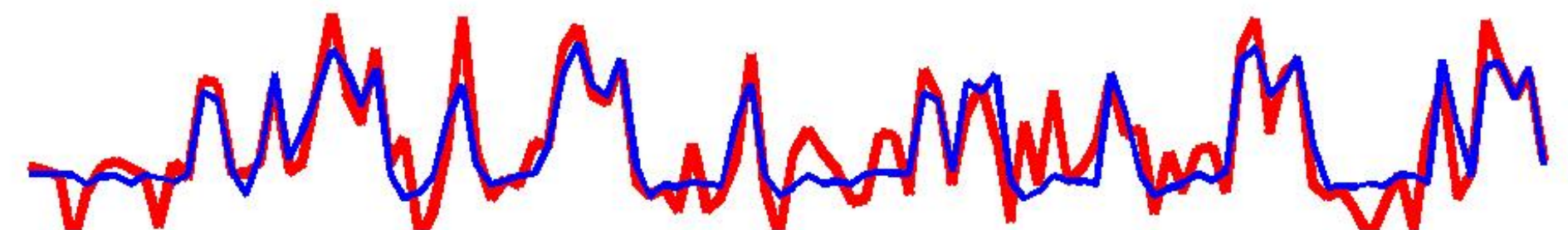
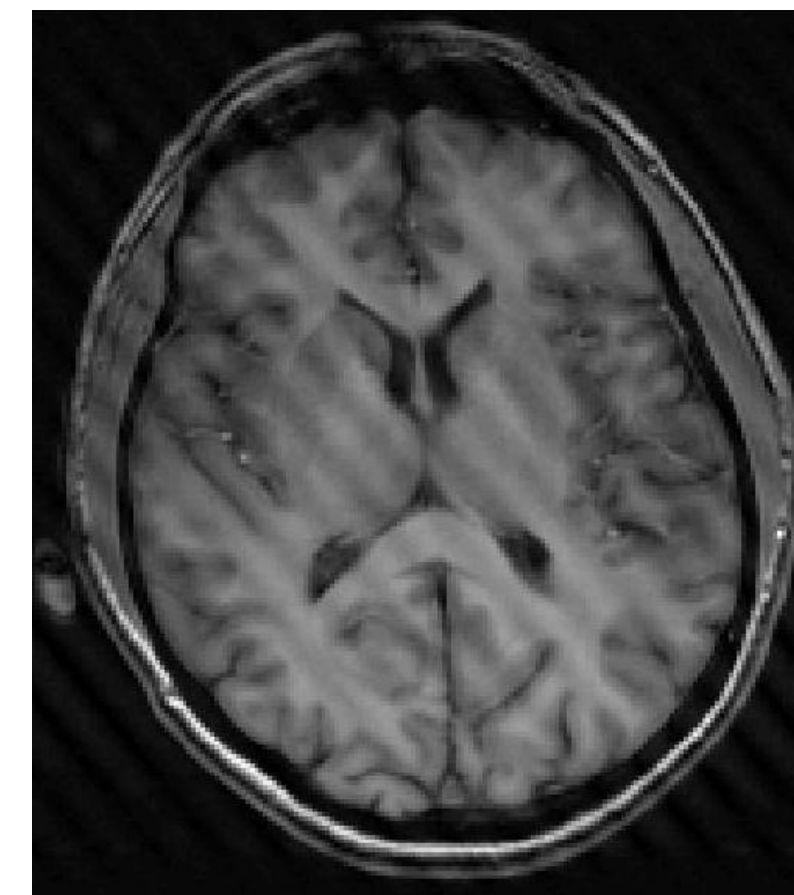


# FMRI single subject analysis

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





# Generic study blueprint

1. Data acquisition

2. Data preprocessing

3. Single-subject analysis

4. Group-level analysis

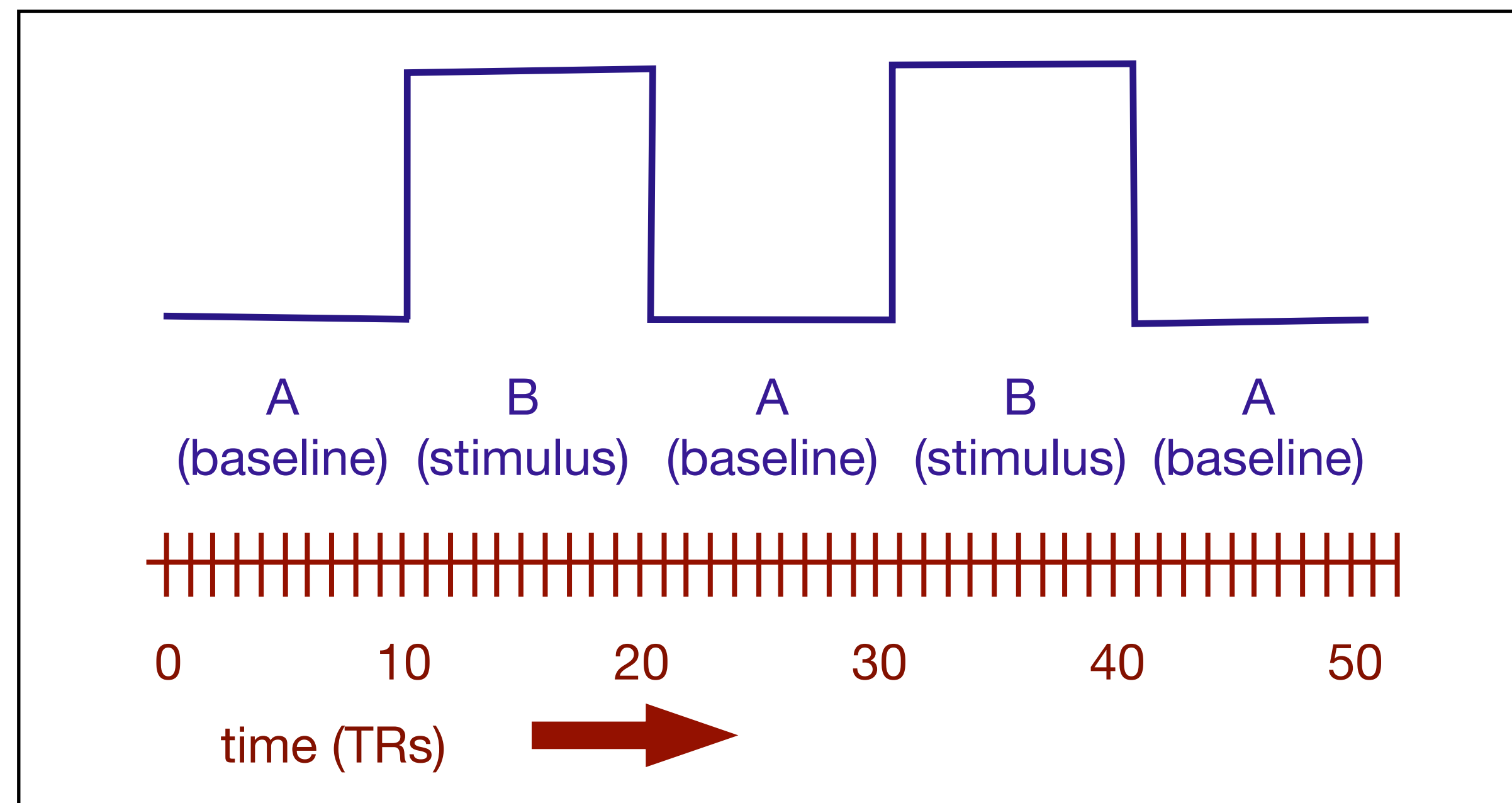
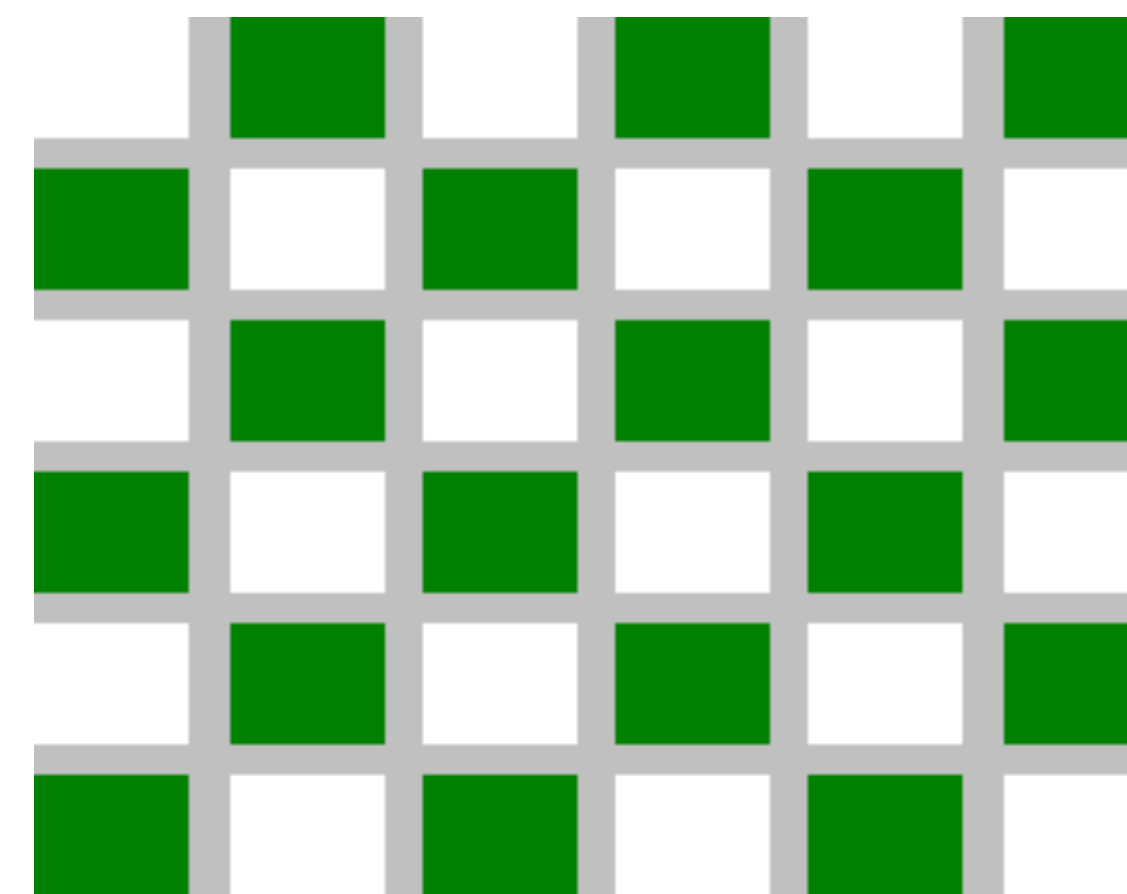
5. Statistical inference

**This morning** ←

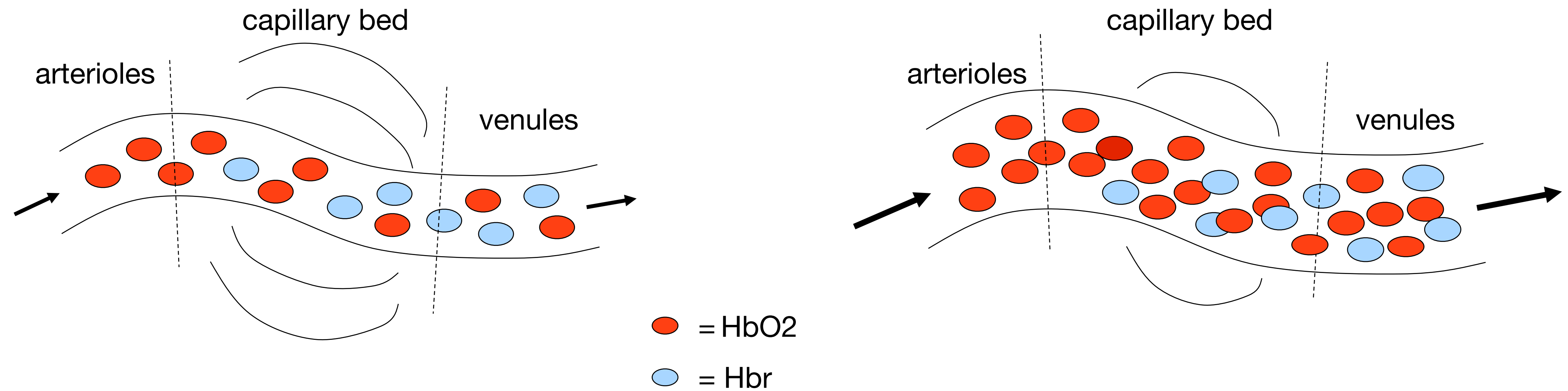
→ **This afternoon**

# Functional MRI experiments

- Measuring change > need baseline condition
- Simple example design
  - Include a stimulus and baseline
  - Keep stimulus “intensity” the same
  - Keep block length the same
  - Many repetitions (ABABAB)



# The Hemodynamic Response



Activation leads to:

↑  
CBF

↑  
CBV

↑  
CMRO<sub>2</sub>

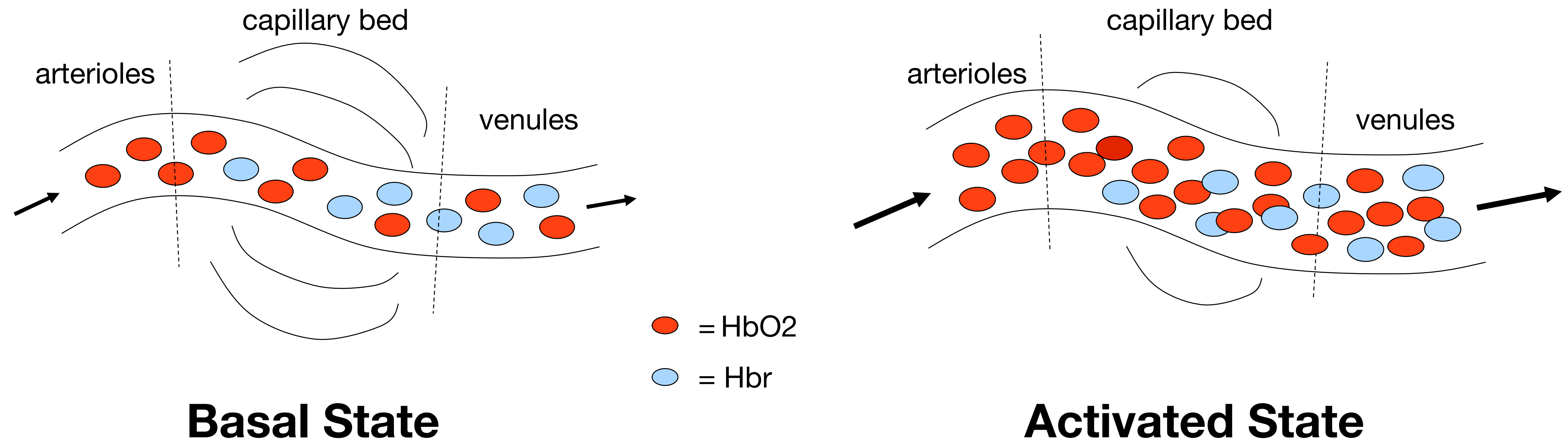
↓  
[Hbr]

