The general linear model and Statistical Parametric Mapping
II: GLM for fMRI

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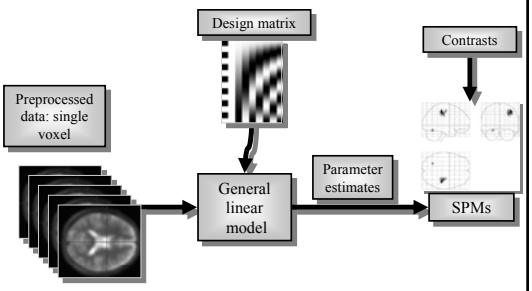
Overview

- Introduction
- General linear model(s) for fMRI
  - Time series
  - Haemodynamic response
  - Low frequency noise
  - Two GLMs fitted in 2-stage procedure
- Summary

Modelling with SPM



GLM review

- Design matrix – the model
  - Effects of interest
  - Confounds (aka effects of no interest)
  - Residuals (error measures of the whole model)
- Estimate effects and error for data
  - Specific effects are quantified as contrasts of parameter estimates (aka betas)
- Statistic
  - Compare estimated effects – the contrasts – with appropriate error measures
  - Are the effects surprisingly large?

fMRI analysis

- Data can be filtered to remove low-frequency (1/f) noise
- Effects of interest are convolved with haemodynamic (BOLD) response function (HRF), to capture sluggish nature of response
- Scans must be treated as a timeseries, not as independent observations
  - i.e. typically temporally autocorrelated (for TRs<8s)

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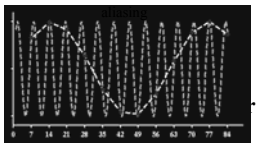
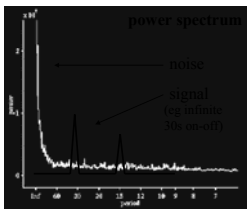
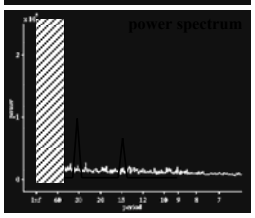
Low frequency noise

Physical (scanner drifts)
Physiological (aliased)
–cardiac (~1 Hz)
–respiratory (~0.25 Hz)







fMRI example

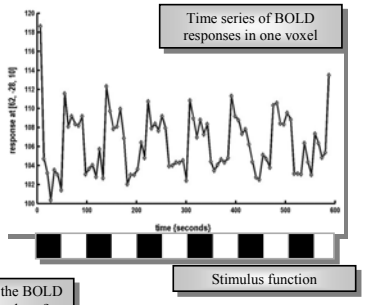
One session

Passive word listening versus rest

7 cycles of rest and listening

Each epoch 6 scans with 7 sec TR

Question: Is there a change in the BOLD response between listening and rest?

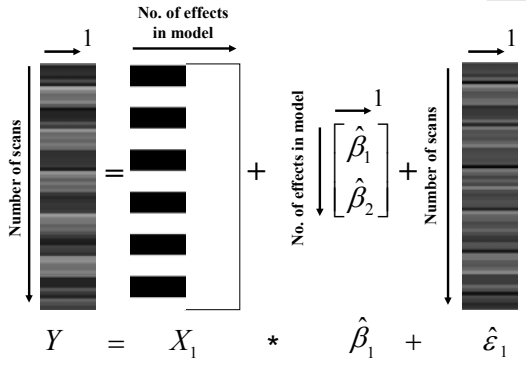


Time series of BOLD responses in one voxel

Stimulus function

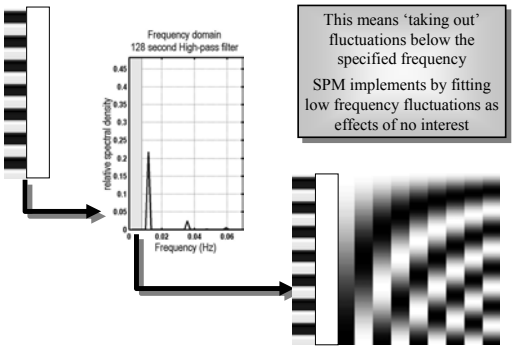
Regression model

Single subject



Add high pass filter

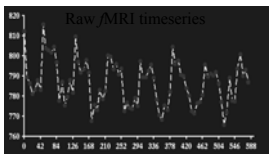
Single subject



This means 'taking out' fluctuations below the specified frequency

SPM implements by fitting low frequency fluctuations as effects of no interest

Fitted & adjusted data



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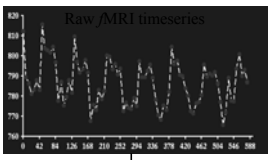

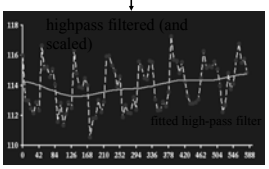

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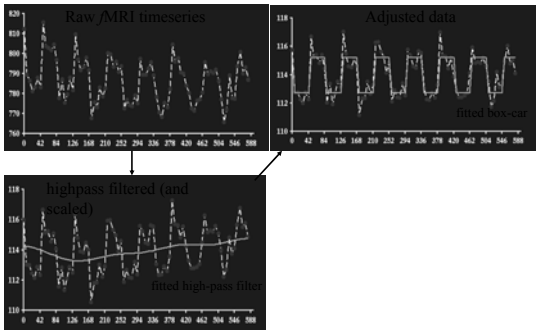

