The general linear model and Statistical Parametric Mapping

II: GLM for fMRI

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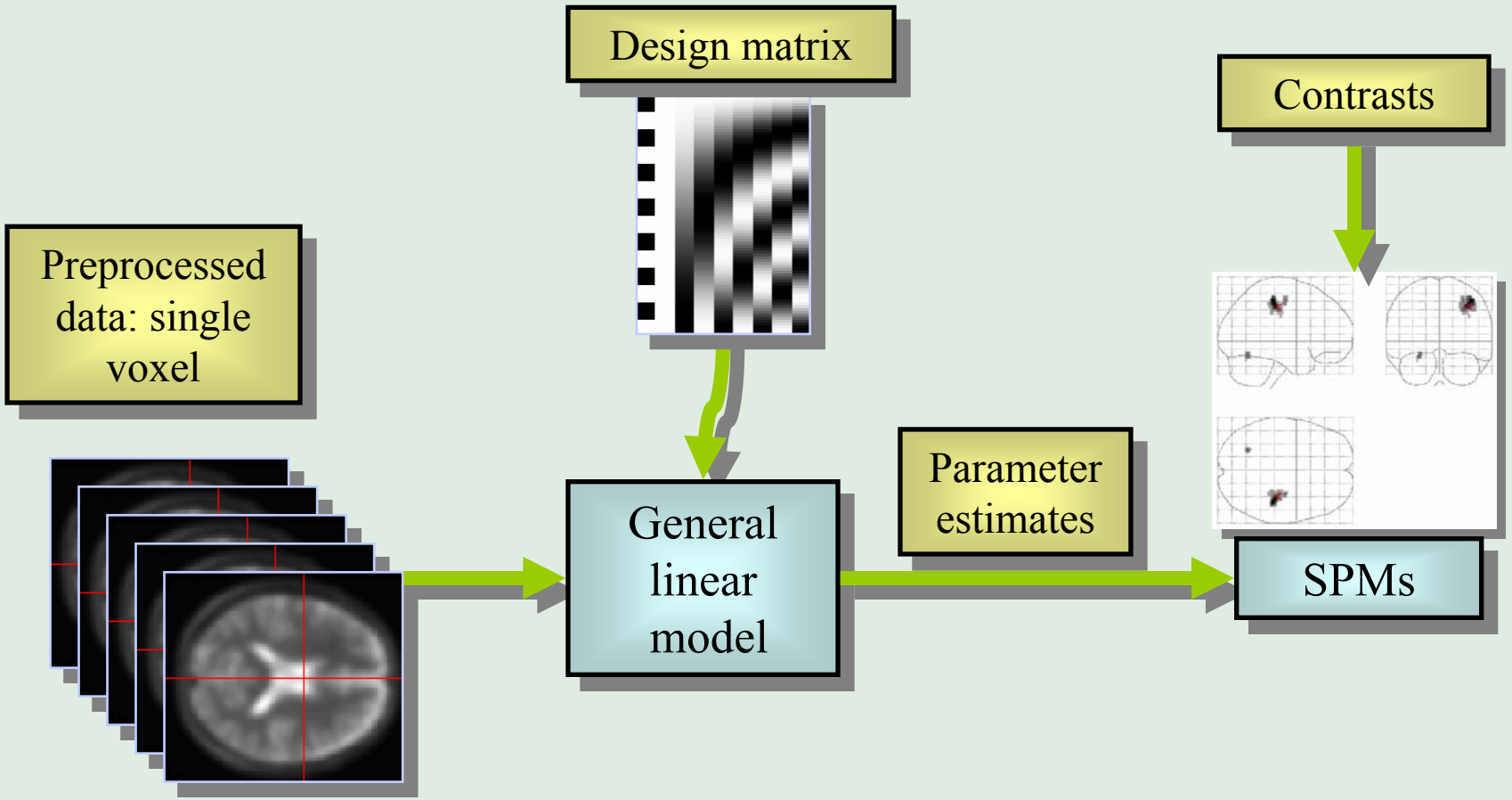
Overview

- 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
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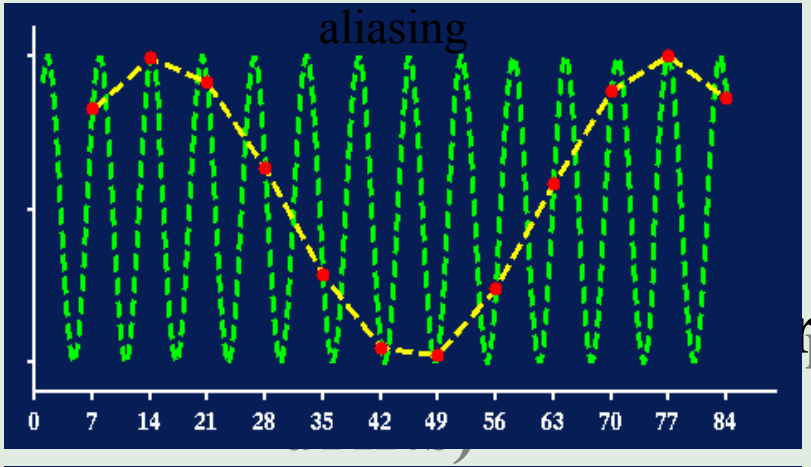
Low frequency noise

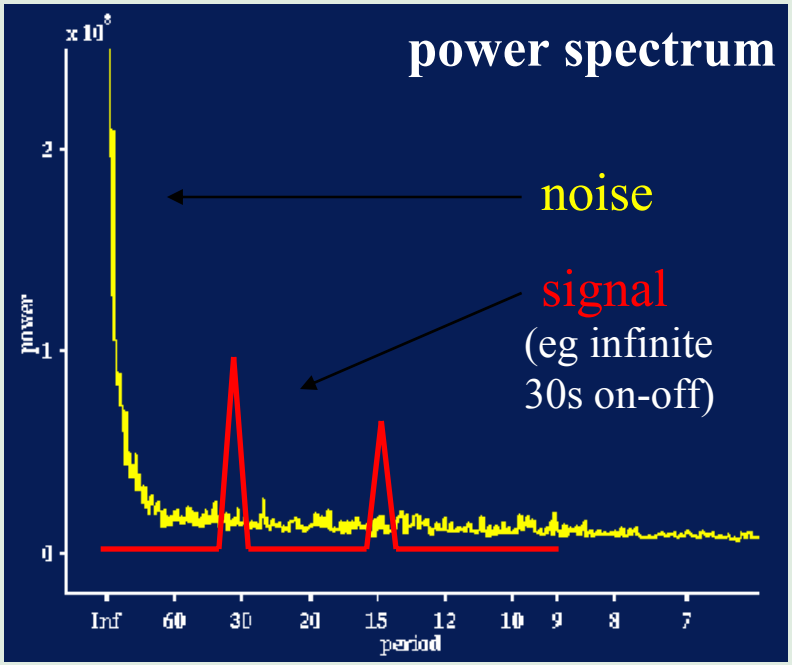
Physical (scanner drifts)

