

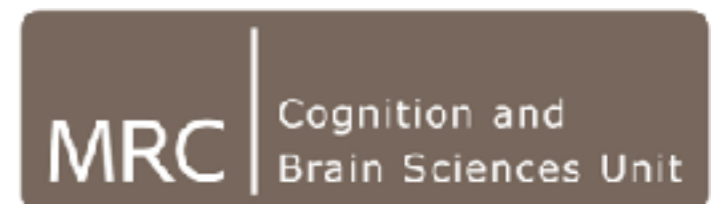
# fMRI 1: preprocessing and BIDS conversion

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Acknowledgment: Tibor Auer, Rik Henson

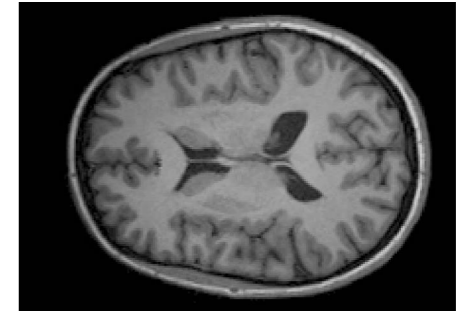


# Outline

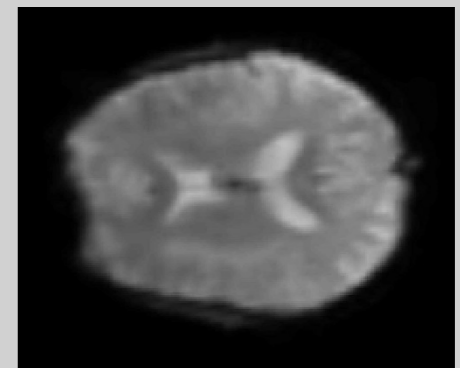
- Typical problems with raw fMRI data
- Fixing these problems with pre-processing (to some extent)
- Workshop: How to convert a typical functional MRI dataset to the BIDS standard

# A typical fMRI dataset

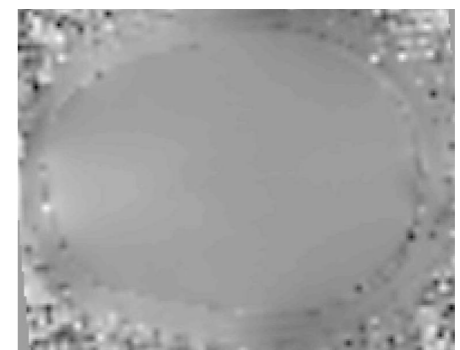
- Anatomical data: T1-weighted, 3D, 1 per subject or session
  - (ME)MPRAGE sequence, minimally distorted
  - High spatial resolution ( $\sim 1$  mm isotropic)
  - Optimised for structural contrast (grey vs white matter)
  - Acquisition time  $\sim 5$  minutes



- Functional data: T2\*-weighted, 4D, 1 per scan
  - EPI sequence, distorted
  - Lower spatial resolution (2-3 mm, perhaps non-isotropic)
  - Optimised for functional contrast (oxy- vs de-oxy haemoglobin)
  - Acquisition time  $\sim 2$  seconds per image (20-30 slices)