↓  
Field  
change

↑  
MRI  
signal



# The Hemodynamic Response

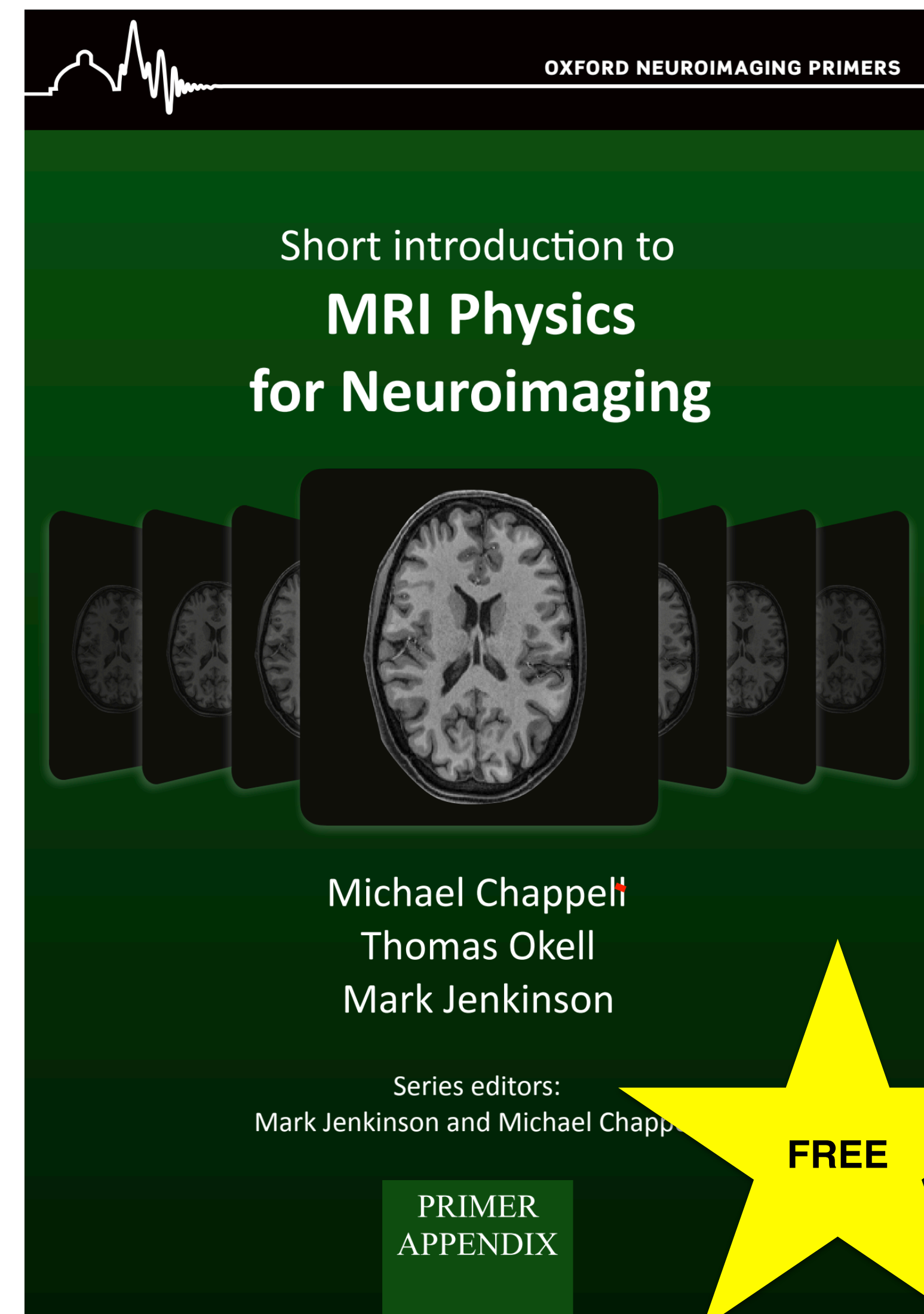
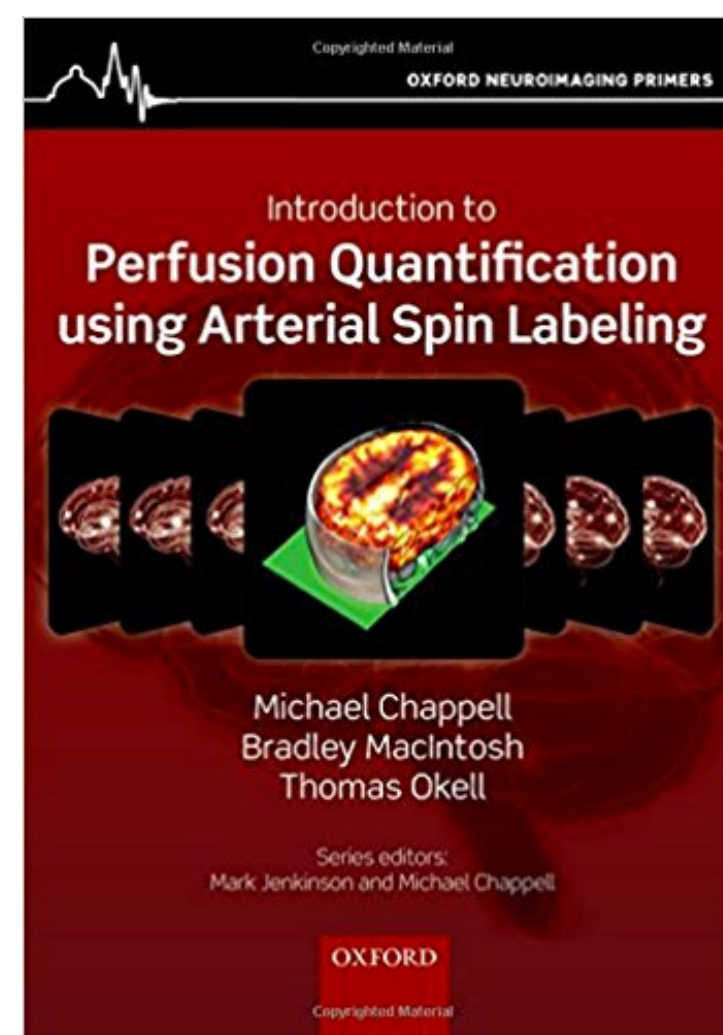
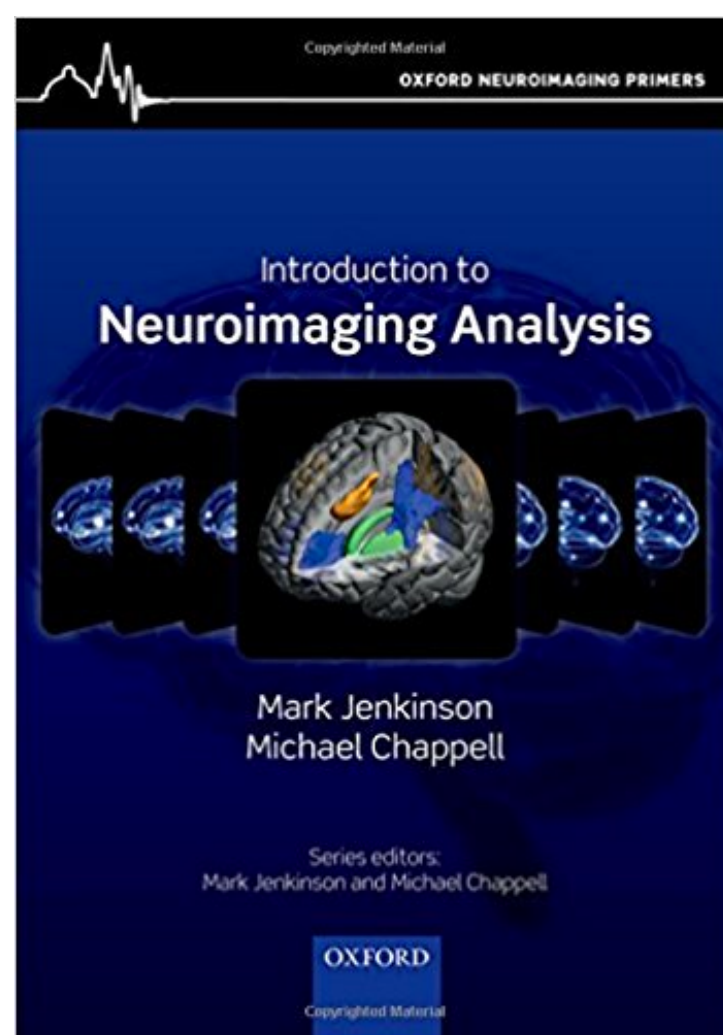


Field changes (perturbations) → de-phasing →  $T_2^*$  effect

BOLD MRI =  $T_2^*$ -weighted

# The free online appendix

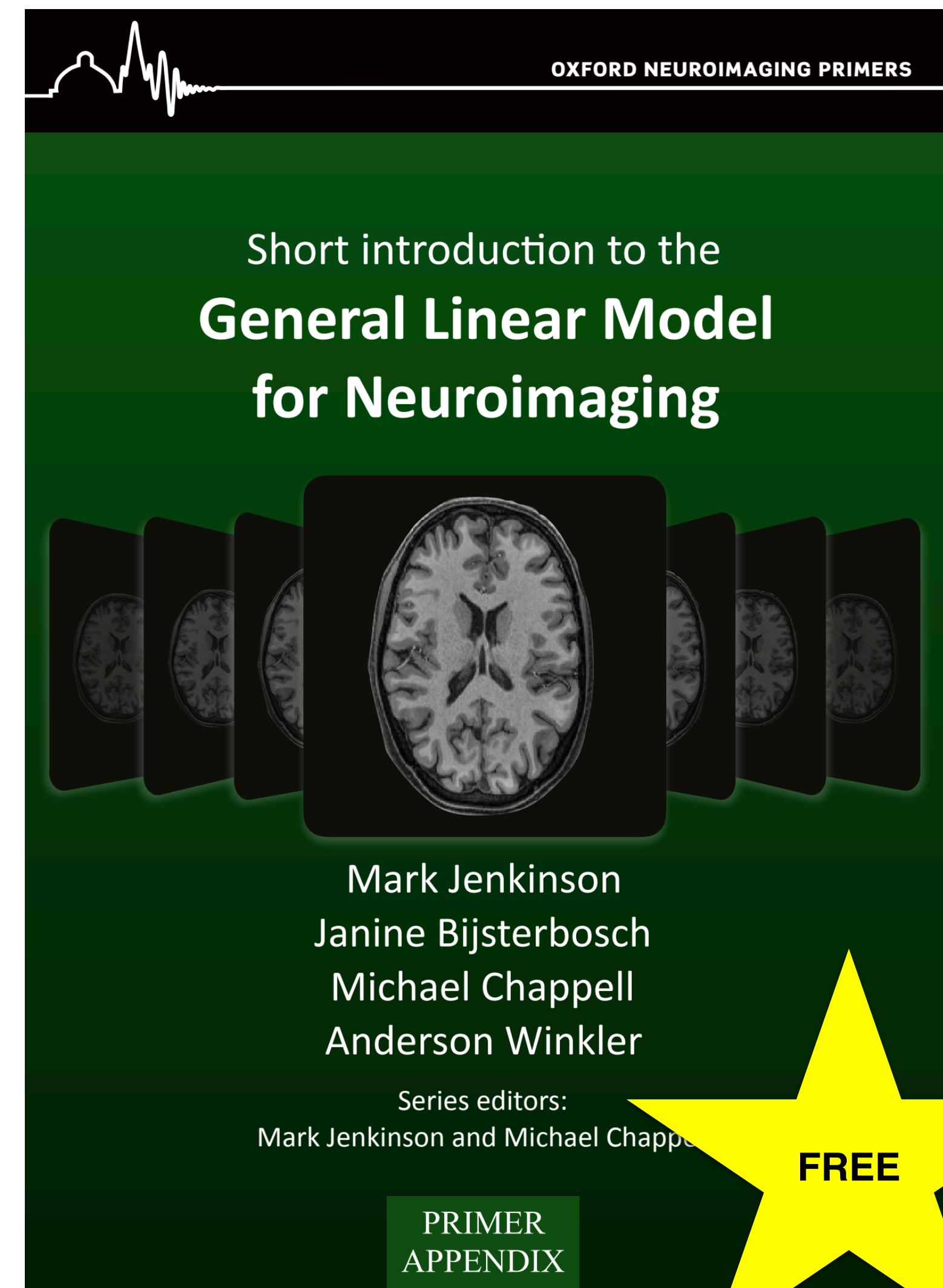
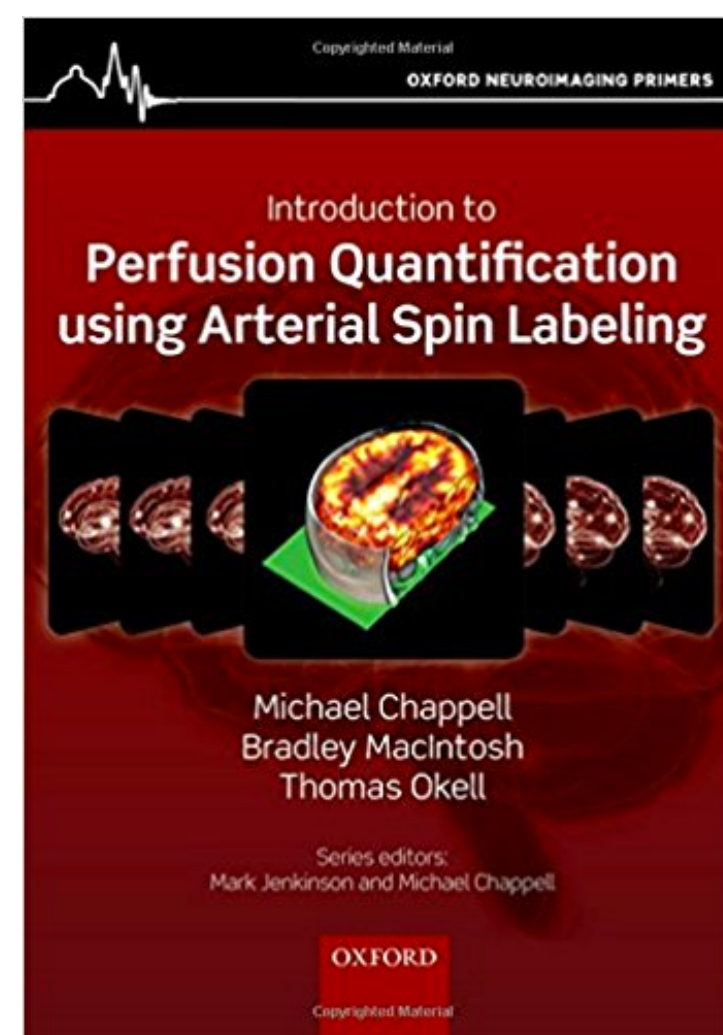
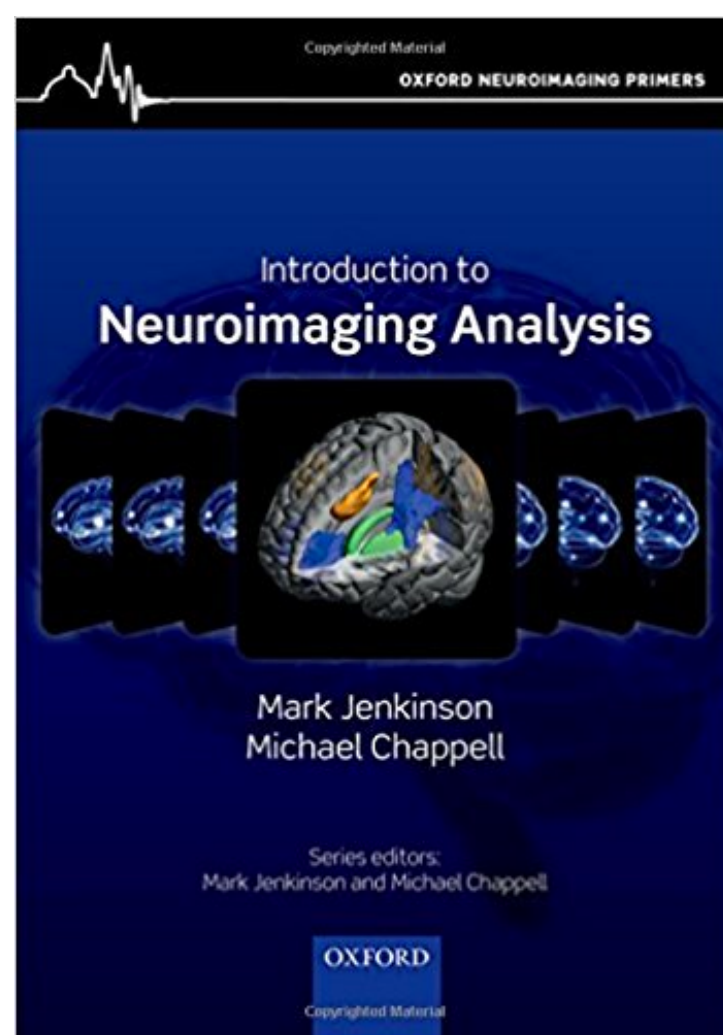
- Part of a series of Oxford Neuroimaging Primers
- [https://www.fmrib.ox.ac.uk/primers/appendices/mri\\_physics.pdf](https://www.fmrib.ox.ac.uk/primers/appendices/mri_physics.pdf)





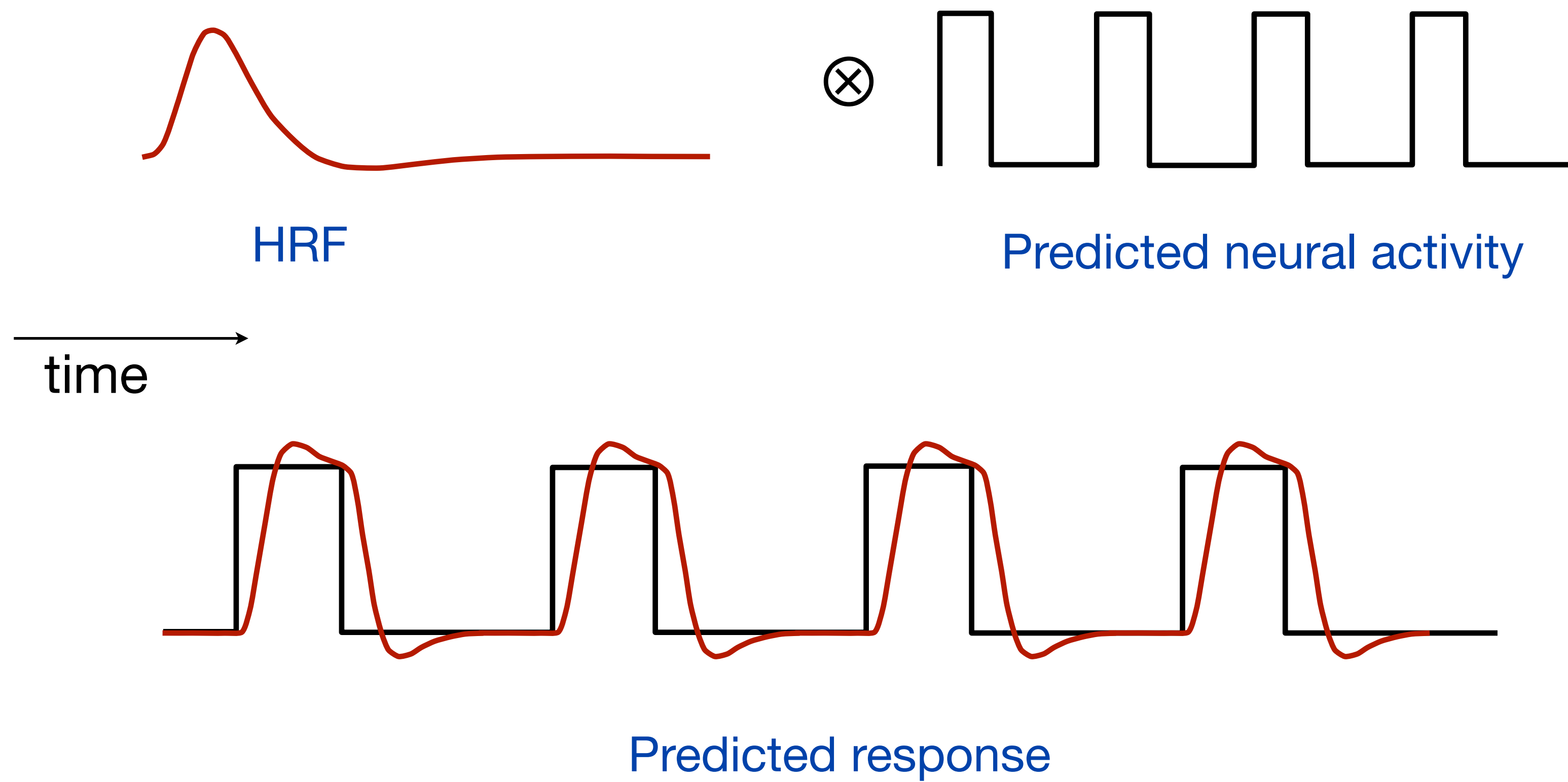
# The free online appendix

- Part of a series of Oxford Neuroimaging Primers
- <https://www.fmrib.ox.ac.uk/primers/appendices/glm.pdf>