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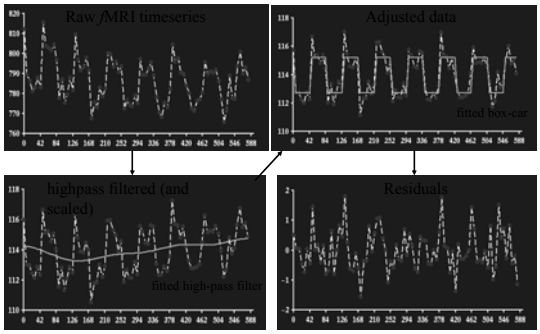
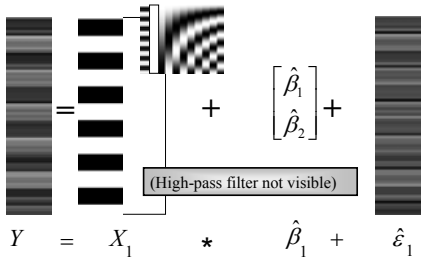


Regression model

Single subject



$$Y = X_1 * \hat{\beta}_1 + \hat{\varepsilon}_1$$

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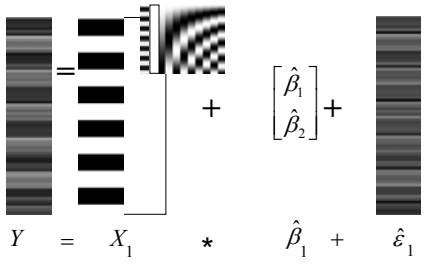

$$Y = X_1 * \hat{\beta}_1 + \hat{\varepsilon}_1$$

What's wrong with this model?

1. Stimulus function is not expected BOLD response
2. Data is serially correlated

fMRI analysis

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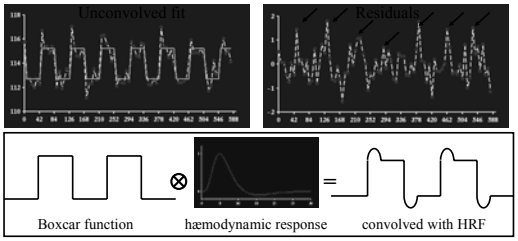
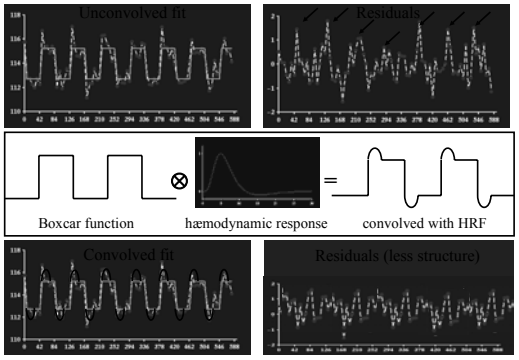
Convolution with HRF



Convolution with HRF



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Temporal autocorrelation

- Because scans are not independent measures, the number of degrees of freedom is less than the number of scans
- This means that under the null hypothesis the data are less free to vary than might be assumed
- A given statistic, e.g. T value, is therefore less surprising and so less significant than we think…

…the next talk

2-stage GLM

'Summary statistic' random effects method

Single subject

Each has an independently acquired set of data
These are modelled separately
Models account for **within subjects variability**
Parameter estimates apply to individual subjects

1st level

Single subject **contrasts of parameter estimates** taken forward to 2nd level as (spm_con*.img) **'con images'**

2-stage GLM

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Single subject **contrasts of parameter estimates** taken forward to 2nd level as (spm_con*.img) **'con images'**

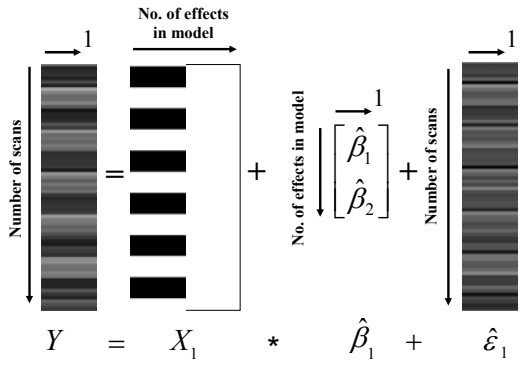
Group/s of subjects

To make an inference that generalises to the population, must also model the **between subjects variability**
1st level betas measure each subject's effects
2nd level betas measure group effect/s

2nd level

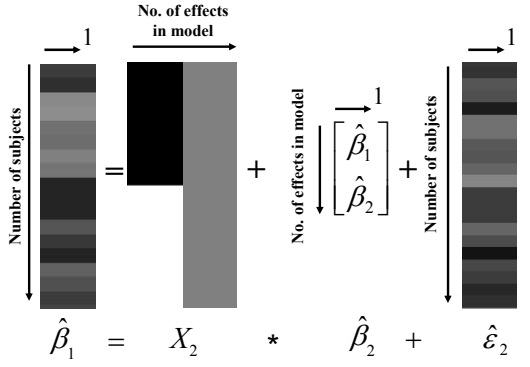
Statistics compare **contrasts of 2nd level parameter estimates to 2nd level error**

Single subject design matrix



Group level design matrix

Group analysis



Summary

- For fMRI studies the GLM specifically needs to take account of
  - Low frequency noise
  - The sluggish haemodynamic response
  - The temporally autocorrelated nature of the timeseries of scans
- A computationally efficient 2-stage GLM is used
  - Continued in next talk