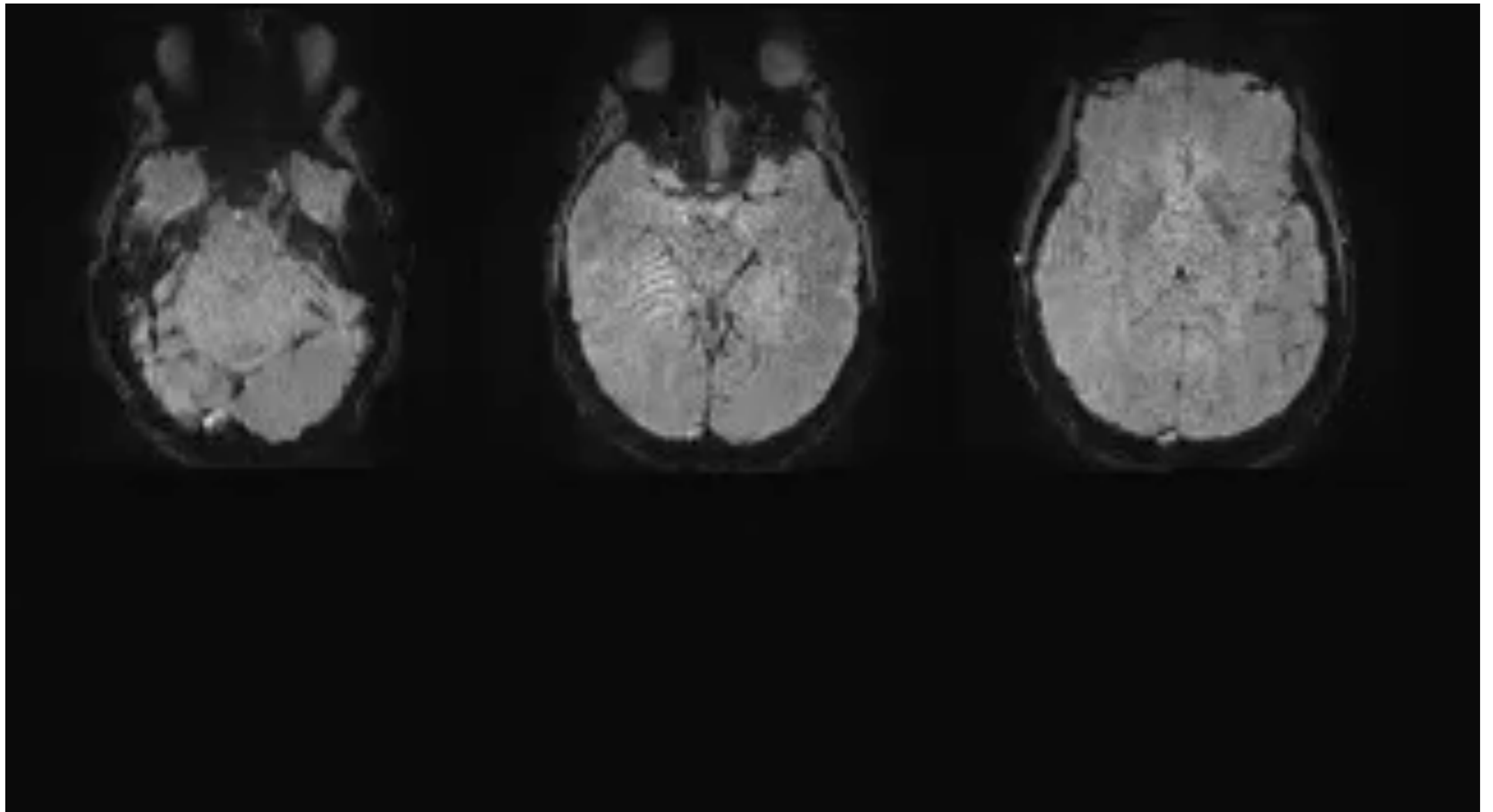


- Fieldmaps: 2x3D, 1 per session
  - Dual-echo GE sequence, undistorted
  - Lower spatial resolution (similar to fMRI)
  - Map of magnetic field inhomogeneities
  - Acquisition time  $\sim 1-2$  minutes.



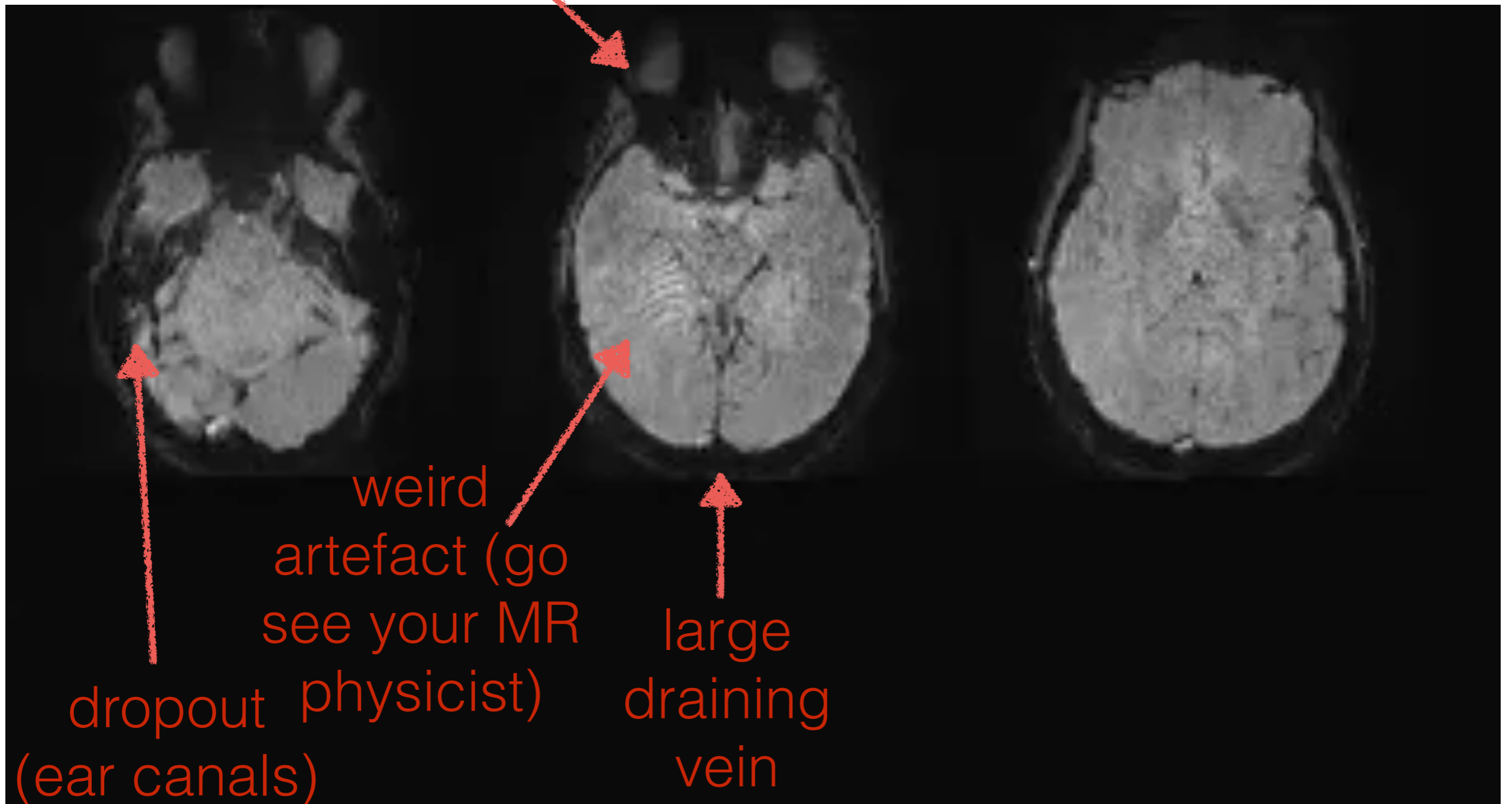
# What does fMRI data look like?

