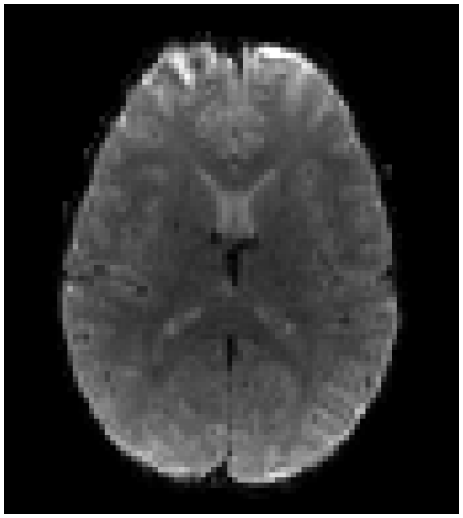
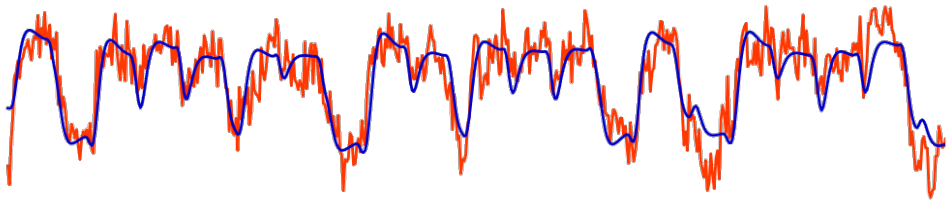
FMRI single subject analysis

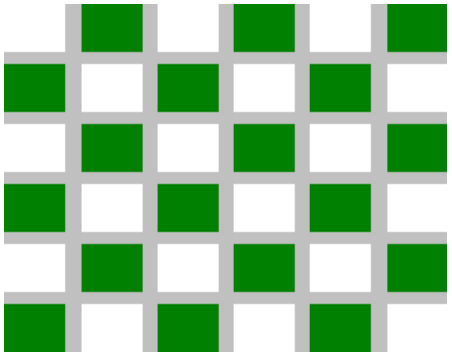
- Overview
- Preprocessing
- Setting up a GLM model
- Contrasts and statistics



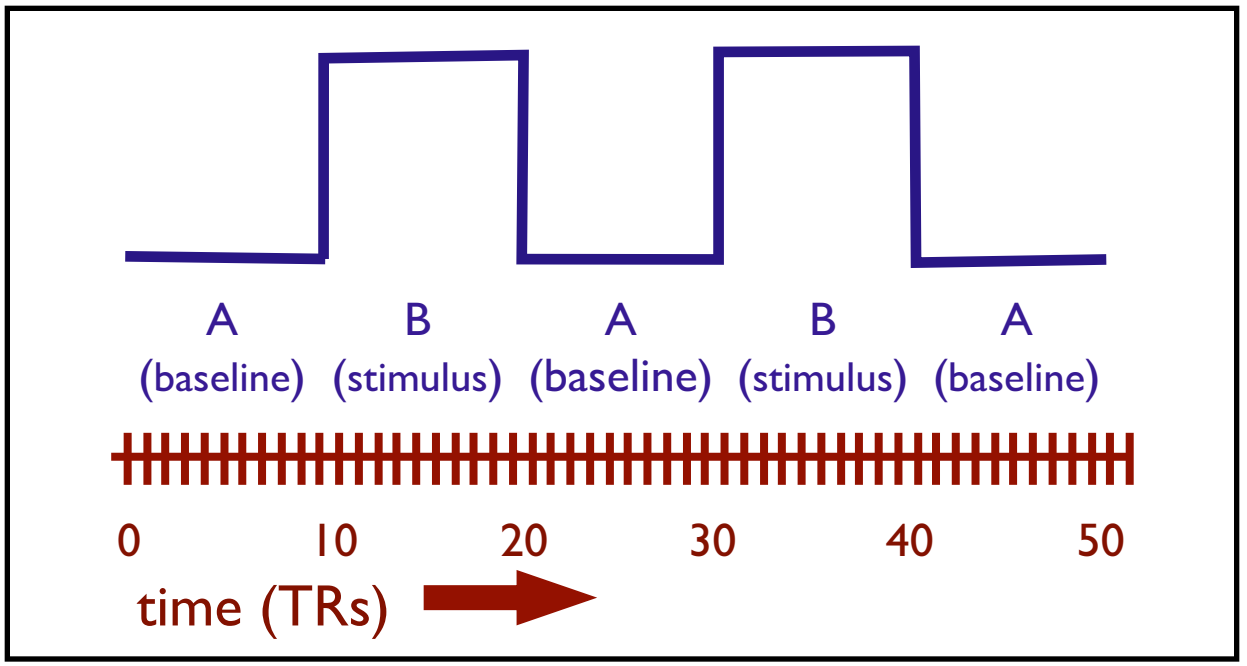


FMRI Experiments

Stimulus



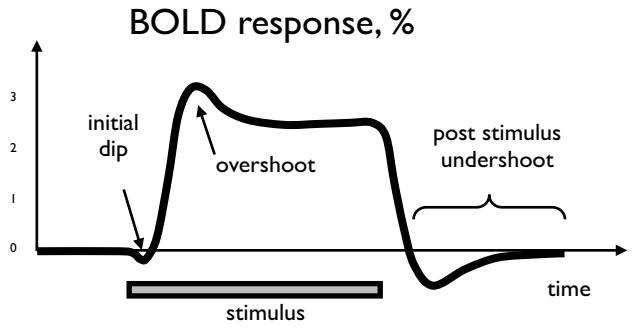
e.g. flashing chequerboard



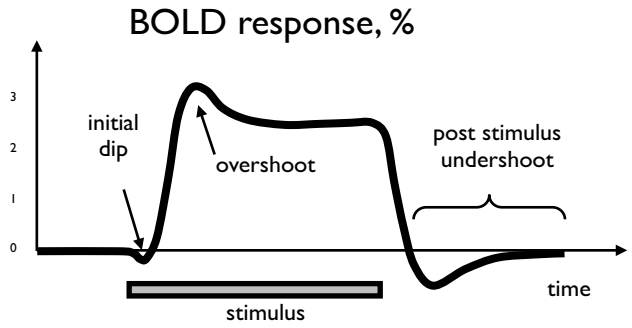
- Simple paradigm design:
  - stimulus vs baseline
  - constant stimulus "intensity"
  - constant block lengths
  - many repetitions: ABABA

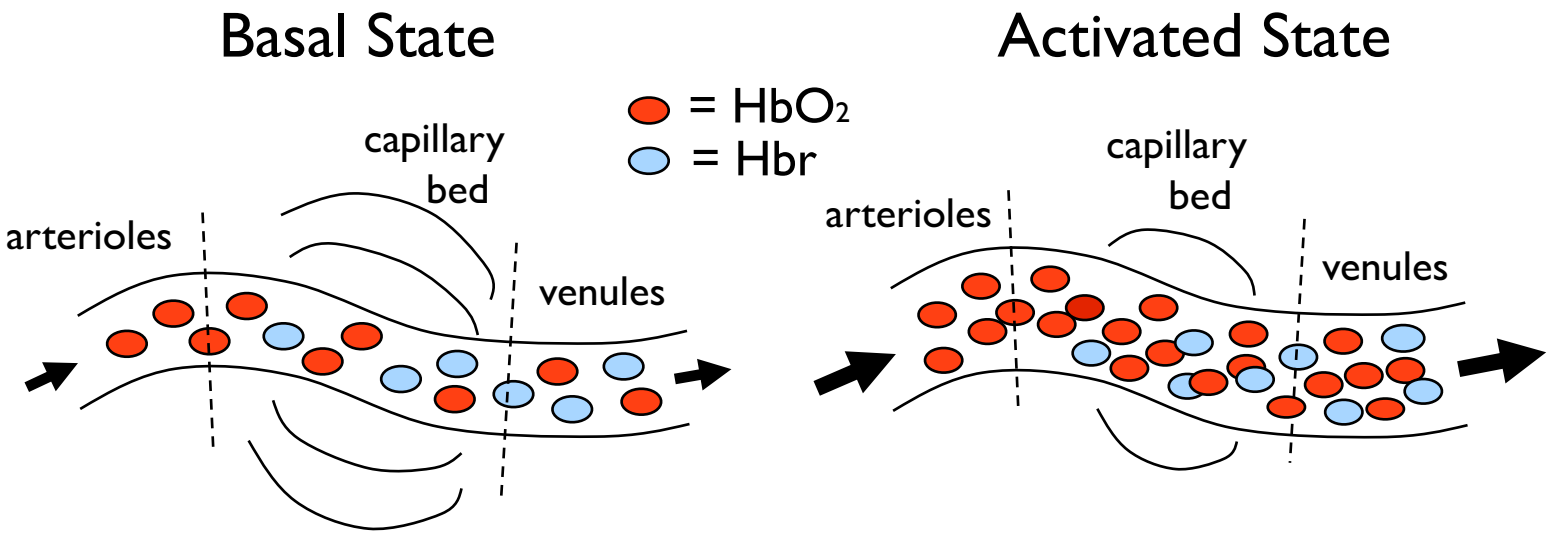
- Need baseline (rest) condition to measure *change*

The Haemodynamic Response

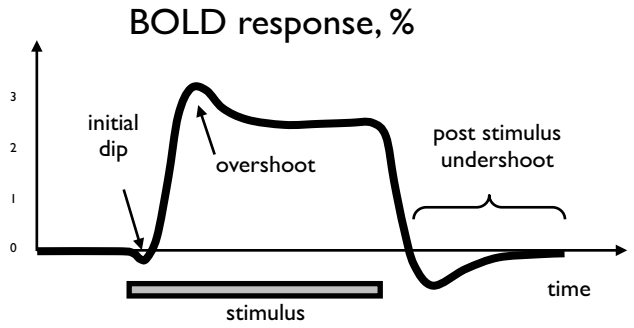


The Haemodynamic Response





The Haemodynamic Response

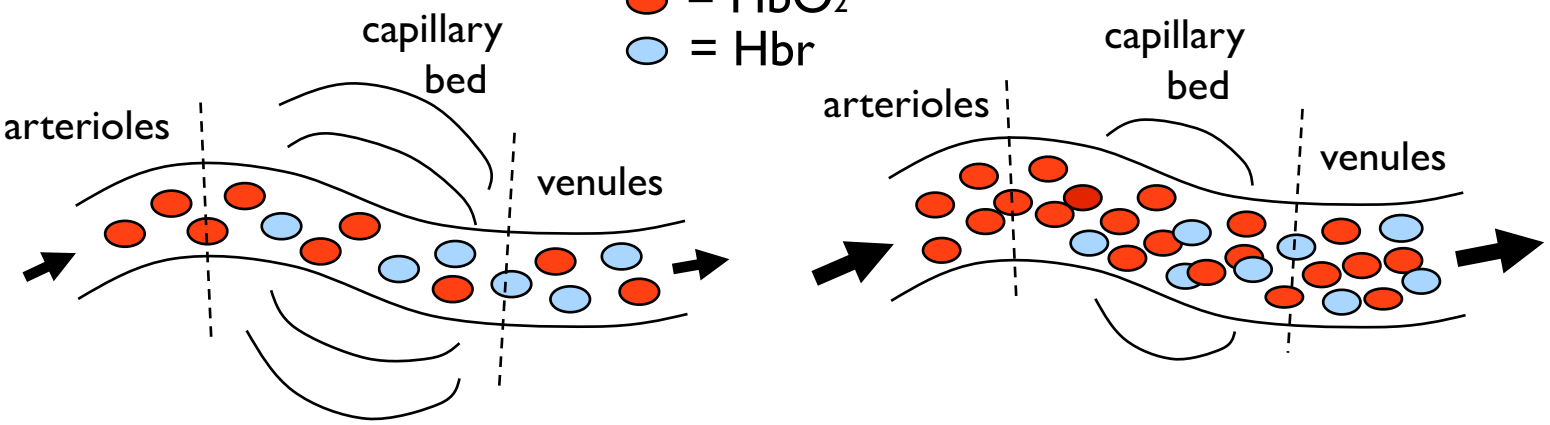


Basal State

Activated State

= HbO_2

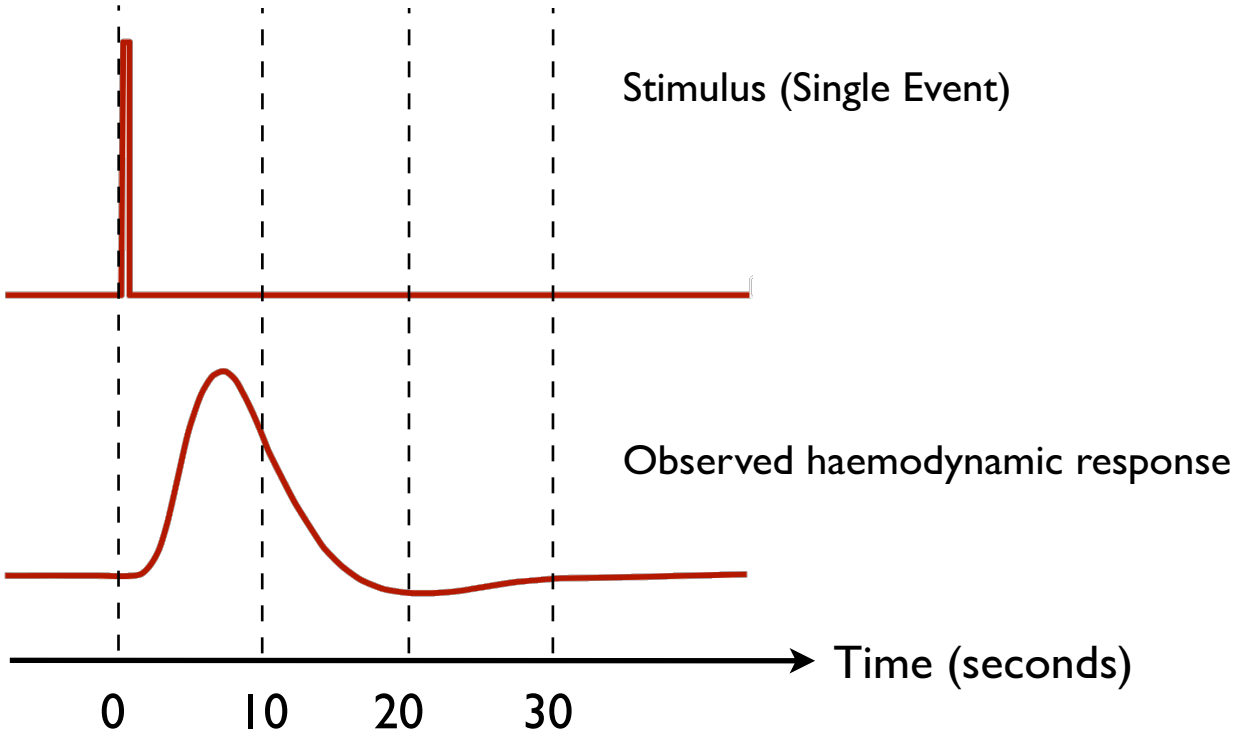
= Hbr



Activation leads to:

CBF ↑ CBV ↑ $CMRO_2$ ↑ [Hbr] ↓ Field change ↓ MRI signal ↑

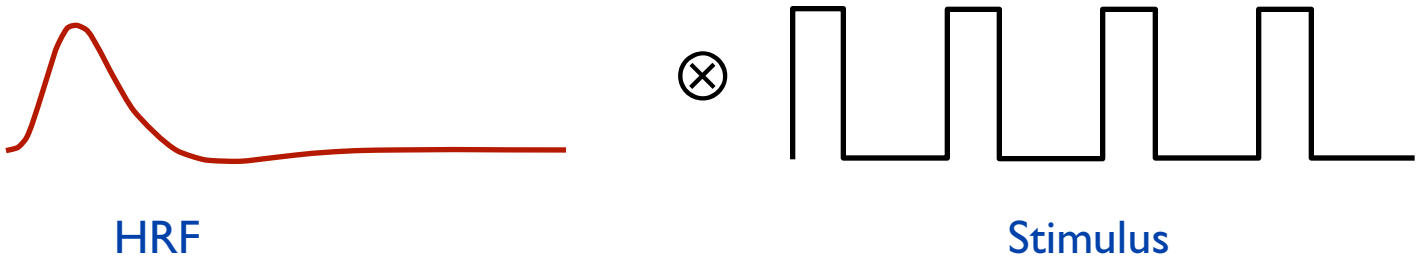
The Haemodynamic Response



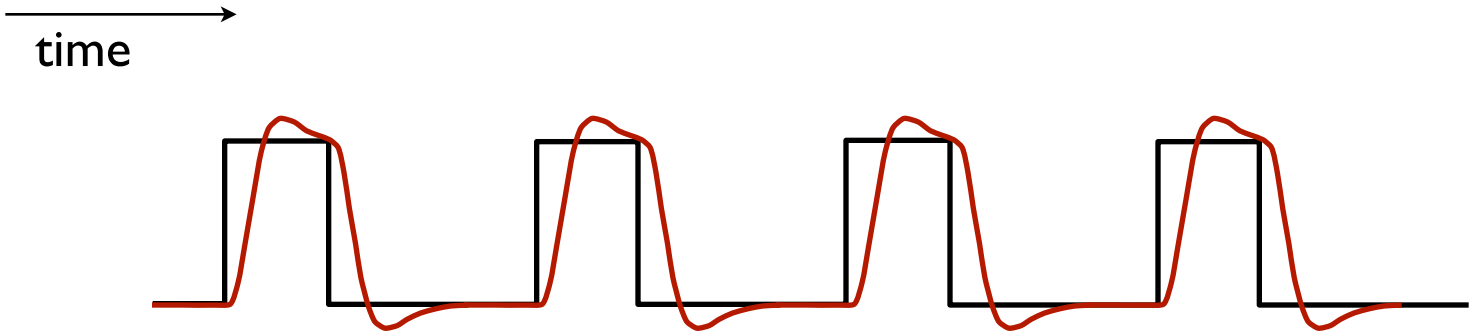
The haemodynamic response to a stimulus is blurred and delayed

