

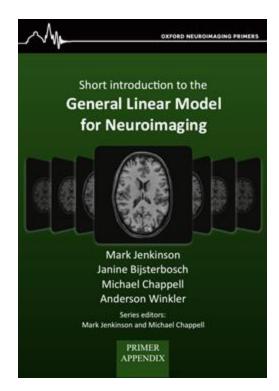
GENERAL LINEAR MODEL FOR FMRI ANALYSIS

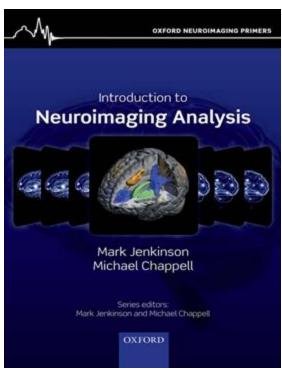
Turku PET Centre Brain Imaging Course 2025

Maya Rassouli, Turku PET Centre



Resources

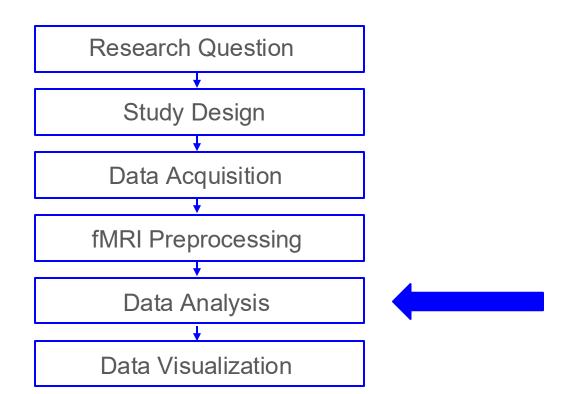






<u>Principles of fMRI Part 1 Module 15: The</u> General Linear Model - Intro

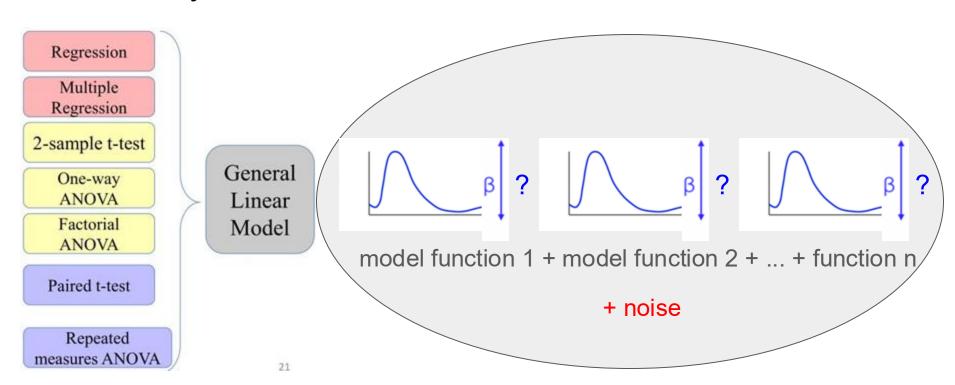
Principles of fMRI Part 1, Module 16: GLM applied to fMRI



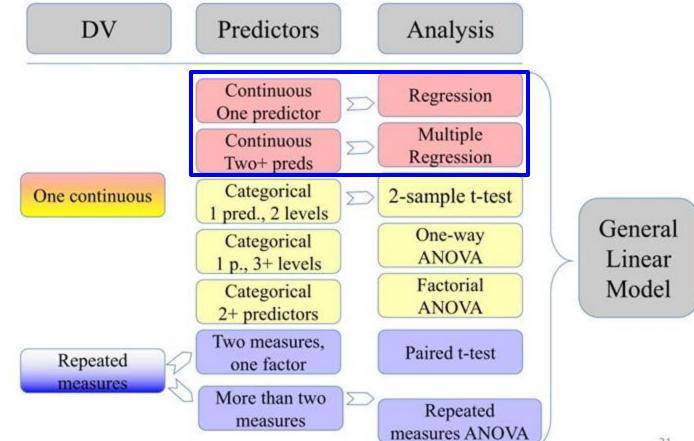
Outline

- 1. General Linear Model (GLM) family
- 2. GLM for fMRI Analysis
 - a. Simple Regression
 - b. Multiple Regression
 - c. Covariates and Confounds
 - d. Limitations
- 3. Case Study & Quiz