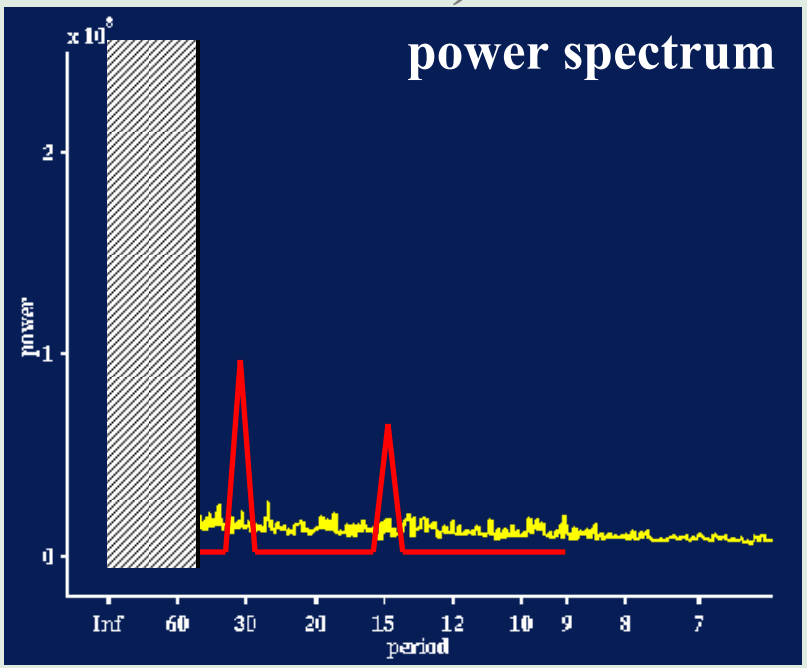
Physiological (aliased)

–cardiac (~1 Hz)

–respiratory (~0.25 Hz)







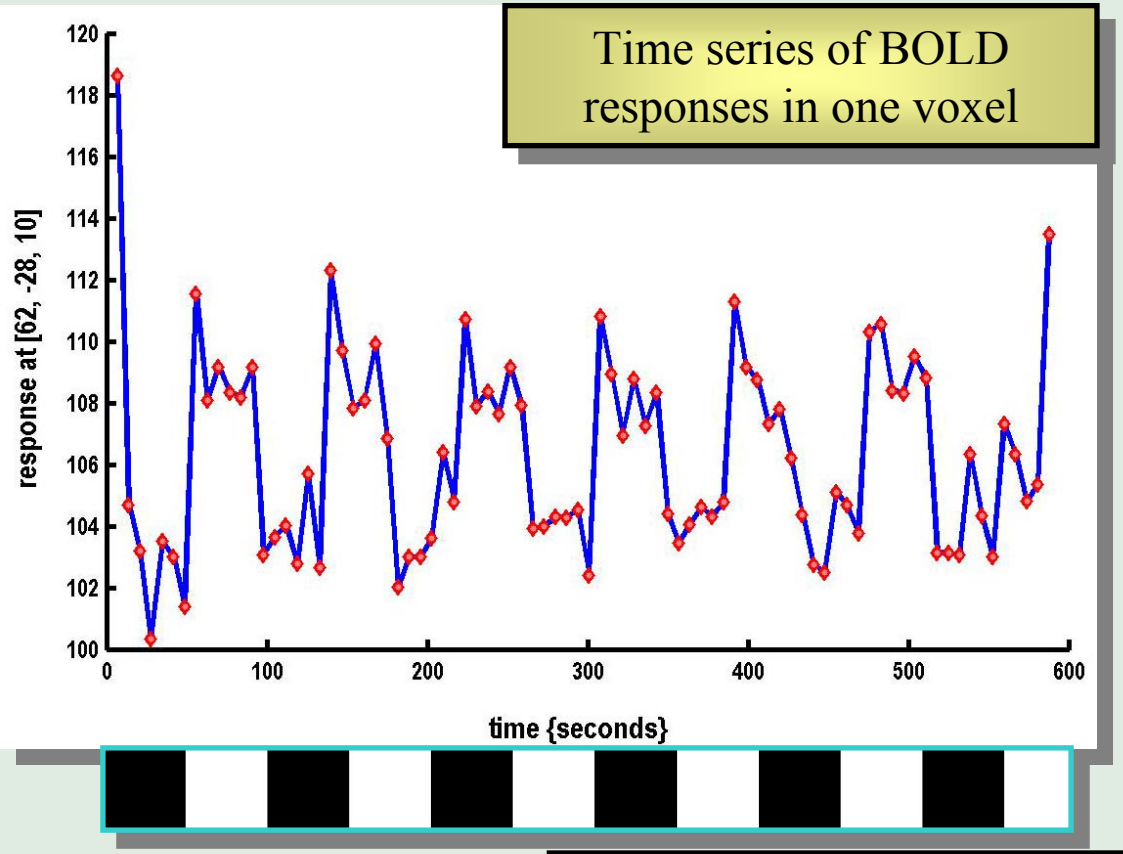
fMRI example

One session

Passive word listening versus rest

7 cycles of rest and listening

Each epoch 6 scans with 7 sec TR



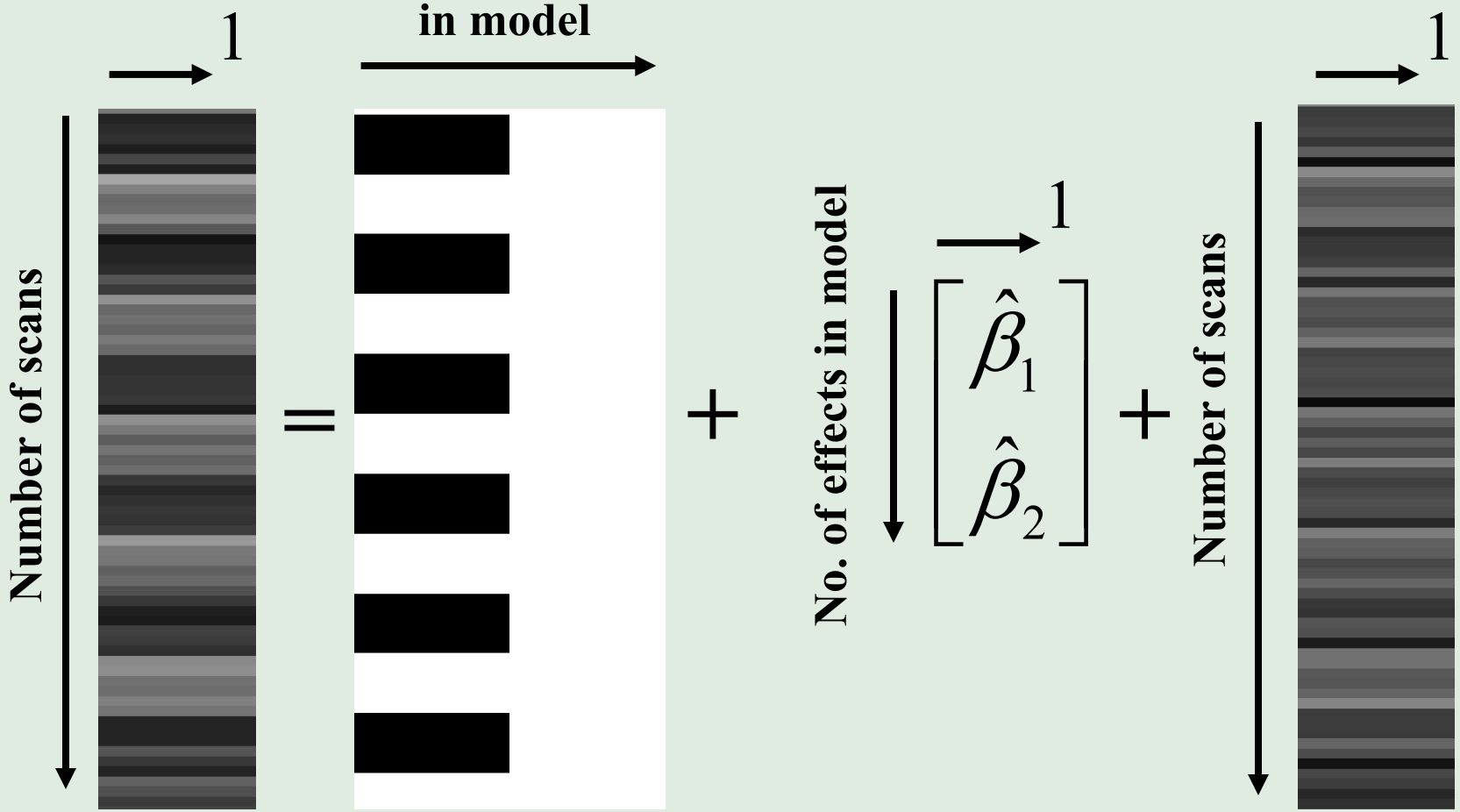
Time series of BOLD responses in one voxel