Predicted Response

We can form our predicted response (our model) by convolving the stimulus timing with a "haemodynamic response function" or HRF



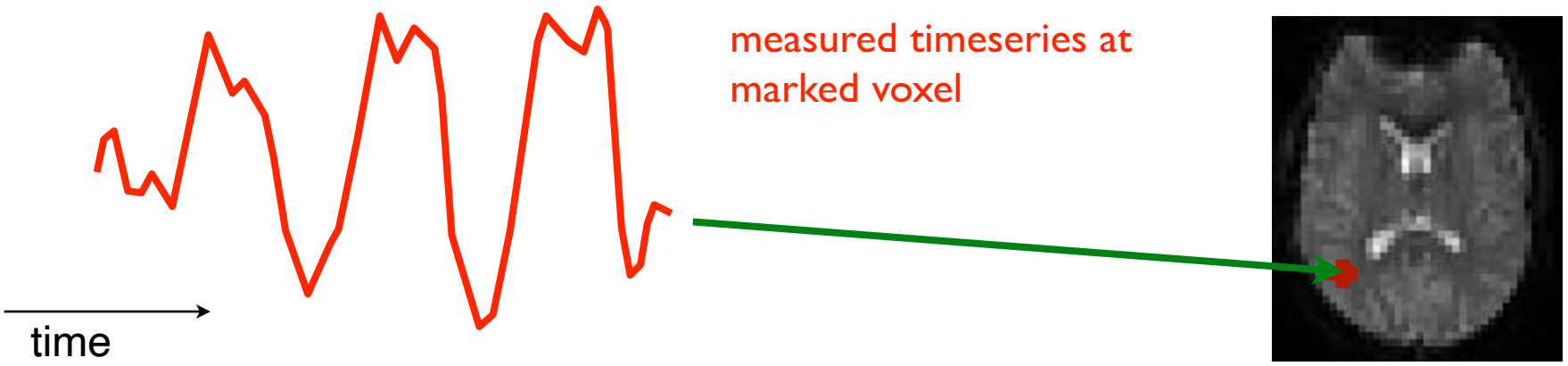
HRF ⊗ Stimulus



Predicted response

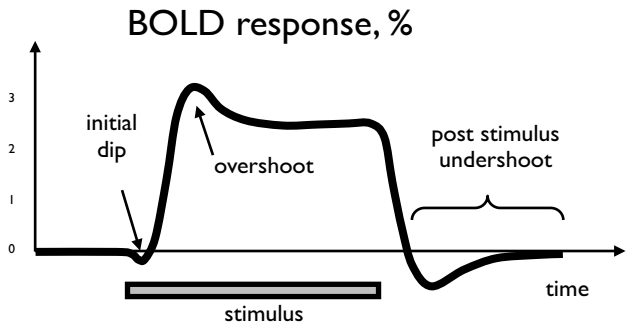
FMRI Analysis

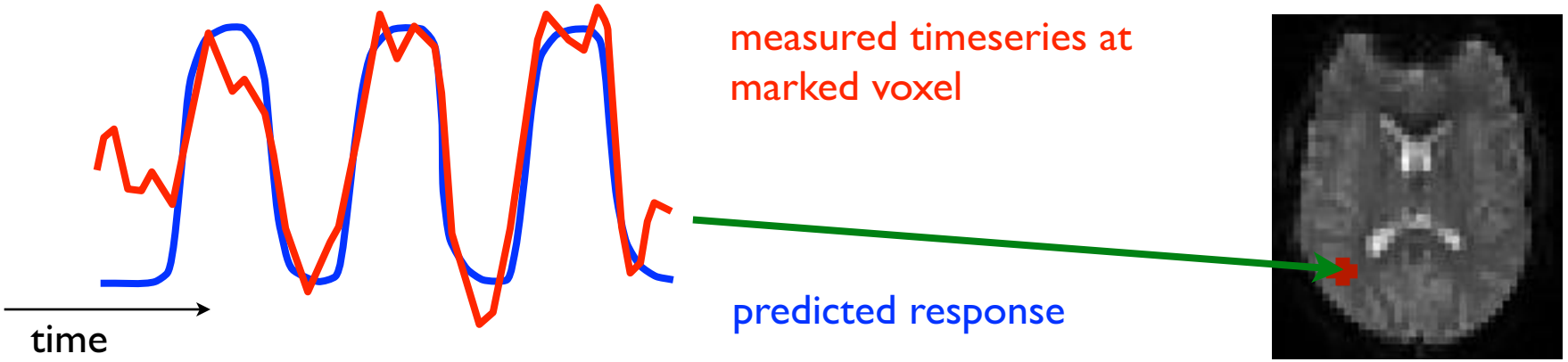
- Each voxel contains a time-varying signal (BOLD signal)

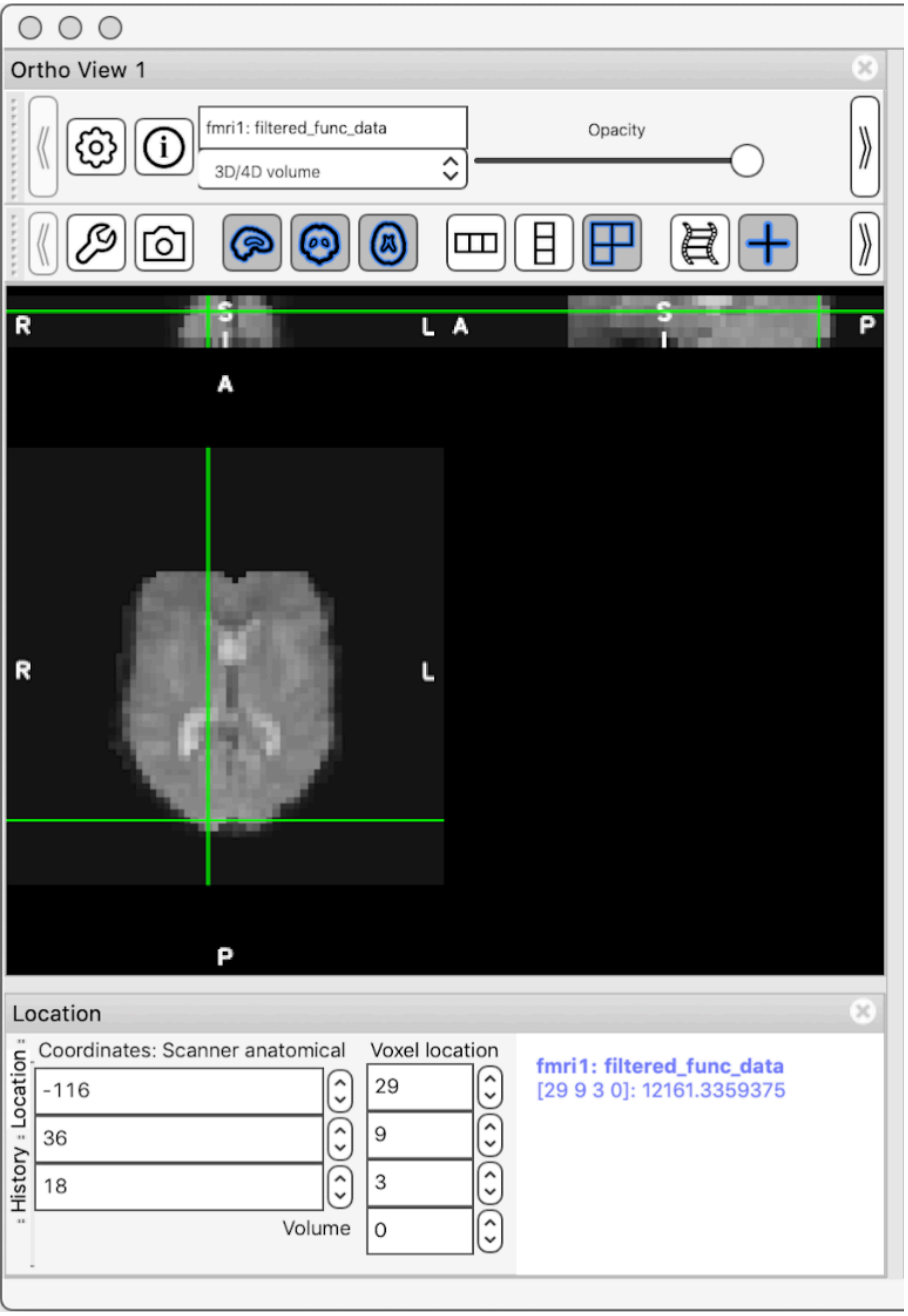


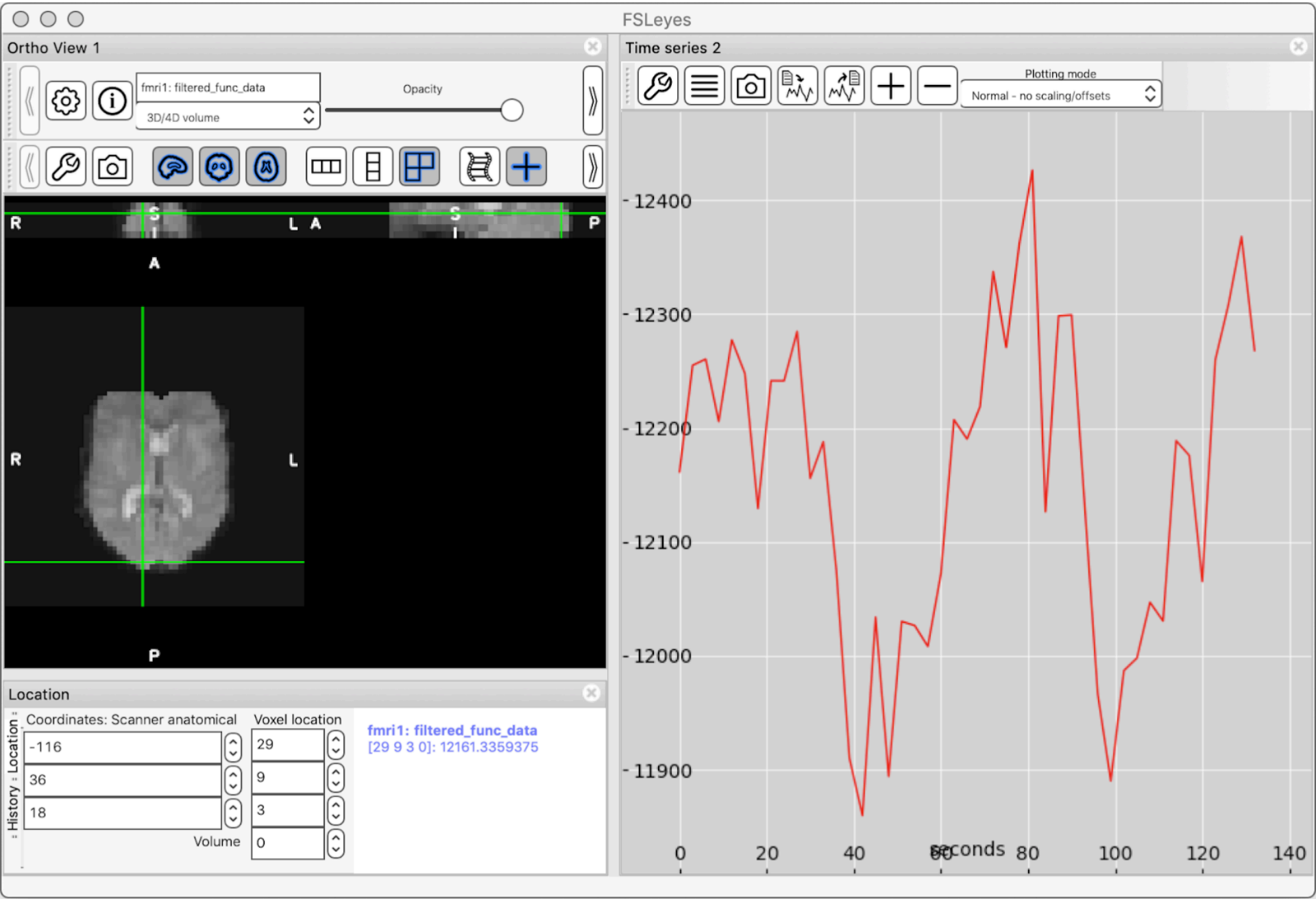
FMRI Analysis

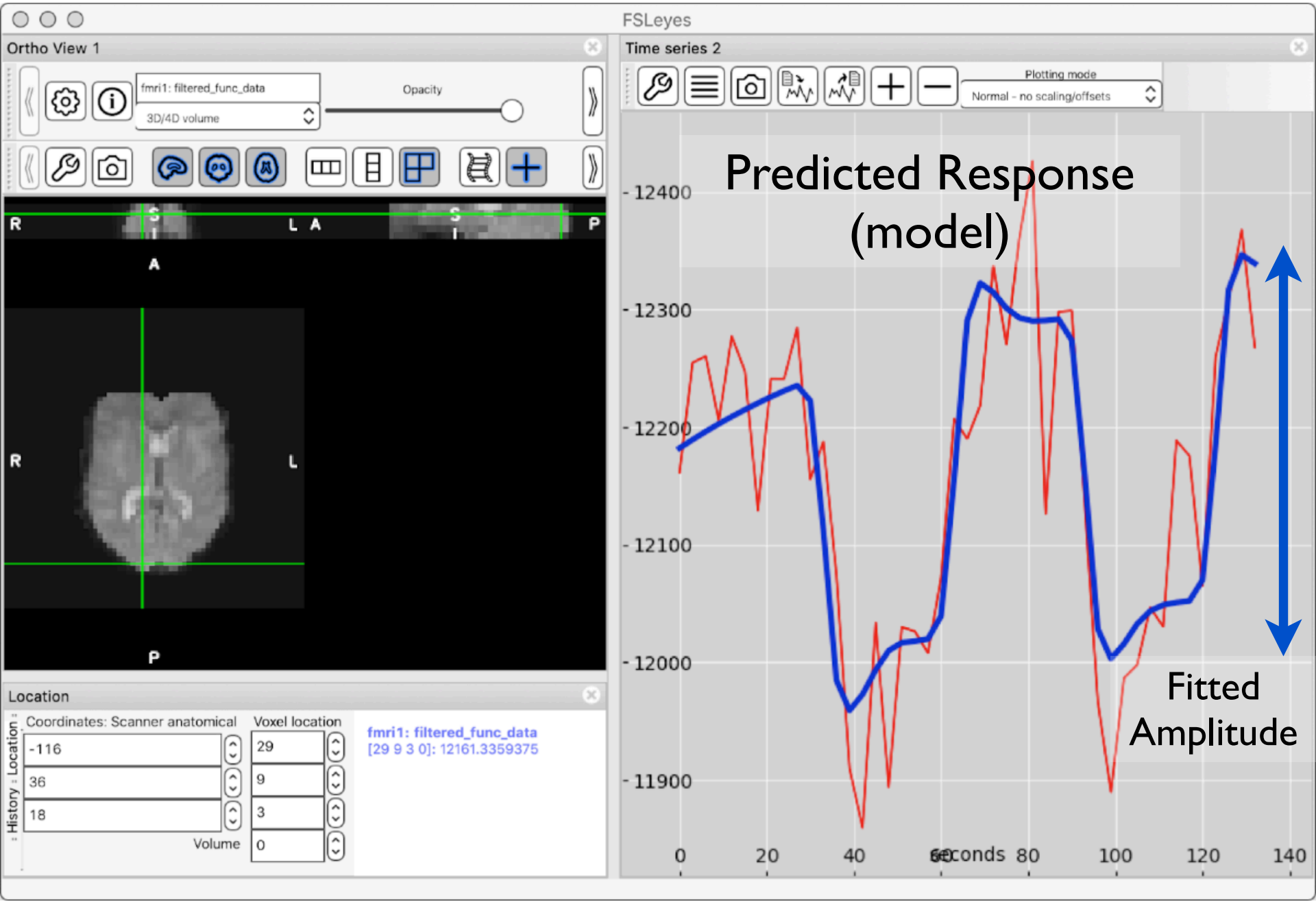
- Each voxel contains a time-varying signal (BOLD signal)
- Model the stimulus-induced change in BOLD signal (predicted response)
- Find which voxels have signals that match the model
- Good match implies activation related to stimulus