3D EPI, GRAPPA R=2, 2mm iso voxels, TR=1.06s

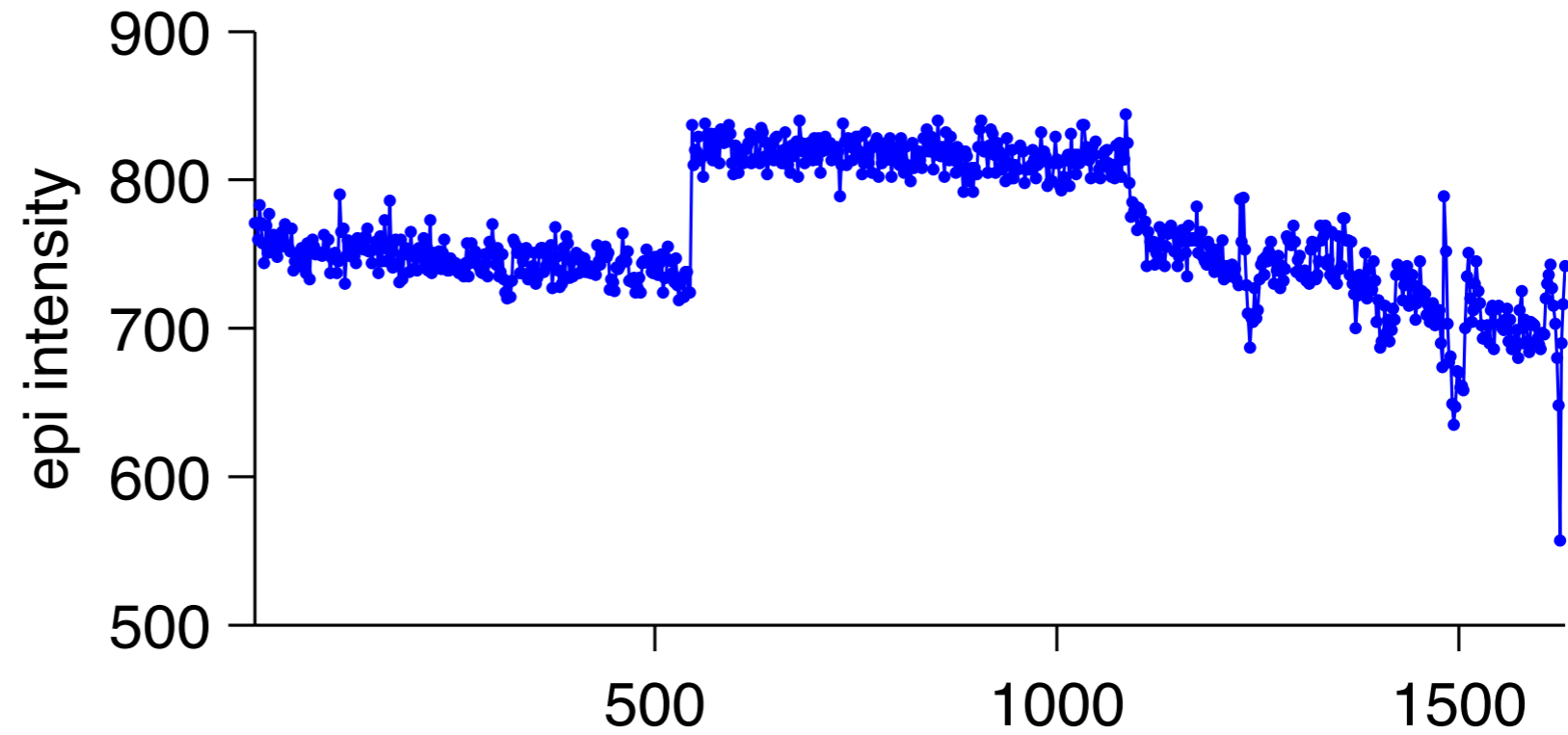


# What does fMRI data look like?

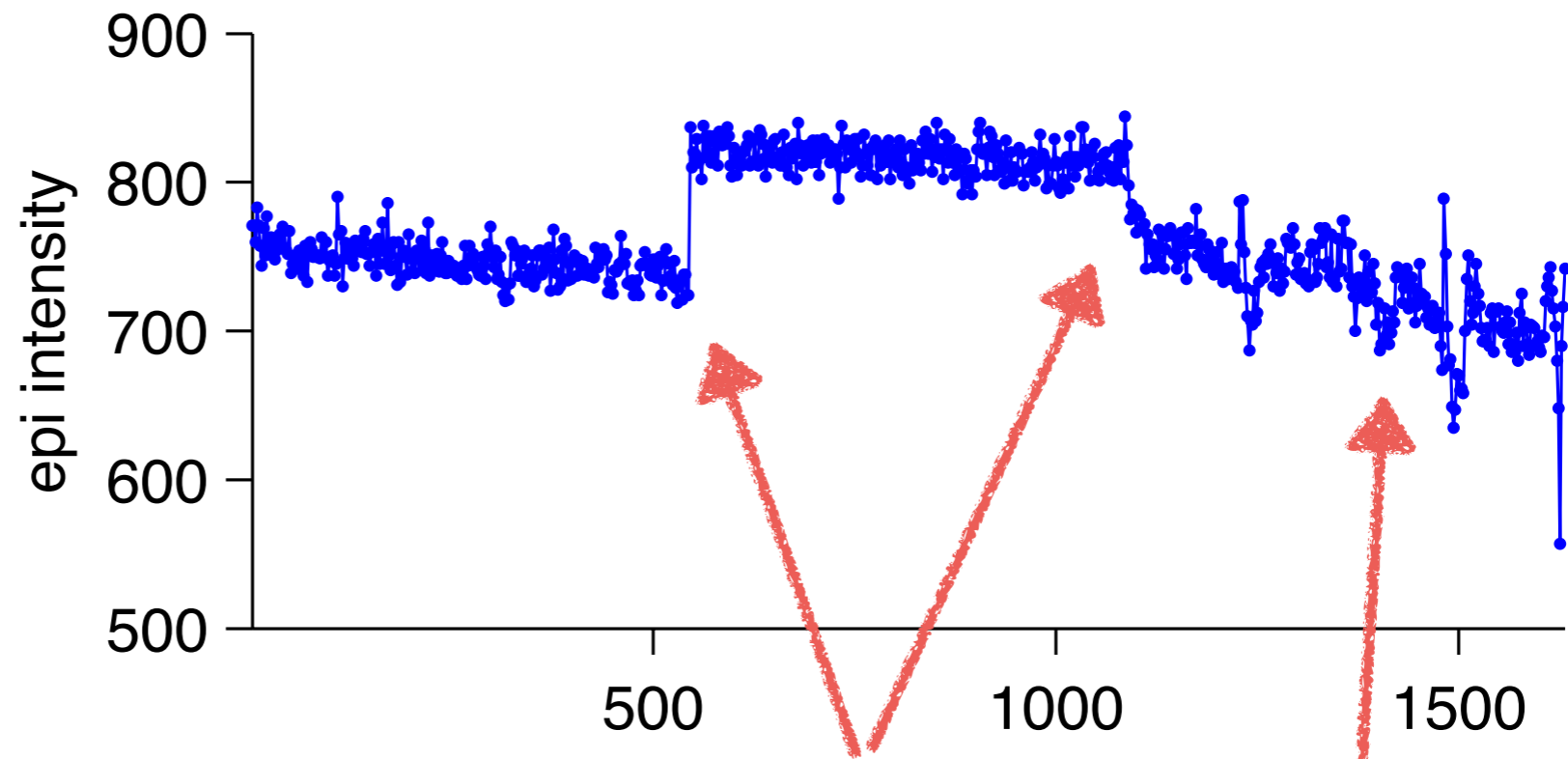
eye blink / movement effect  
(not just in eye balls!)



