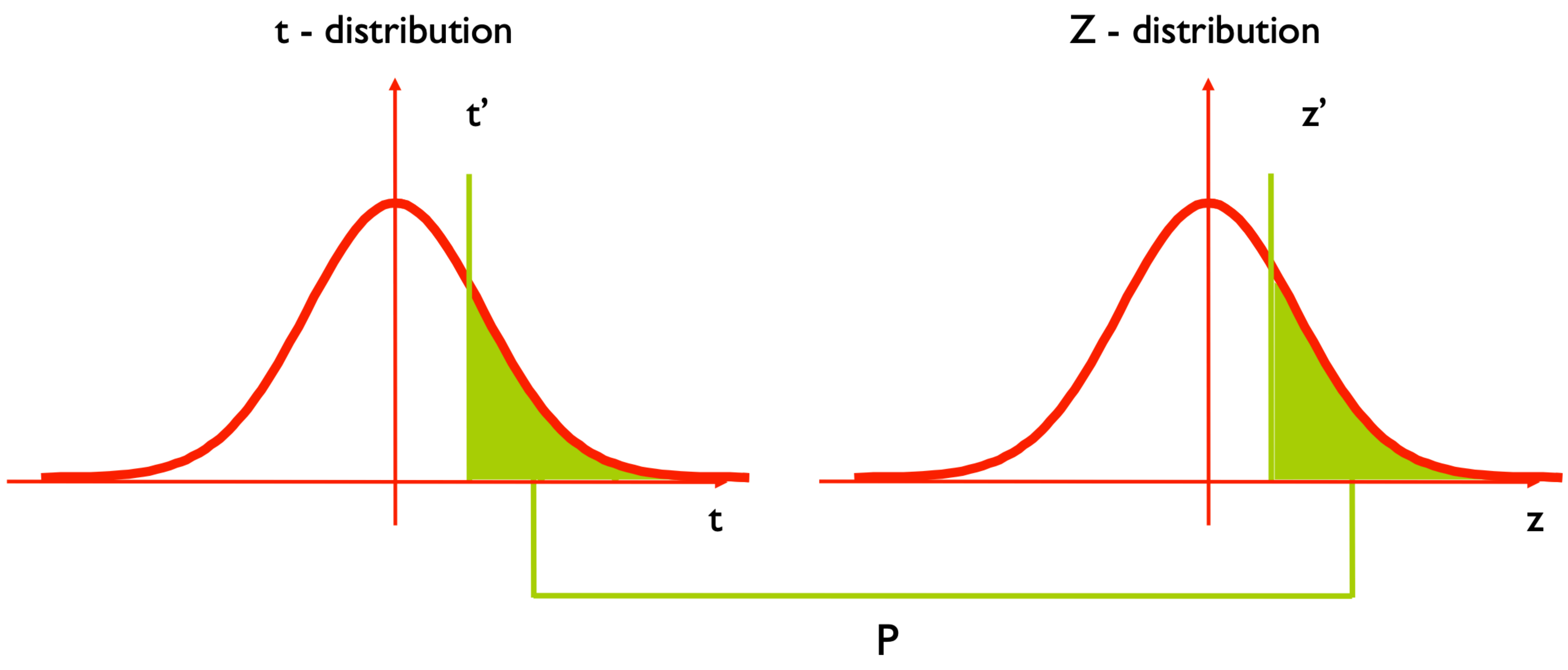
$$[1 \;\; 0]$$



The Model the Contrast and the Residual Error

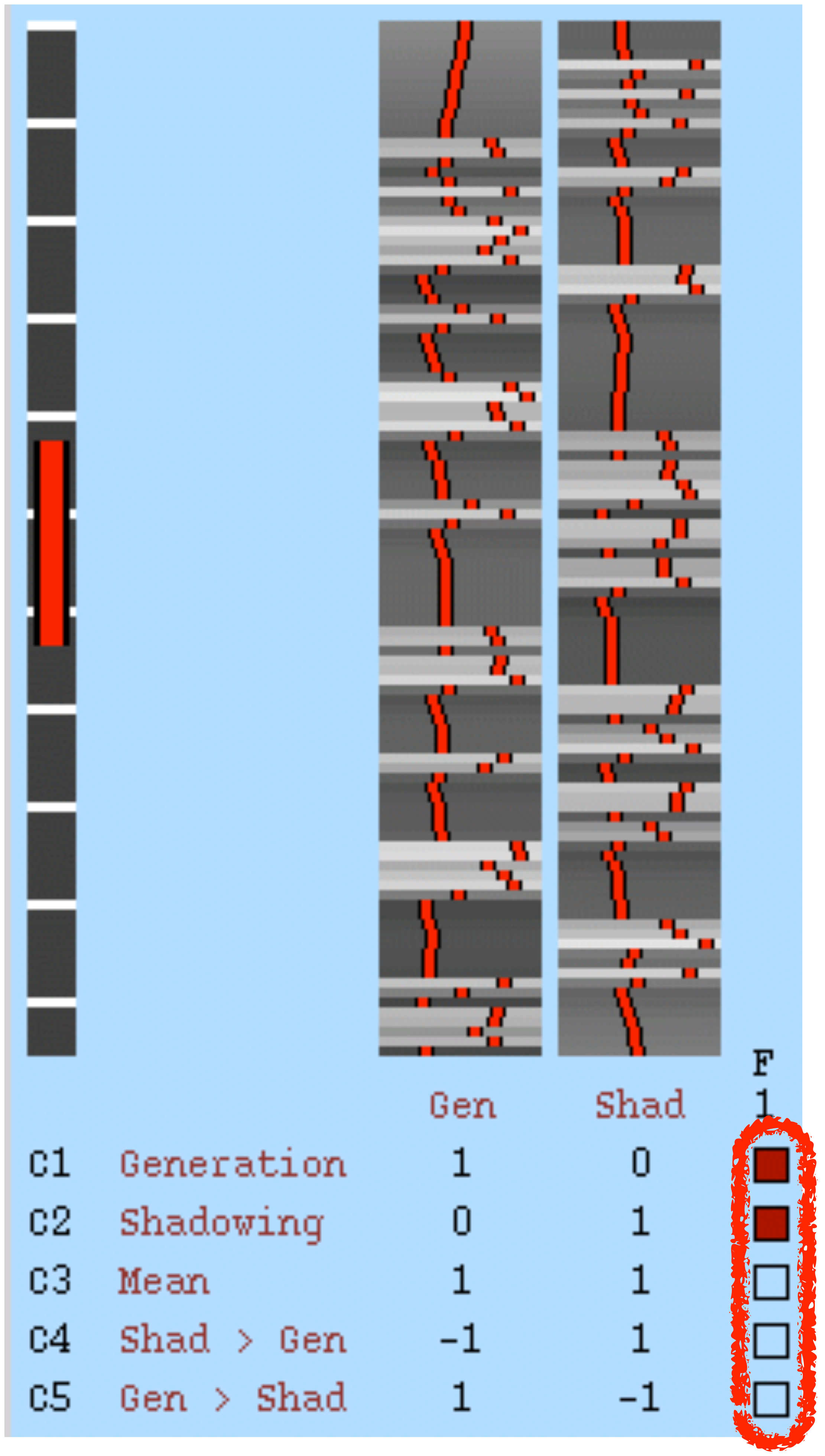
t-statistic

$$t = \frac{COPE}{std(COPE)}$$