Stimulus function

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

Regression model

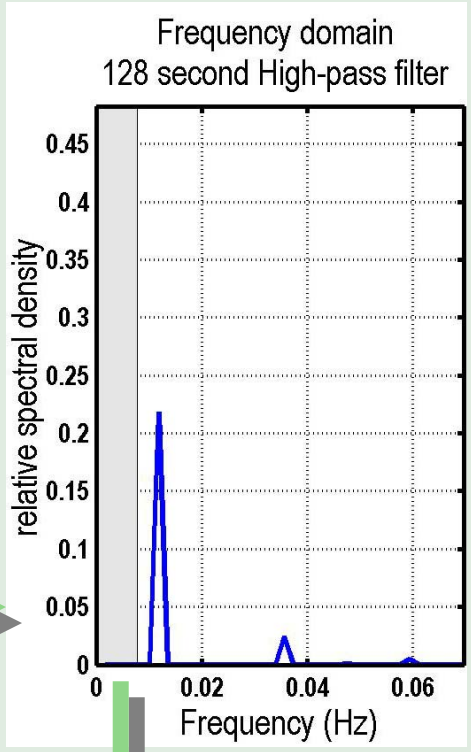
Single subject



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

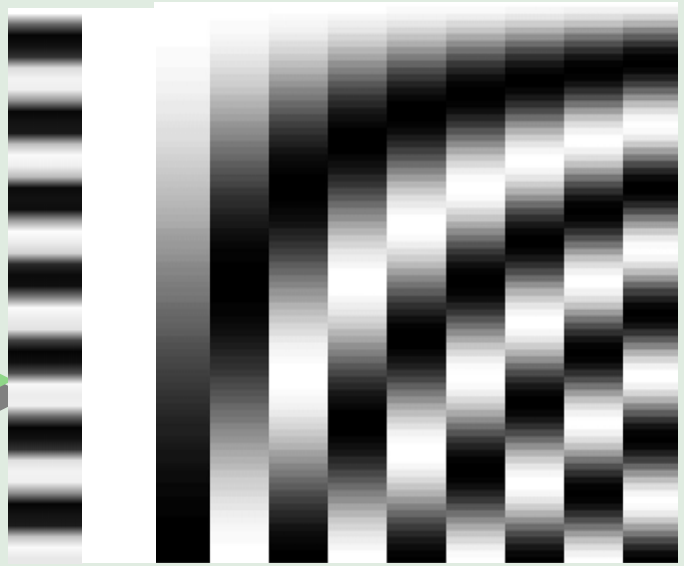
Add high pass filter

Single subject

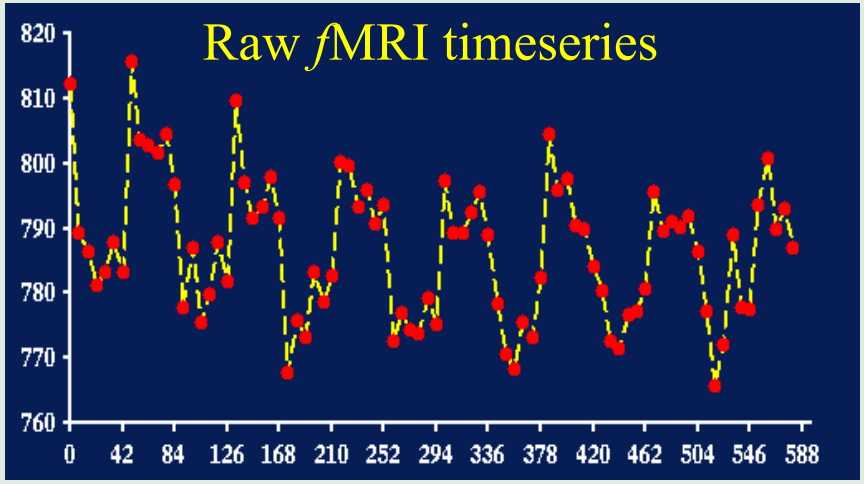


This means 'taking out' fluctuations below the specified frequency

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



Fitted & adjusted data



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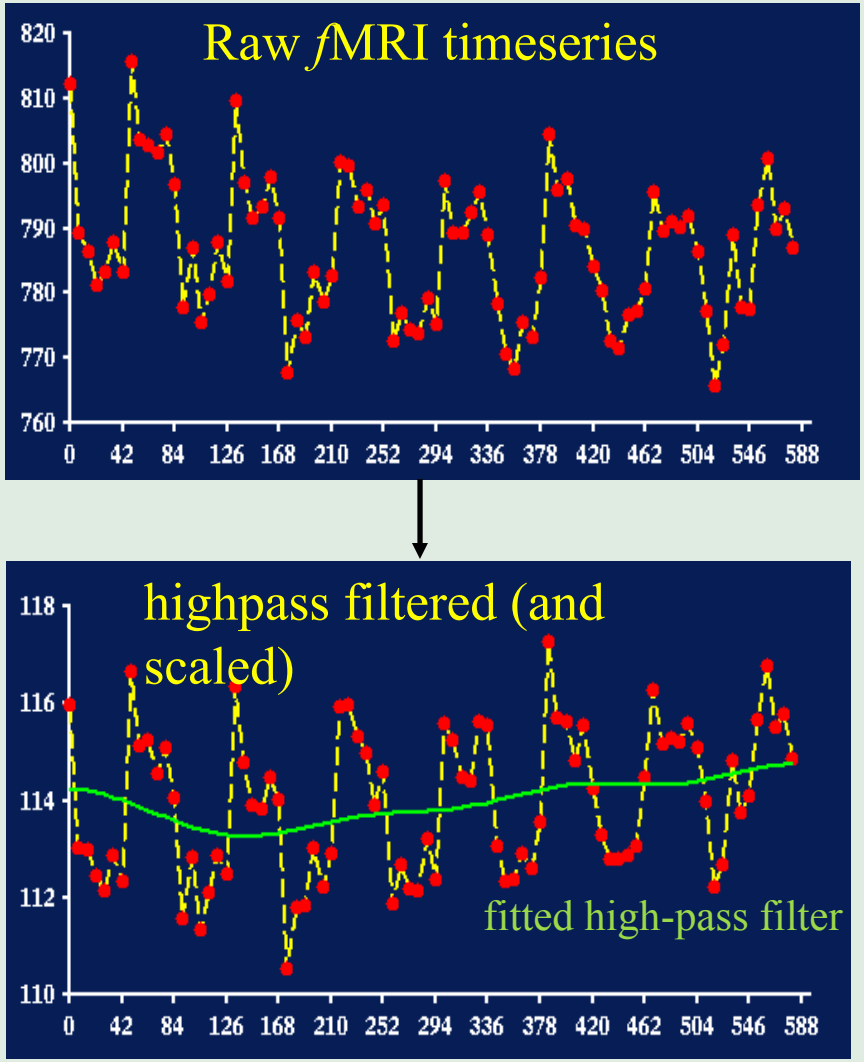

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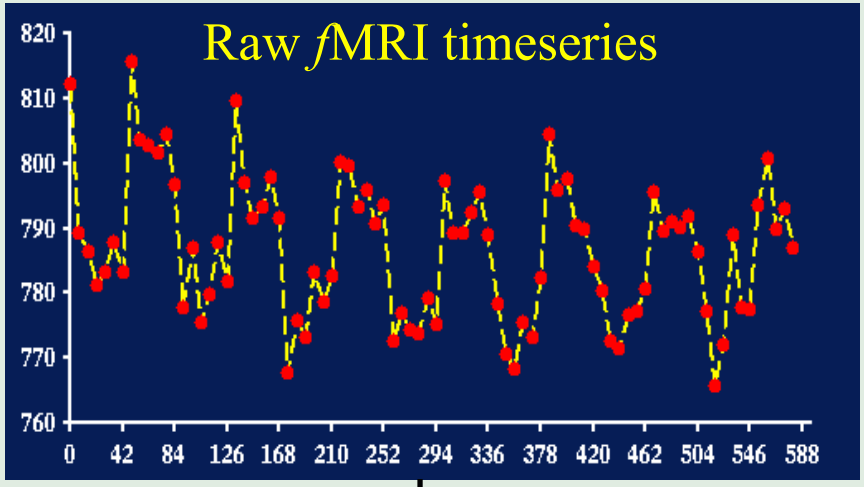