# Example voxel - raw data



# Example voxel - raw data

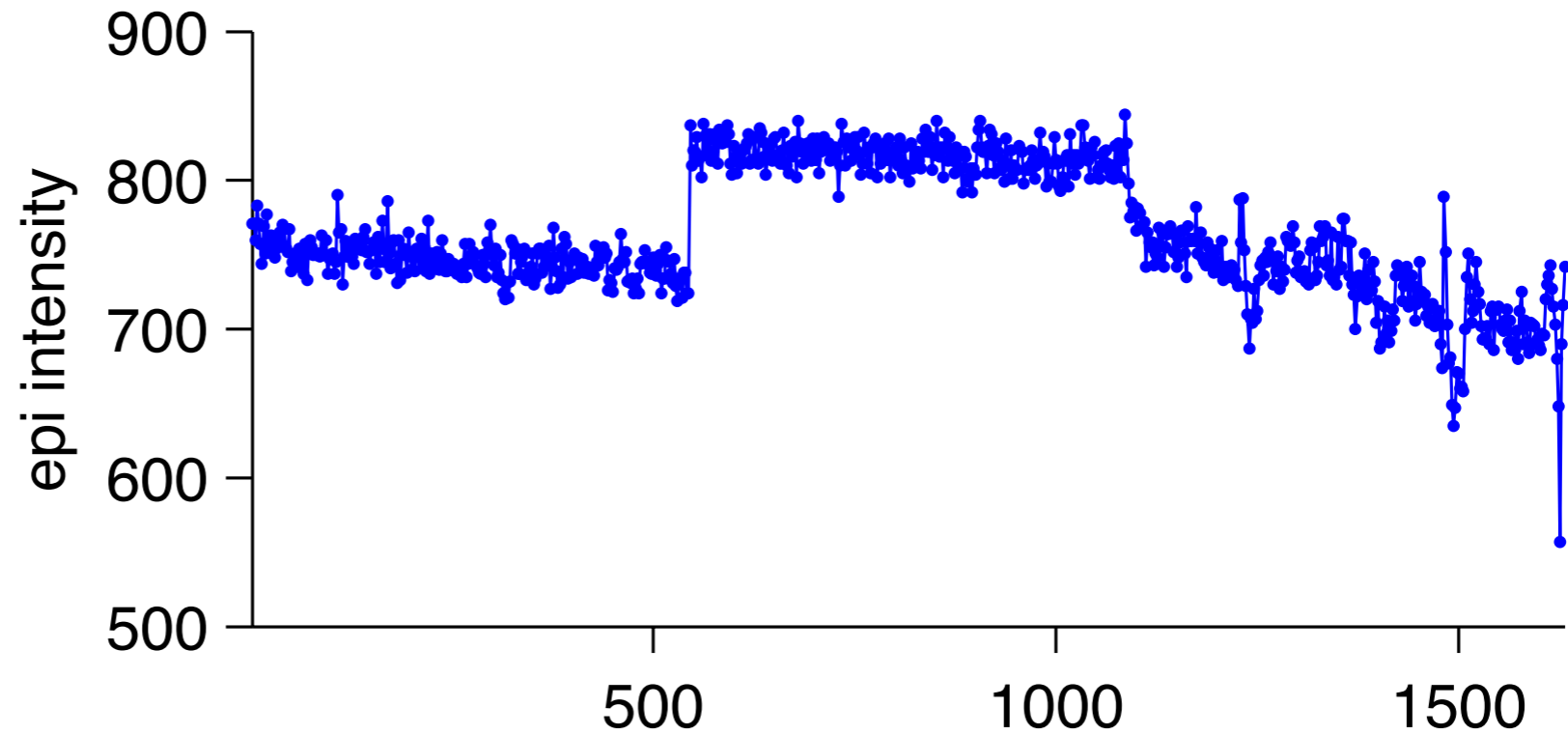


run transitions  
(head movement  
between scans?)

lots of signal drift  
vs other runs  
(head movement  
during this scan?)