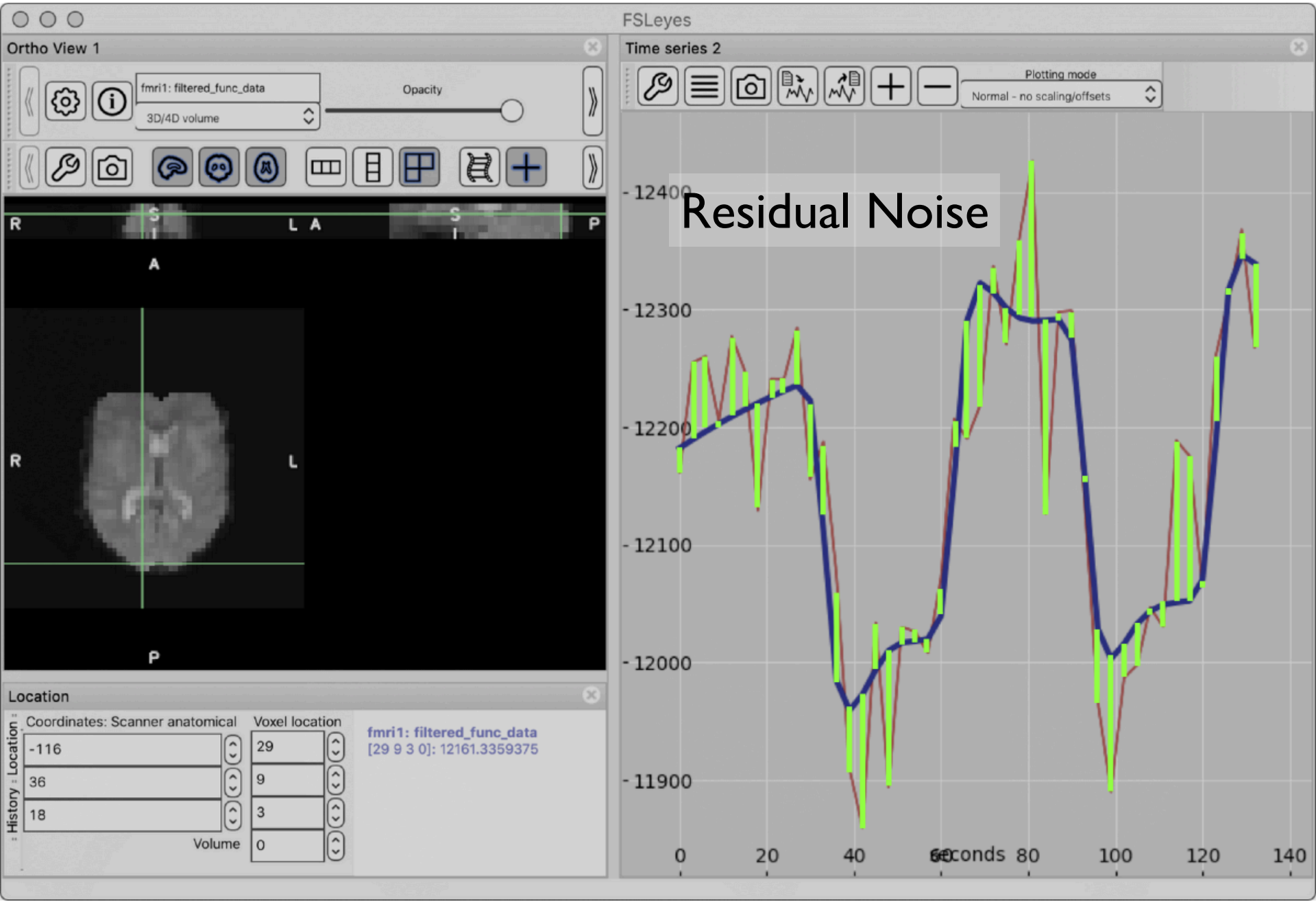


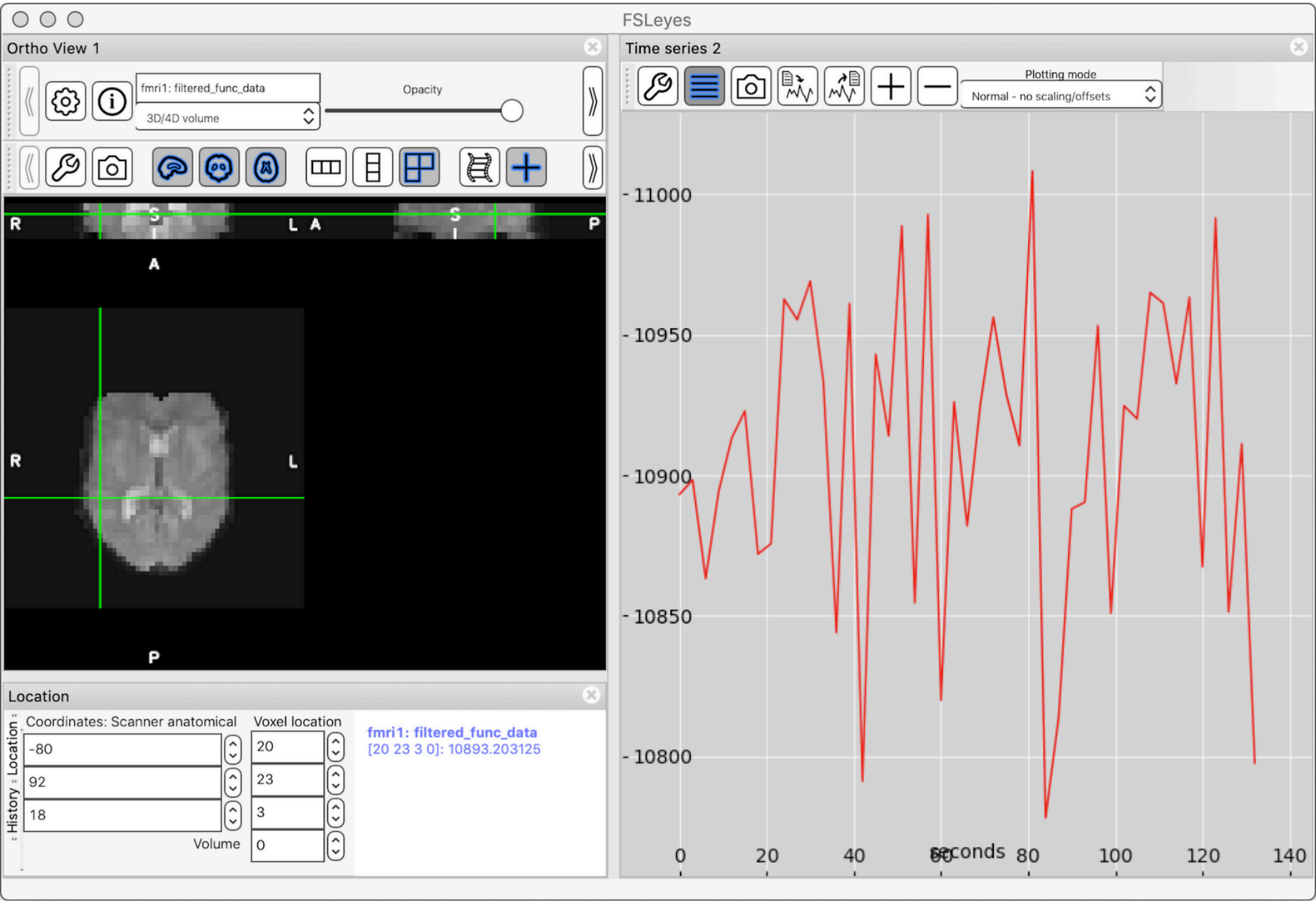


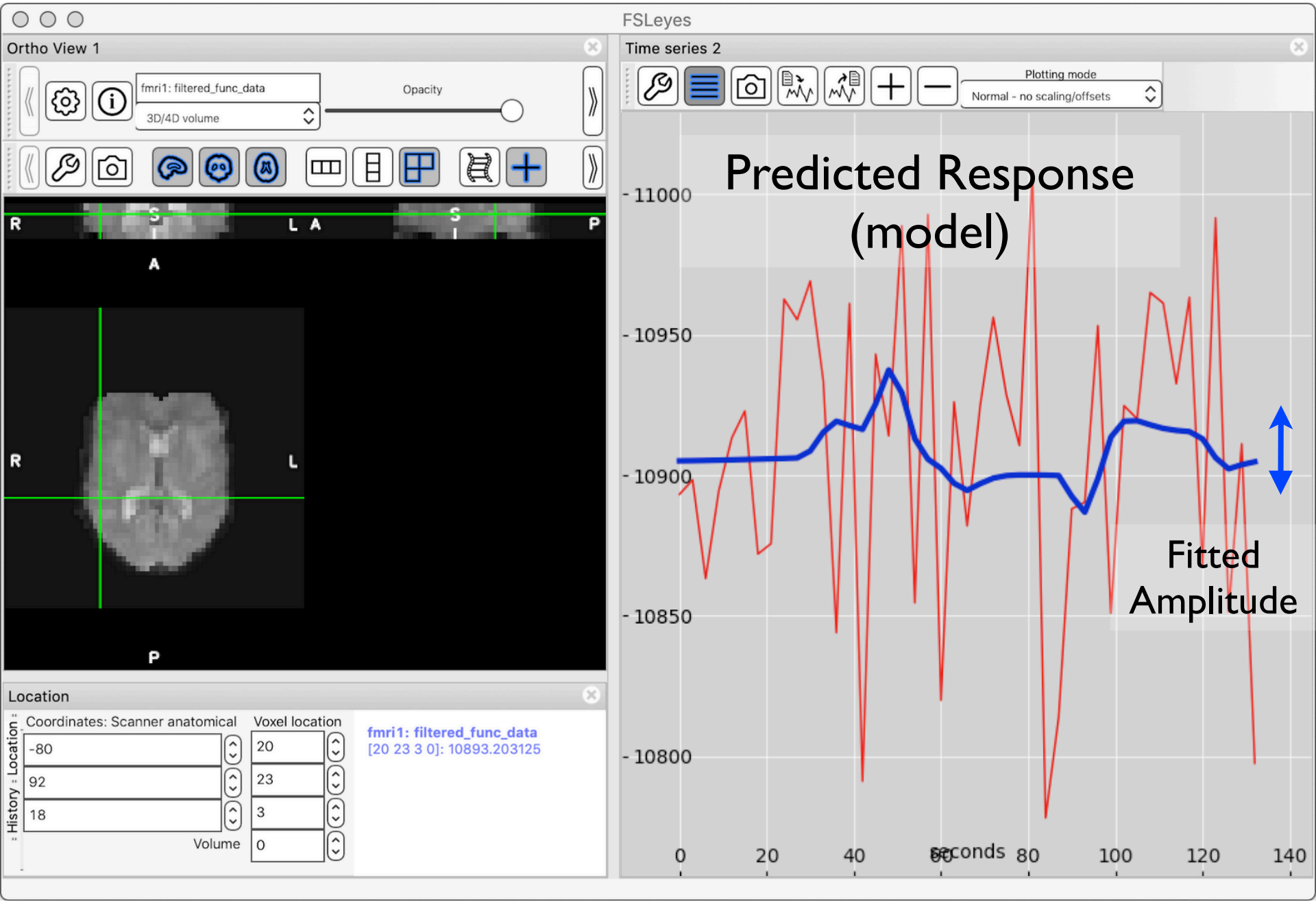

Ortho View 1
fmri1: filtered_func_data
3D/4D volume
Opacity
R
S
I
L A
S
I
P
A
R
L
P
Location
Coordinates: Scanner anatomical
Voxel location
-116
36
18
Volume
29
9
3
0
fmri1: filtered_func_data
[29 9 3 0]: 12161.3359375
History
Location


FSLeyes
Ortho View 1
fmri1: filtered_func_data
3D/4D volume
Opacity
R
L A
S
I
P
A
R
L
P
Location
Coordinates: Scanner anatomical
Voxel location
-116
36
18
29
9
3
Volume
0
fmri1: filtered_func_data
[29 9 3 0]: 12161.3359375
History
Location
Time series 2
Plotting mode
Normal - no scaling/offsets
12400
12300
12200
12100
12000
11900
0
20
40
seconds
80
100
120
140

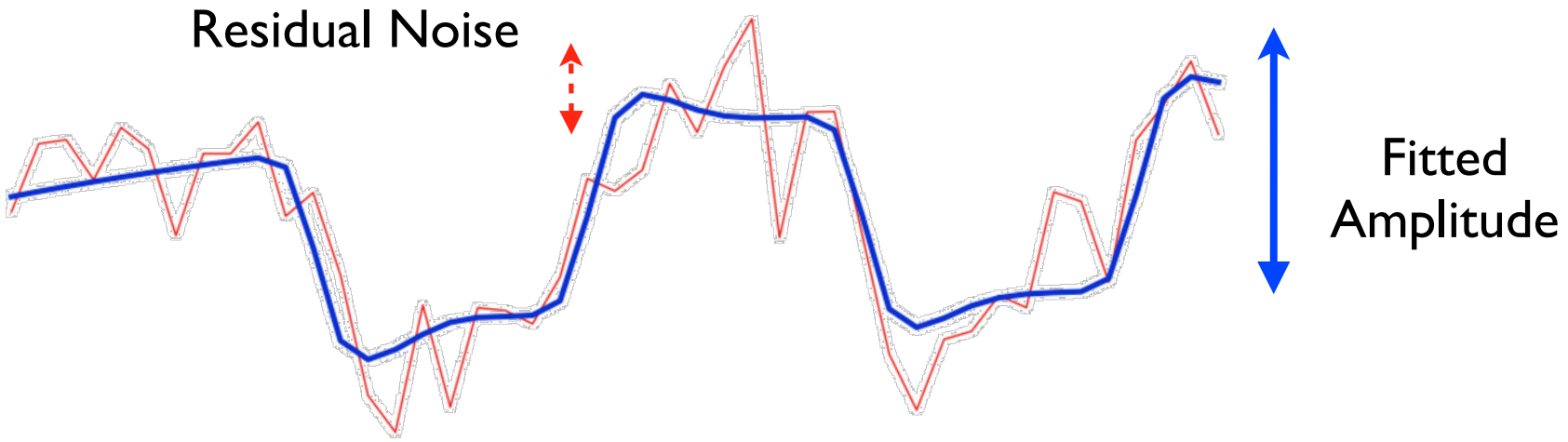

FSLeyes
Ortho View 1
fmri1: filtered_func_data
3D/4D volume
Opacity
R
L A
P
A
R
L
P
Location
Coordinates: Scanner anatomical
Voxel location
-116
36
18
Volume
29
9
3
0
fmri1: filtered_func_data
[29 9 3 0]: 12161.3359375
History
Location
Time series 2
Plotting mode
Normal - no scaling/offsets
Predicted Response
(model)
Fitted
Amplitude
12400
12300
12200
12100
12000
11900
0
20
40
60
80
100
120
140
seconds


FSLeyes
Ortho View 1
fmri1: filtered_func_data
3D/4D volume
Opacity
R
L A
S
I
P
A
R
L
P
Time series 2
Plotting mode
Normal - no scaling/offsets
Residual Noise
12400
12300
12200
12100
12000
11900
0
20
40
60
80
100
120
140
seconds
Location
Coordinates: Scanner anatomical
Voxel location
-116
36
18
29
9
3
Volume
0
fmri1: filtered_func_data
[29 9 3 0]: 12161.3359375
History
Location

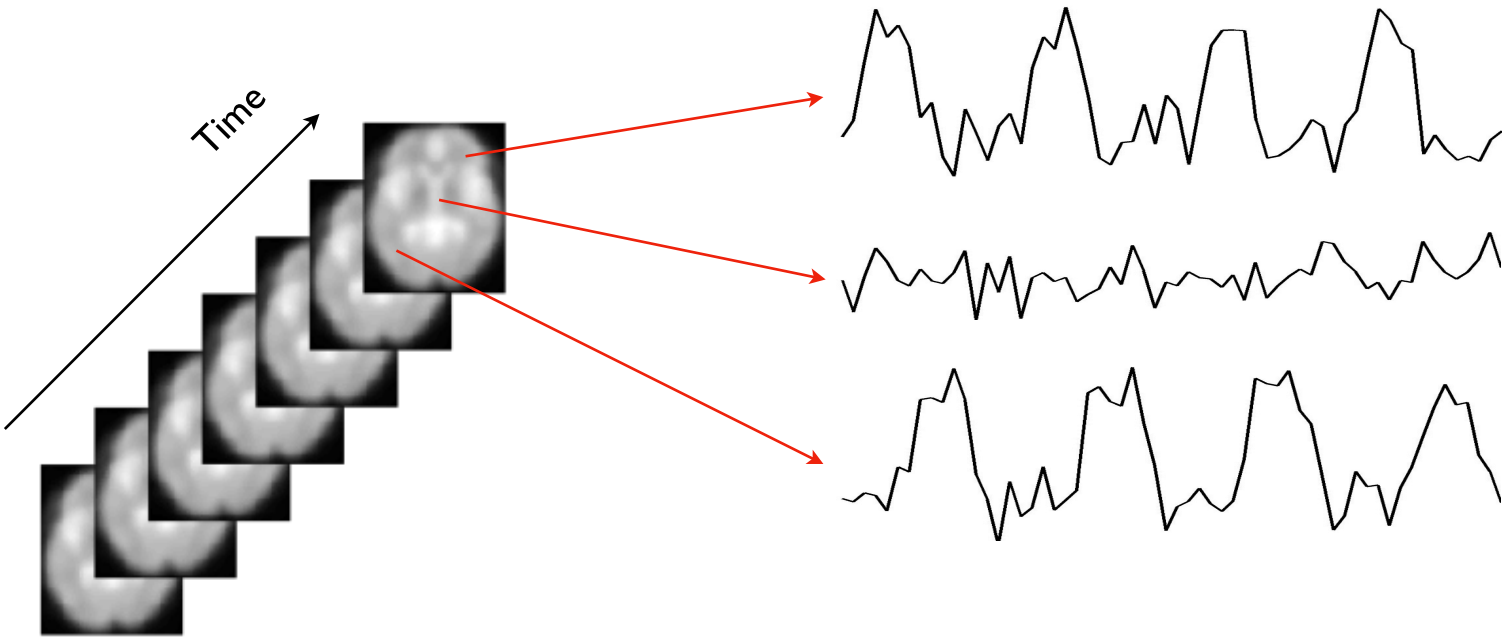

FSLeyes
Ortho View 1
fmri1: filtered_func_data
3D/4D volume
Opacity
R
L A
S
I
P
A
R
L
P
Location
Coordinates: Scanner anatomical
Voxel location
-80
92
18
20
23
3
Volume
0
fmri1: filtered_func_data
[20 23 3 0]: 10893.203125
History
Location
Time series 2
Plotting mode
Normal - no scaling/offsets
11000
10950
10900
10850
10800
0
20
40
60
80
100
120
140
seconds


FSLeyes
Ortho View 1
fmri1: filtered_func_data
3D/4D volume
Opacity
R
L A
P
A
R
L
P
Location
Coordinates: Scanner anatomical
Voxel location
-80
92
18
20
23
3
Volume
0
fmri1: filtered_func_data
[20 23 3 0]: 10893.203125
History
Location
Time series 2
Plotting mode
Normal - no scaling/offsets
Predicted Response
(model)
Fitted
Amplitude
11000
10950
10900
10850
10800
0
20
40
60
80
100
120
140
seconds

Is my data signal or is it noise?