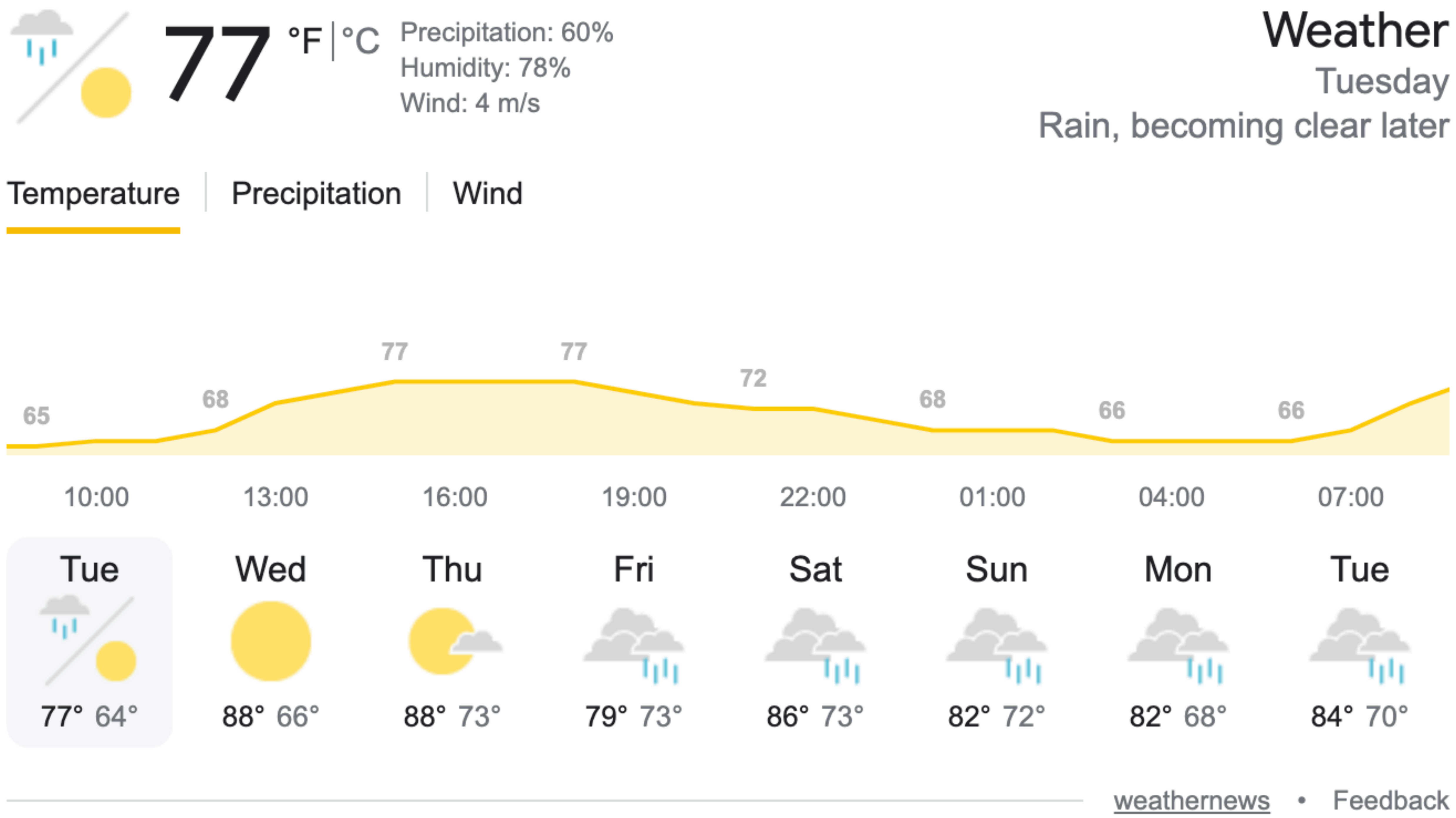


F-contrasts

- Allows you to ask if any condition is significant
    - Is there activation to any condition?
    - Does any regressor explain variance in the data?