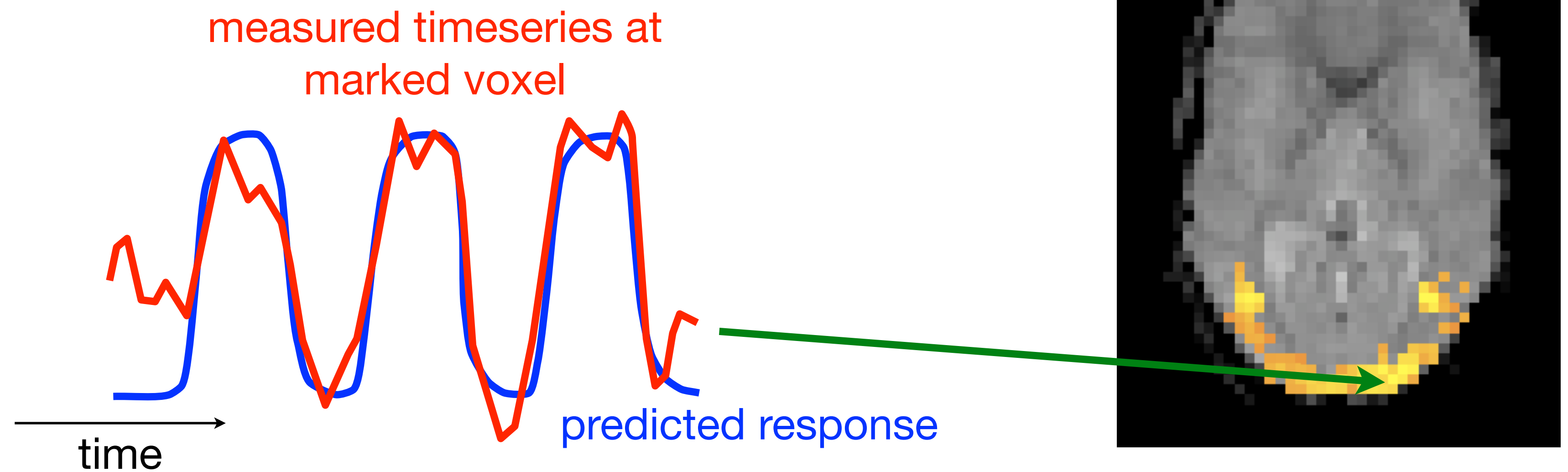
# Model

Convolution



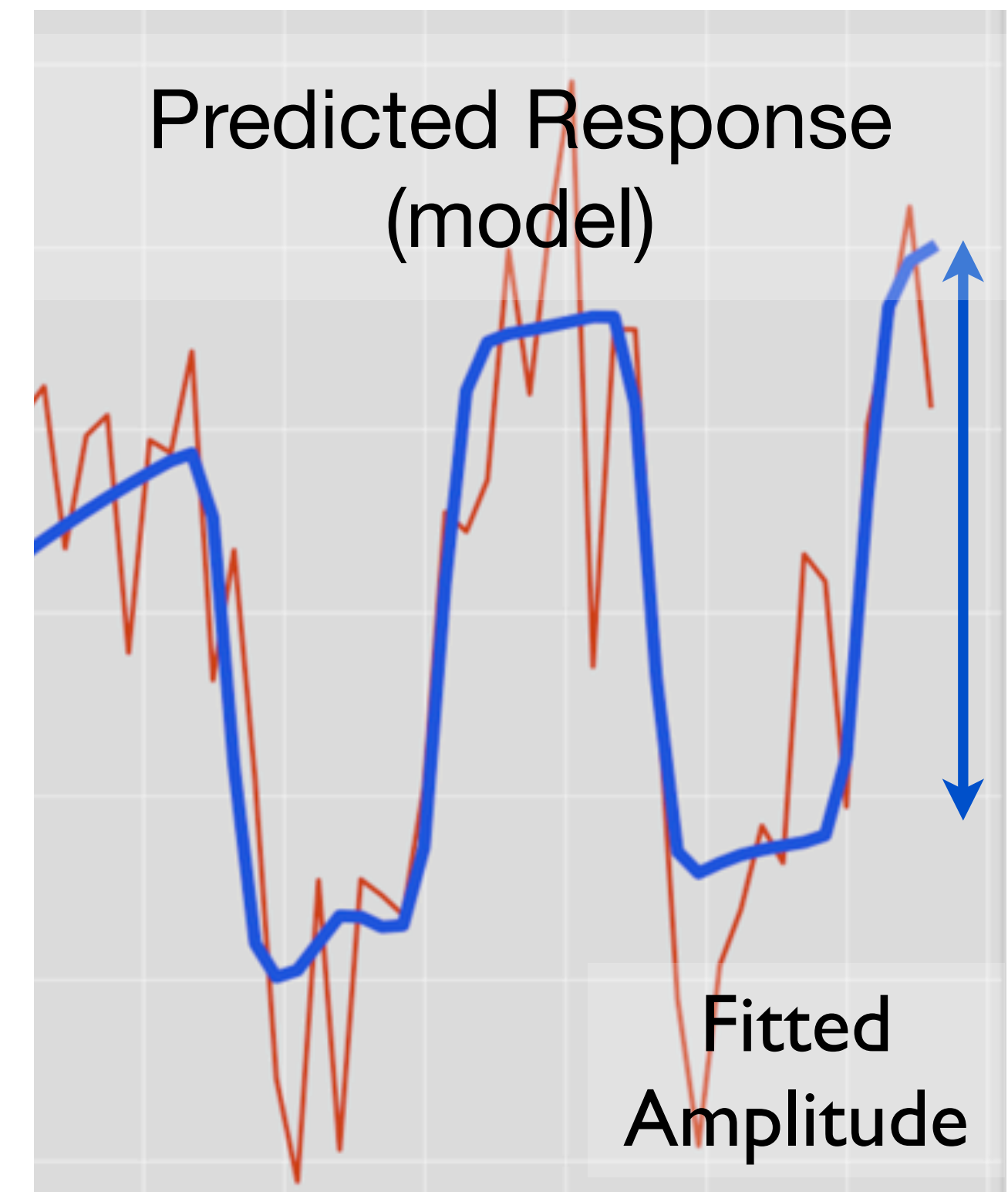
# Fit model to data

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



# Standard GLM statistics

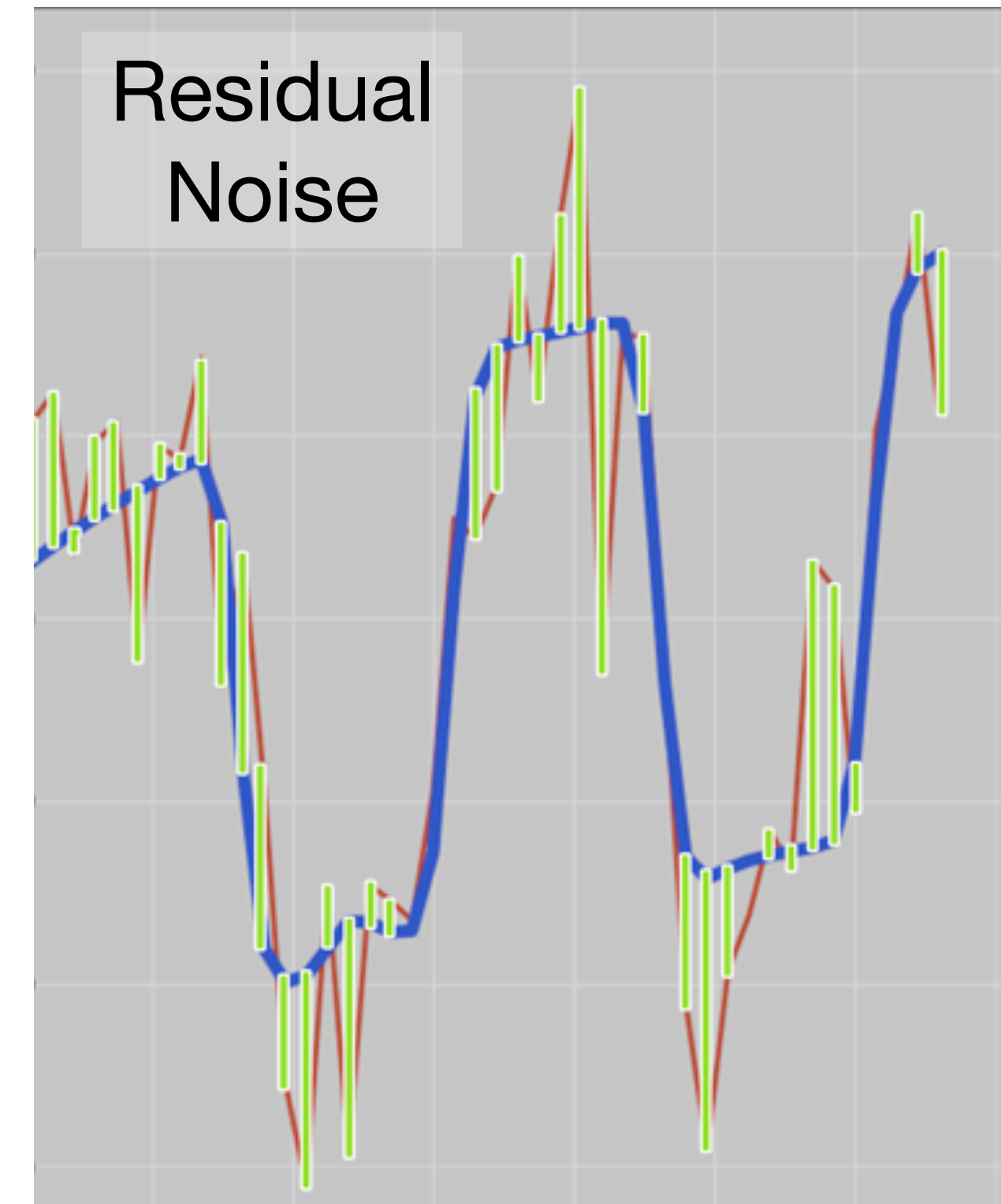
- Fit model to each voxel separately





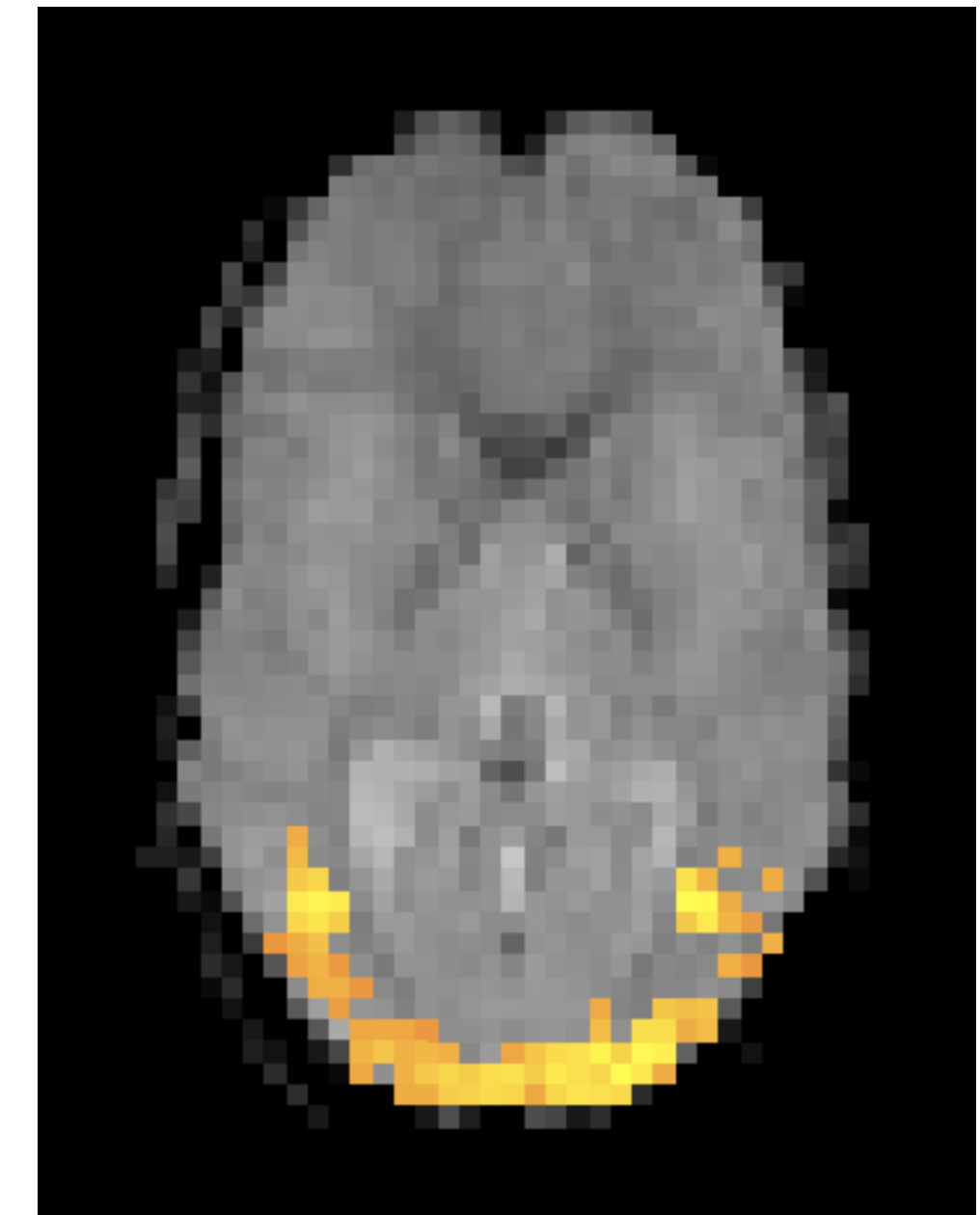
# Standard GLM statistics

- Fit model to each voxel separately
- Measure residual noise variance



# Standard GLM statistics

- Fit model to each voxel separately
- Measure residual noise variance
- Voxel t-statistic = model fit / noise amplitude
- Threshold t-statistics and display map