Two different views of the data

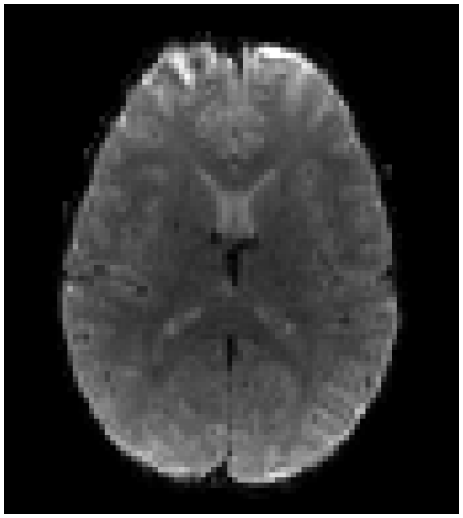


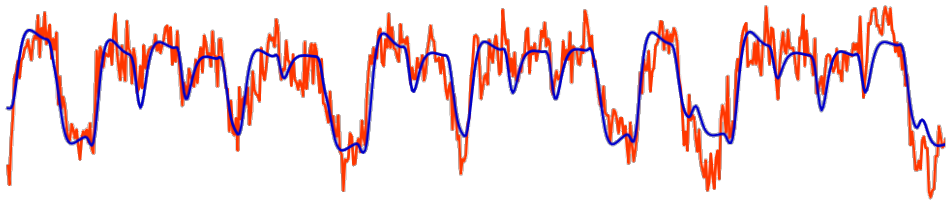
A "smallish" number of volumes

A **large** number of timeseries

FMRI single subject analysis

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





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- Motion correction
- Slice timing correction
- Spatial smoothing
- Temporal filtering
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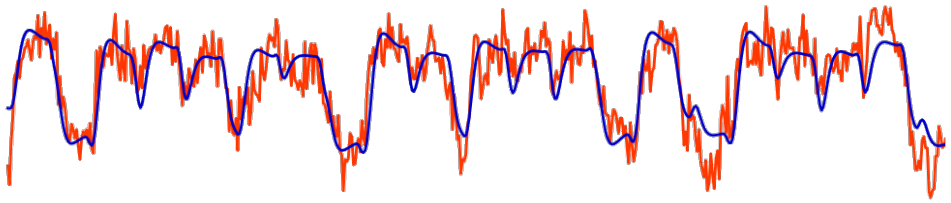
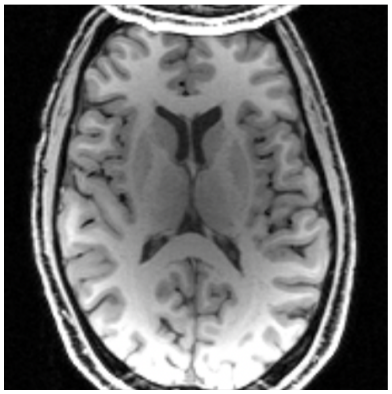
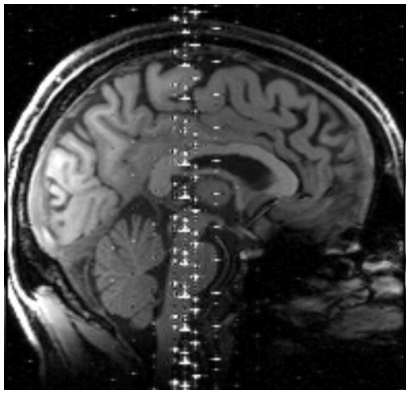


Image Reconstruction

- Convert k-space data to image - done automatically on the scanner

Image Reconstruction

- Convert k-space data to image - done automatically on the scanner
- Occasionally get problematic data
  - e.g. RF spikes, wrap-around, RF interference

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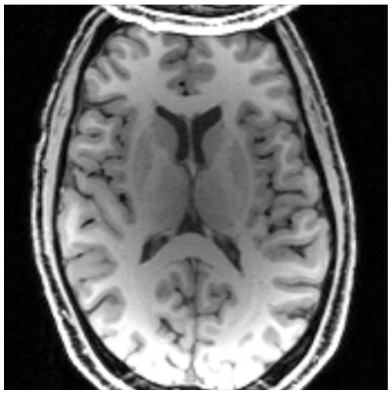
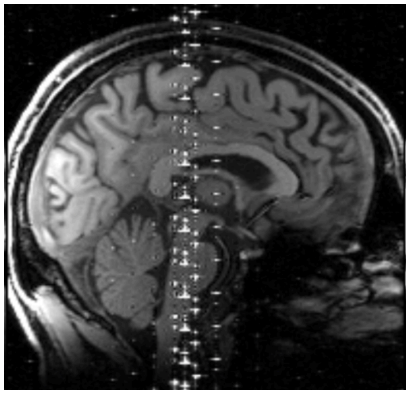
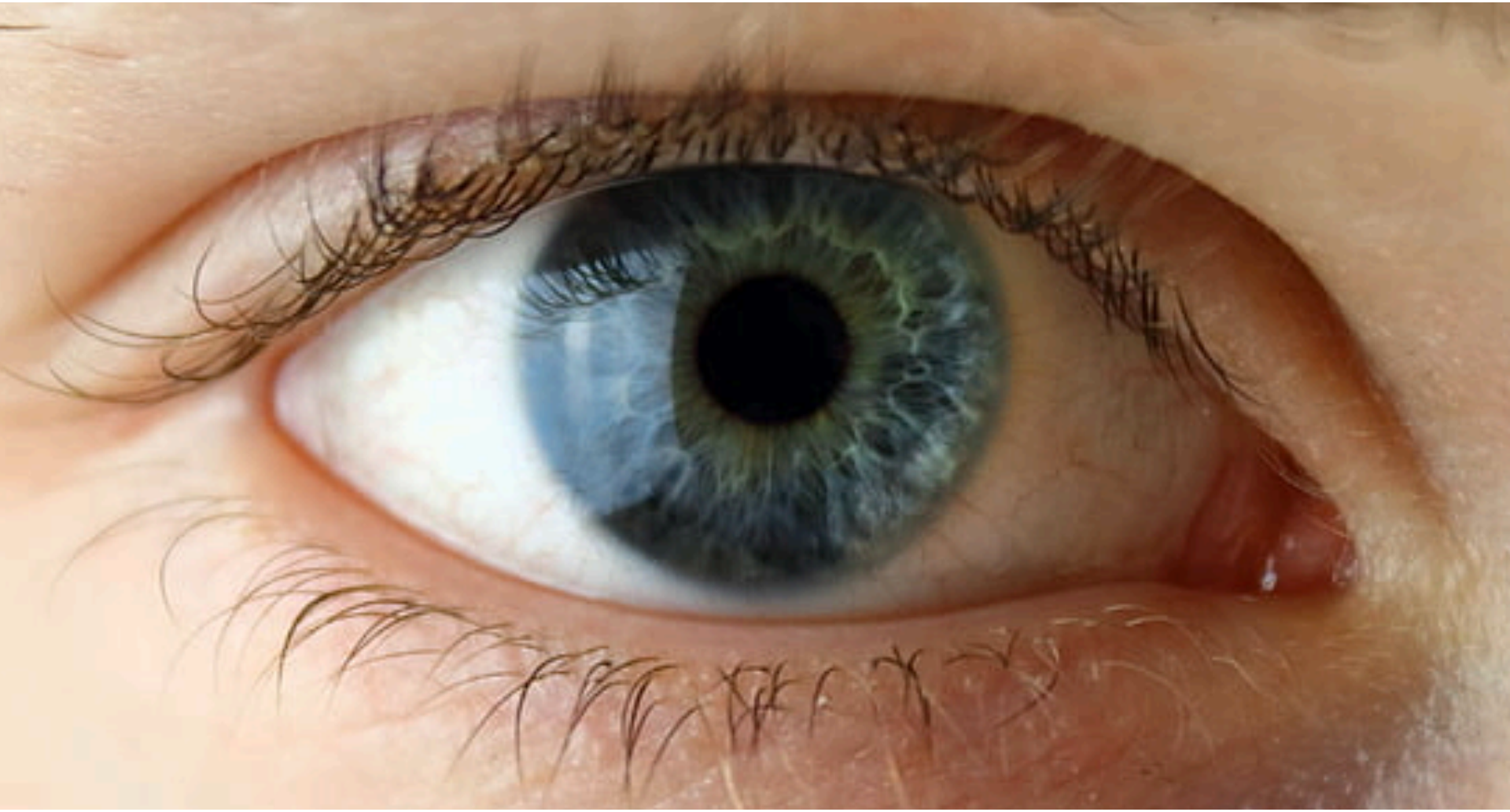



- Scanner artefacts can be found by:

LOOK AT YOUR DATA!

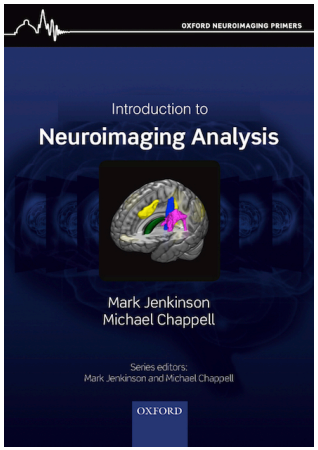


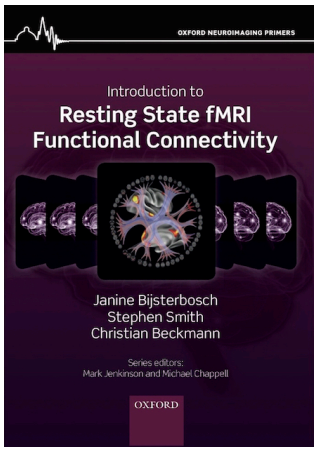
www.pickpik.com

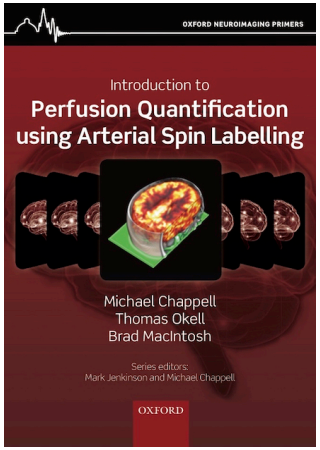
Free online appendix

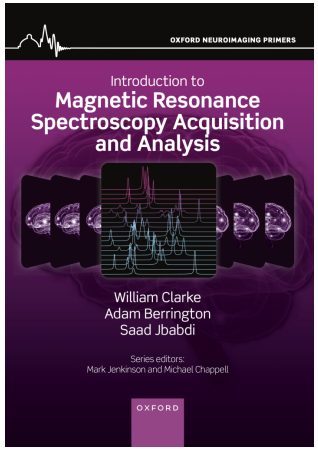
Oxford Neuroimaging Primers

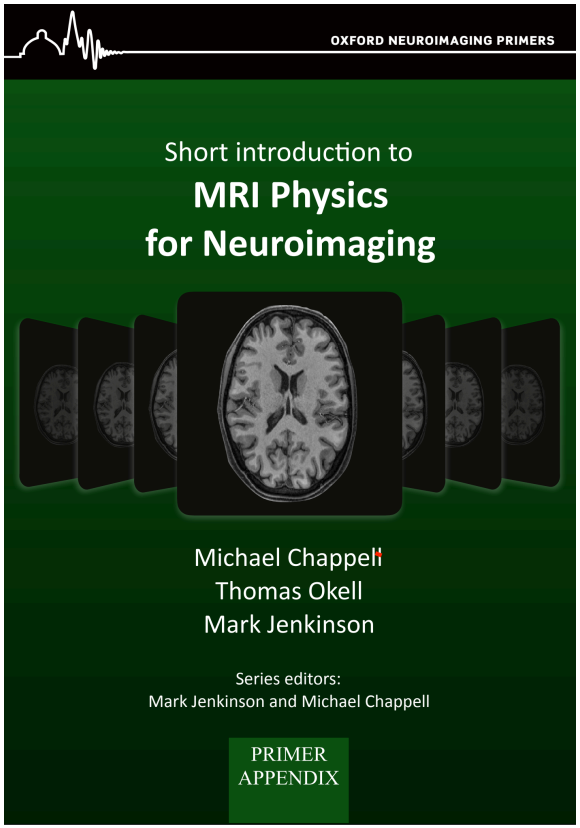
https://www.fmrib.ox.ac.uk/primers/appendices/mri_physics.pdf











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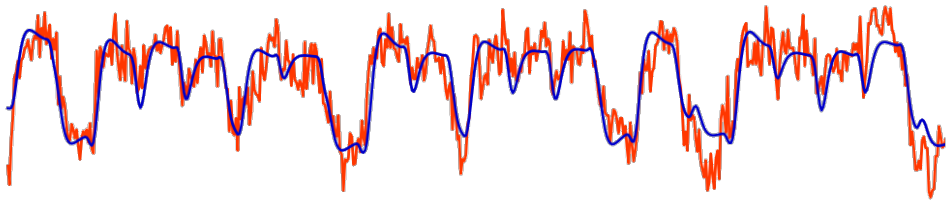
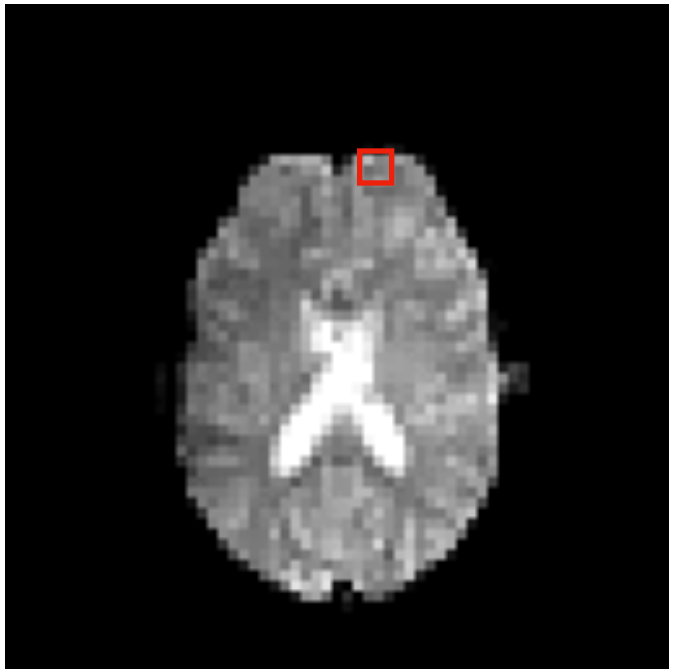


Motion Correction

People move in the scanner



Motion Correction

Many manual correction methods have been attempted over the years ...