- F-contrasts are not directional
- F-statistic compares full model to reduced model



Temporal autocorrelation



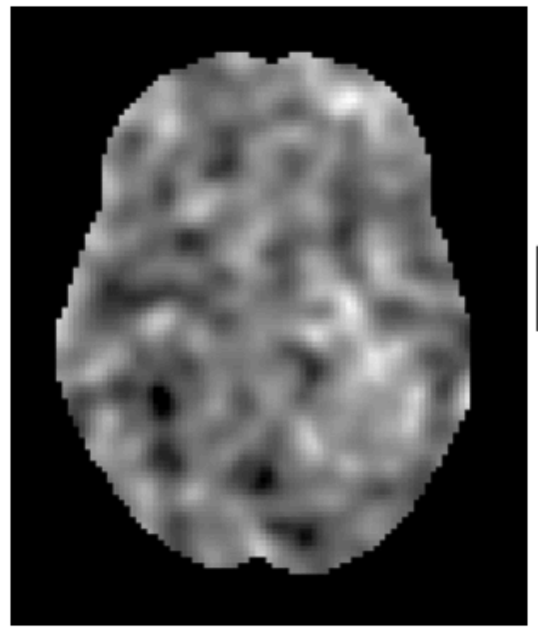
Uncorrected, this causes:

- biased stats (increased false positives)
- decreased sensitivity

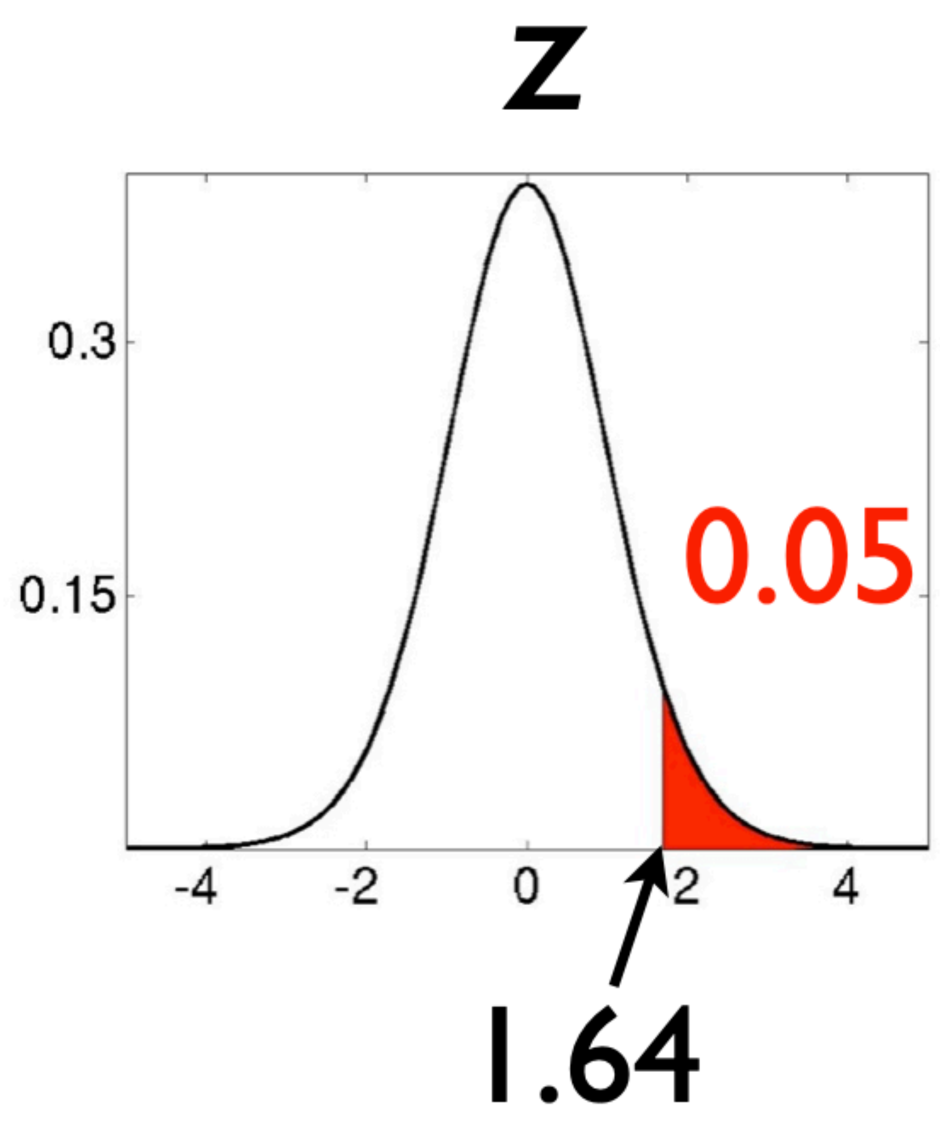
FSL fixes it for you in FEAT!