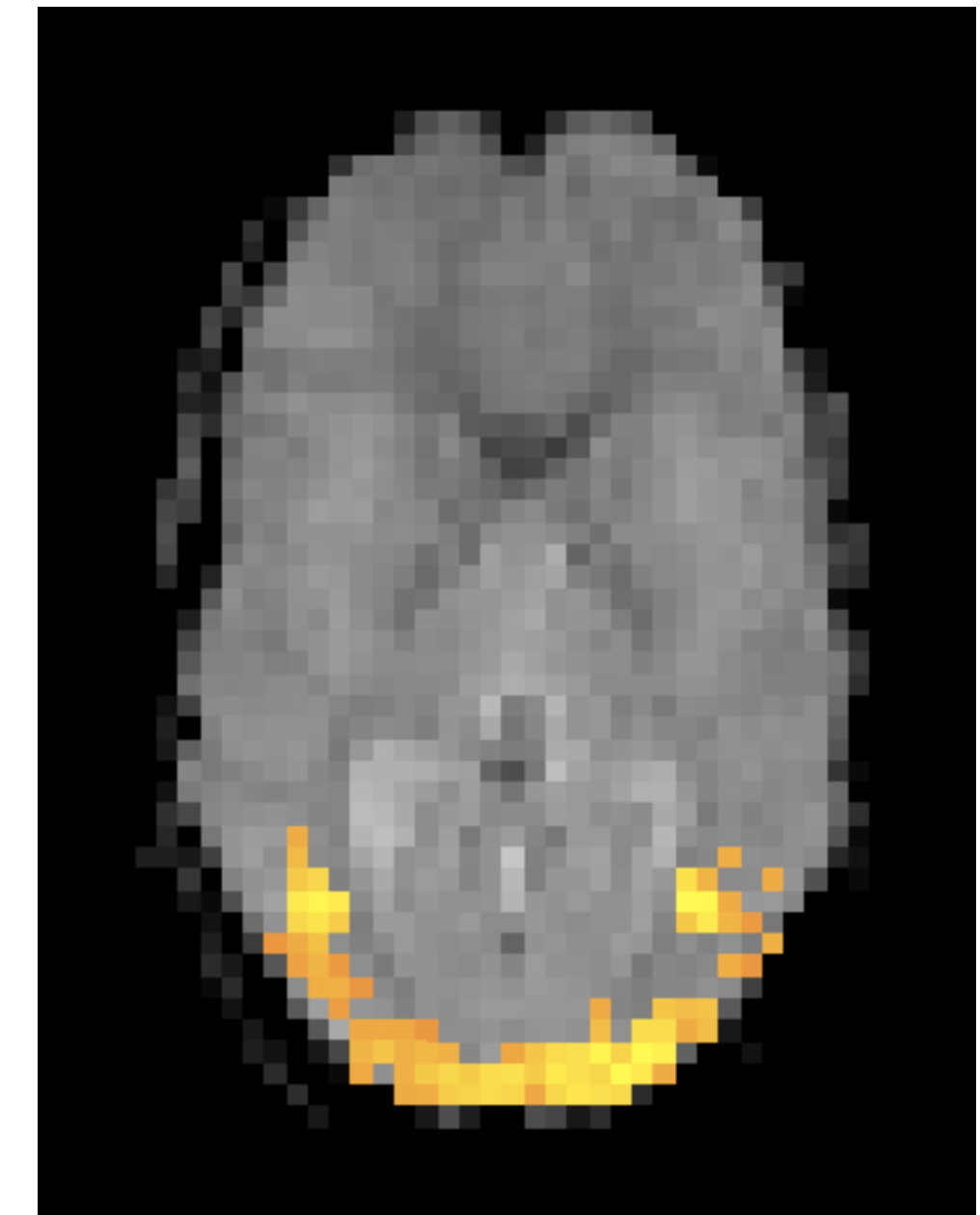


# Standard GLM statistics

- Fit model to each voxel separately
- Measure residual noise variance
- Voxel t-statistic = model fit / noise amplitude
- Threshold t-statistics and display map

BUT artifacts can affect model fit and noise amplitude

NEED preprocessing to reduce artifacts

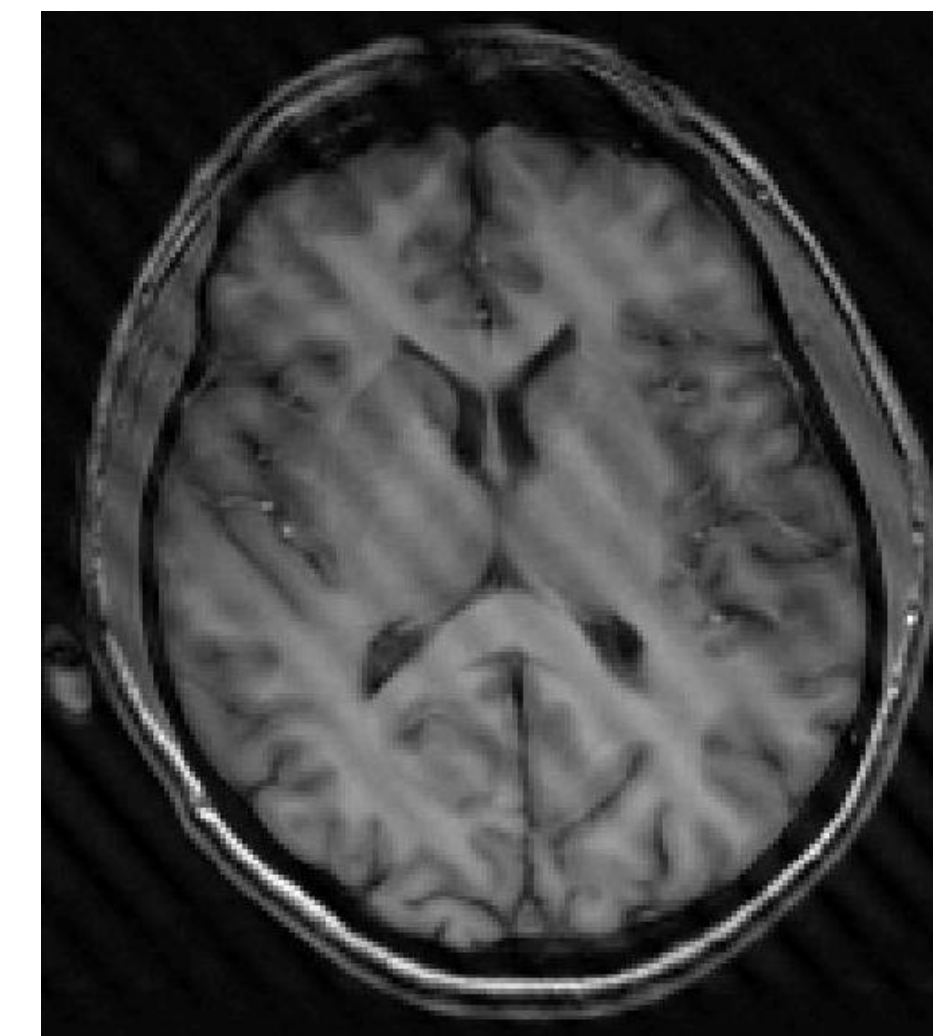
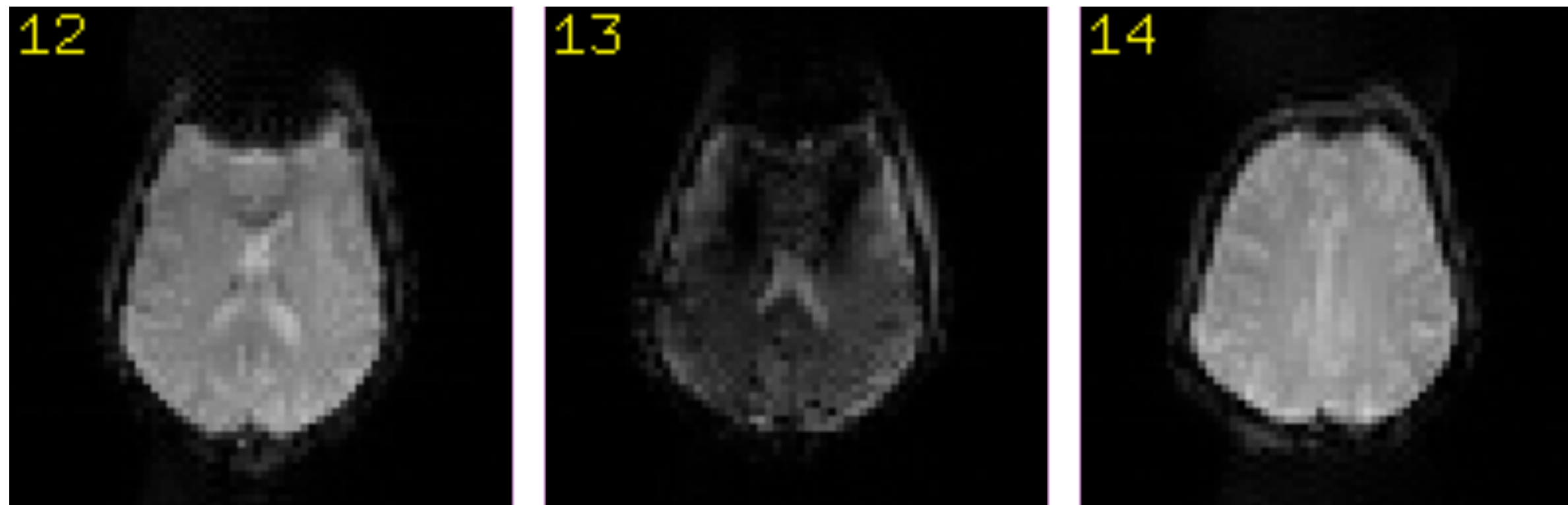




# Preprocessing

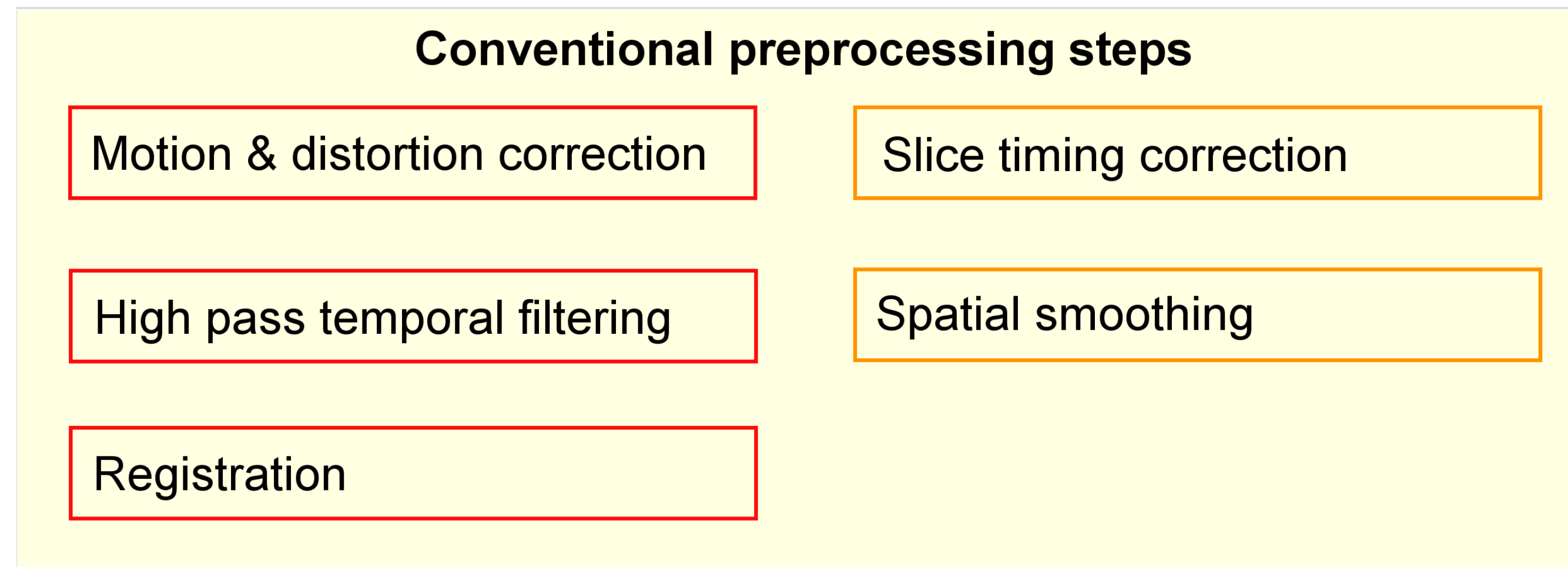
# Image reconstruction

- Convert k-space data to images using reconstruction algorithm
- Problematic data due to e.g., slice timing errors, RF spikes or RF interference





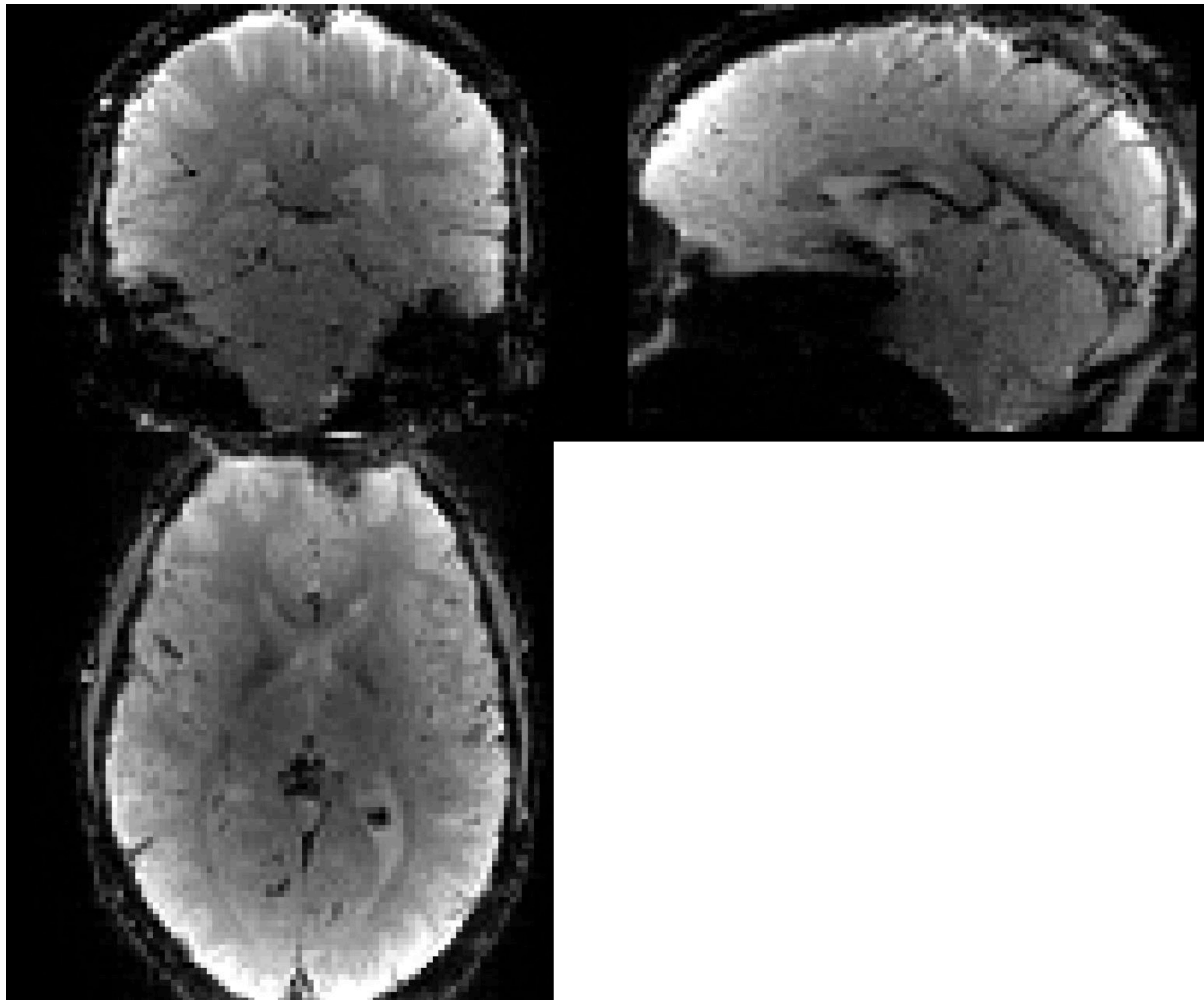
# Preprocessing overview



These same concepts are applied across all imaging modalities (task, rest, diffusion, ASL etc)



# Motion correction



- Biggest source of noise
- Correction is always necessary
- Linear correction may leave motion effects in data (e.g. partial volume)
- Additional motion correction methods will be discussed later in the course

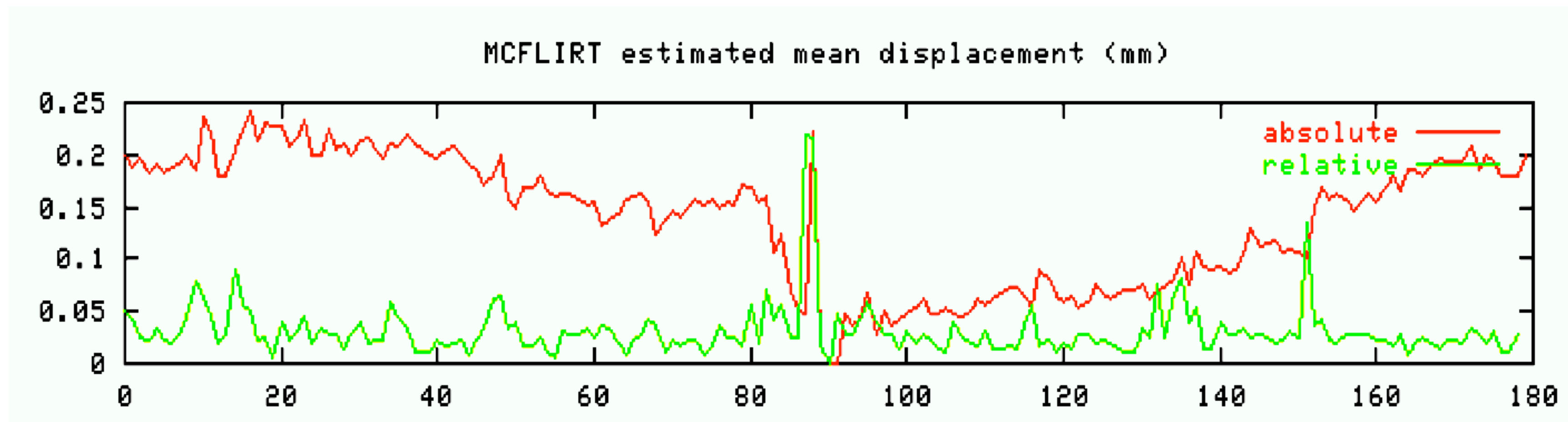
# Motion correction

- Uses rigid body registration
- Select reference timepoint = target
- Register each fMRI volume to target separately
- Use rigid body (6 DOF)