Motion Correction

Try to make your participants as comfortable as possible

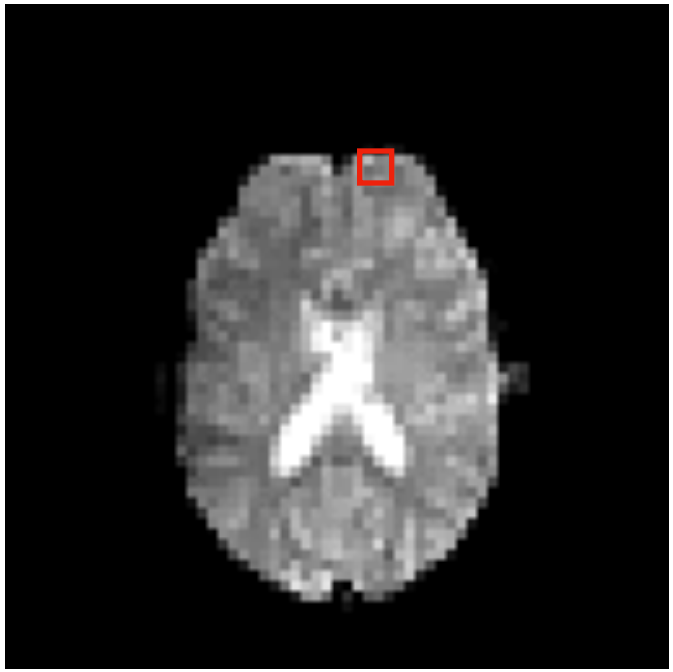
Motion Correction

People move in the scanner

Even with padding around the head there is still some motion

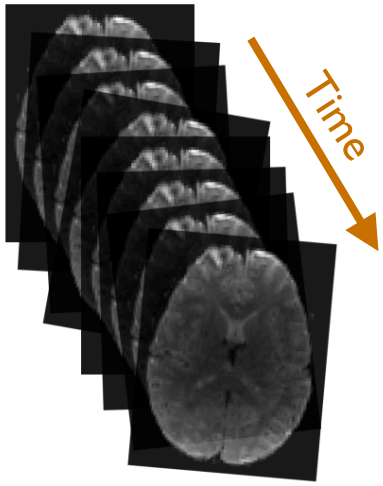
Through time each voxel should be located at a consistent anatomical point

ALWAYS do motion correction



Motion Correction

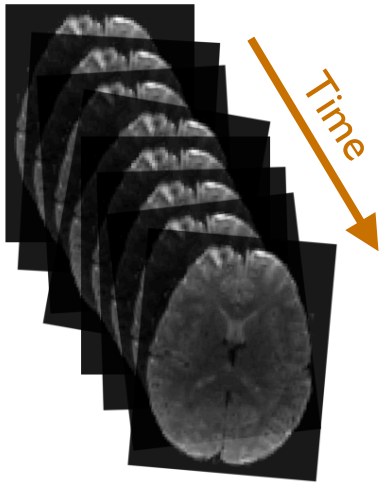
Corrected using linear registration



1. Take the raw FMRI data

Motion Correction

Corrected using linear registration



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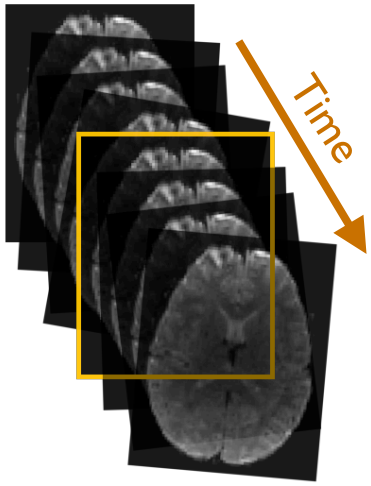
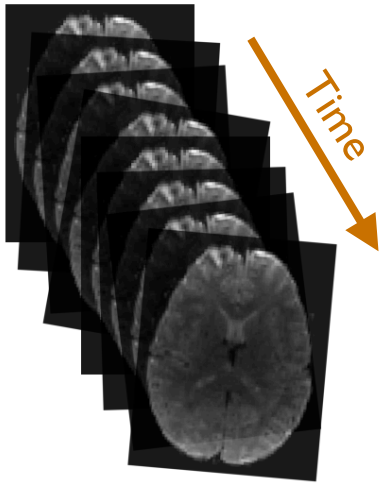


2. Choose a reference volume (usually the middle time point)

Motion Correction

Corrected using linear registration



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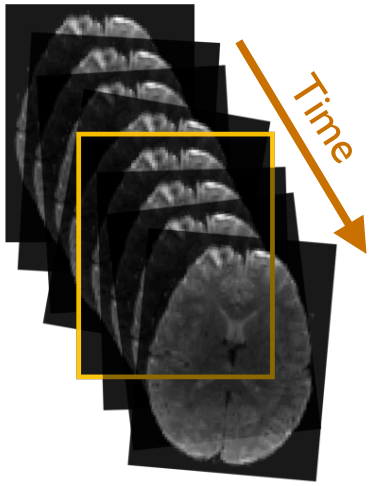

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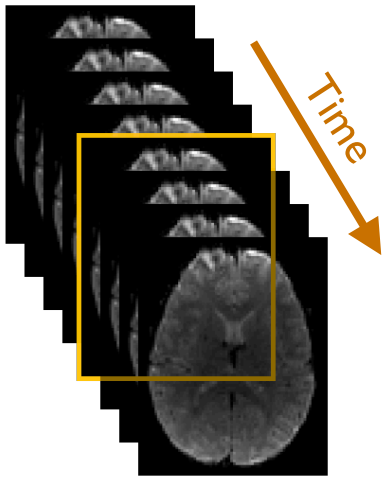
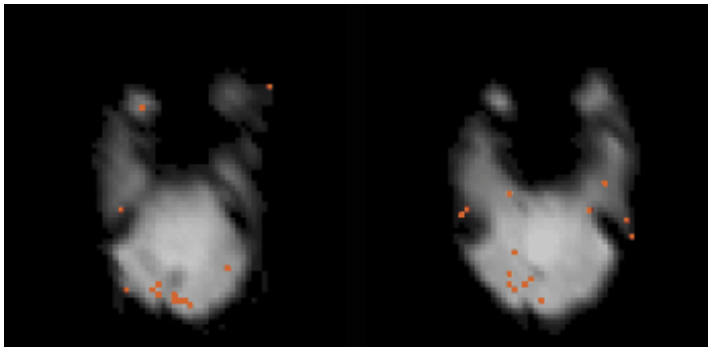
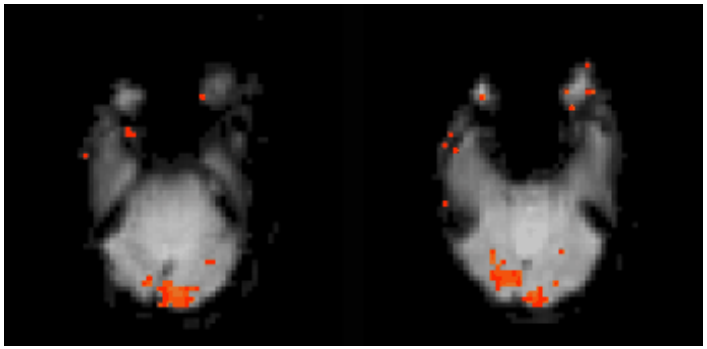


3. Rotate and shift all other volumes so they are aligned with the reference (using 6 DOF linear registration)

Effect of Motion Correction

Uncorrelated Motion



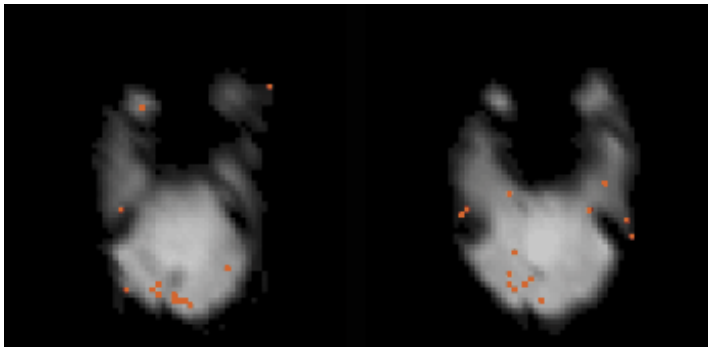


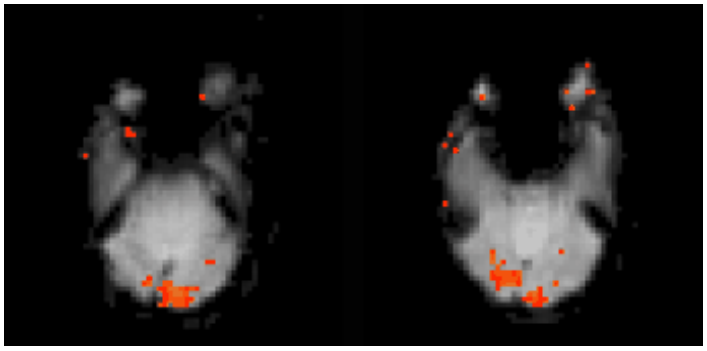
Without MC

With MC

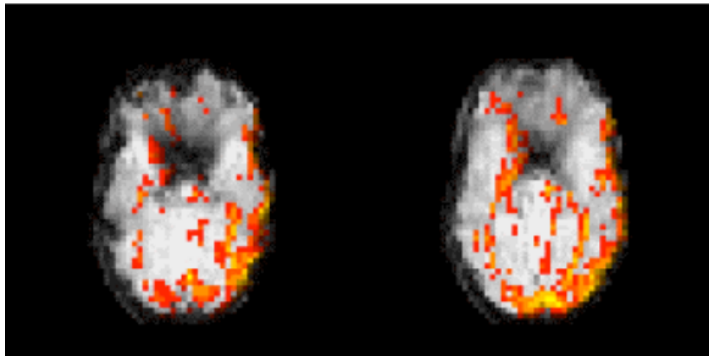
Effect of Motion Correction

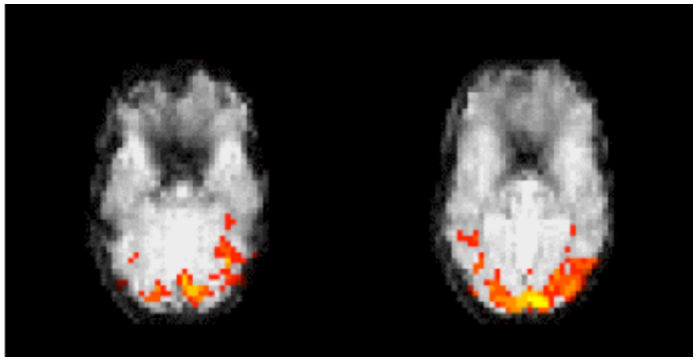
Uncorrelated Motion





Stimulus Correlated Motion





Without MC

With MC

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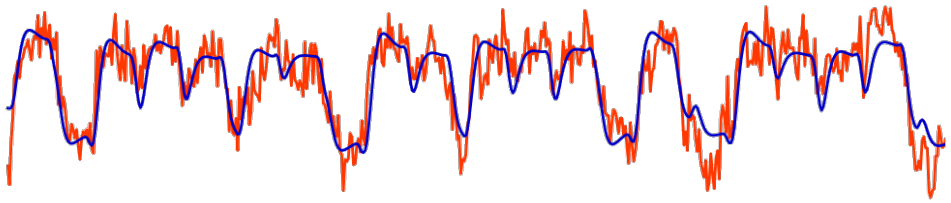
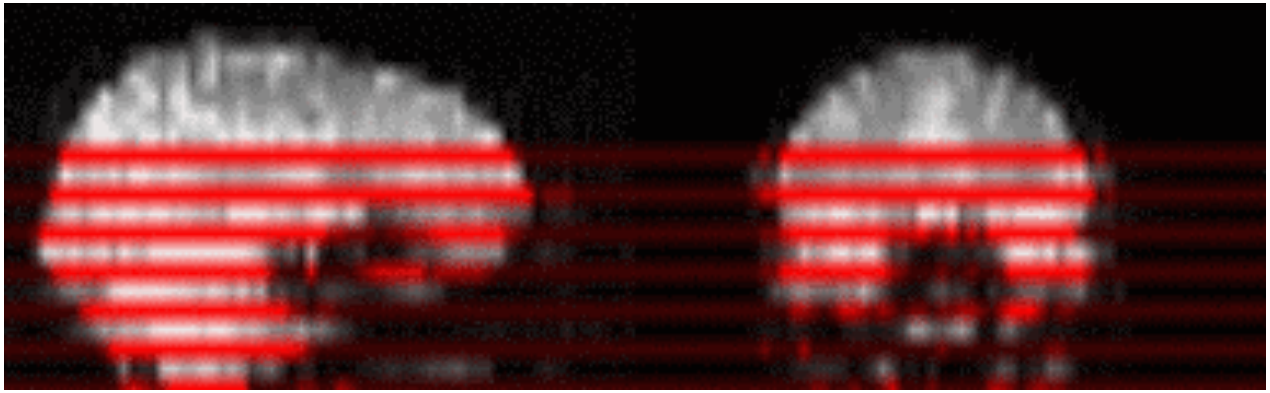


Slice Timing Correction

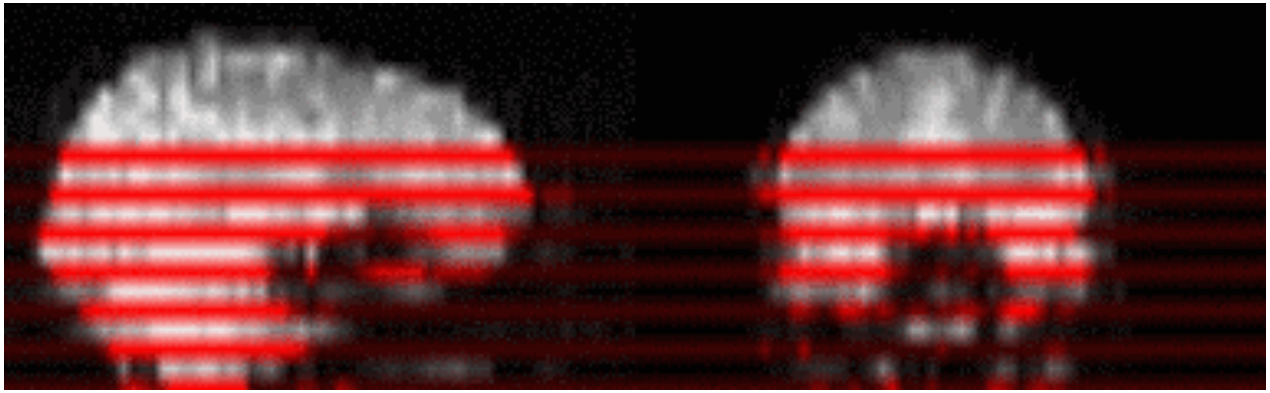


Almost all FMRI scanning takes each slice separately

Each slice is scanned at a slightly different time

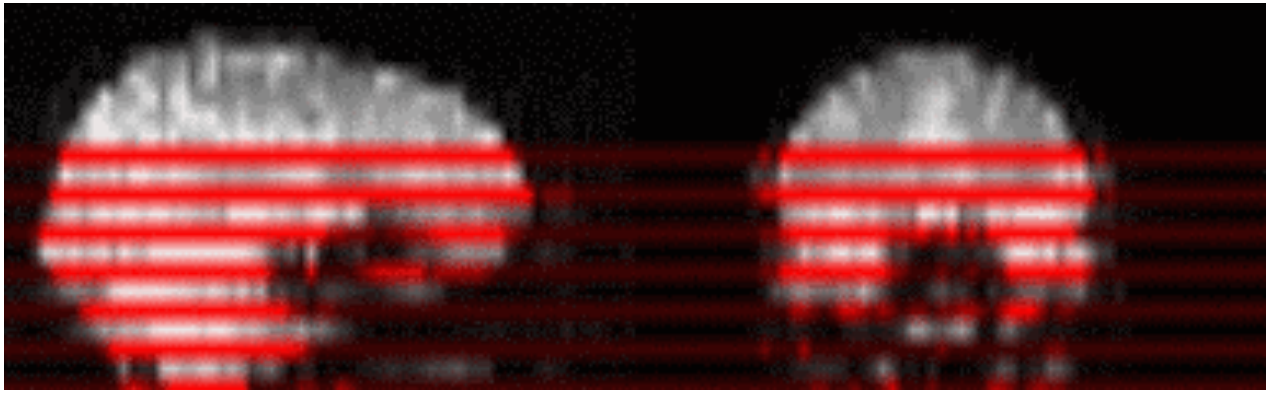
Slice order can be interleaved (as shown) or sequential (up or down)

Slice Timing Correction



Can deal with timing change by:

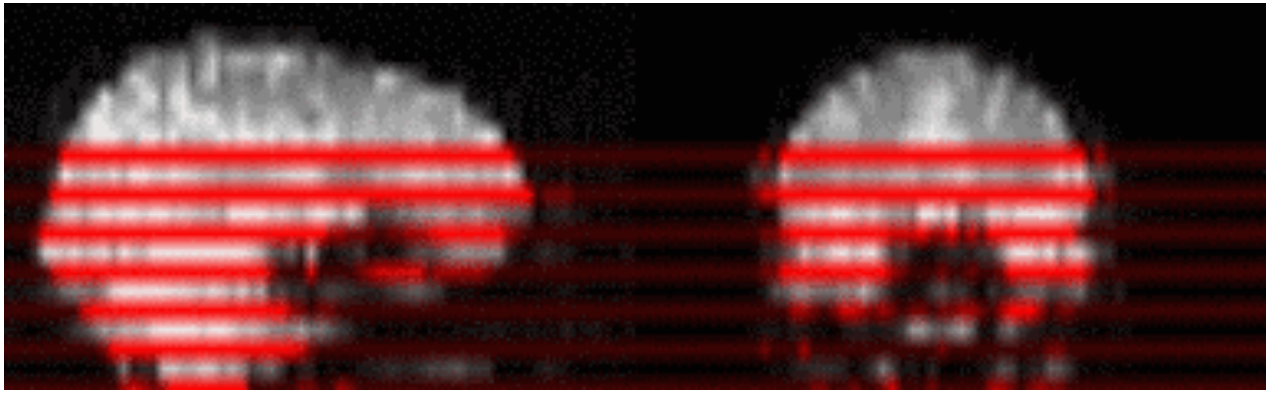
Slice Timing Correction



Can deal with timing change by:

Shifting the **data** timing
= slice timing correction
(not recommended)

Slice Timing Correction



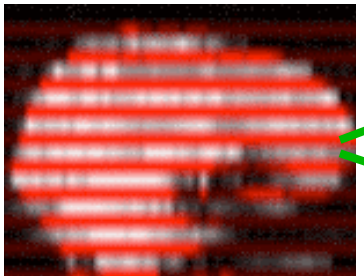
Can deal with timing change by:

Shifting the **data** timing
= slice timing correction
(not recommended)

Shifting the **model** timing
using temporal derivative
(recommended)