Cannot use randomise (see later) because of autocorrelation

Multiple comparisons



z-map where each voxel ~*N*.
Null-hypothesis true everywhere, i.e.
NO ACTIVATIONS



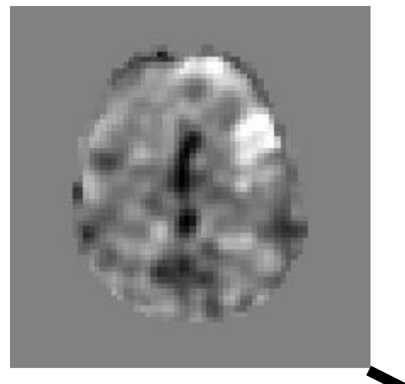
z-map
thresholded at
1.64

16 clusters
288 voxels
~5.5% of the voxels

That's a LOT of false positives

This afternoon: inference

β_1



/stats/pe1

β_2

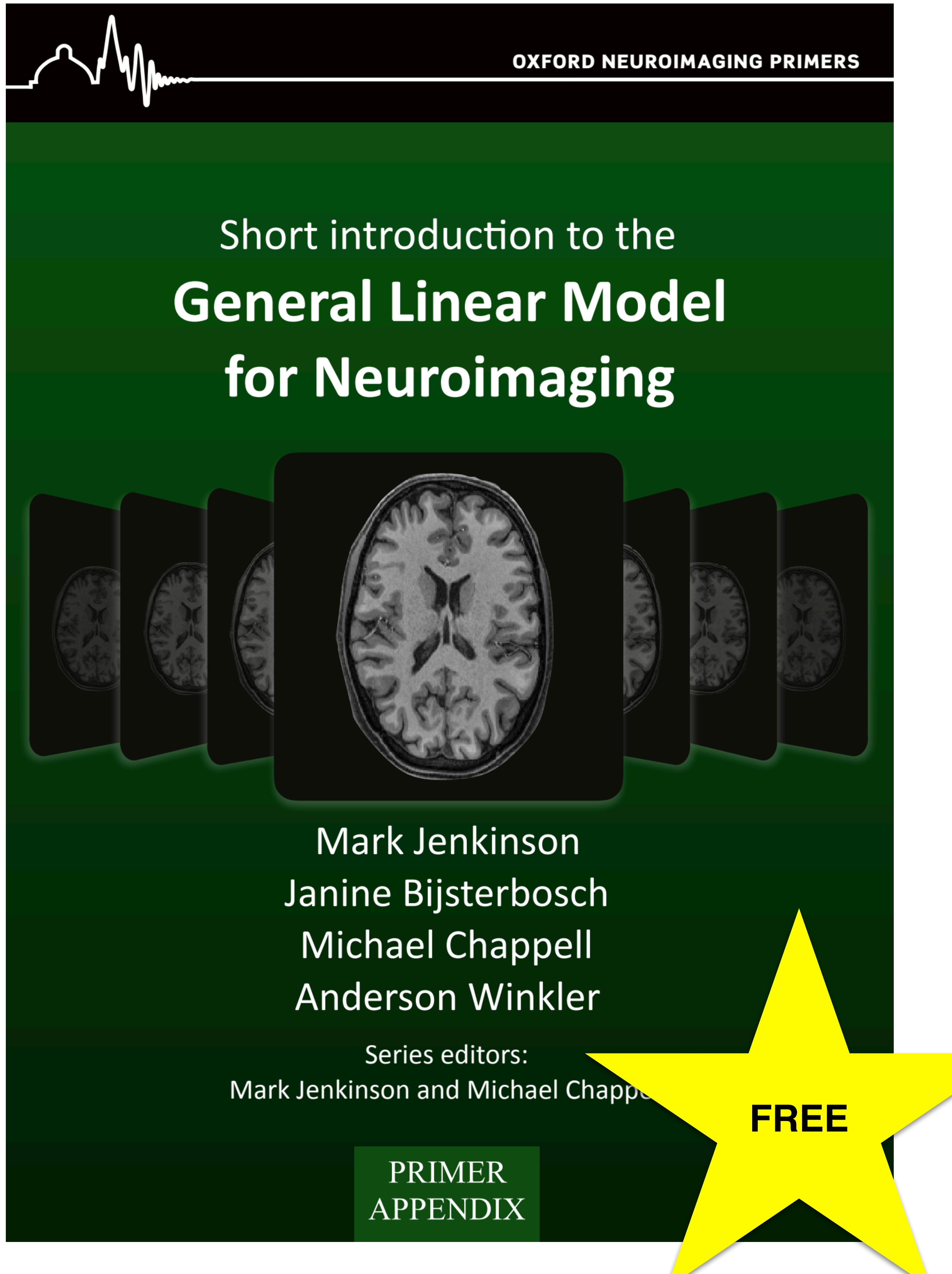
/stats/pe2

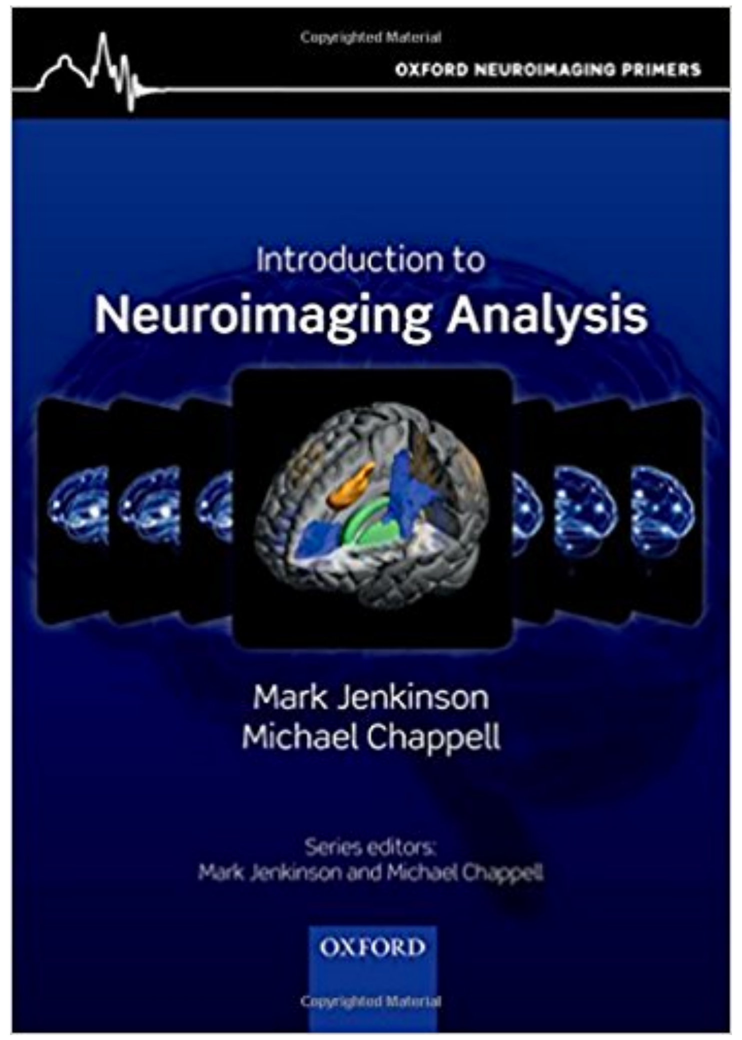
Which areas of the brain are **significantly** activated during word generation compared to baseline?