GLM family



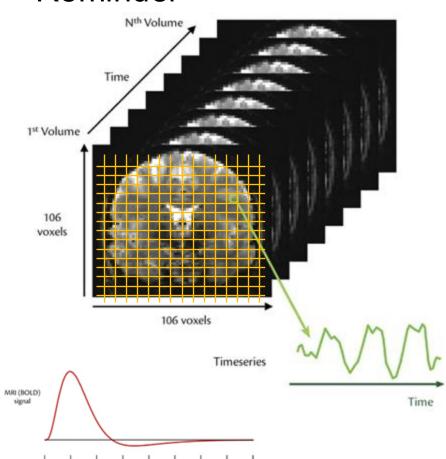
GLM family

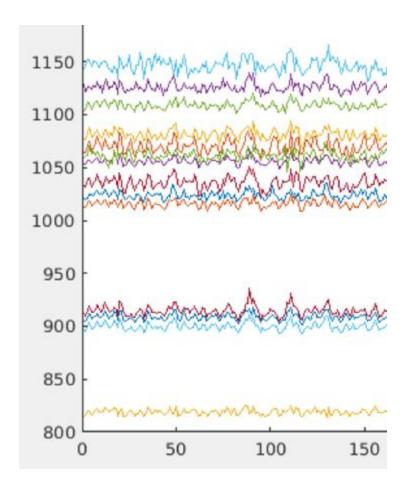


Reminder

onset

Time (seconds)



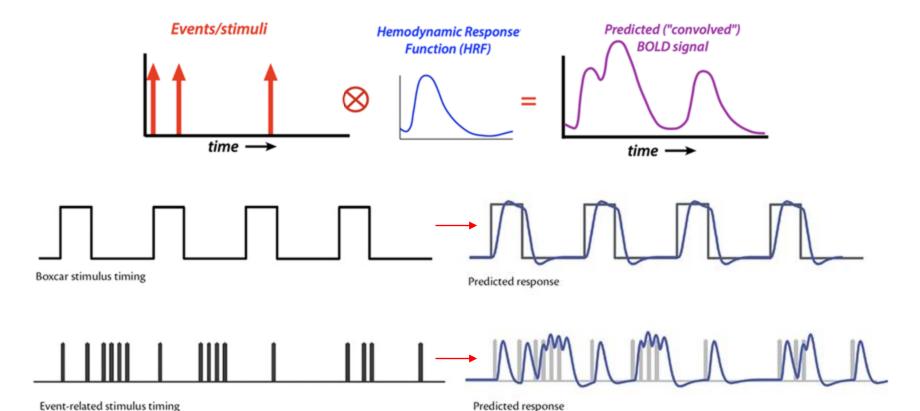


GLM for fMRI Analysis

GLM

looks for the predicted responses in the measured fMRI signal.

Predicted response model



GLM for fMRI Analysis

GLM

looks for the predicted responses in the measured fMRI signal.

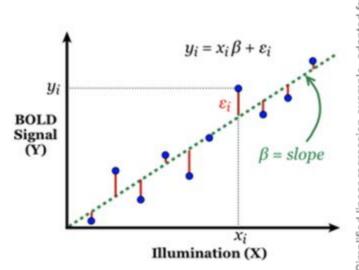
 helps determine where there is significant relationship between the measured signal and the predicted response

Simple Regression

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

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ \vdots \\ y_n \end{bmatrix} = \begin{bmatrix} x_1 \\ x_2 \\ x_3 \\ \vdots \\ x_n \end{bmatrix} [\beta] + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \\ \vdots \\ \varepsilon_n \end{bmatrix}$$

- Y = BOLD timeseries
- X = regressor
- β = scaling parameter
- ε = residual error / residuals