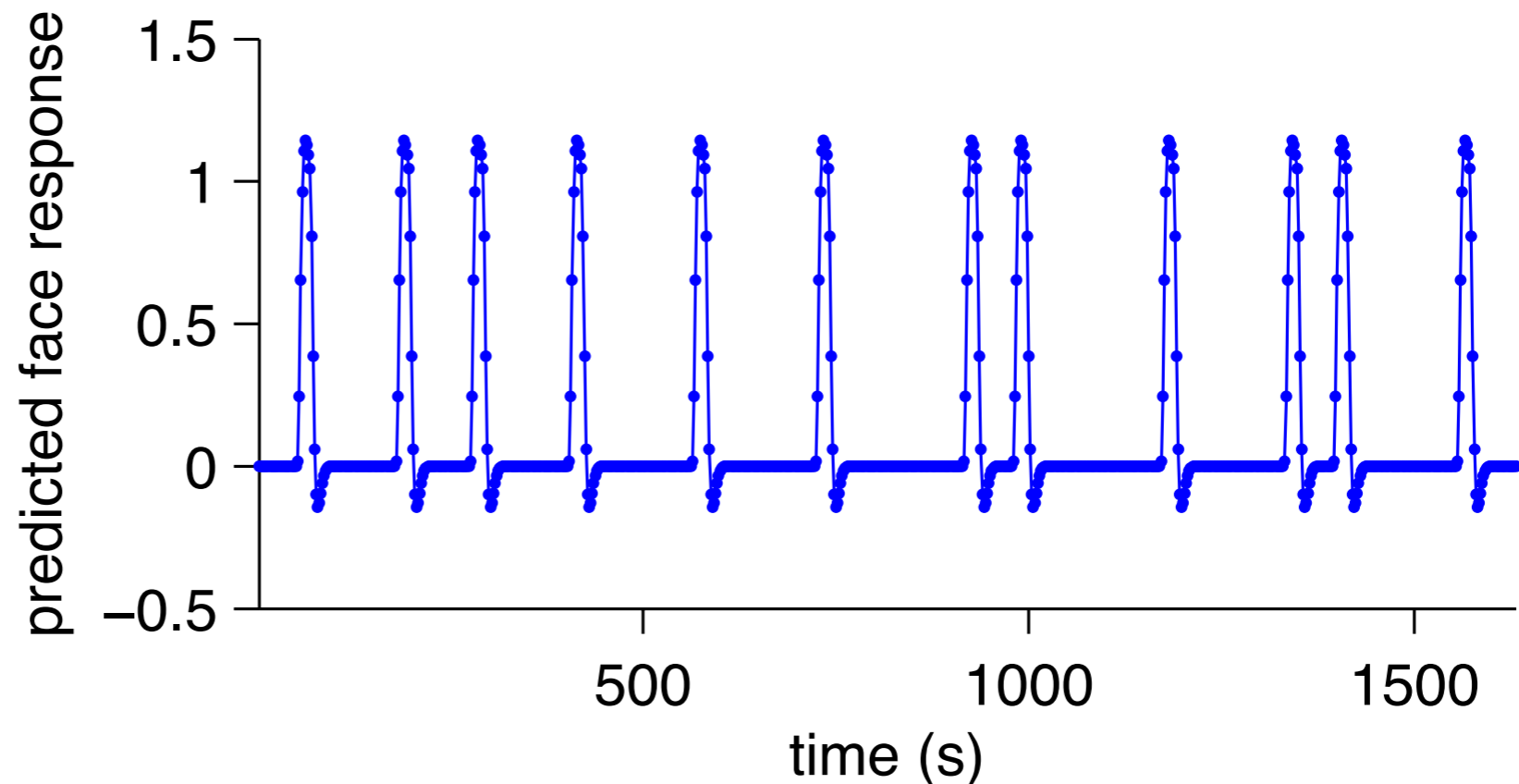
# Example voxel - raw data

The (raw) fMRI data



The cognitive model

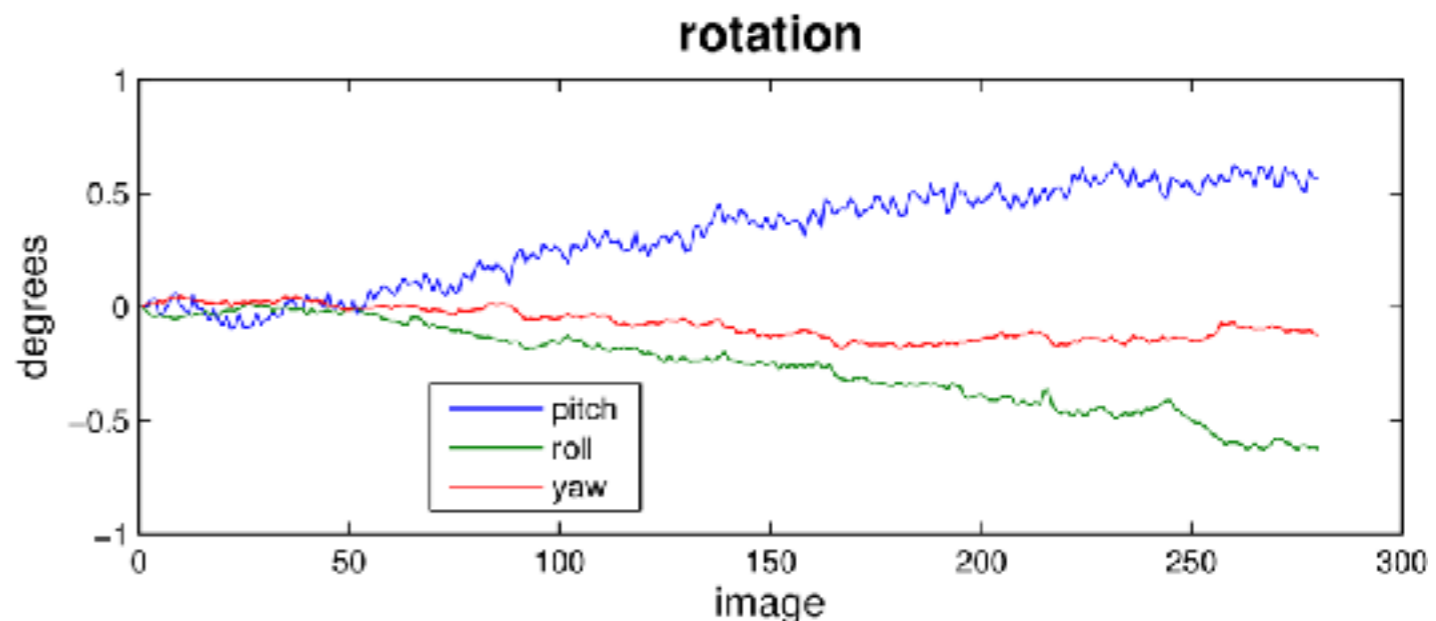
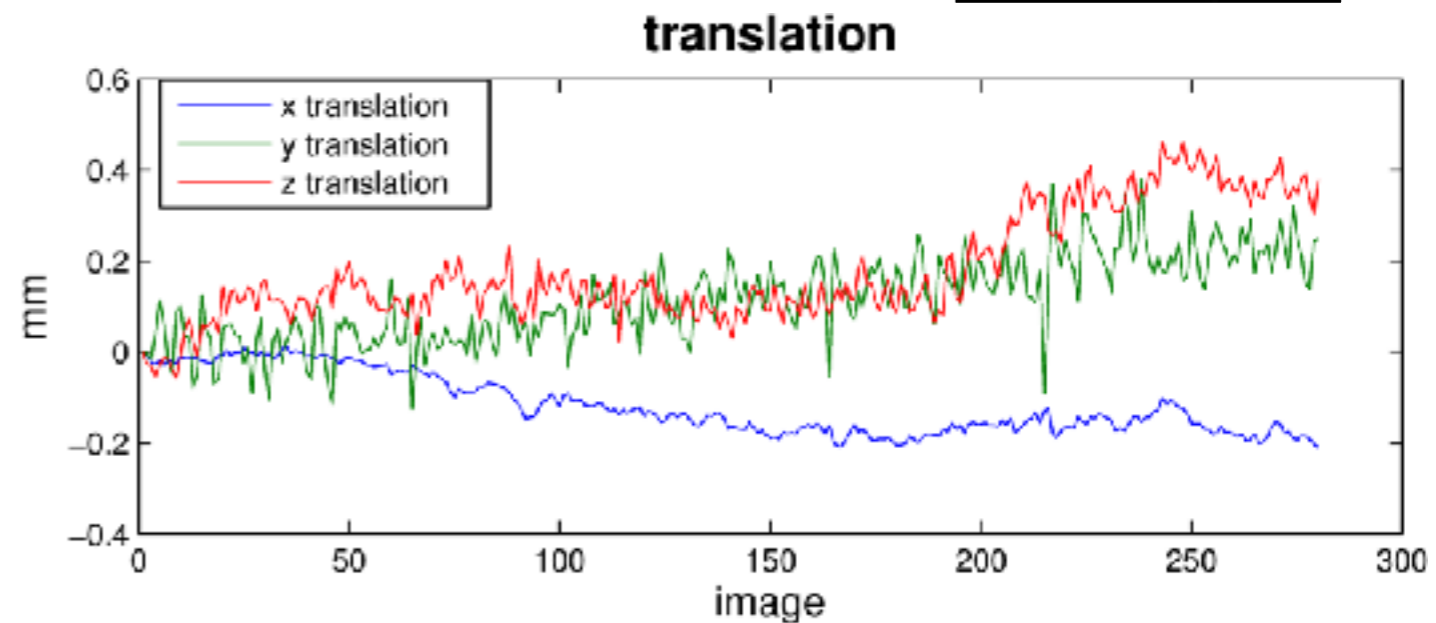
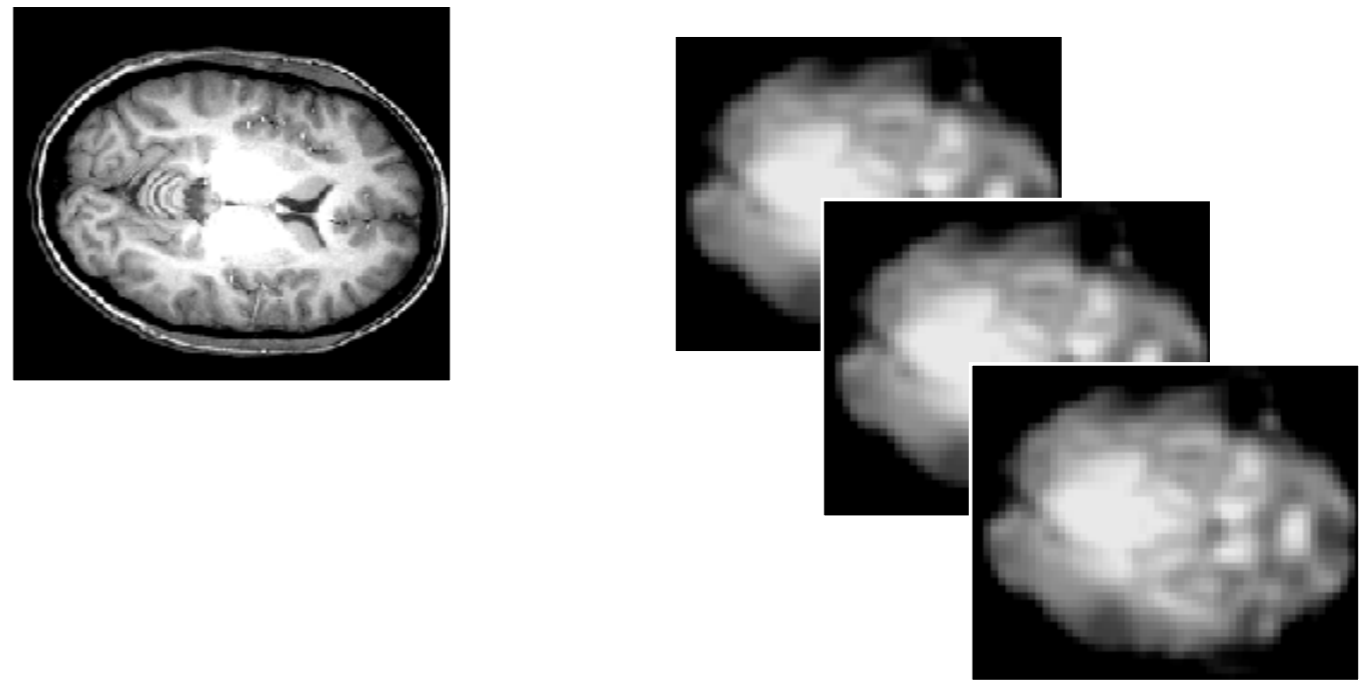
Not much hope of this working without signal processing





# So many problems

- HRF is delayed and temporally smooth
- Signal intensity drifts over time
- EPI images are distorted
- The head is likely to move during the fMRI scan
- Slices within the same image come from different time points (assuming standard 2D EPI)
- Head movements between fMRI scans and structural scans
- Signal is typically spatially extended
- Even if we can correct the above, different people's brains are different shapes, so how do you do group analysis?