Slice Timing Correction

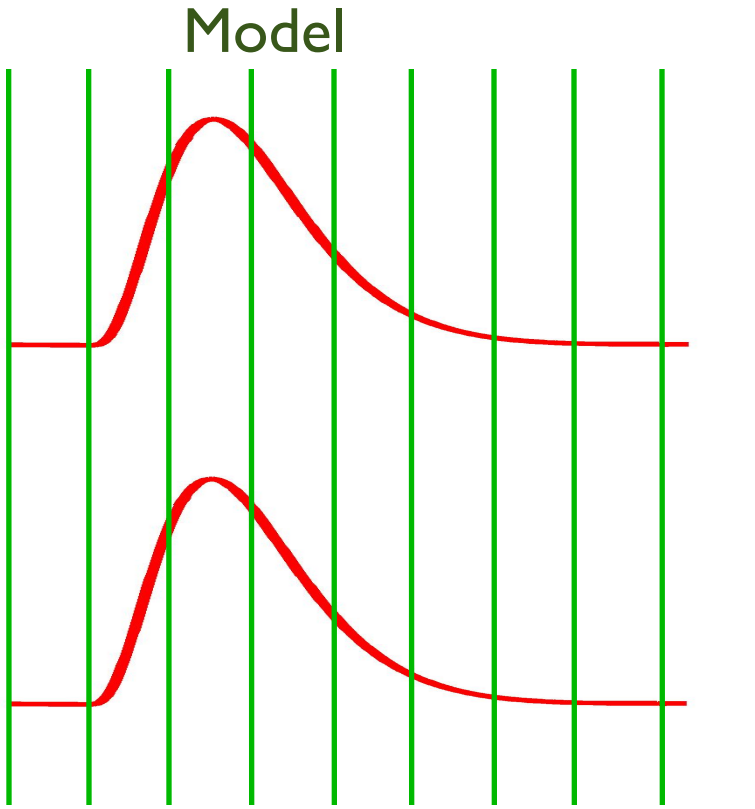
Without any adjustment, the model timing is always the same



slice 10

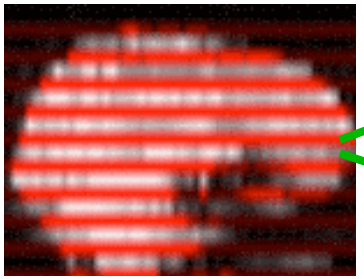
slice 9

Slice 9 acquired 1.5 secs after slice 10



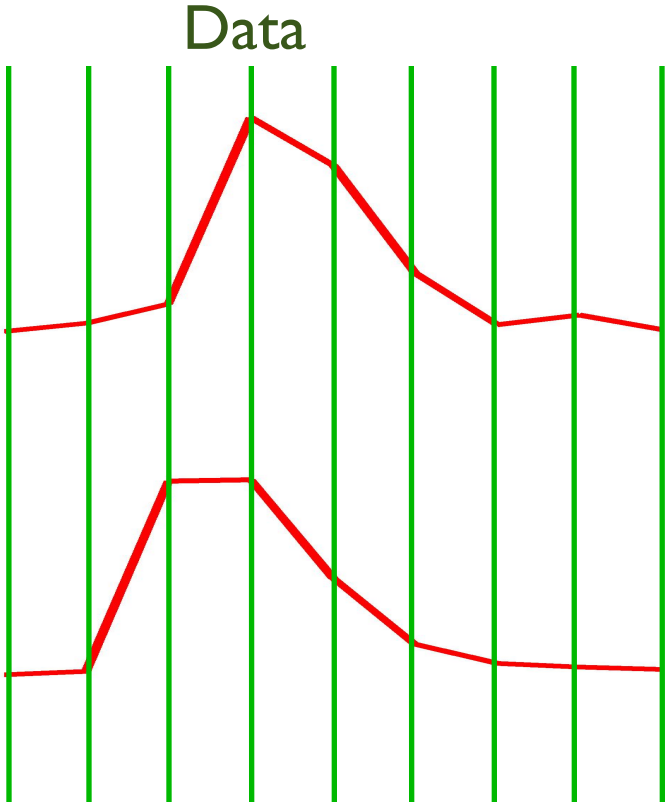
Slice Timing Correction

... but the timing of each slice's data is *different*



slice 10

slice 9

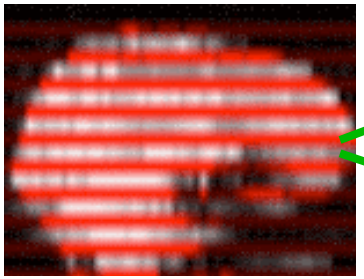


Slice 9 acquired 1.5 secs after slice 10

acquisition timing (TRs)

Slice Timing Correction

Can get consistency by shifting the ***data***



slice 10

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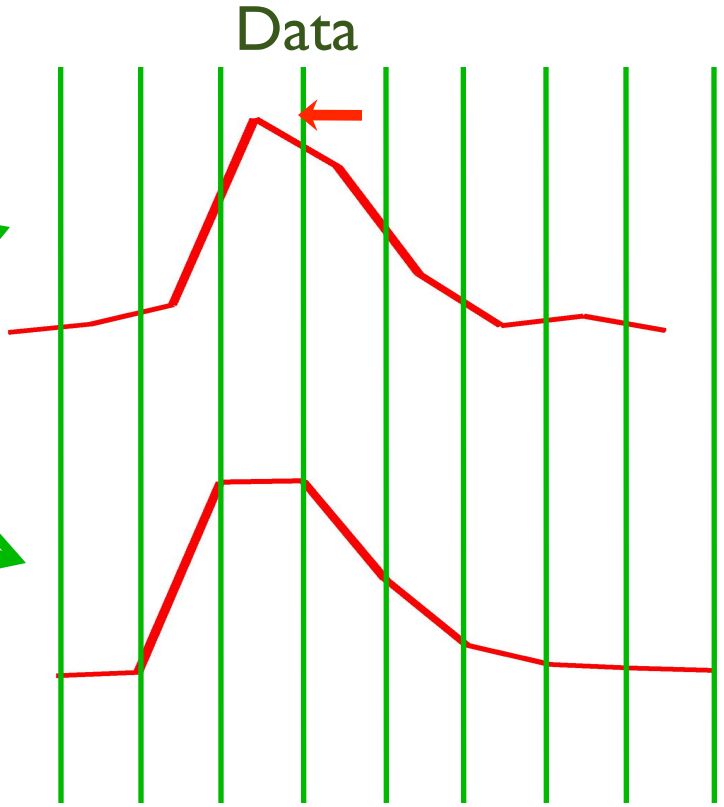
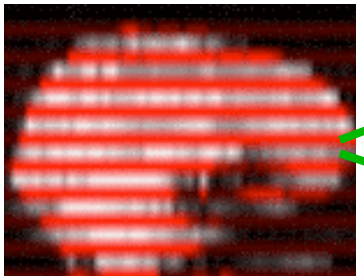
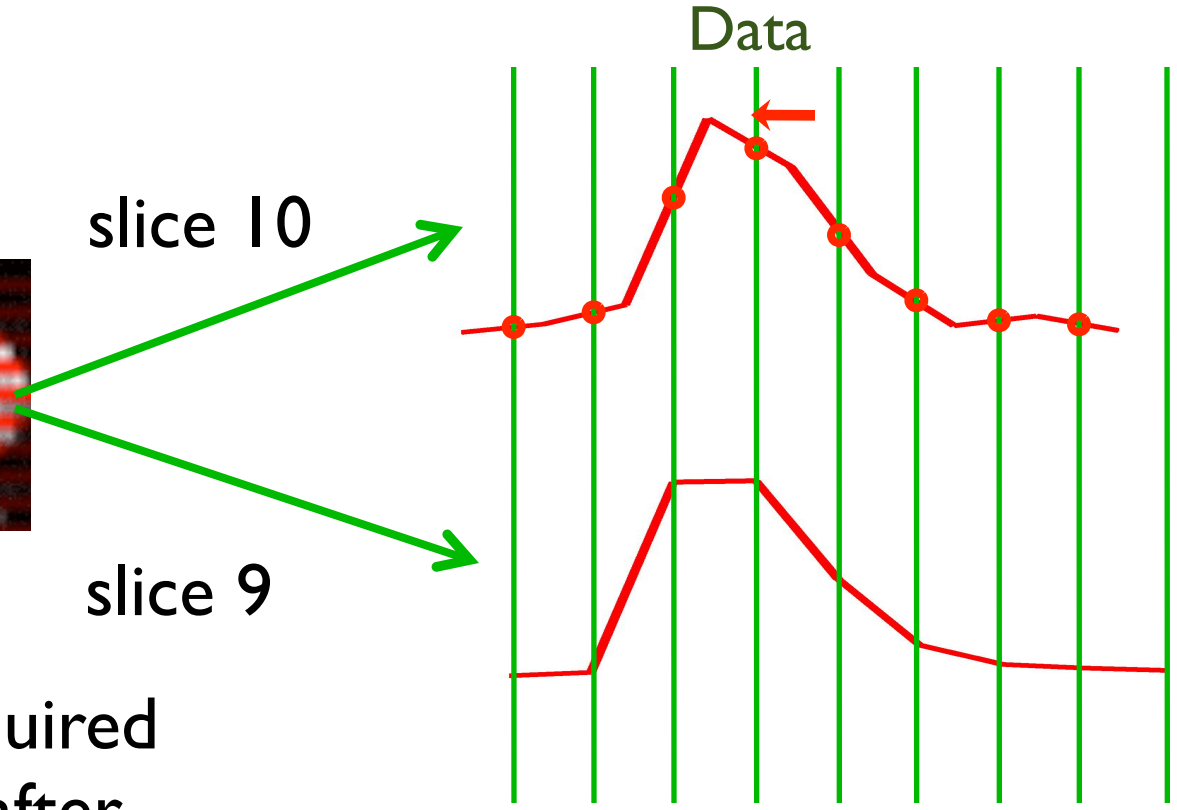


Slice 9 acquired 1.5 secs after slice 10

Slice Timing Correction

... and then interpolating the data
= ***slice timing correction***

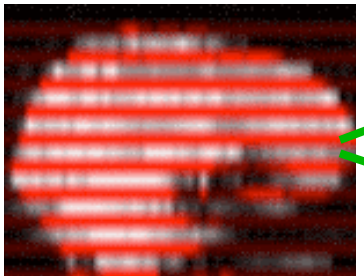


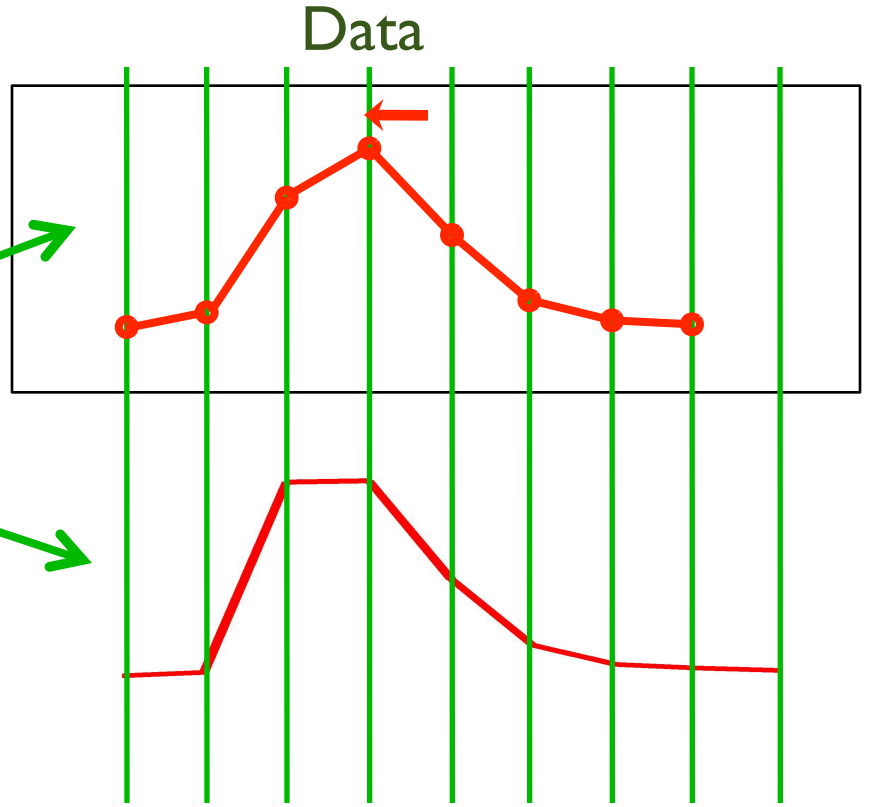


Slice 9 acquired
1.5 secs after
slice 10

Slice Timing Correction

... and then interpolating the data
= ***slice timing correction***

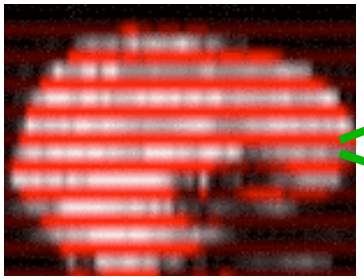




Slice 9 acquired
1.5 secs after
slice 10

Slice Timing Correction

The result of slice timing correction is that the data is changed (degraded) by interpolation



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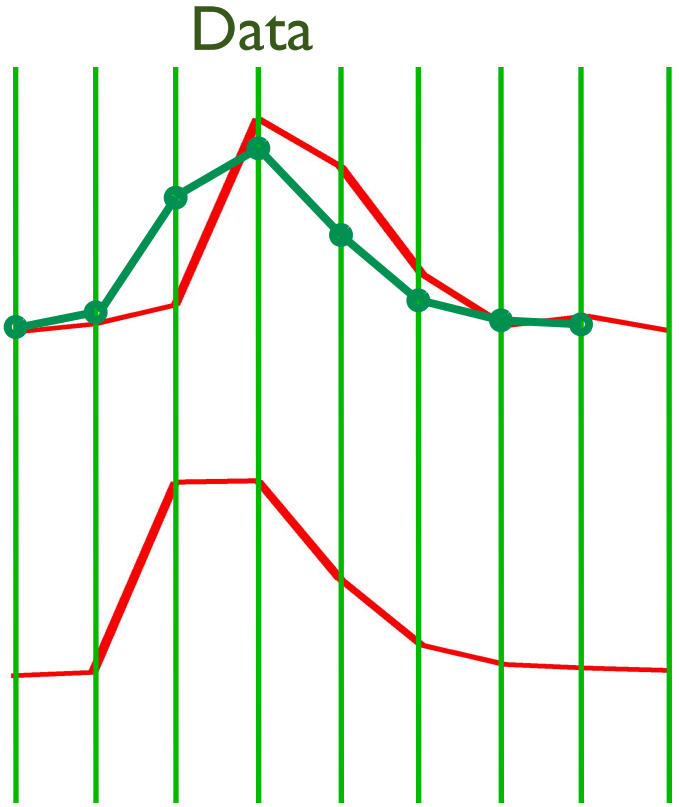
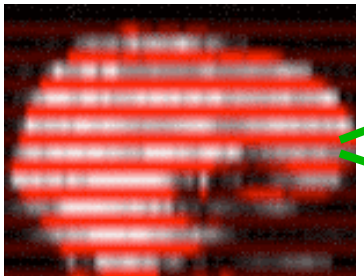


Slice Timing Correction

Alternatively, can get consistency by shifting the ***model***



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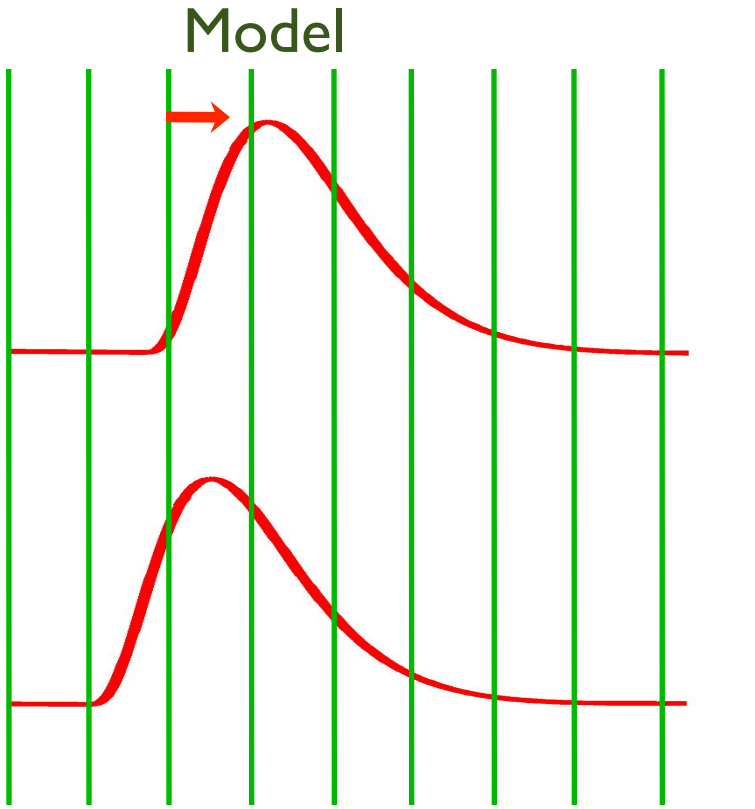