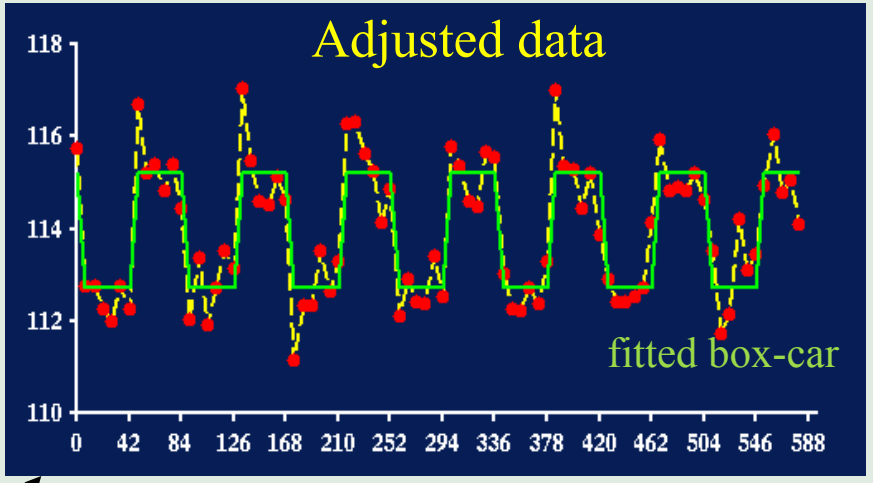

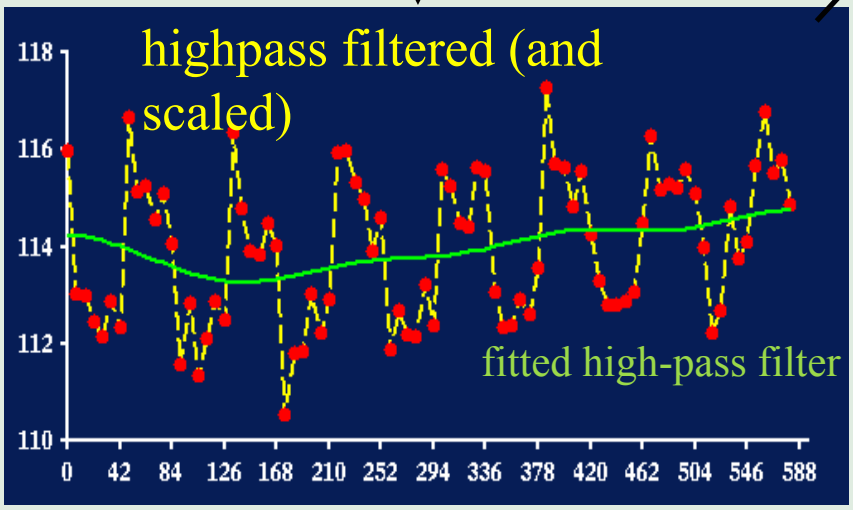

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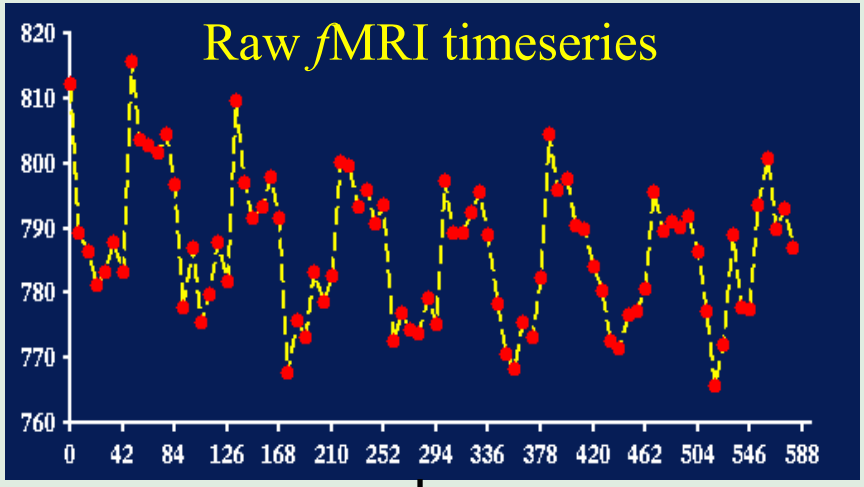
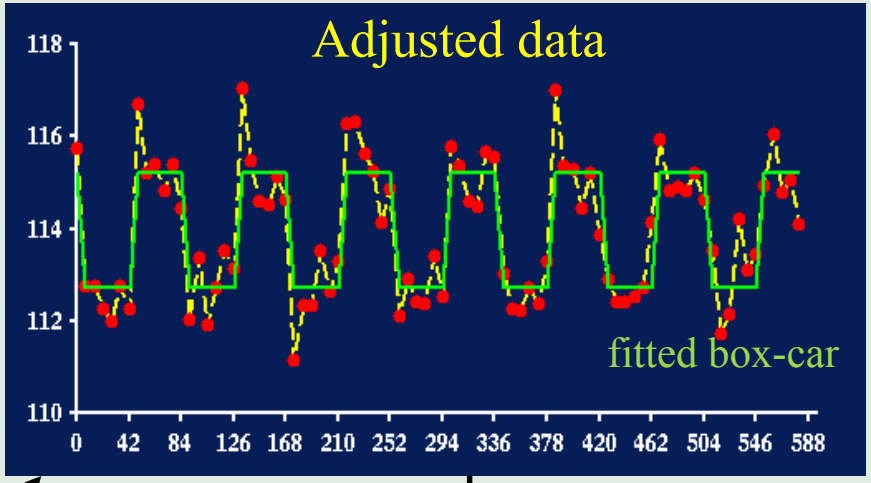
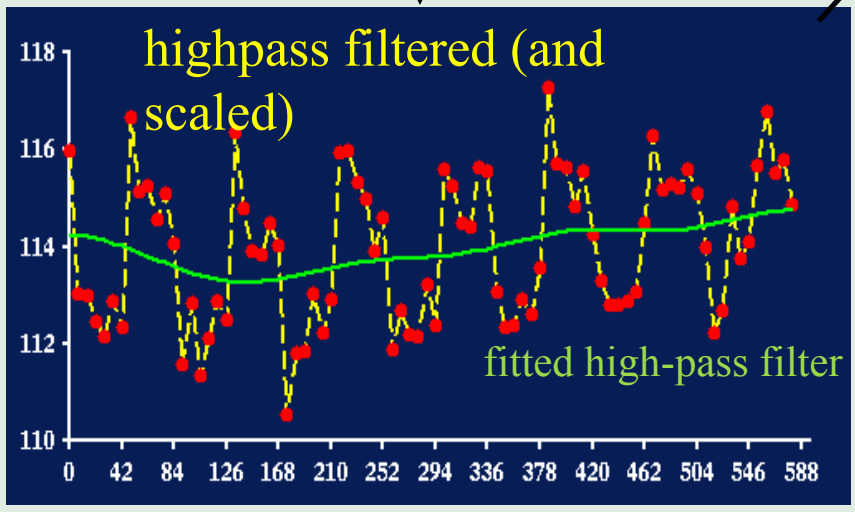
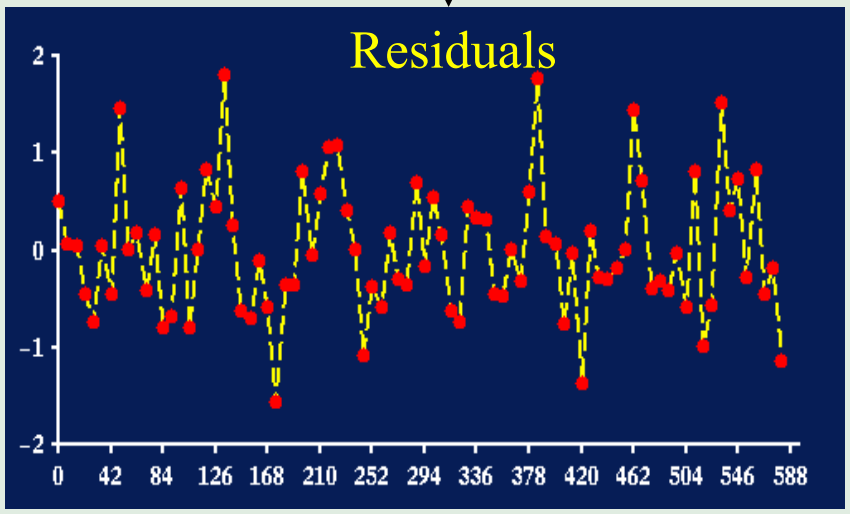