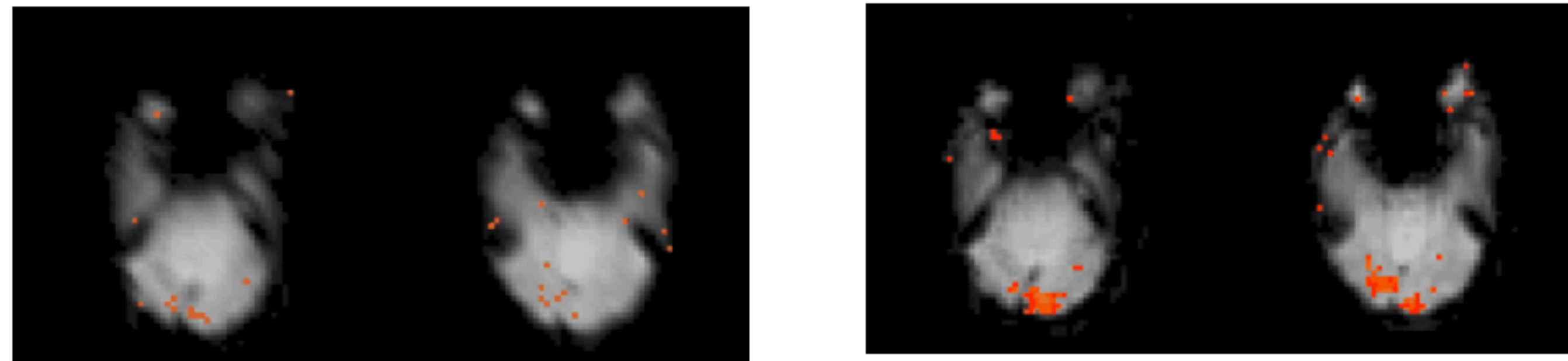
# Motion correction

- Results in 6 summary measures (rotations and translations)
- **Absolute** = timepoint to reference (shows jumps & drifts)
- **Relative** = timepoint to next timepoints (shows jumps)
- Large jumps are more important than slow drifts (especially in **relative** motion plot)

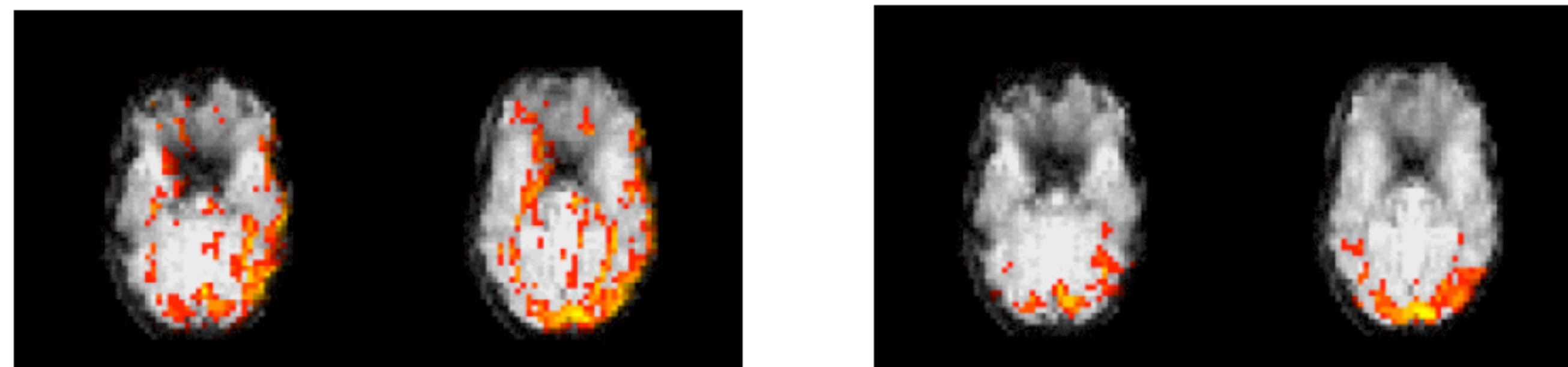


# Effect of motion correction

Uncorrelated Motion



Stimulus Correlated Motion



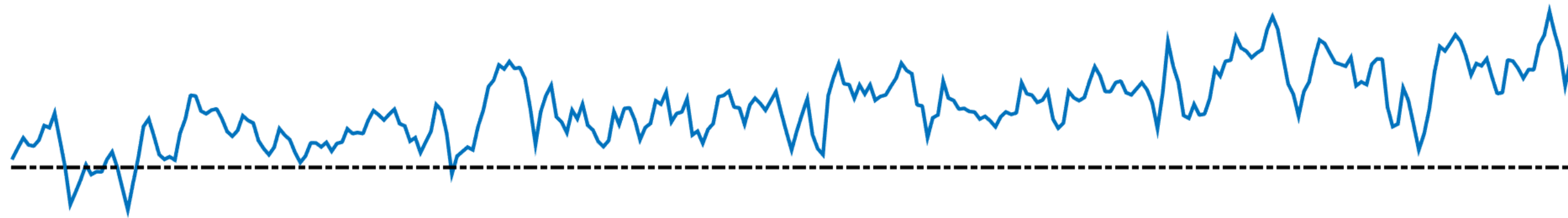
Without MC

With MC

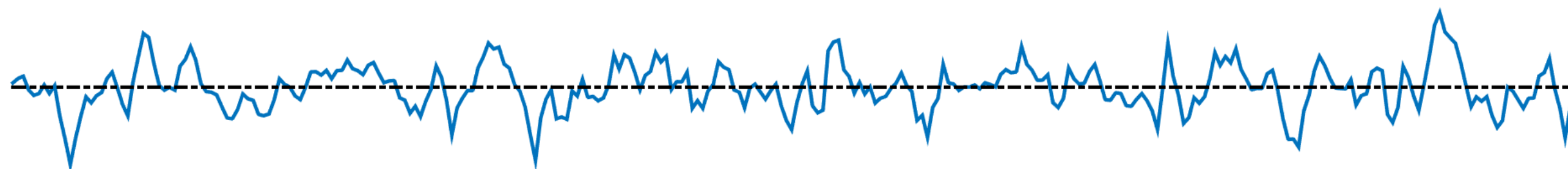


# Temporal filtering

Original BOLD data

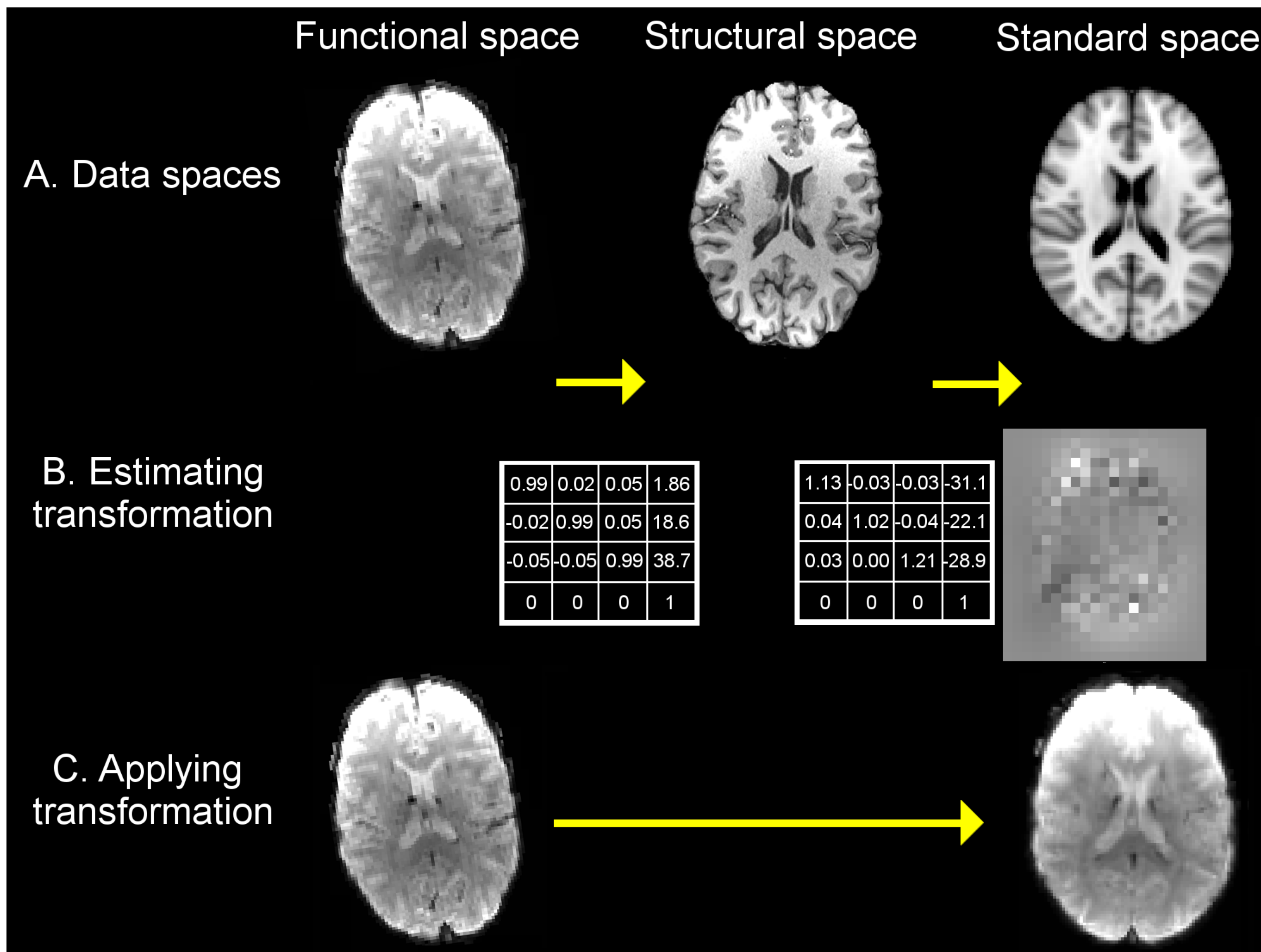


Highpass filtered data (>0.01 Hz)



- Correct for gradual drift in the data
- High-pass filtering recommended
- Need to choose cutoff frequency carefully
- Lower frequency (i.e. longer period) than task frequencies of interest
- Should be >90 seconds for autocorrelation estimation

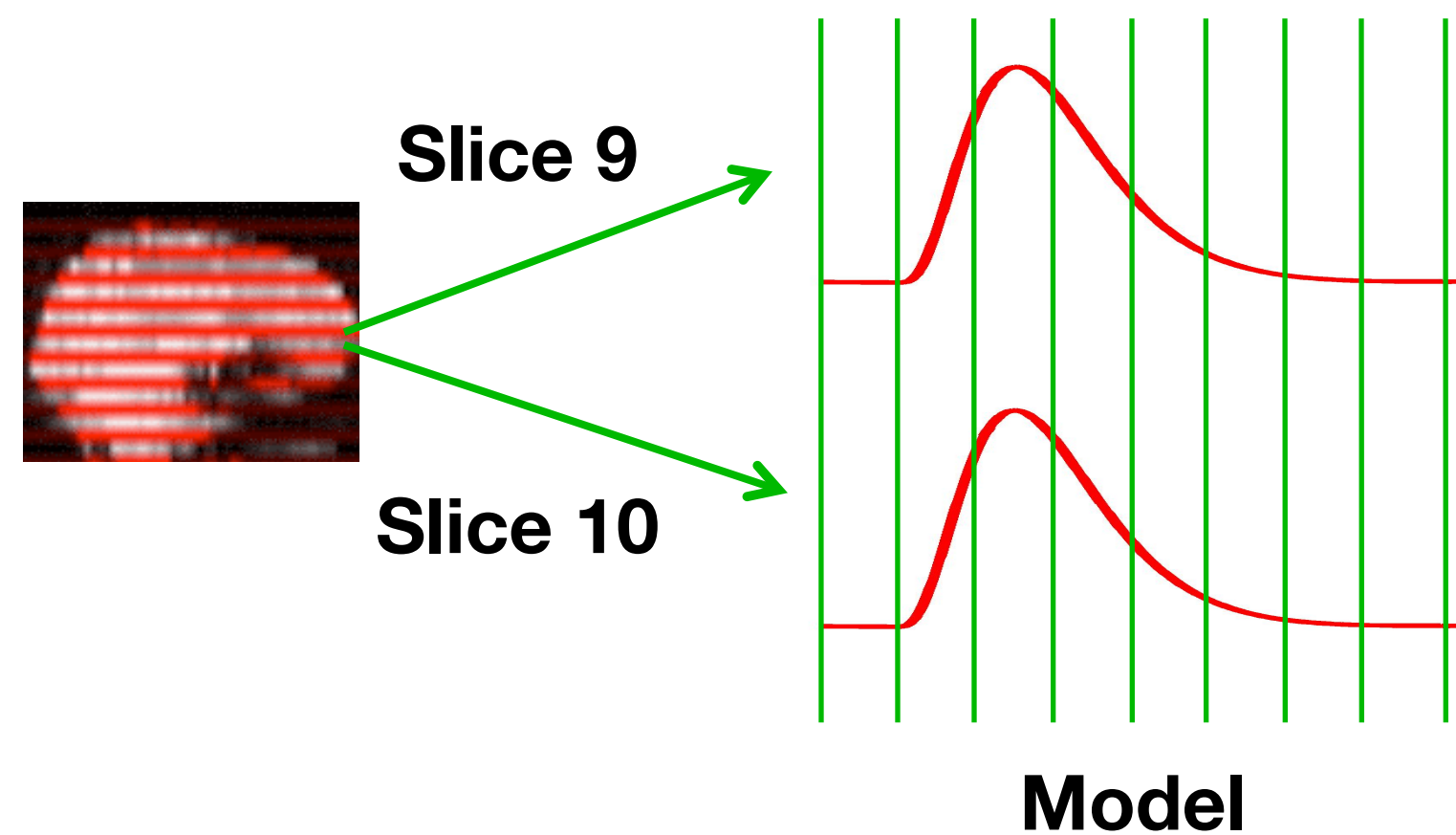
# Registration



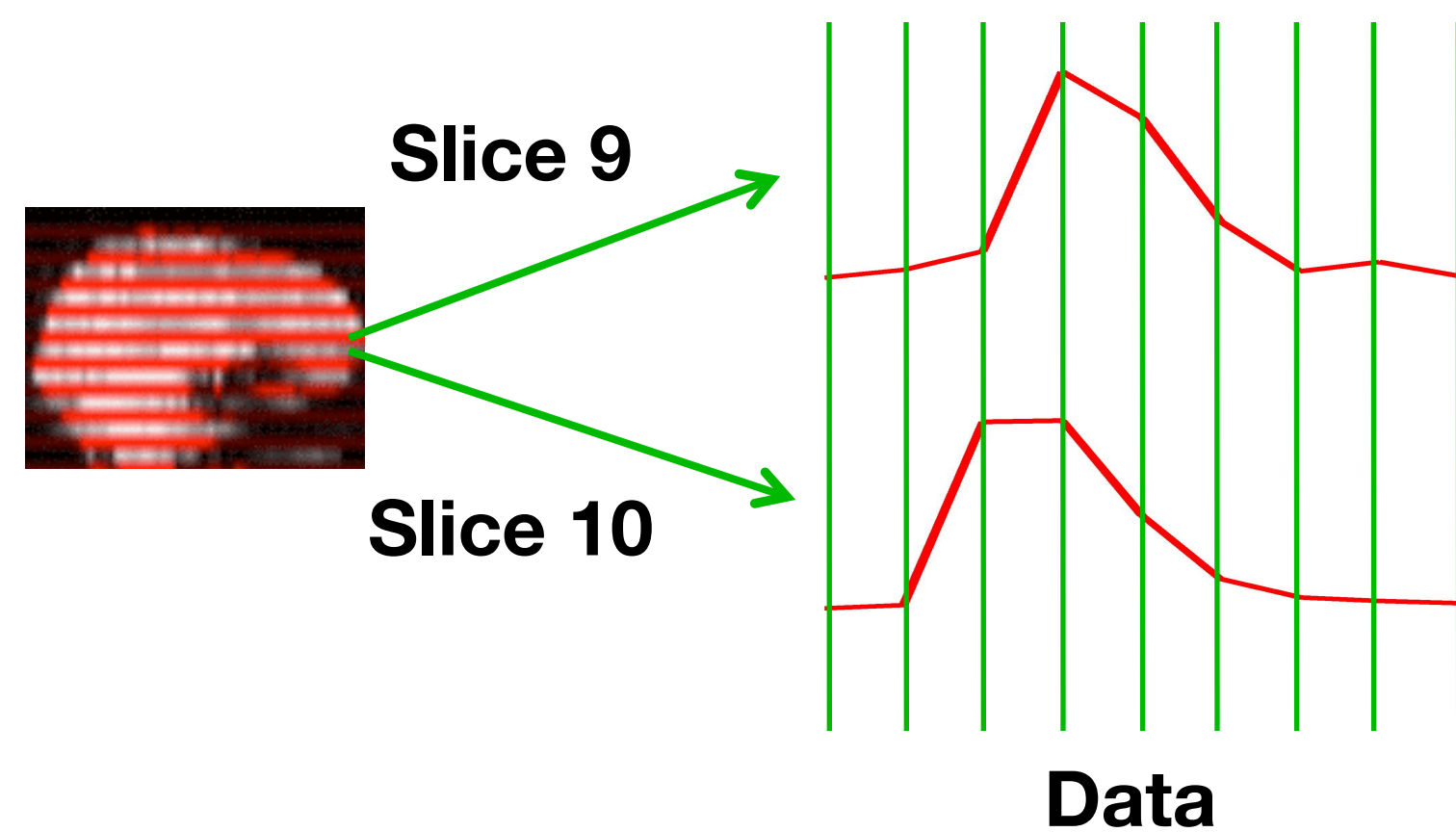
- Needed to compare different subjects
- Needed to compare pre vs post (or longitudinal data) of same subject
- Needed as a universal coordinate system (even in single subject)