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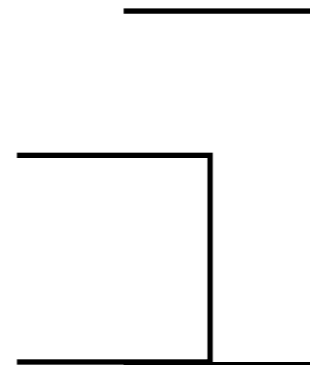
# Solutions

- ← Just model it! Next lecture
- ← Just model it! Next lecture
- ← Use a B0 fieldmap to undistort
- ← Rigid-body motion correction (realign)
- ← Slice timing correction
- ← Coregister headers
- ← Spatial smoothing
- ← Normalisation to template (MNI) brain, or ROI analysis

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# Interactions are harder to fix

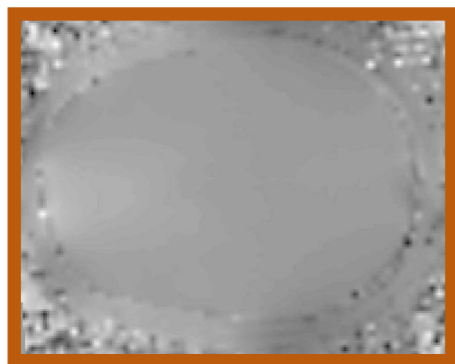


head motion x b0 field interaction

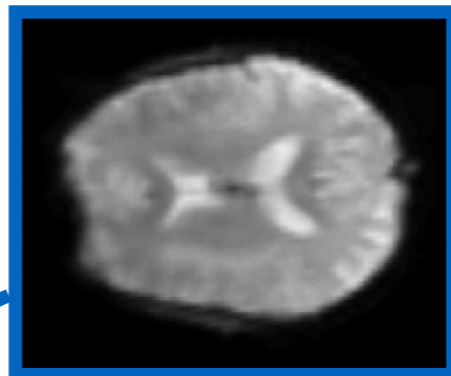
head motion x slice time interaction

**Preprocessing is no substitute for collecting high quality (low head-motion) data**

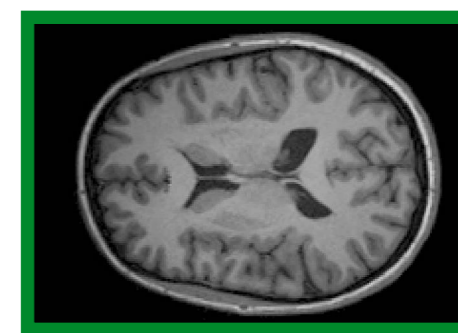
**fieldmap**



**functional**



**structural**



combined  
undistort and  
realign (unwarp)

fieldmap  
undistortion

coregistration

tissue class  
segmentation

slice time  
correction

motion correction  
(realign)