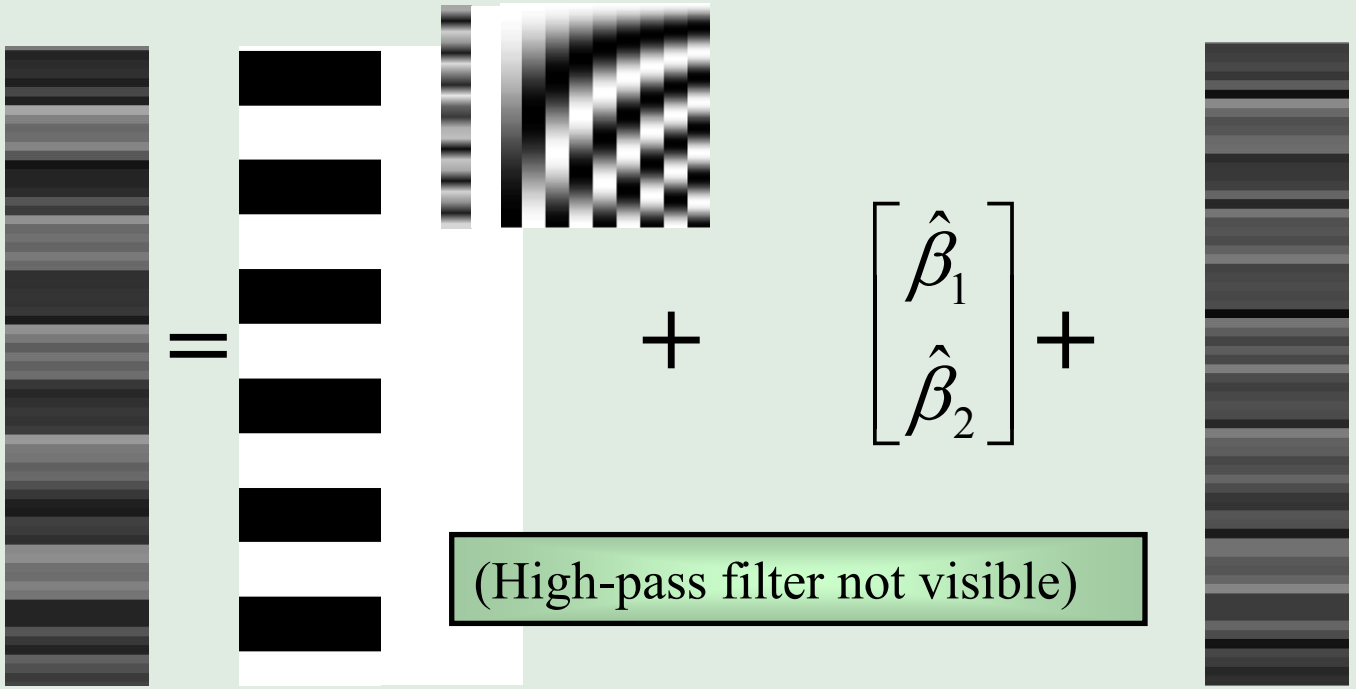






Regression model

Single subject



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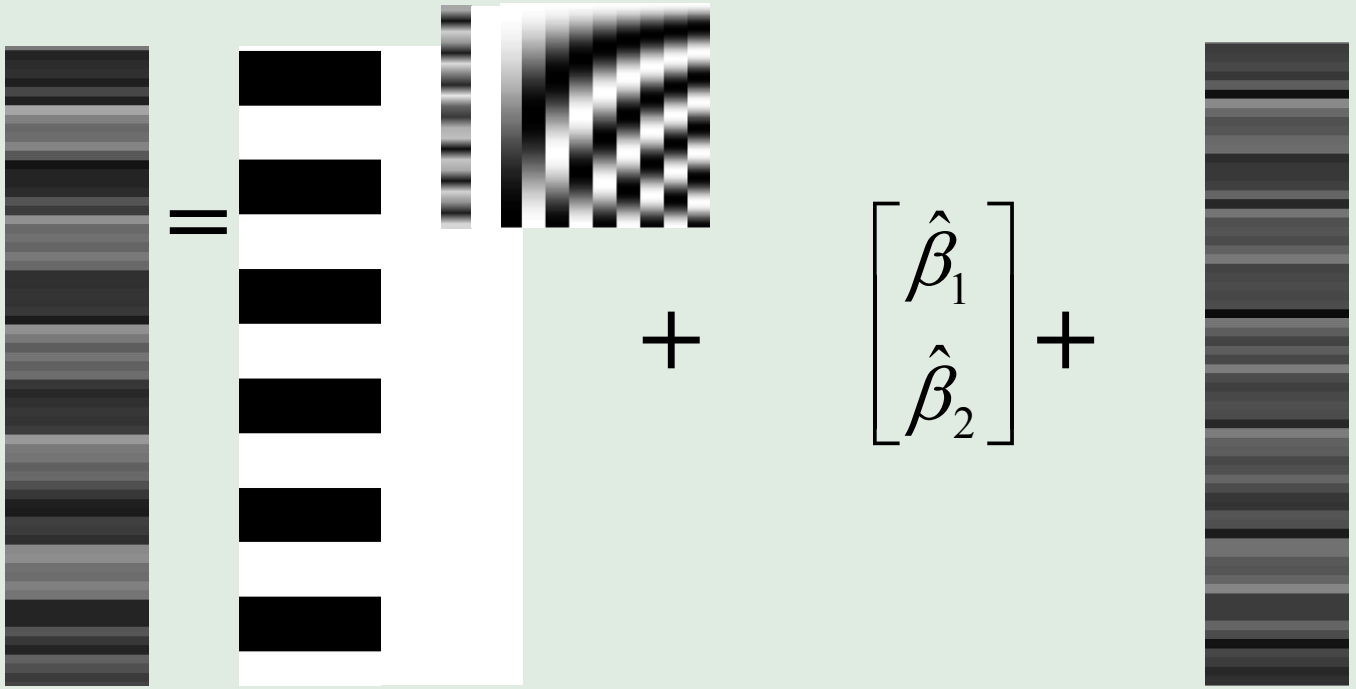

$$Y = X_1 * \hat{\beta}_1 + \hat{\varepsilon}_1$$

What's wrong with this model?