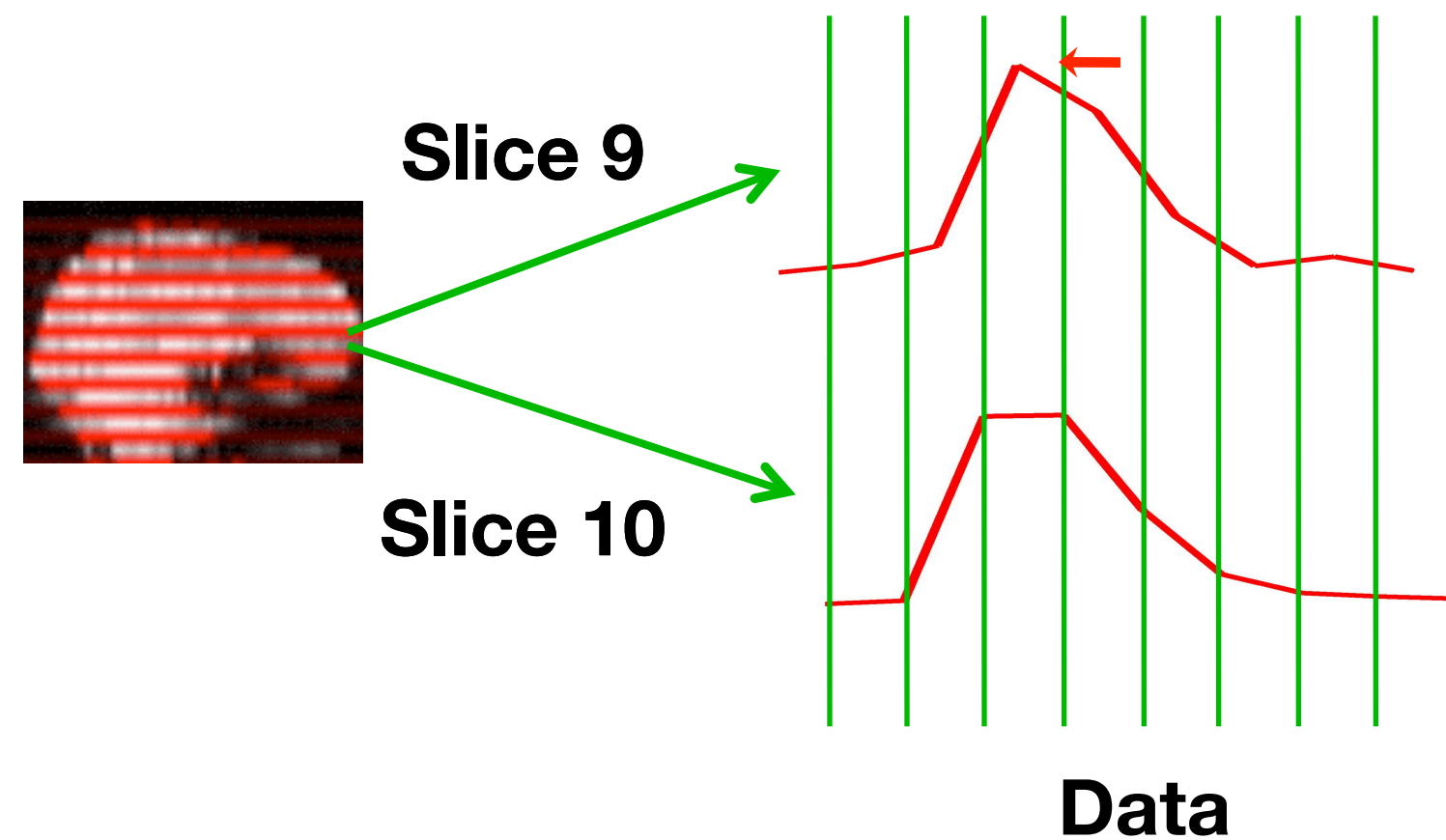
# Slice timing correction



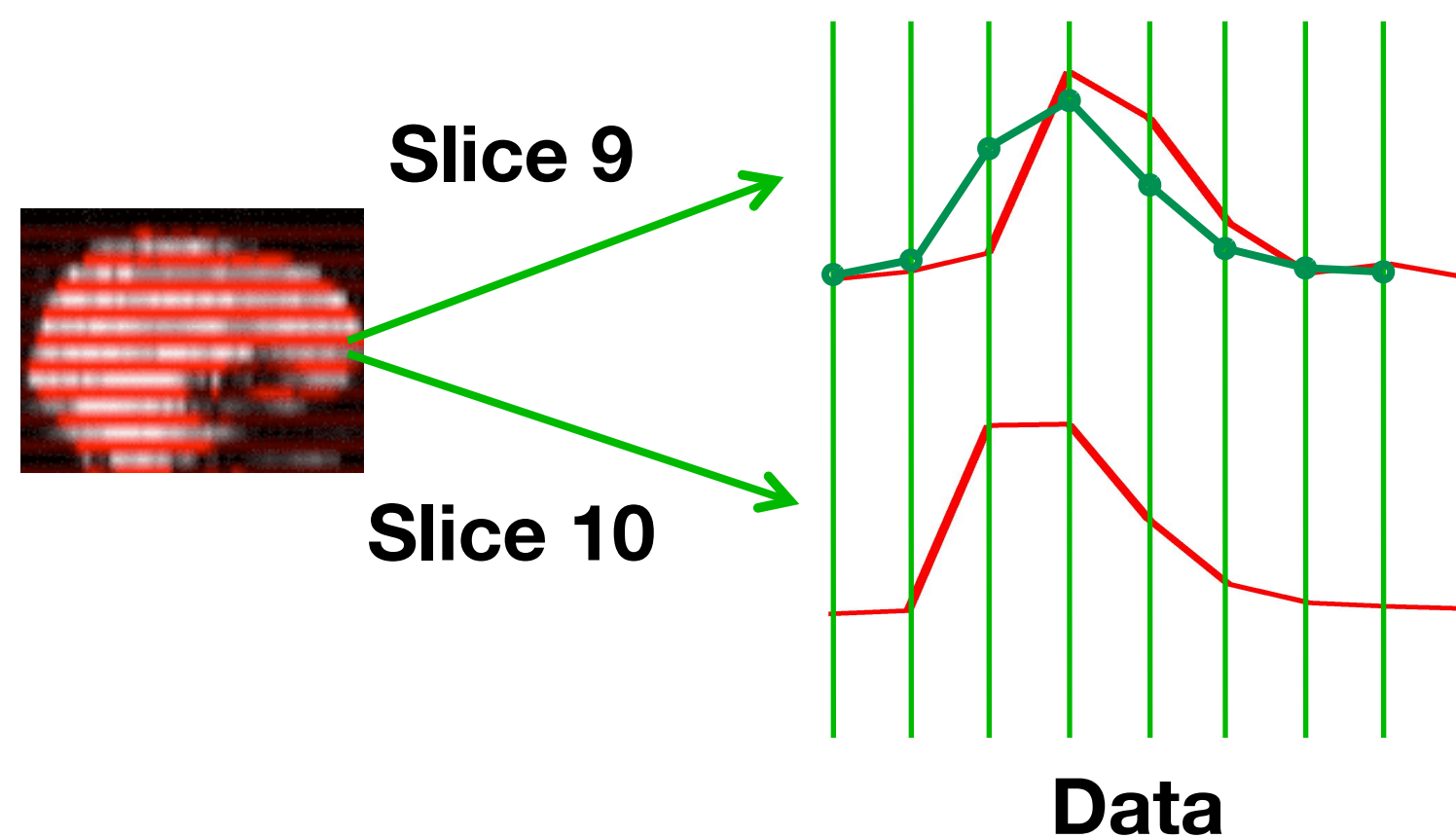
- Need to adjust for differences in acquisition time between different slices



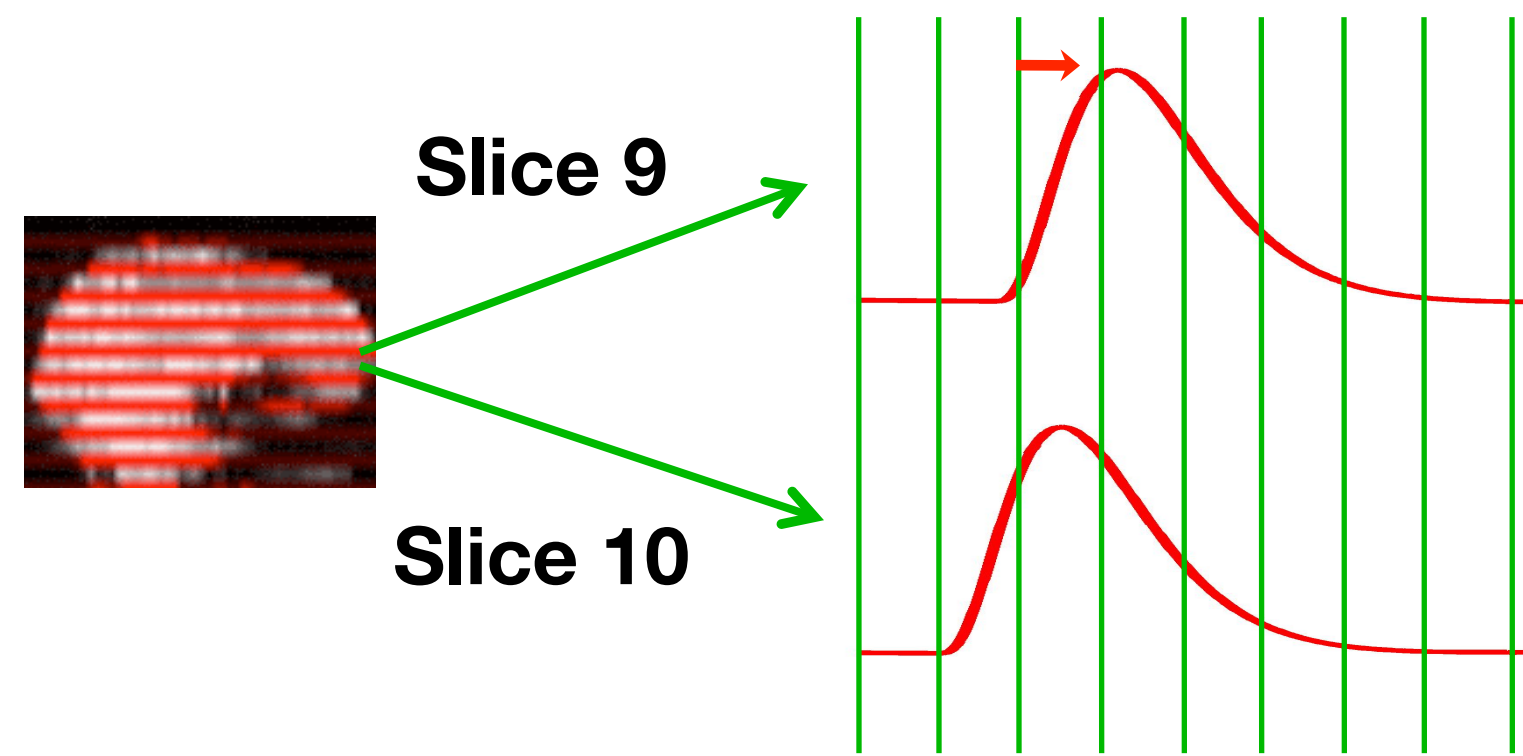
# Slice timing correction



- Need to adjust for differences in acquisition time between different slices
- Can do with slice timing correction (i.e. shifting the data), but interpolation leads to degraded data



# Slice timing correction



Model

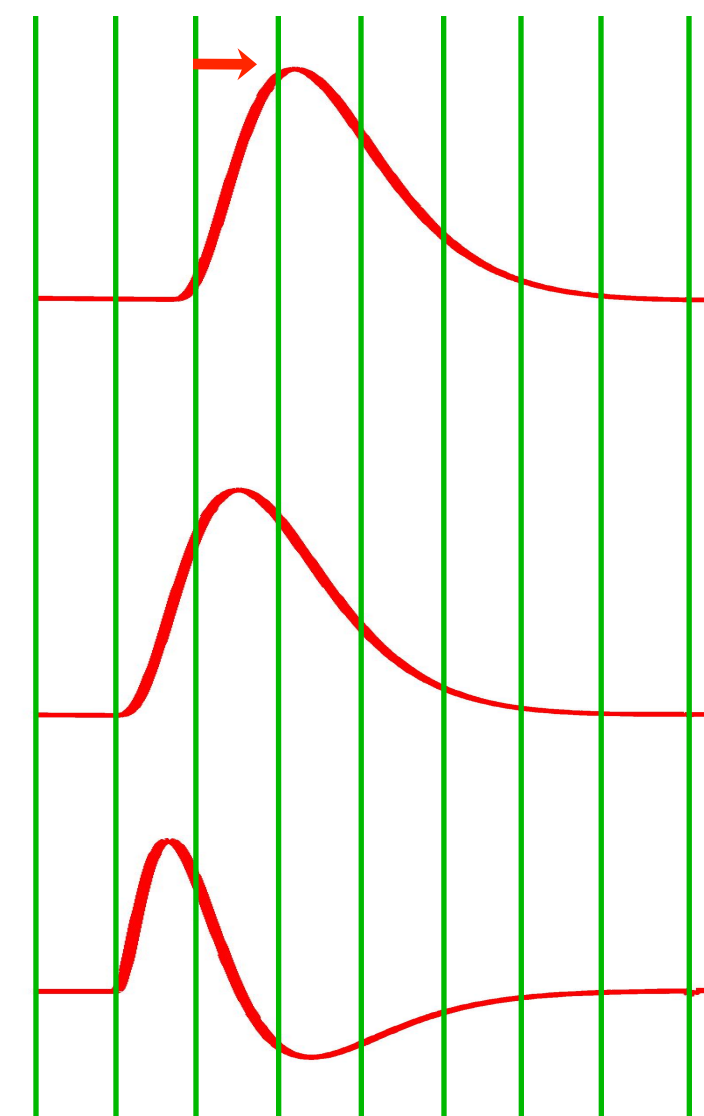
Shifted model

=

Original model

-

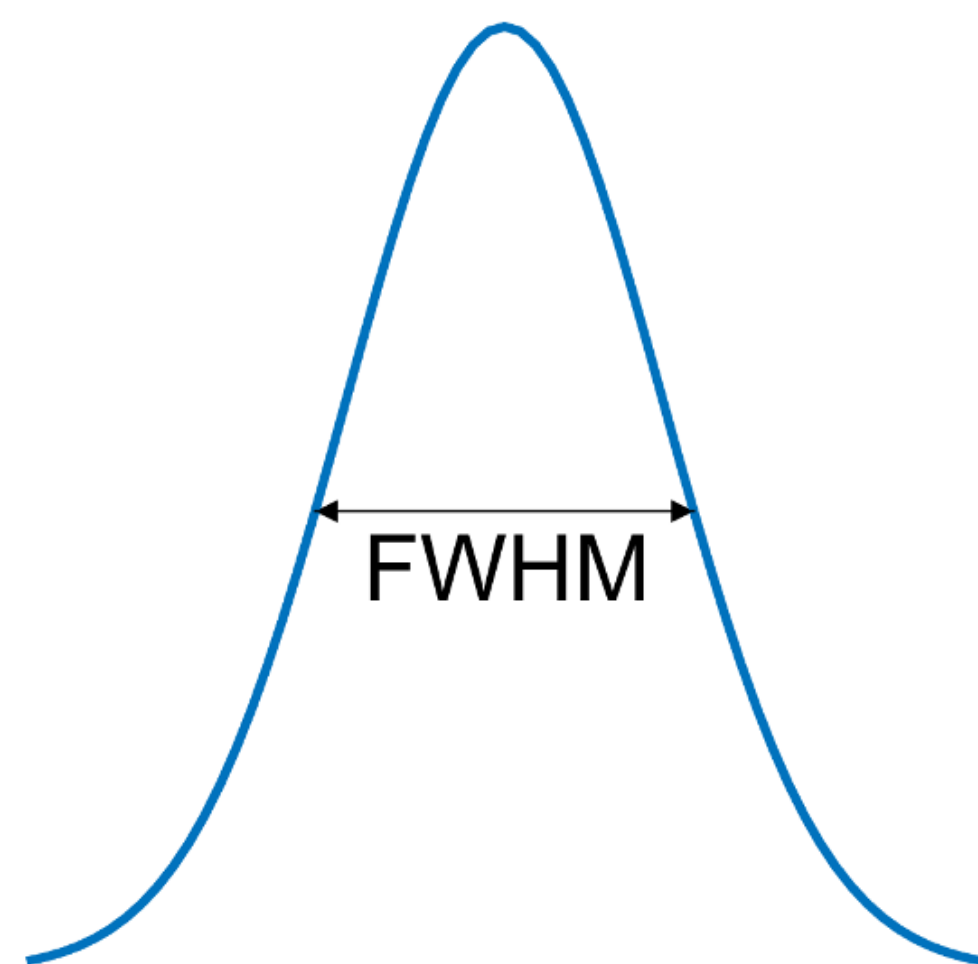
Temporal derivative



- Need to adjust for differences in acquisition time between different slices
- Can do with slice timing correction (i.e. shifting the data), but interpolation leads to degraded data
- Better to shift the model, which we can do by including the temporal derivatives of EVs