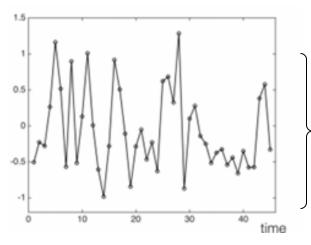


Simplified linear regression

Simple Regression

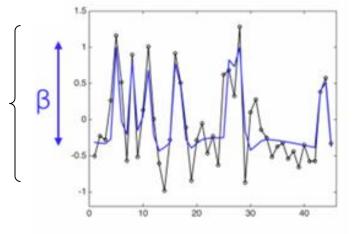
predicted response

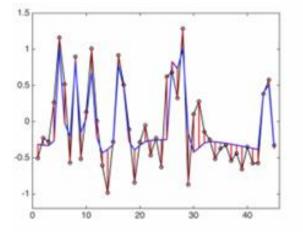




BOLD timeseries

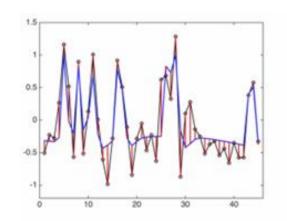






 $Y = X \beta + \varepsilon$

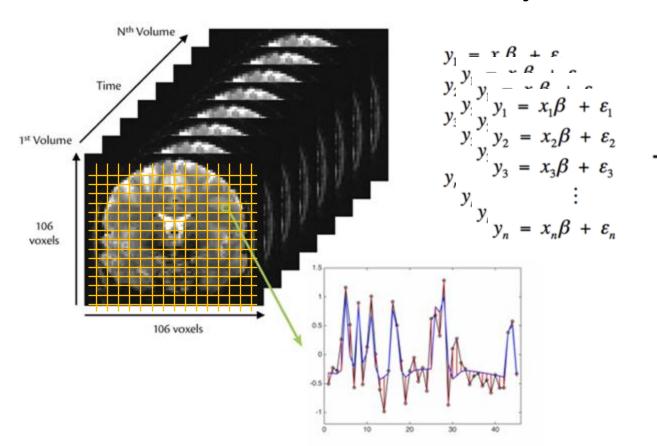
"Best fit"



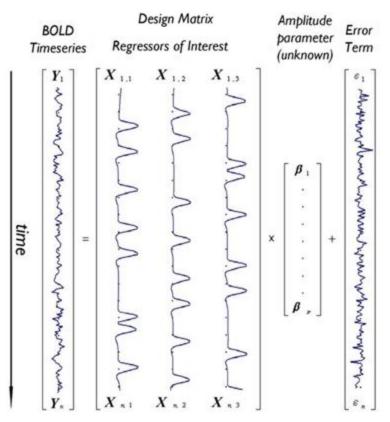
Difference between the residuals are minimised

→ Minimising the residuals / Finding the least squared error

Voxelwise + Mass Univariate Analysis



Multiple Regression



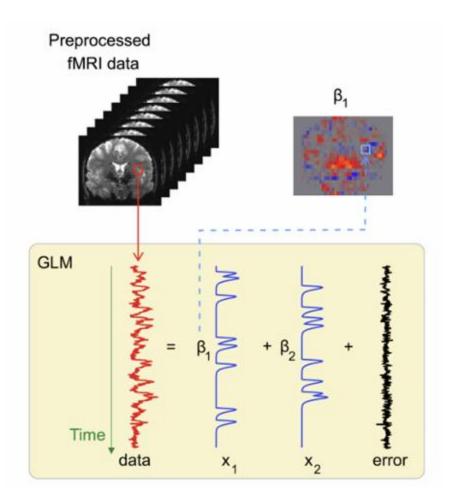
Multiple Regression

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

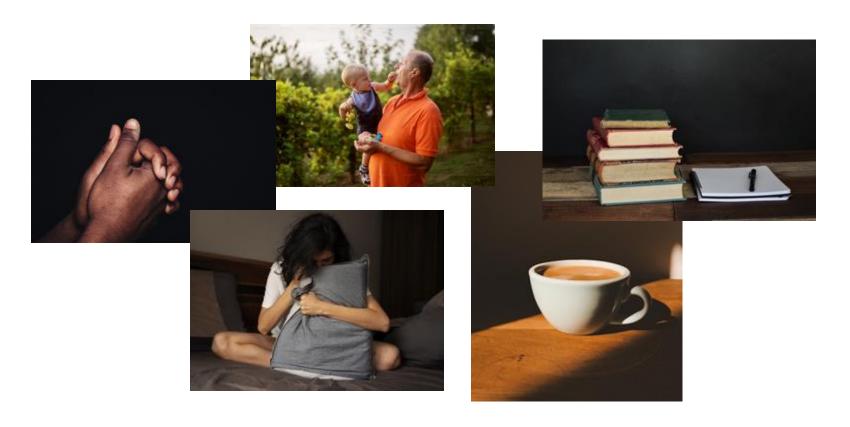
$$\text{time} \quad \left[\begin{array}{c} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{array} \right] = \left[\begin{array}{cccc} 1 & X_{11} & \cdots & X_{1p} \\ 1 & X_{21} & \cdots & X_{2p} \\ \vdots & \vdots & & \vdots \\ 1 & X_{np} & \cdots & X_{np} \end{array} \right] \times \left[\begin{array}{c} \beta_0 \\ \beta_1 \\ \vdots \\ \beta_p \end{array} \right] + \left[\begin{array}{c} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_n \end{array} \right]$$