Slice Timing Correction

One way to shift the model is to use the ***temporal derivative in the GLM***

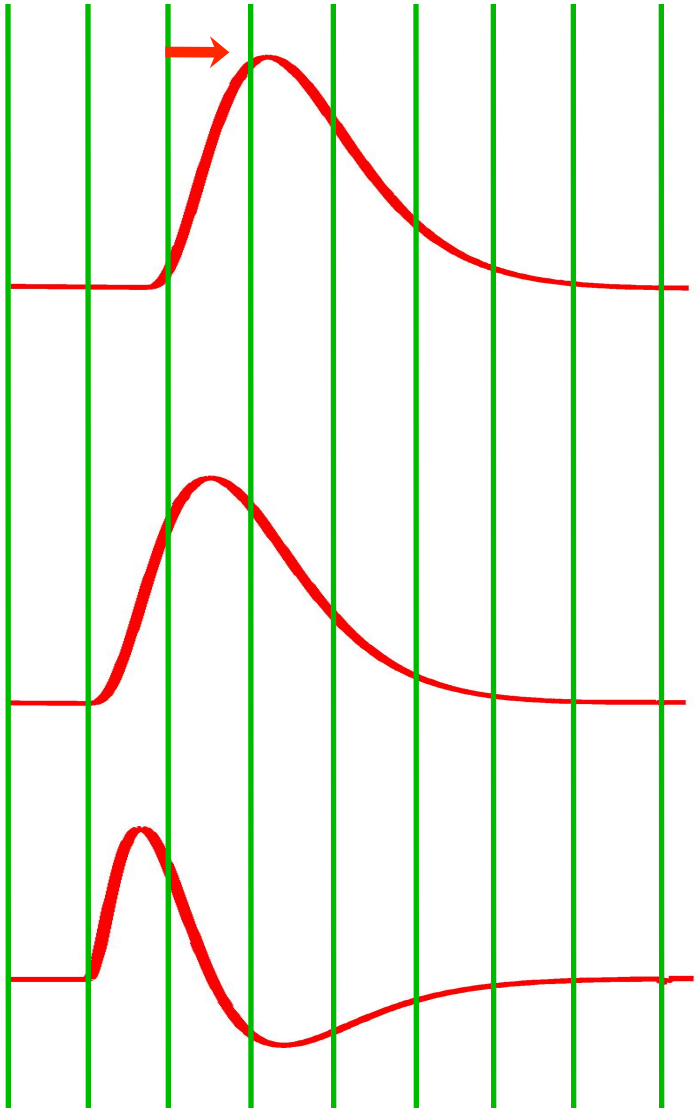
Shifted Model

=

Original Model

-

Temporal Derivative



Based on Taylor approx:

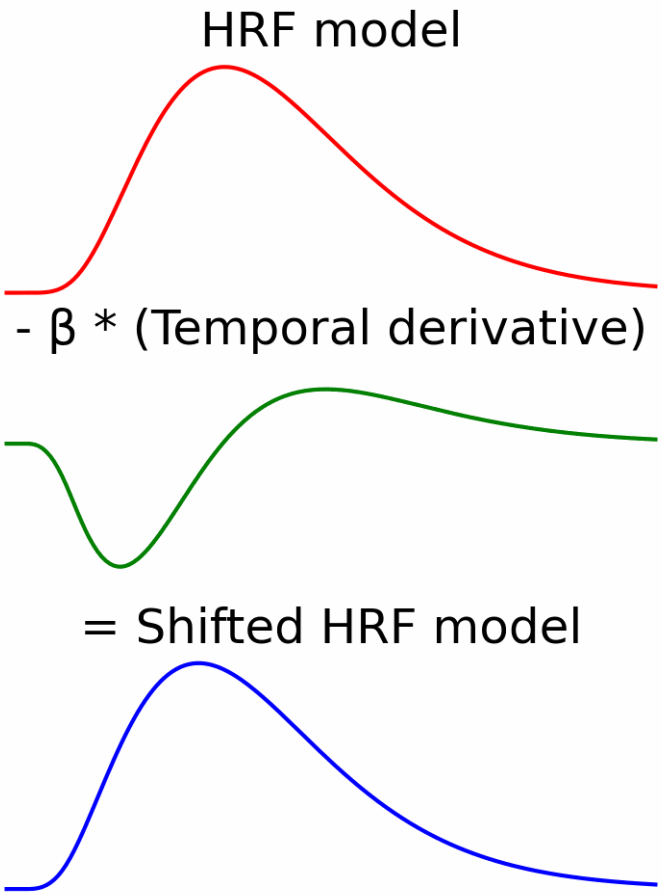
$m(t+a) = m(t) + a.m'(t)$

Slice Timing Correction

Shifting the model also accounts for variations in the HRF delay

as the HRF is known to vary between subjects, sessions, etc.

This is the recommended solution for slice timing



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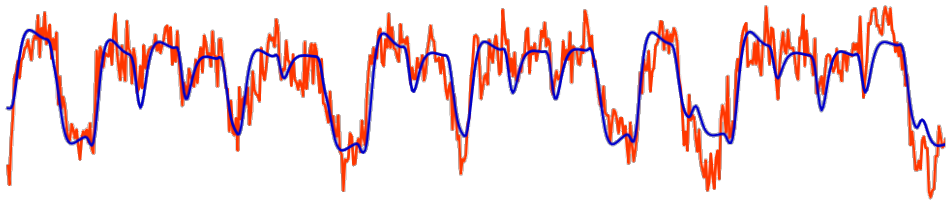
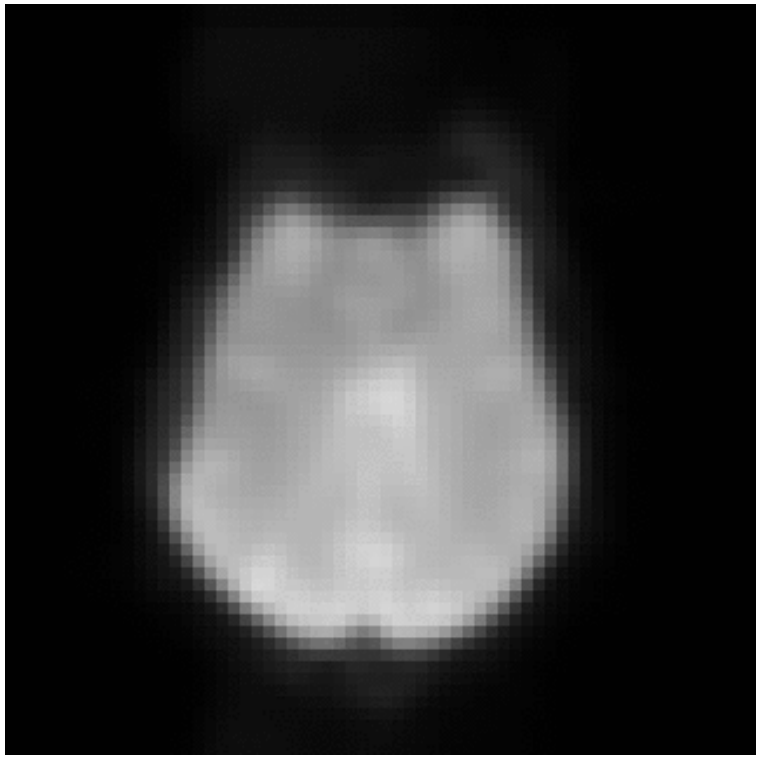


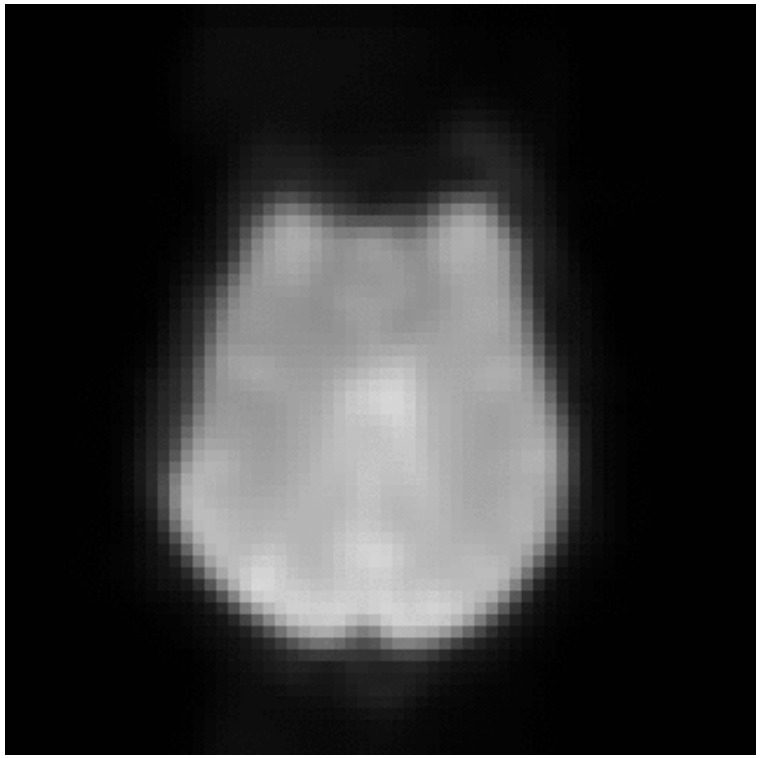
Spatial Smoothing



Spatial Smoothing

Why do it?

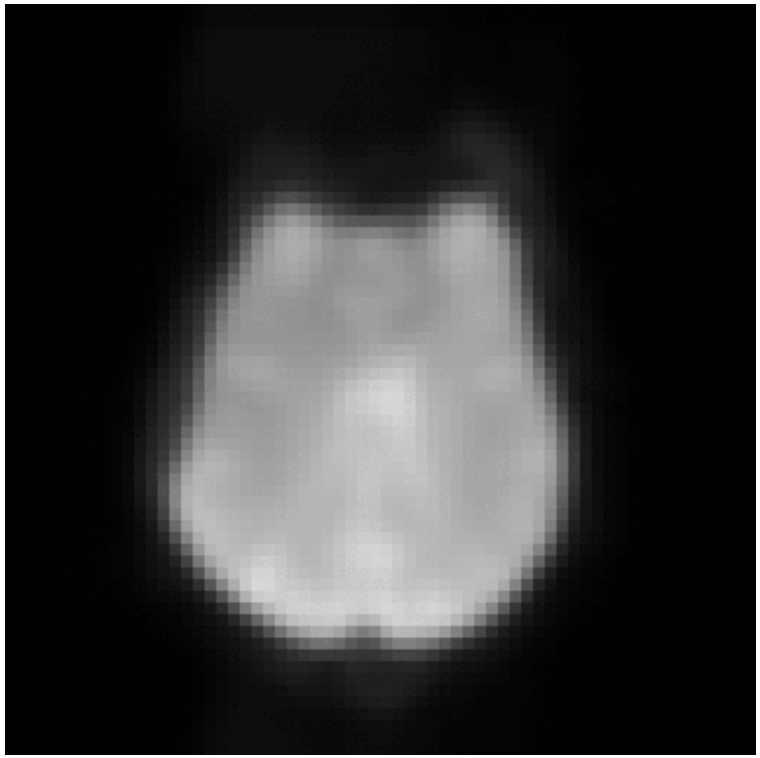
1. Increases signal to noise ratio if size of the blurring is less than size of activation



Spatial Smoothing

Why do it?

1. Increases signal to noise ratio if size of the blurring is less than size of activation
2. Need minimum "smoothness" to use *Gaussian random field theory* for thresholding



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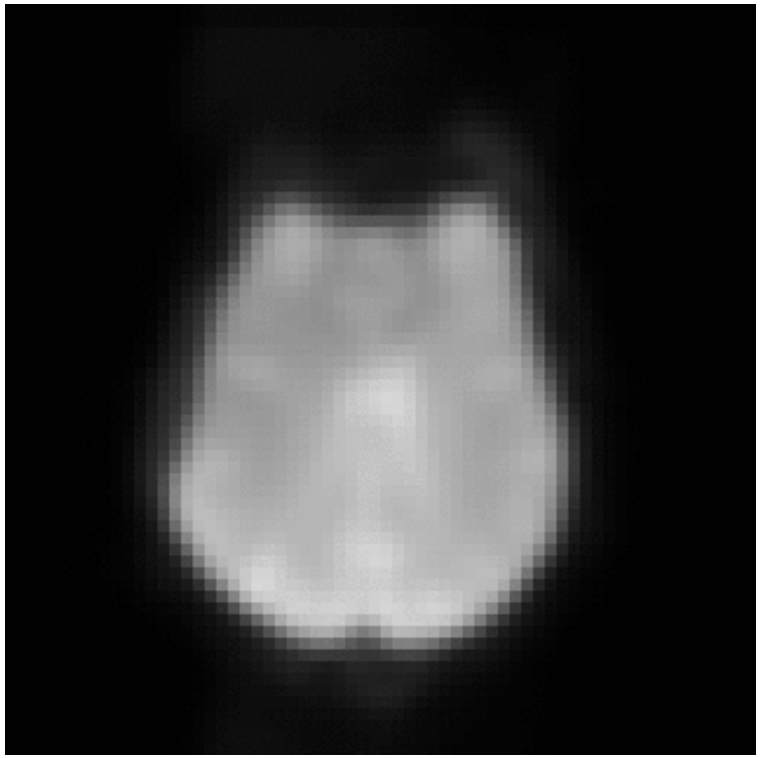

However:

- Reduces small activation areas
- Safest option is to do a small amount of smoothing
- Alternative thresholding/stats eliminates the need for smoothing (e.g. randomise, TFCE)

Spatial Smoothing

Spatial filtering done by a 3D convolution with a Gaussian (cf. 1D convolution with HRF for model)

Each voxel intensity is replaced by a *weighted* average of neighbouring intensities

A Gaussian function in 3D specifies weightings and neighbourhood size

Weights

0.1	0.3	0.4	0.3	0.1
0.3	0.6	0.8	0.6	0.3
0.4	0.8	1.0	0.8	0.4
0.3	0.6	0.8	0.6	0.3
0.1	0.3	0.4	0.3	0.1

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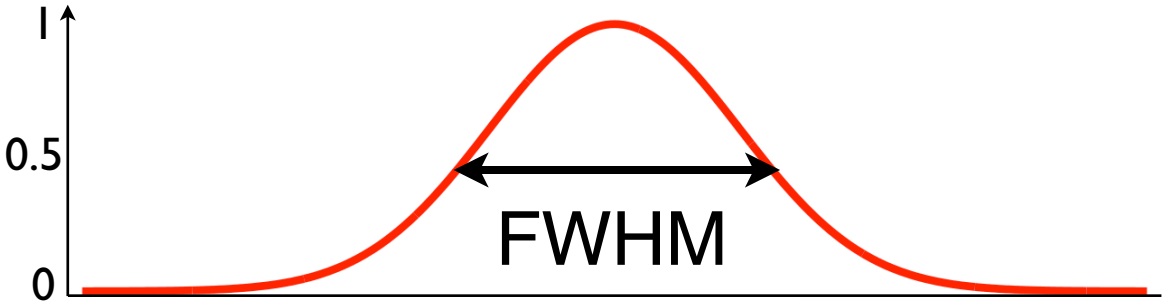

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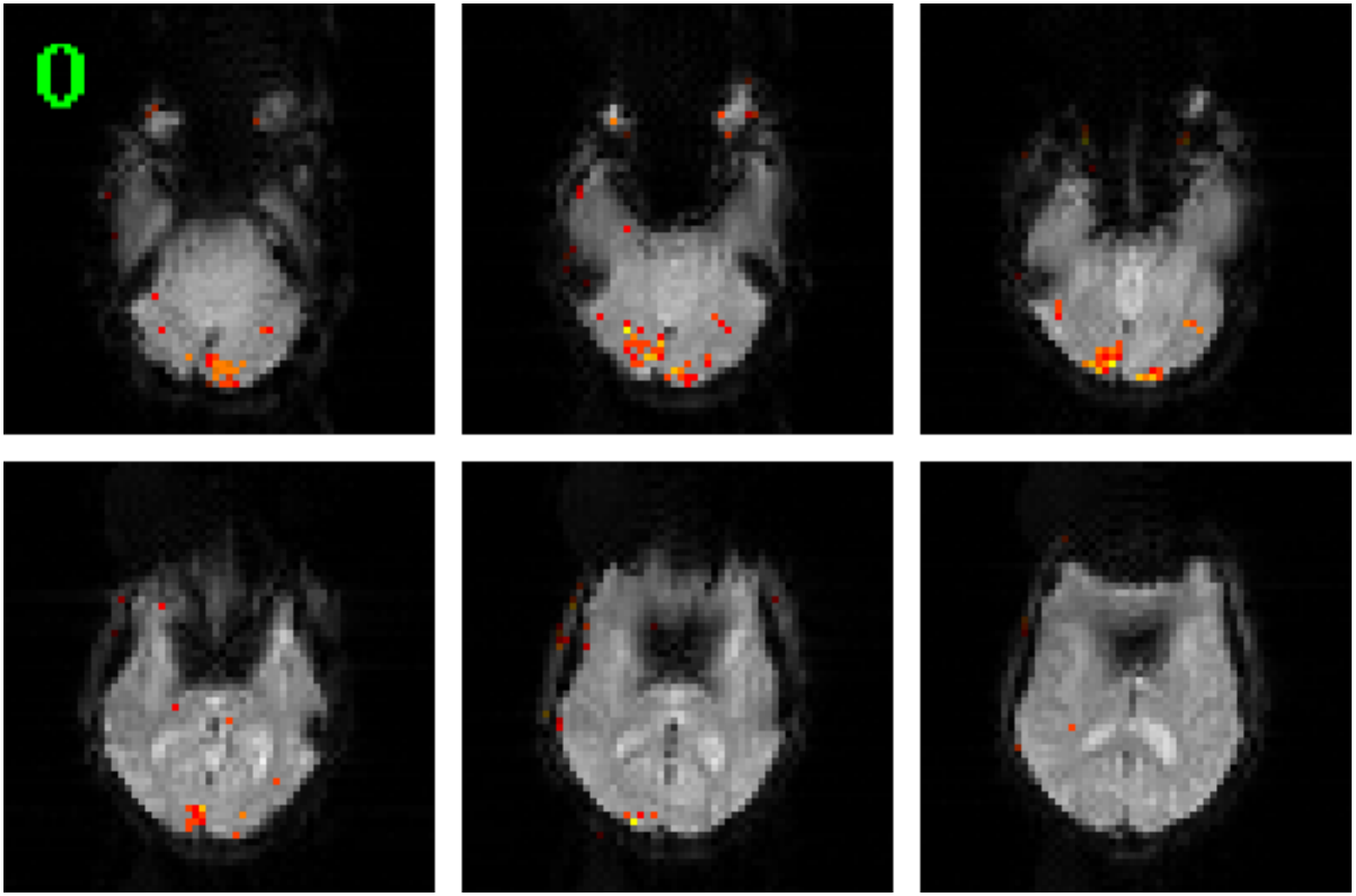
0.3	0.6	0.8	0.6	0.3
0.1	0.3	0.4	0.3	0.1