Based on  
Taylor approximation:  
 $m(t+a) = m(t) + a.m'(t)$

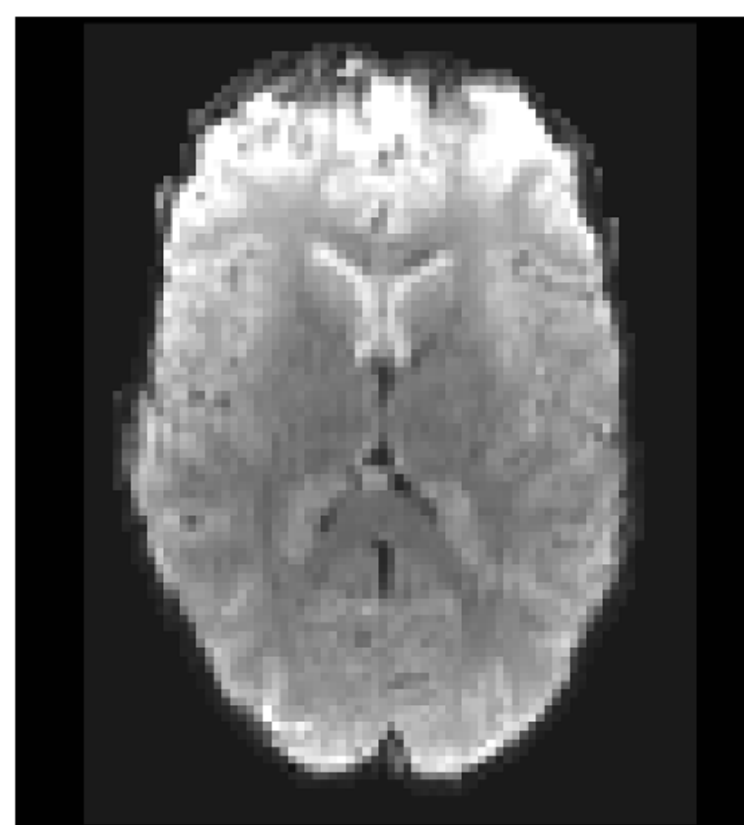
# Smoothing (spatial filtering)



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

← FWHM →

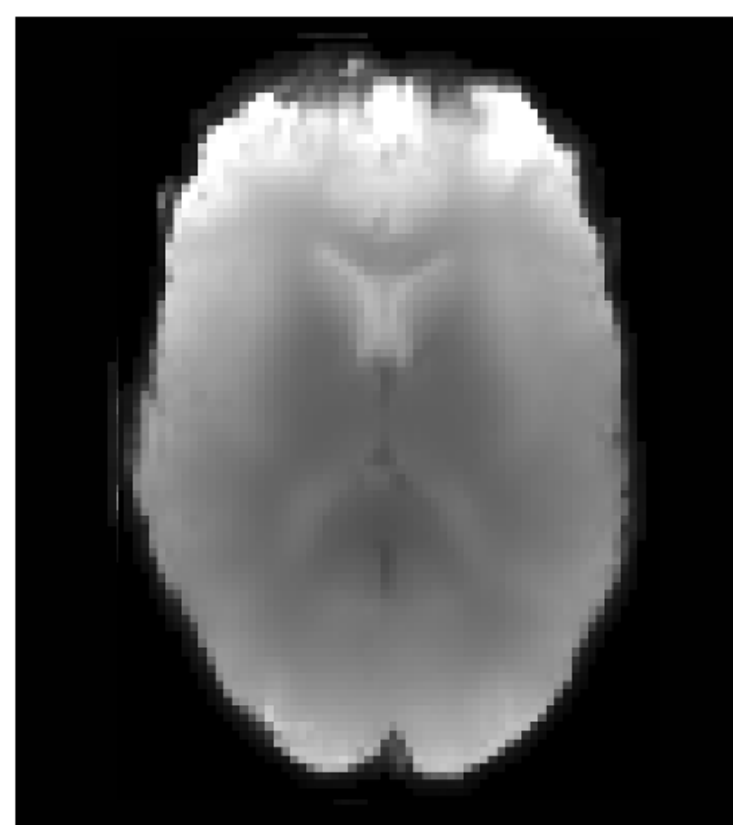
- Increase signal to noise ratio by blurring the image
- Averaging leads to less noisy voxel values
- Keep in mind:
  - Size of expected activation
  - Desired spatial specificity
  - May not need to do any



No smoothing

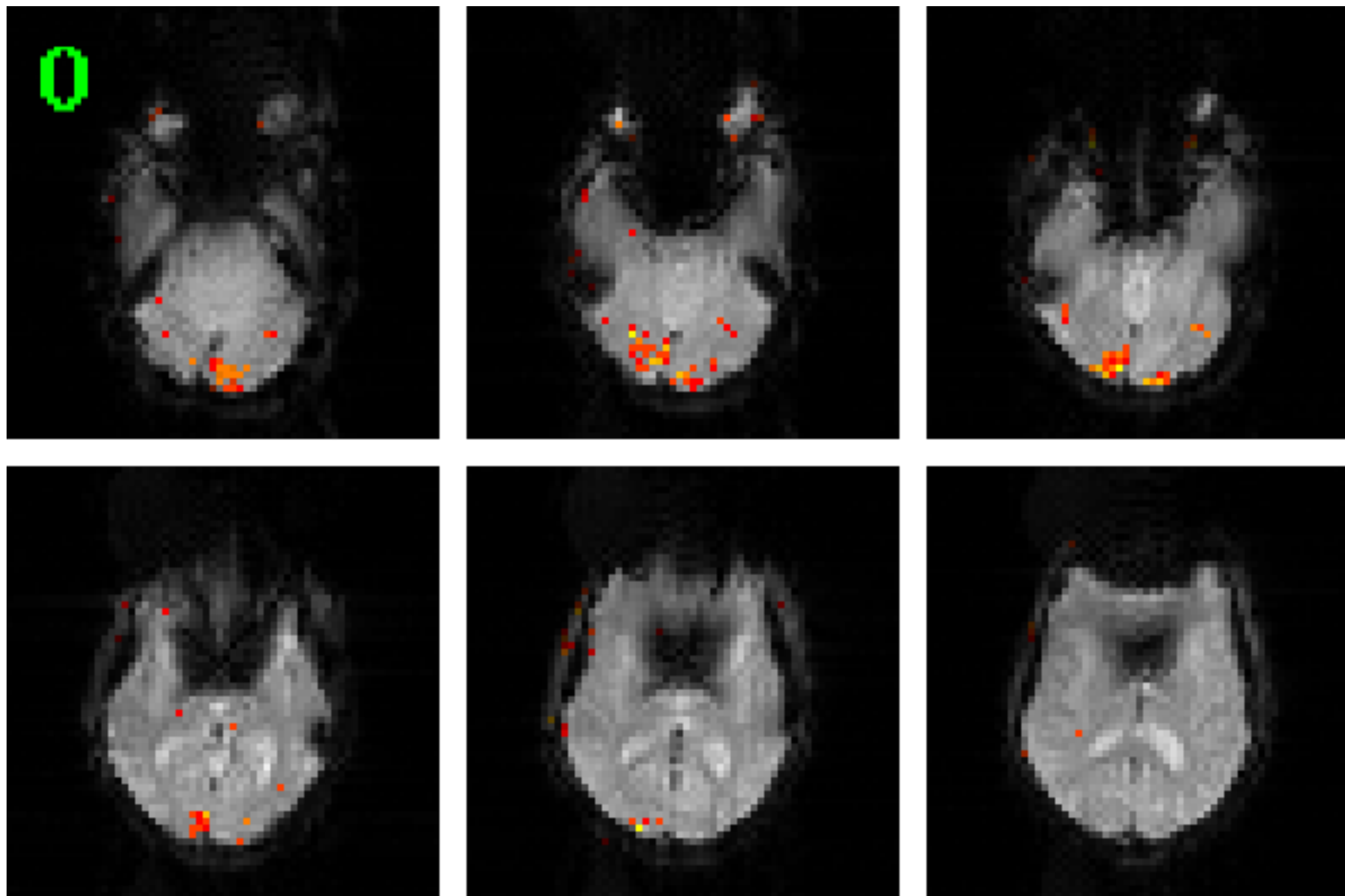


5 mm smoothing



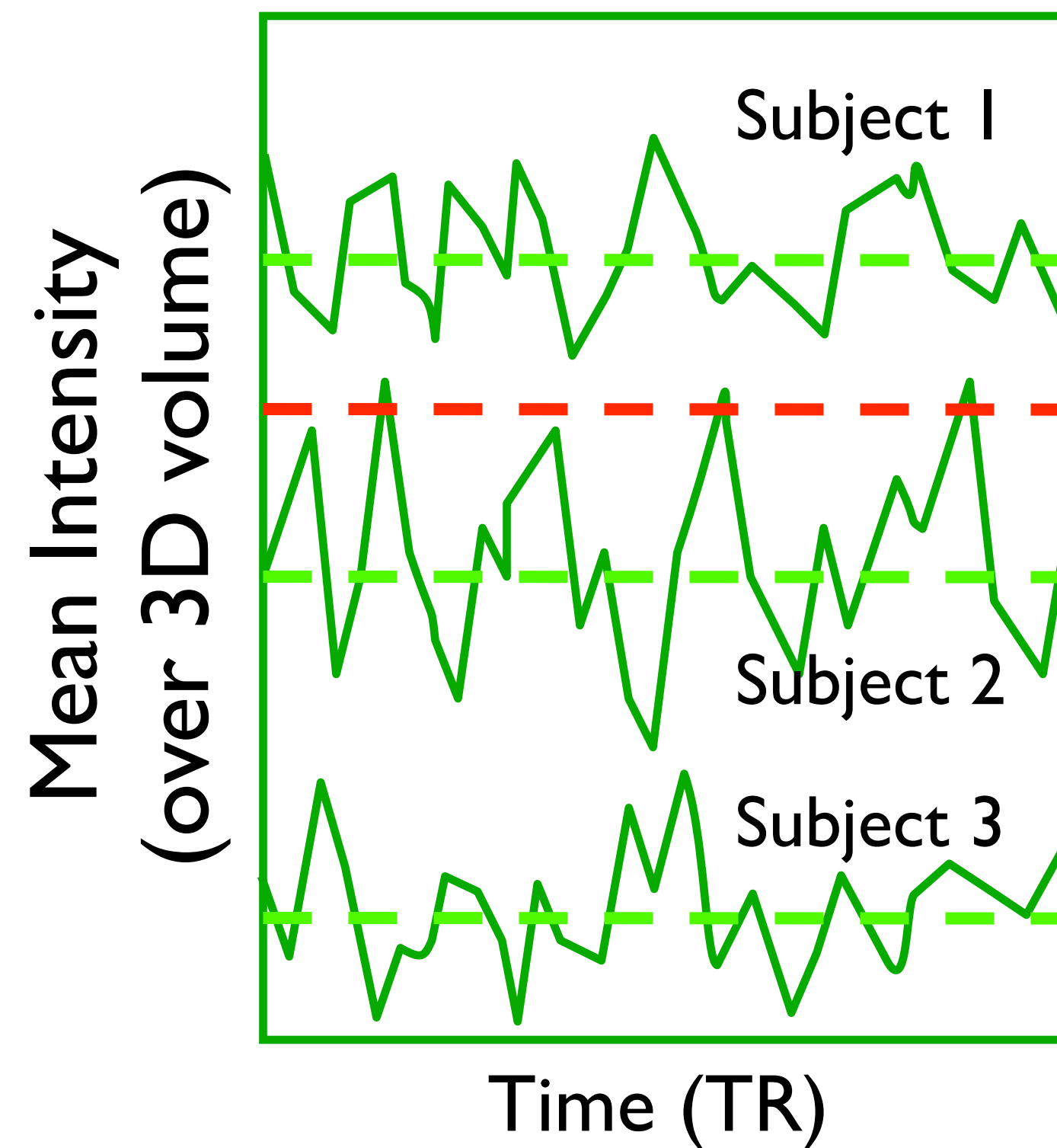
10 mm smoothing

# Effect of smoothing





# Global Intensity Normalisation



- Need to remove uninterested offsets between subjects and sessions
- Scale (i.e. multiply) each 4D dataset by a single value
- Automatically done in all software packages
- Not the same as global signal regression!

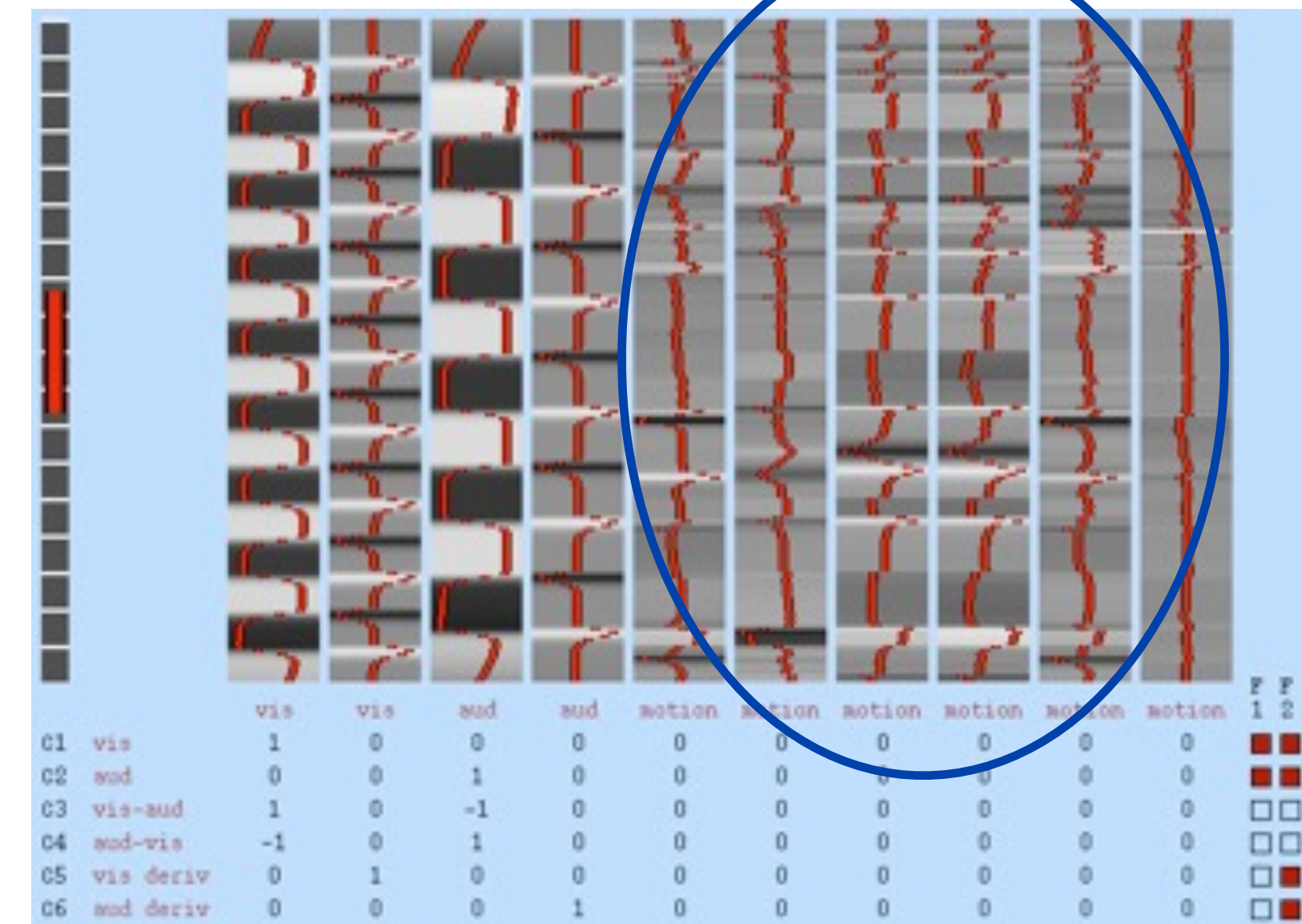




# Summary of preprocessing

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 <i>slow</i> drifts Lowpass: Avoid for autocorr est.
Intensity Normalisation	4D: Keeps overall signal mean constant across sessions

- Removes any correlated signals (since they are confounds)
- Assumes a linear relationship between **motion parameters** and intensity of motion artefact
- Assumes that MCFLIRT estimation is accurate
- Problematic if motion parameters and EVs of interest are highly correlated (stimulus-correlated motion)

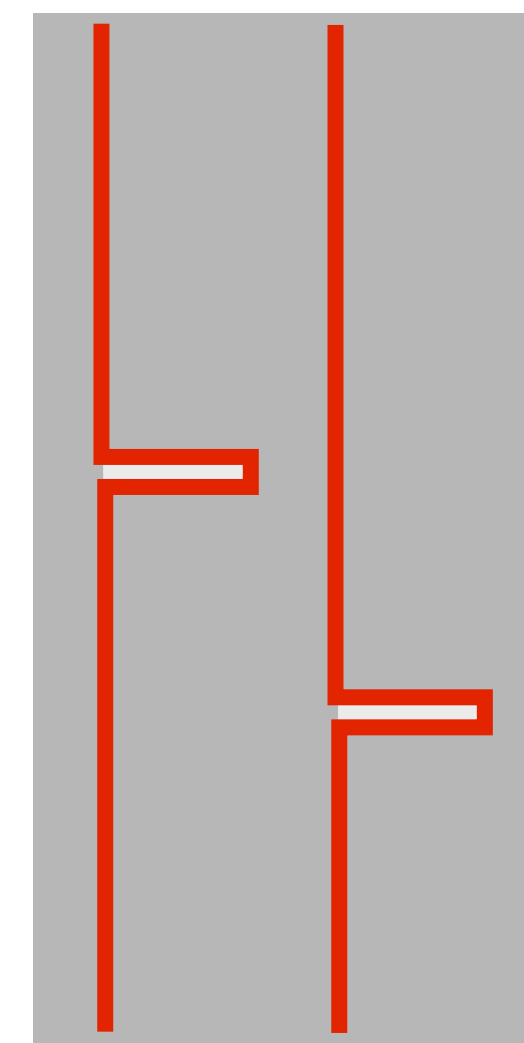




# Outlier Timepoint Detection

- Also known as scrubbing or volume censoring
- Removes ***all*** influence of the timepoints
- Uses one extra confound regressor per outlier timepoint
- `fsl_motion_outliers` creates confound matrix for GLM
- Can cope with very extreme motion effects
- But leaves other timepoints uncorrected