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

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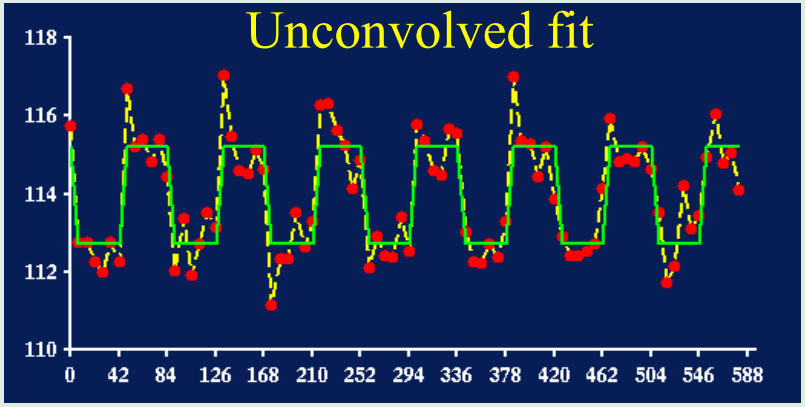
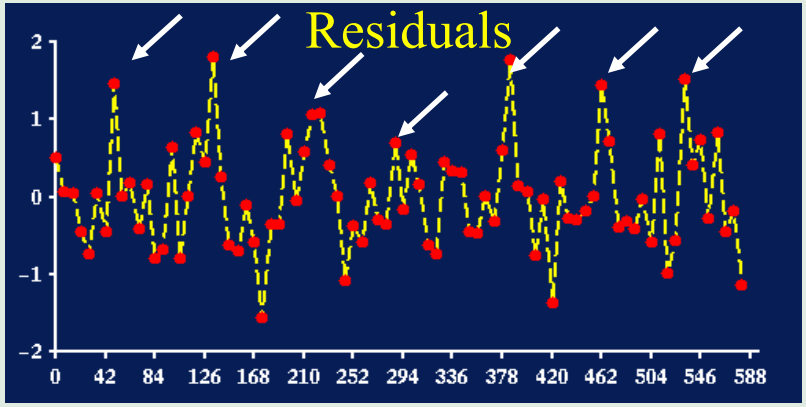
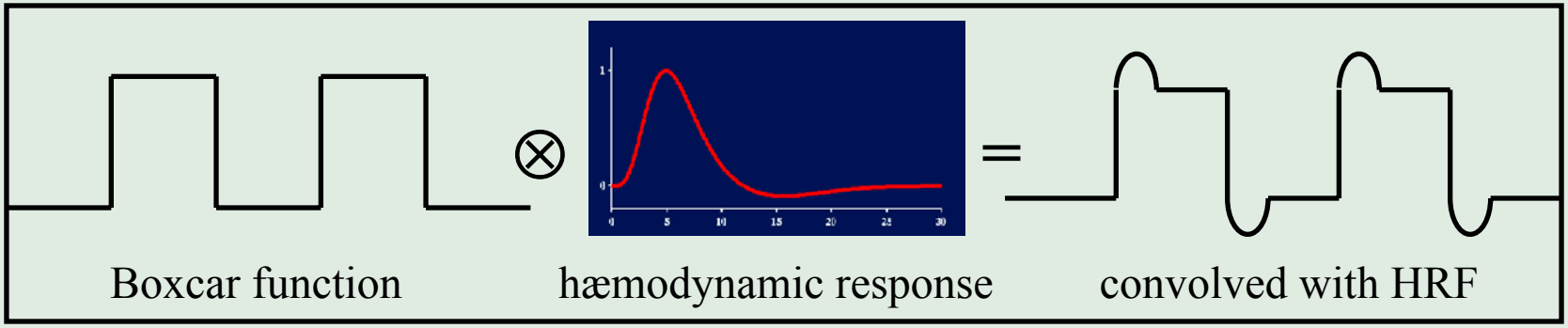
Convolution with HRF