- Y = BOLD timeseries
- X = design matrix of all the regressors each regressor = one column
- β = vector of all the individual scaling parameters
- ε = residual error / residuals

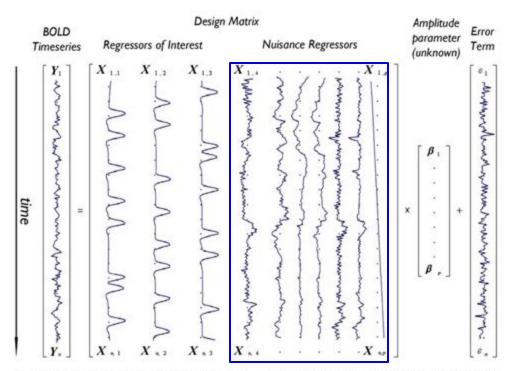
Results



Covariates of (no) Interests



Confounds / Nuisance Regressors



Depiction of the General Linear Model (GLM) for a voxel with time-series Y predicted by a design matrix X including 10 effects (three regressors of Interest - e.g., tasks A,B,C - and seven nuisance regressors - e.g., six motion parameters and one linear drift). Calculated weighting factors ($\beta_1 - \beta_{10}$) corresponding to each regressor are placed in amplitude vector β_1 while column vector β_2 contains calculated error terms (β_3) for the model corresponding to each time point β_3 . (From Monti, 2011, under CC BY license)

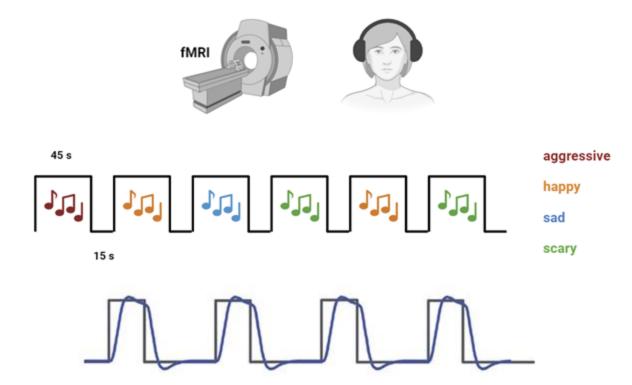
Limitations

 The model is the same for each voxel (mass univariate), but the haemodynamic response might differ across the brain regions.

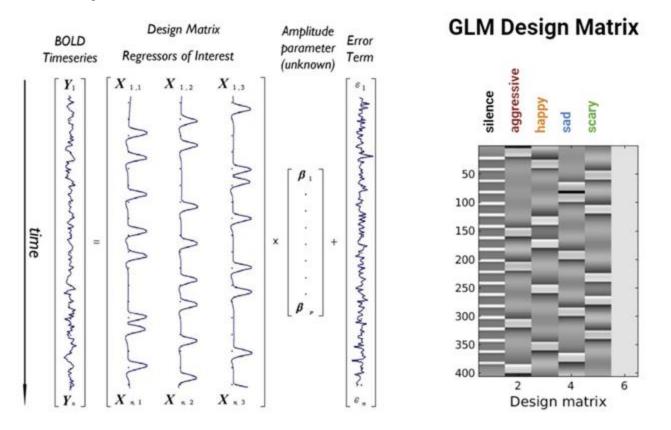
 The model assumes that noise varies with a normal distribution in each voxel in each time point, but e.g. noise differs greatly close to large arteries.

 The model assumes independent statistical test for each voxel, but voxels in the same vicinity have similar properties.

Case Study



Case Study



Quiz 1

How do you get the predicted response model?

By convolving the known stimuli design with the haemodynamic response function

Quiz 2

How does one fit the best GLModel possible?

- 1) Minimising the residuals
- 2) Including relevant confounds in GLM
- 3) Including relevant covariates

Quiz 3

Will including an additional regressor in the GLM affect the parameter estimates?

Yes

Take Home Messages

fMRI GLM analysis

→ determines where there is a significant relationship between the measured BOLD signal and the predicted response

→ provides a set of whole brain maps of beta values (one for each regressor)



Thank you for your attention!

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