FWHM

Specify amount by Full Width Half Maximum (FWHM)
= distance between 0.5 values

Spatial Smoothing: Results at Different FWHM



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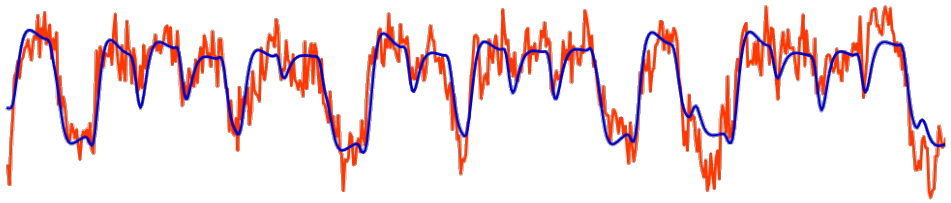


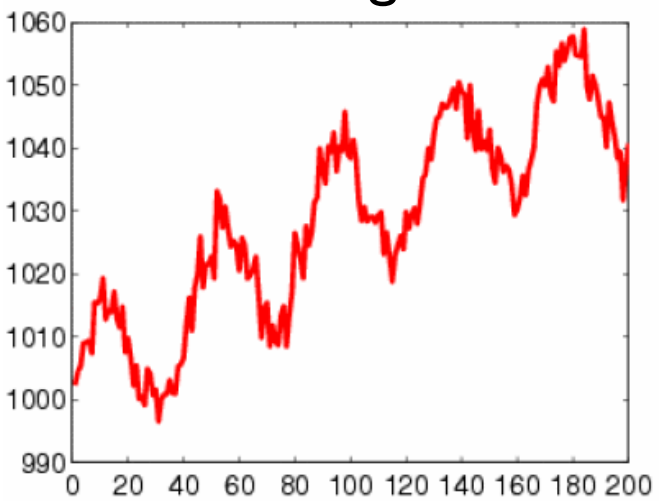
Temporal Filtering

- Time series from each voxel contains low frequency drifts and high frequency noise
- Drifts are scanner-related and physiological (cardiac cycle, breathing etc)
- Both high and low frequency noise hide activation

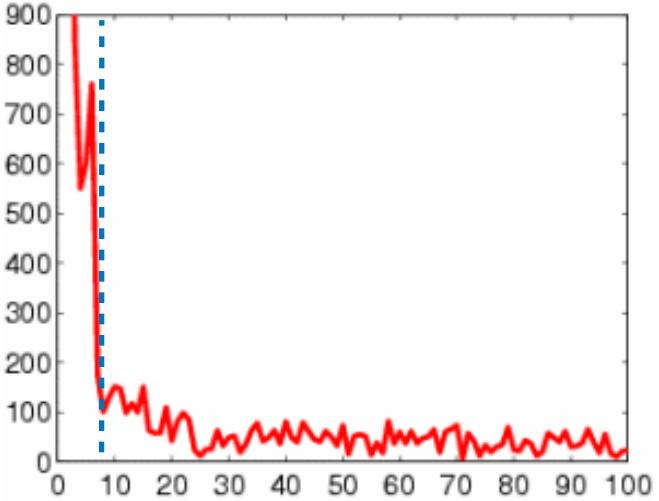
What is temporal filtering?

Removal of high frequencies, low frequencies or both, without removing signal of interest

Raw Signal

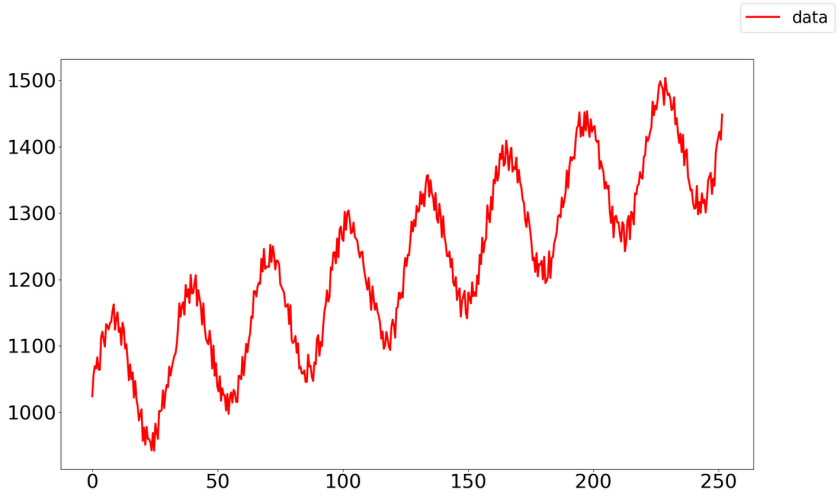


Frequency content

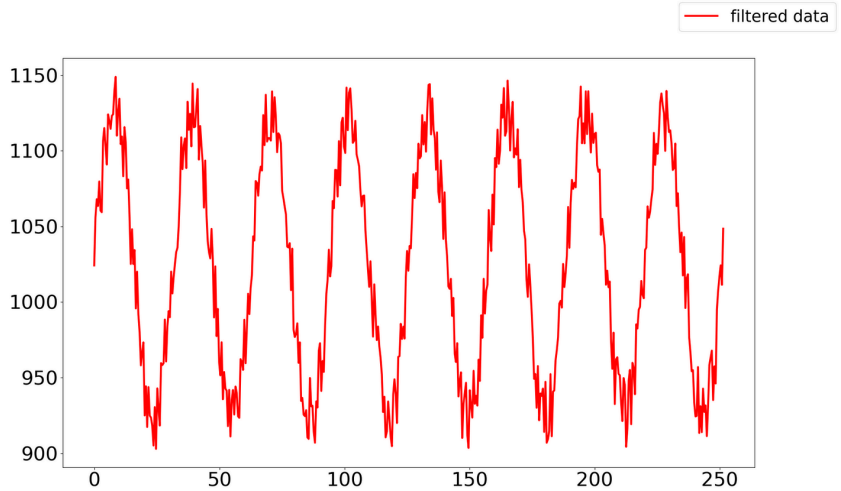


Temporal Filtering

Raw Signal



High pass Filtered



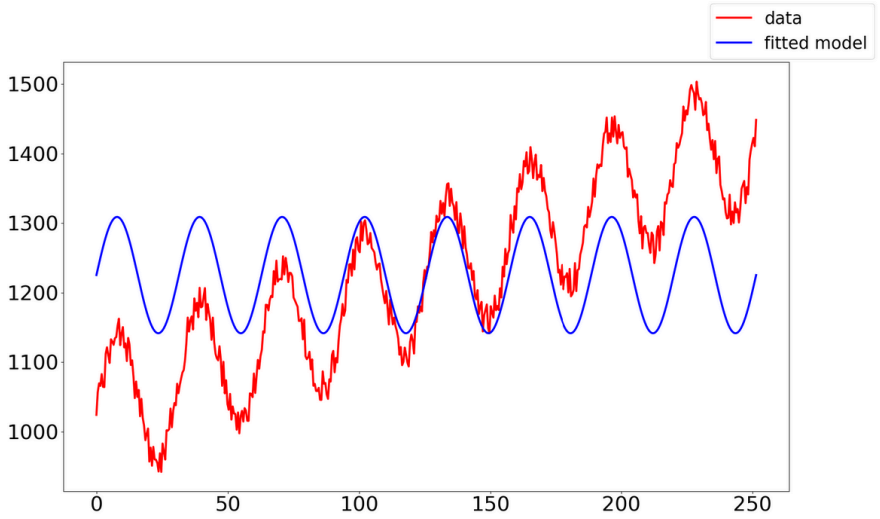
- Can remove low frequencies (*high pass*), high frequency (*low pass*) or both (*band pass*) - high pass is the usually the best option for FMRI
- **High pass**: removes low frequency signals, including linear trend
- Must choose cutoff frequency carefully (lower than frequencies of interest = longer period)

Effect of Temporal Filtering

Without temporal filtering

Poor model fit

Large residual error



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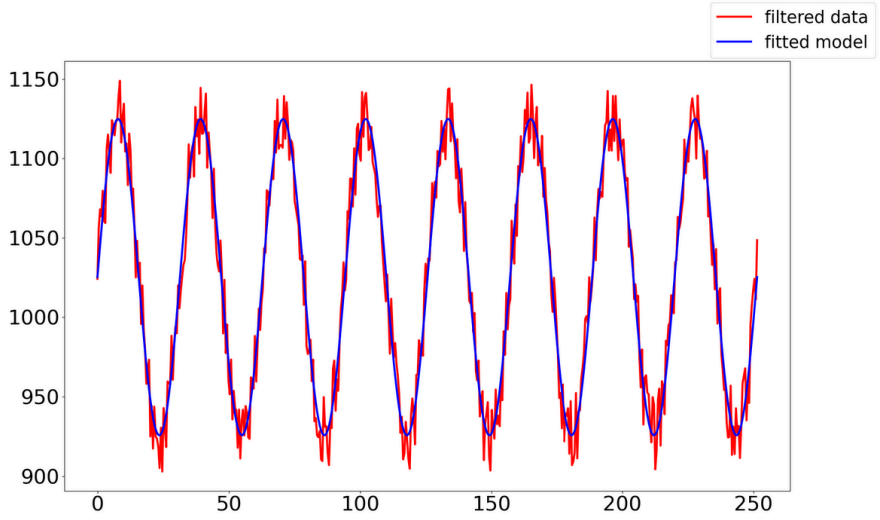
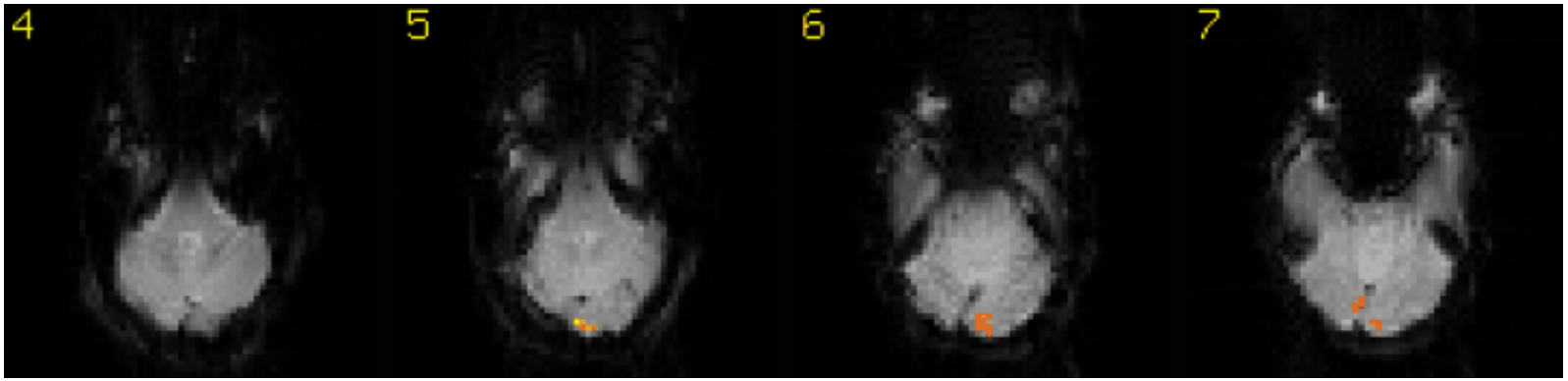
Good model fit

Small residual error

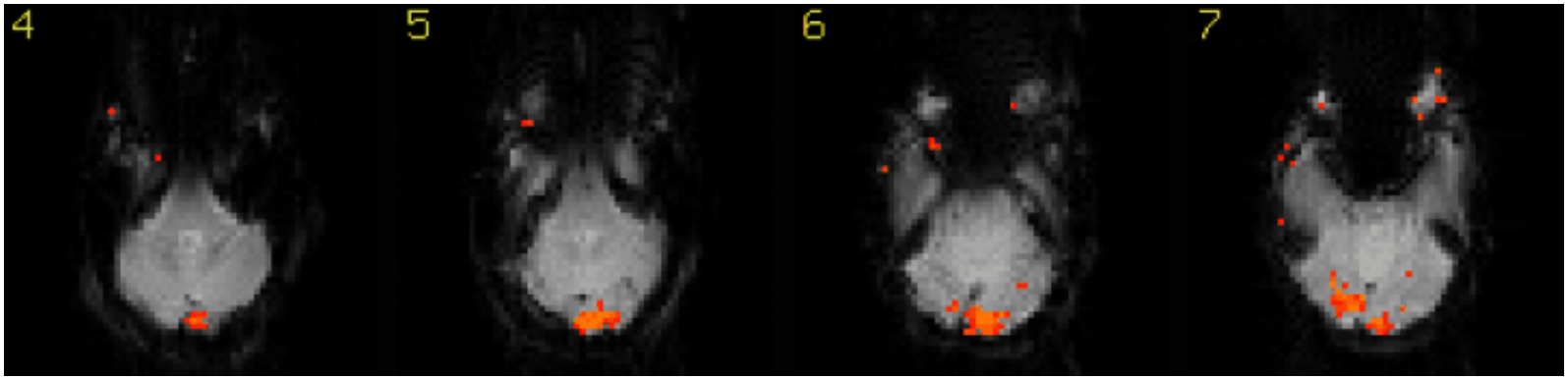


Effect of Temporal Filtering

No Temporal Filtering



High pass Temporal Filtering



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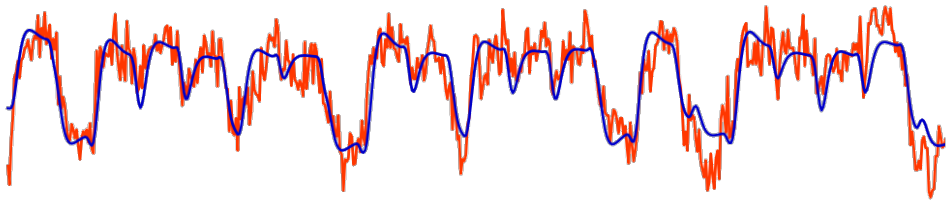
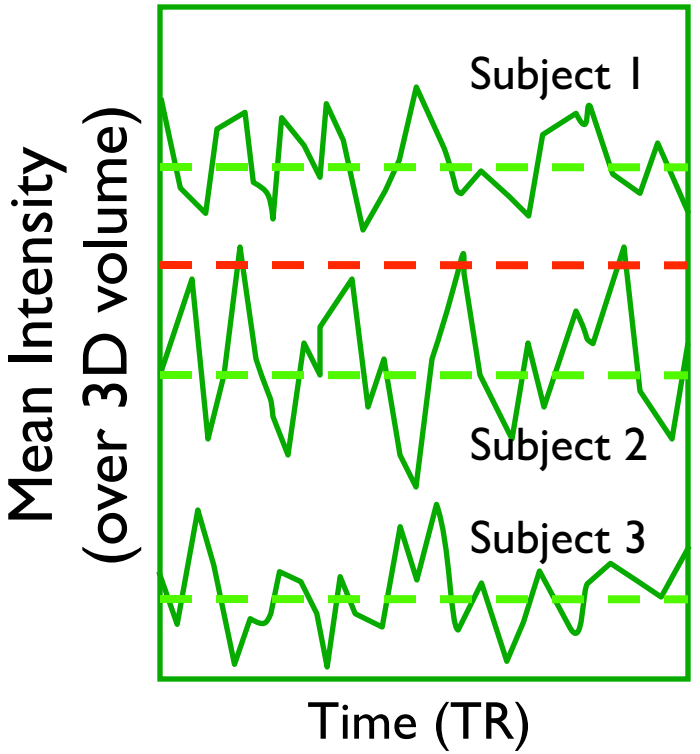


Global Intensity Normalisation

- Mean intensity of the whole dataset changes between subjects and sessions
  - due to various uninteresting factors (e.g. caffeine levels)
- Want the same mean signal level for each subject (taken over all voxels and all timepoints: i.e. 4D)
- Scale each 4D dataset by a *single value* to get the overall 4D mean (dotted line) to be the same
- Automatically done within FEAT



Summary

Reconstruction	Create image and remove gross artefacts
Motion Correction	Get consistent anatomical coordinates (always do this)
Slice Timing	Get consistent acquisition timing (use temporal derivative instead)
Spatial Smoothing	Improve SNR & validate GRF
Temporal Filtering	Highpass: Remove *slow* drifts
Intensity Normalisation	4D: Keeps overall signal mean constant across sessions

Summary

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Intensity Normalisation	4D: Keeps overall signal mean constant across sessions
Registration/unwarping	Align data across sessions, subjects, modalities/EPI distortion correction

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