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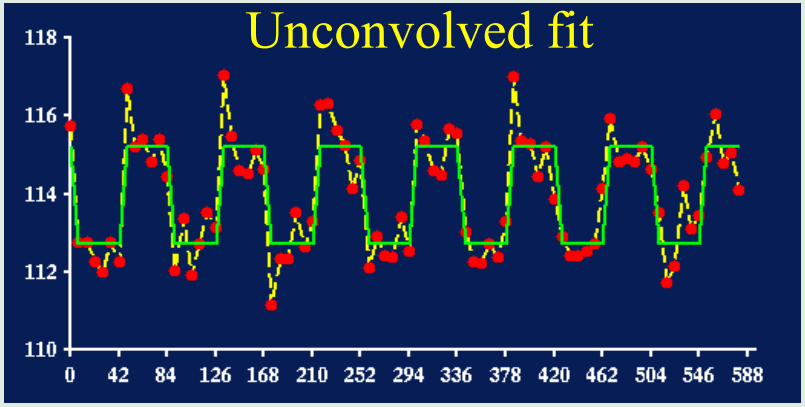

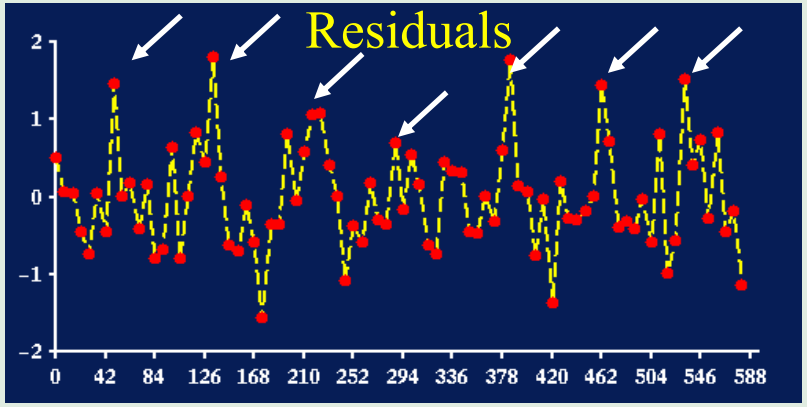

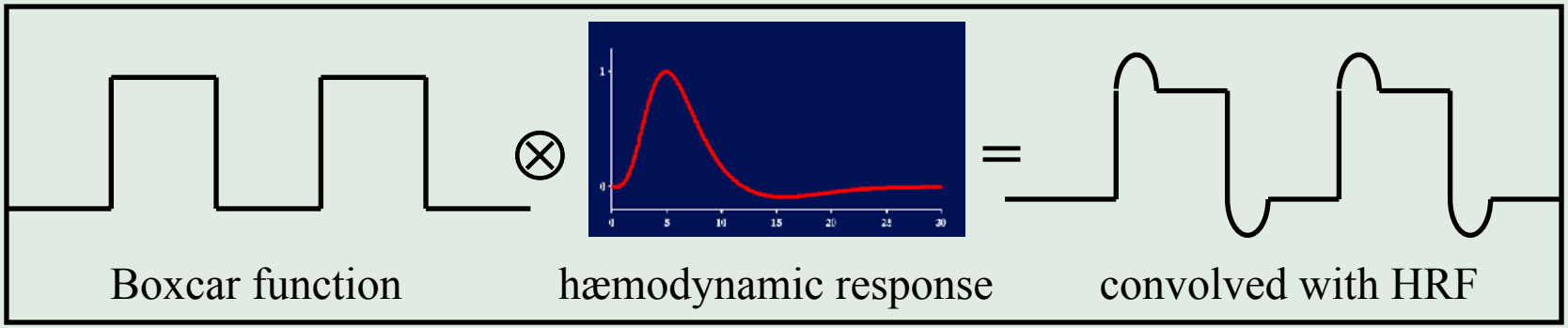

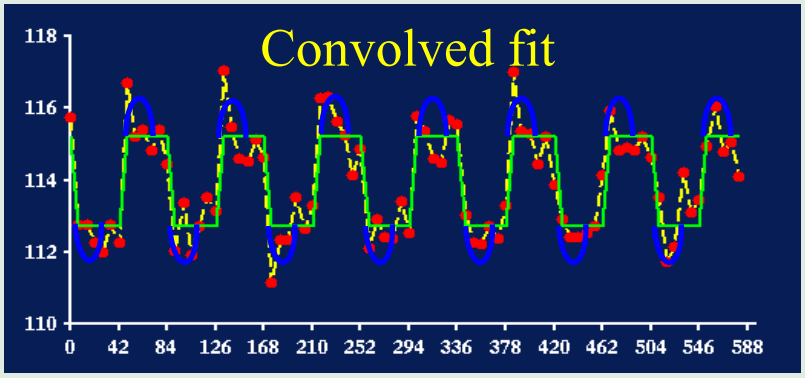

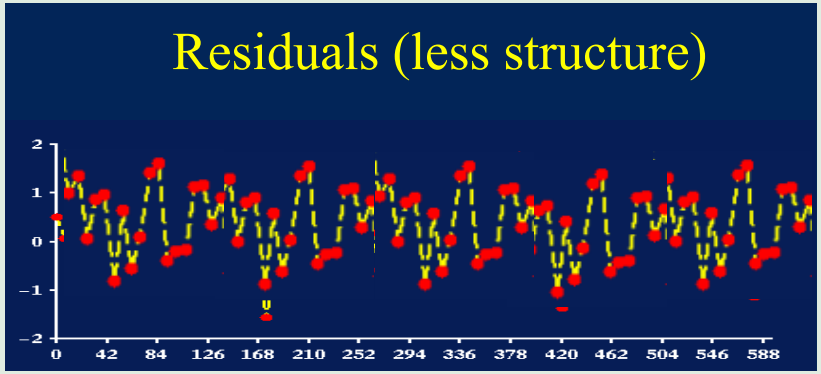

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Temporal autocorrelation