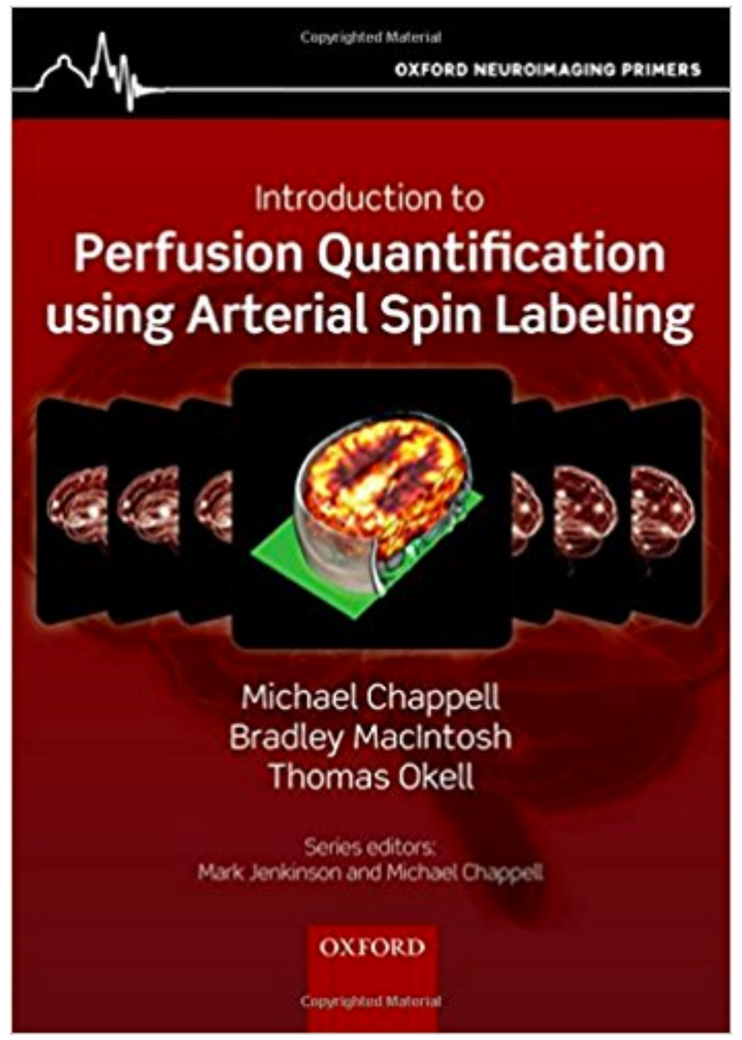
Which areas of the brain are **significantly** more activated during word generation compared to word shadowing?

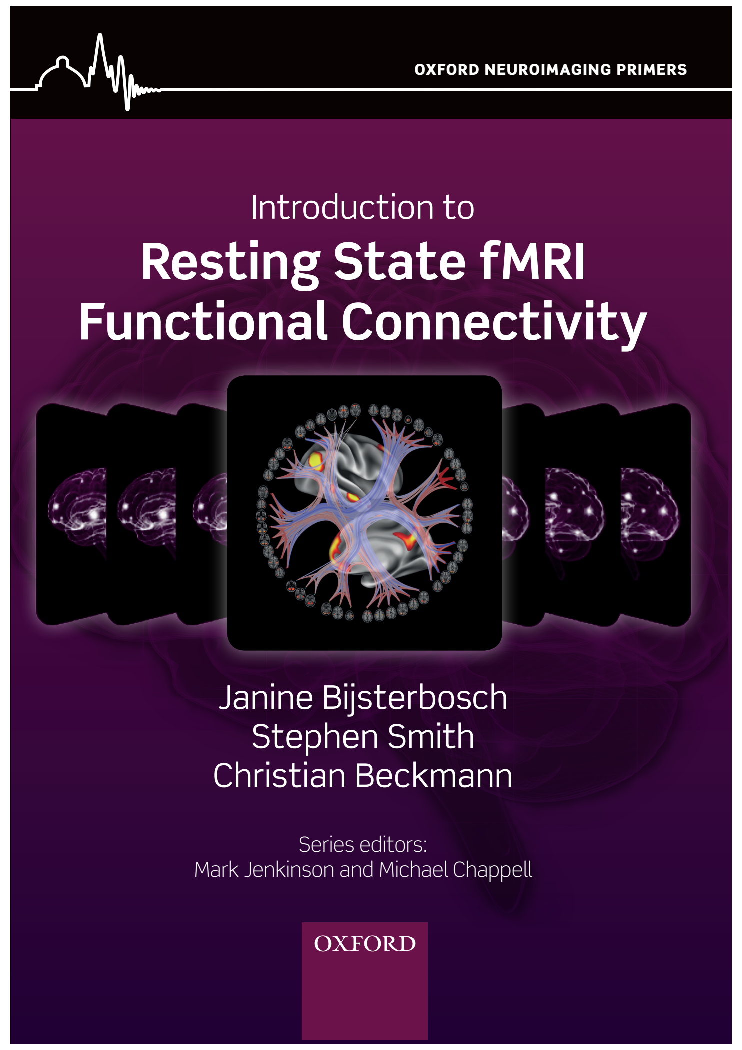
The free online appendix

- Part of a series of Oxford Neuroimaging Primers
- https://www.fmrib.ox.ac.uk/primers/appendices/glm.pdf
- Work on a full primer book on the GLM is in progress!









That’s all folks