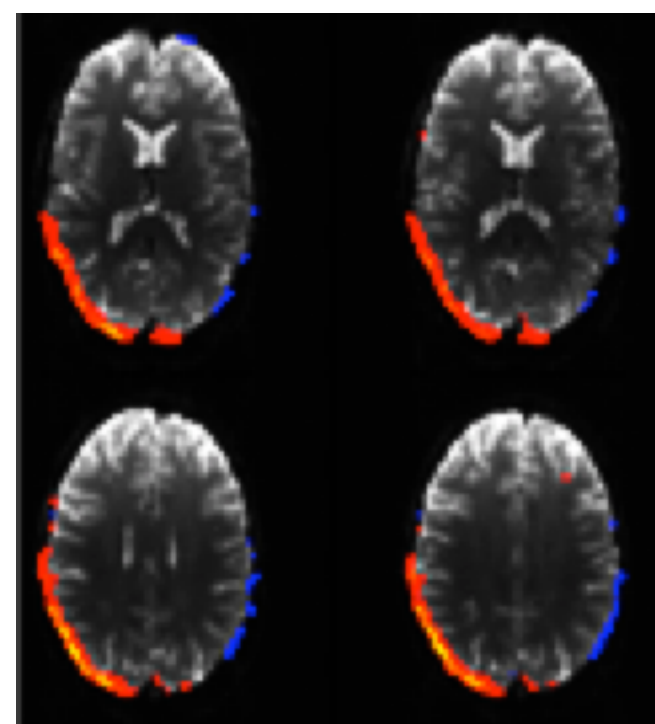
Confound matrix with  
2 outlier timepoints



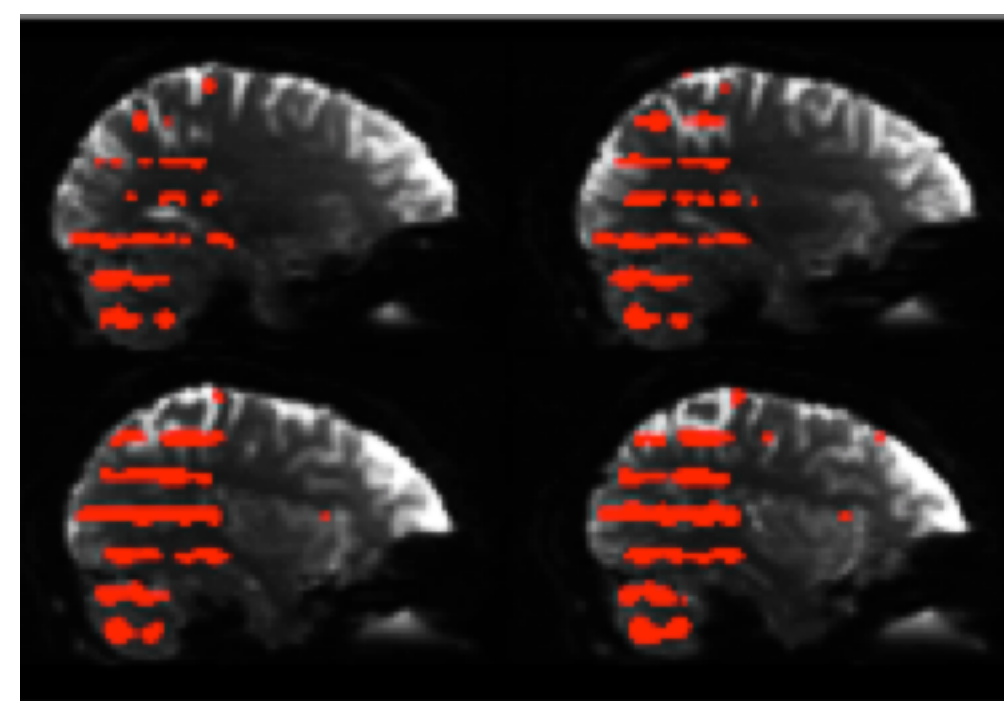


# ICA denoising

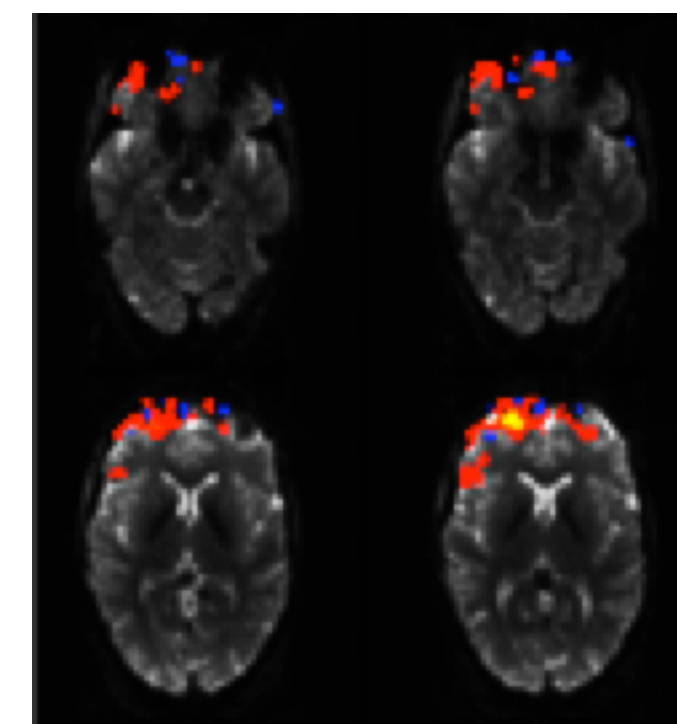
- Use ICA to identify noise components
- More on this during the ICA lecture



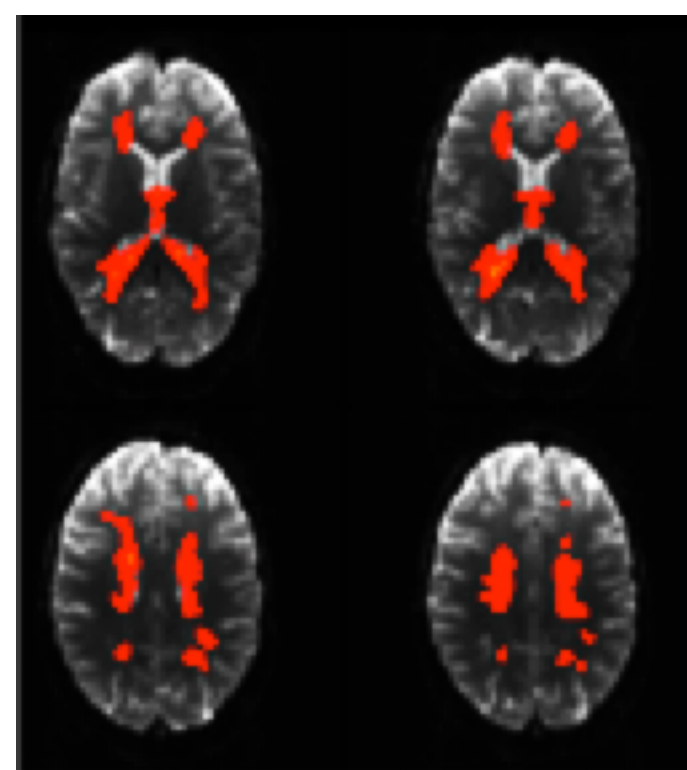
Classic motion



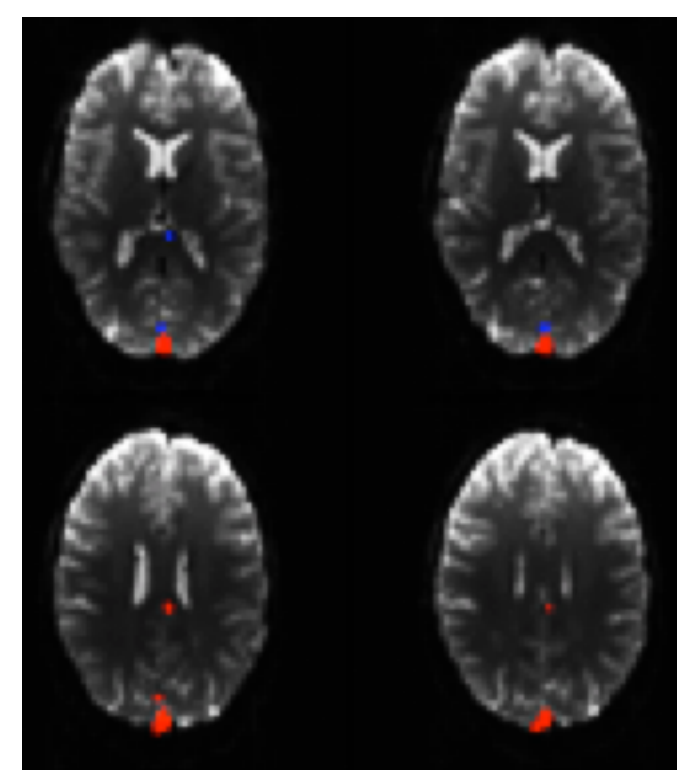
Multiband motion



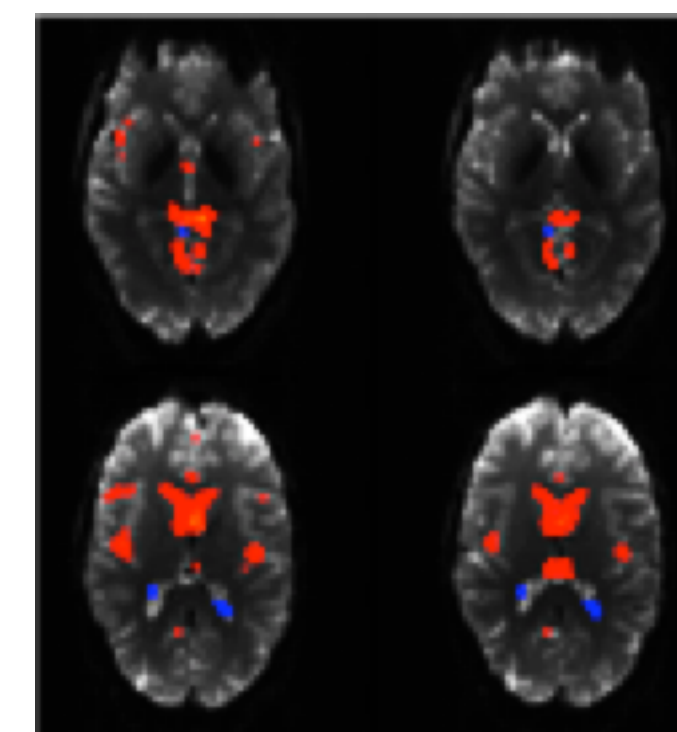
Susceptibility motion



White matter



Sagittal sinus



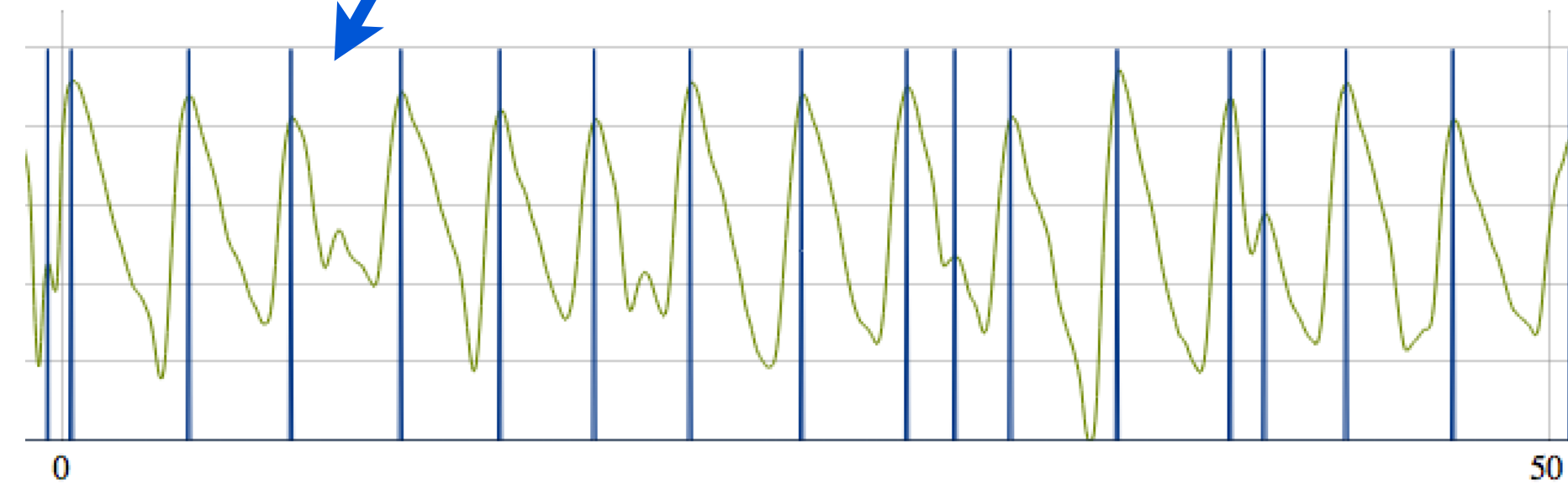
Cardiac/CSF



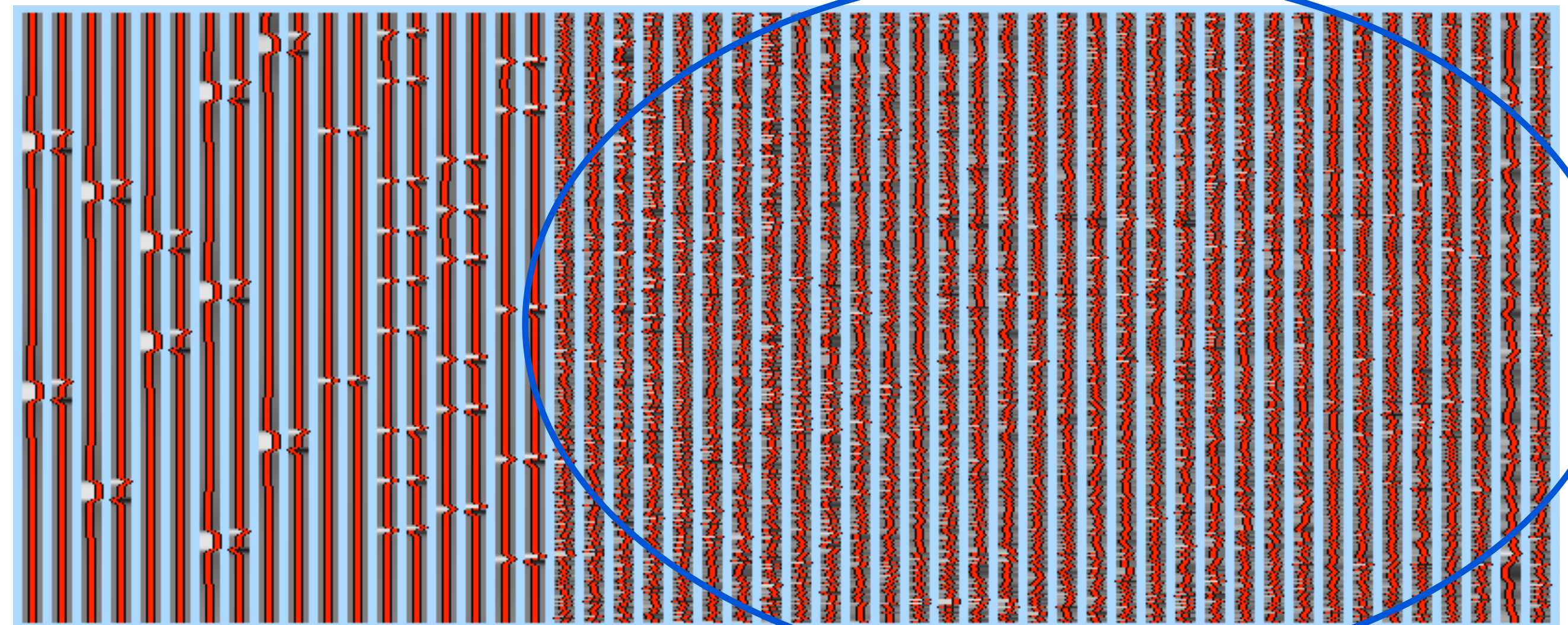
# Physiological Noise Regression



Peak detection in  
physiological trace



PNM GUI creates a  
set of files suitable  
for use as *Voxelwise  
Confounds* in FEAT



Very important for high-risk  
brain regions such as the  
brainstem