- 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'**

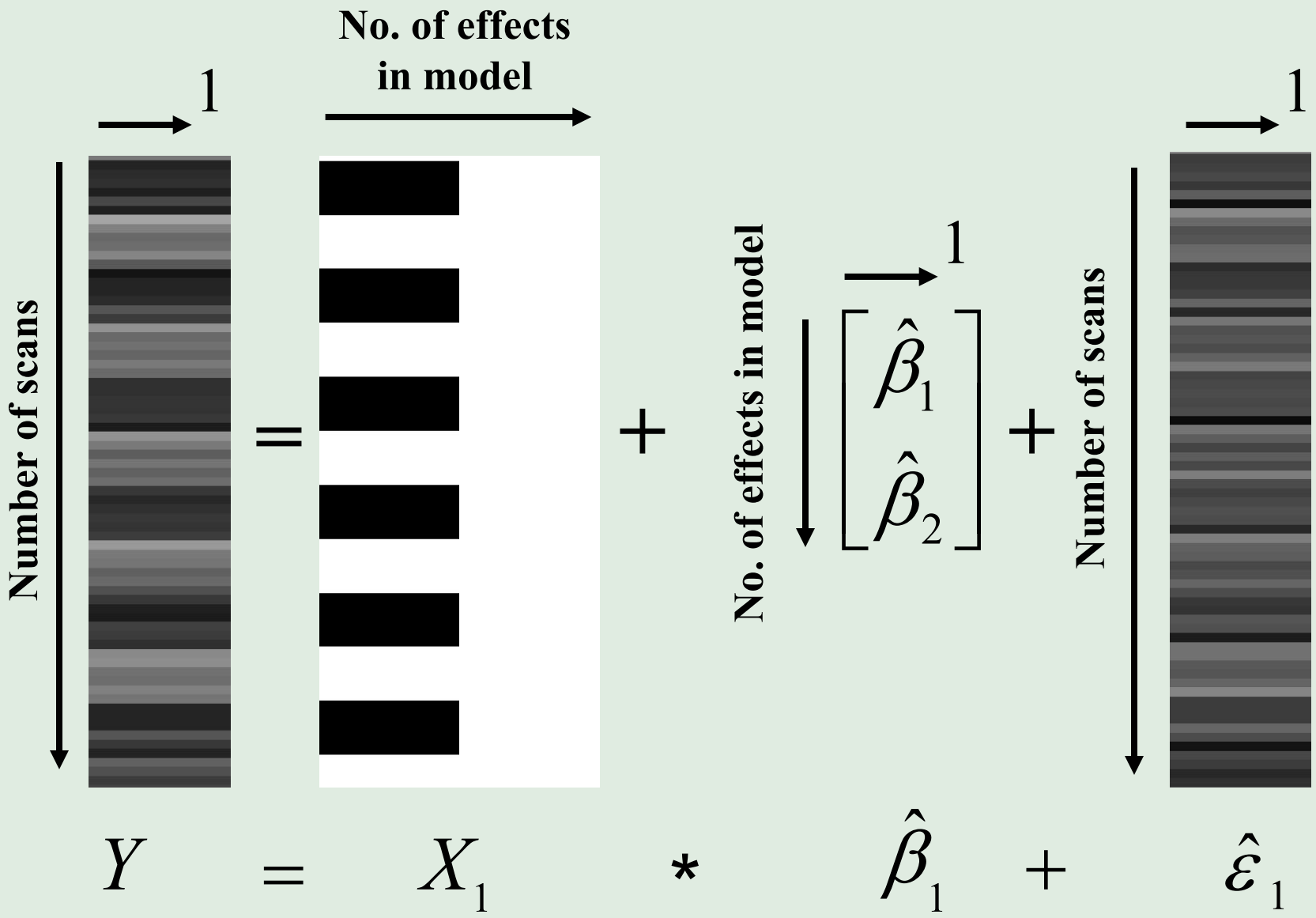
Group/s of subjects

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

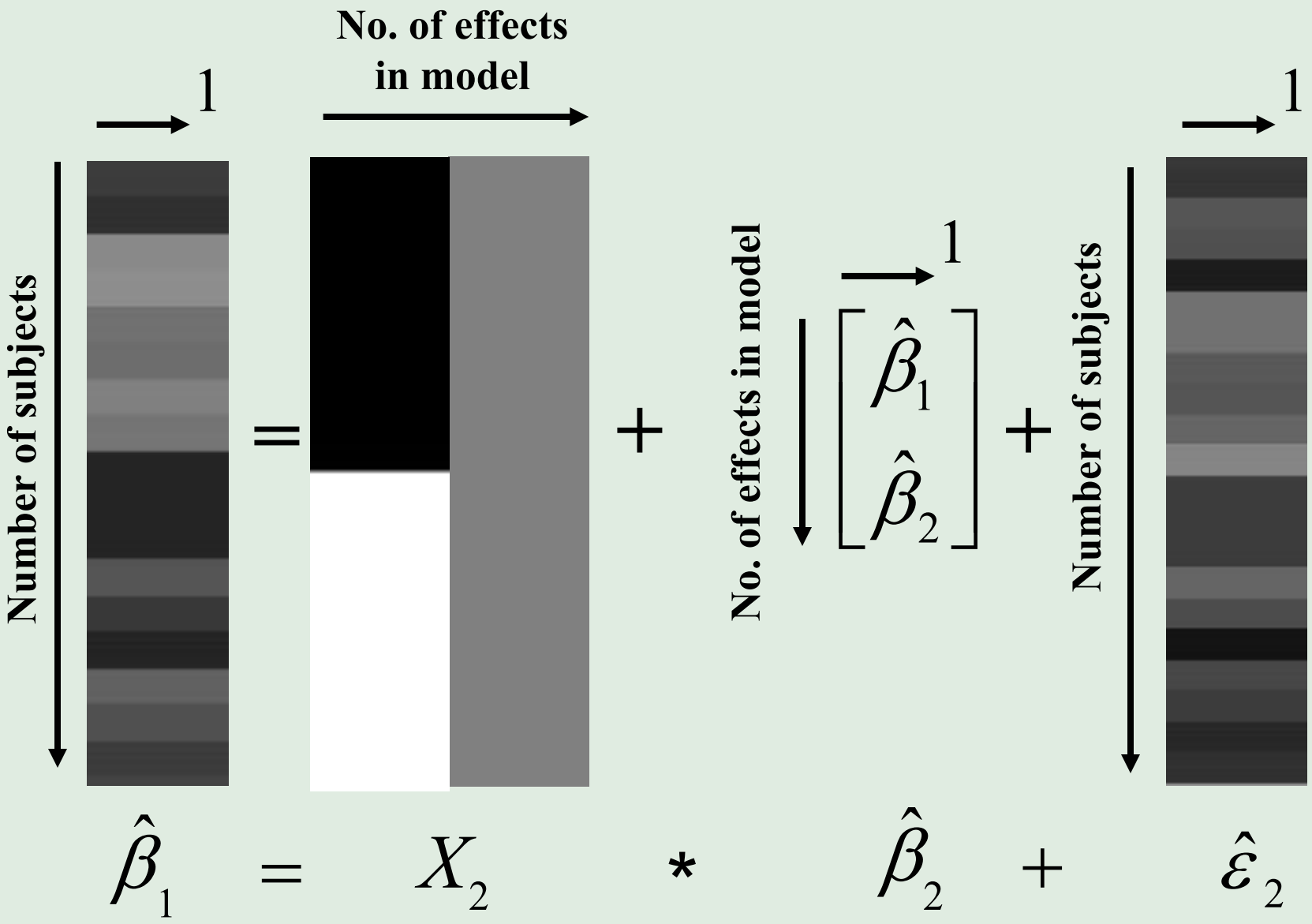
Statistics compare **contrasts of 2nd level parameter estimates to 2nd level error**

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