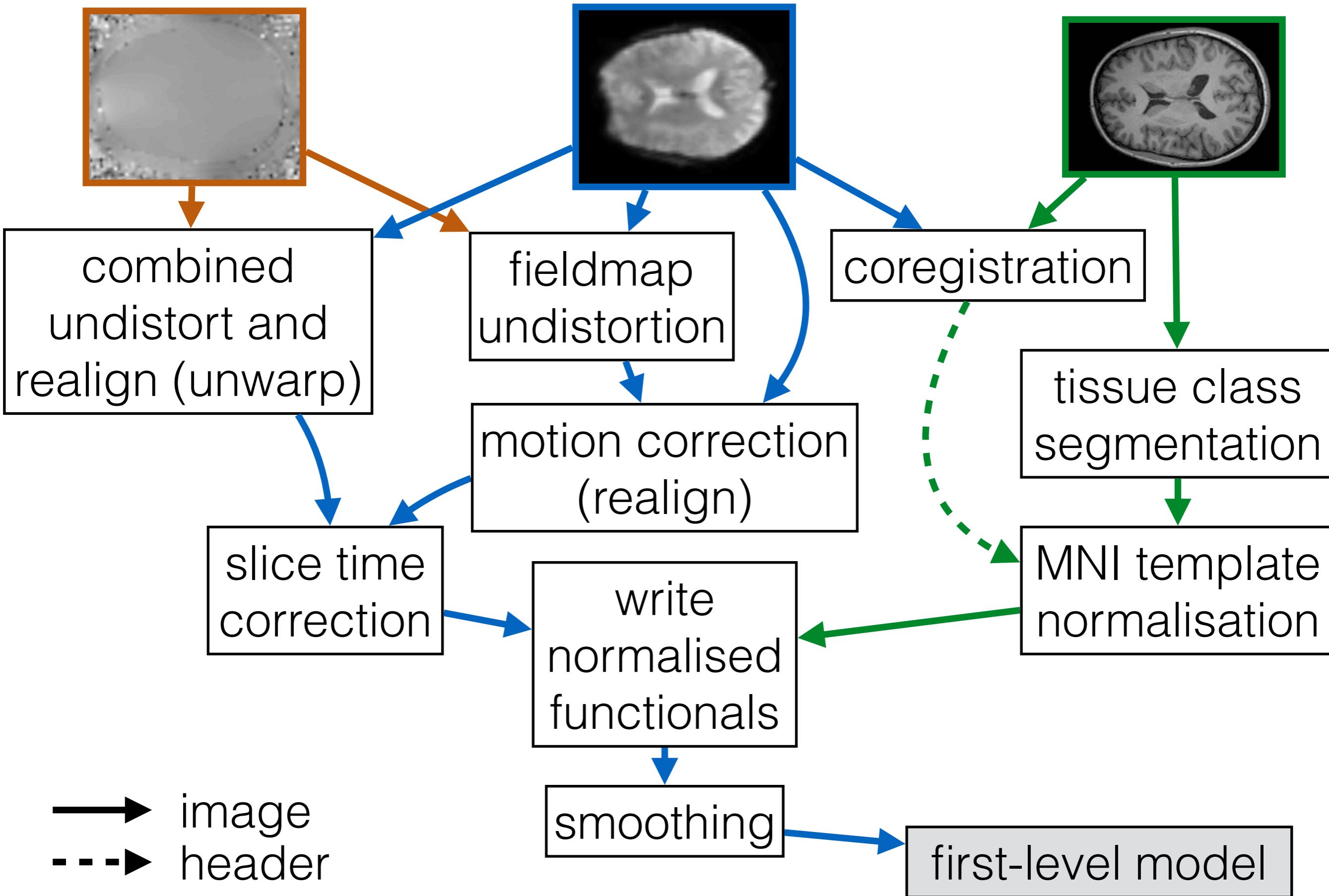
MNI template  
normalisation

write  
normalised  
functionals

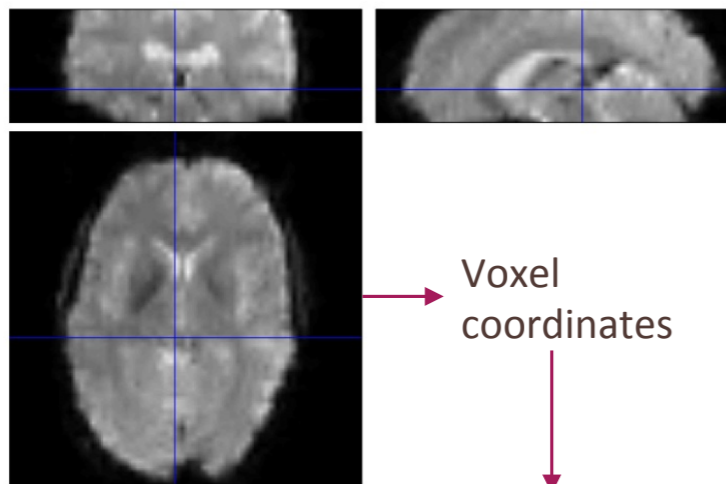
smoothing

first-level model

→ image  
- - -> header

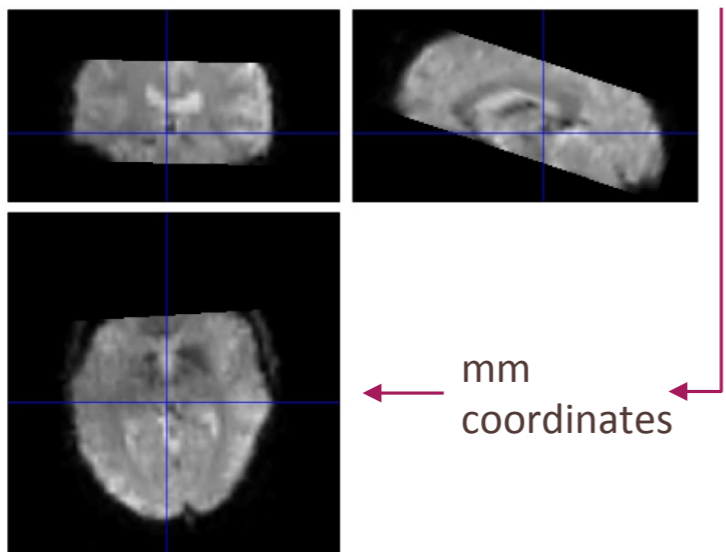


# Coordinate systems



Voxel coordinates

$$\begin{bmatrix} -3.0 & -0.2 & 0.1 & 107.1 \\ -0.3 & 2.8 & -1.3 & -61.7 \\ 0 & 1.0 & 3.8 & -47 \\ 0 & 0 & 0 & 1 \end{bmatrix} \times \begin{bmatrix} 34 \\ 28 \\ 5 \\ 1 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 1 \end{bmatrix}$$



mm coordinates

- **“Spaces”**
  - “Voxel space”: location in the data matrix
  - “World space”: meaningful units (mm) from a POO<sup>1</sup>

- **Transformation matrix: relationship between “voxel space” and “world space”**

$$\begin{matrix} \text{Translations} & \text{Pitch} & \text{Roll} & \text{Yaw} \\ \begin{pmatrix} 1 & 0 & 0 & X_{\text{trans}} \\ 0 & 1 & 0 & Y_{\text{trans}} \\ 0 & 0 & 1 & Z_{\text{trans}} \\ 0 & 0 & 0 & 1 \end{pmatrix} & \times \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & \cos(\Phi) & \sin(\Phi) & 0 \\ 0 & -\sin(\Phi) & \cos(\Phi) & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} & \times \begin{pmatrix} \cos(\Theta) & 0 & \sin(\Theta) & 0 \\ 0 & 1 & 0 & 0 \\ -\sin(\Theta) & 0 & \cos(\Theta) & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} & \times \begin{pmatrix} \cos(\Omega) & \sin(\Omega) & 0 & 0 \\ -\sin(\Omega) & \cos(\Omega) & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}
 \end{matrix}$$

- Changing the transformation matrix<sup>2</sup>
  - ↓
- Changes the relationship
  - ↓
- Transforms the image without having to resample (reslice) it

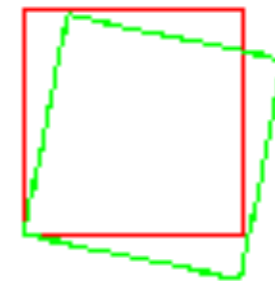
# Coordinate transformations

*The transform can describe a transition*

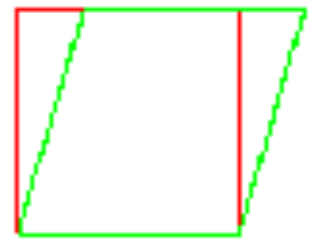
- voxel index  $\gg$  mm (e.g., relative to center of scanner bore)
- mm  $\gg$  mm (e.g., from scanner to MNI)

*Transforms can be*

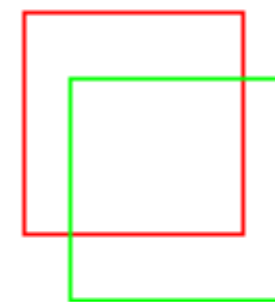
- Linear (ie, same parameters for the entire volume)
  - ‘rigid body’: 6 df - translation (x,y,z), rotation (pitch, roll, yaw). Used for co-registration between structural and EPI, motion correction
  - ‘affine’: 12 df - scale (aka ‘zoom’), shear. Used as initial stage of normalisation.
- Non-linear (ie, different parameters for different voxels) - for normalisation to template brains



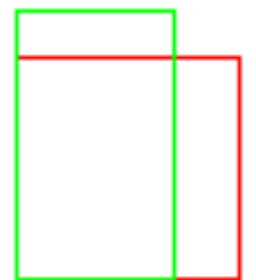
rotation



shear



translation



scale

*The transform can be applied to*

- Header only (e.g., in co-registration)
- To reslice a new, transformed image (e.g., in motion correction, normalisation)

# Template brain normalisation

*Goal:* transforming brain so its shape matches that of a template. Useful for:

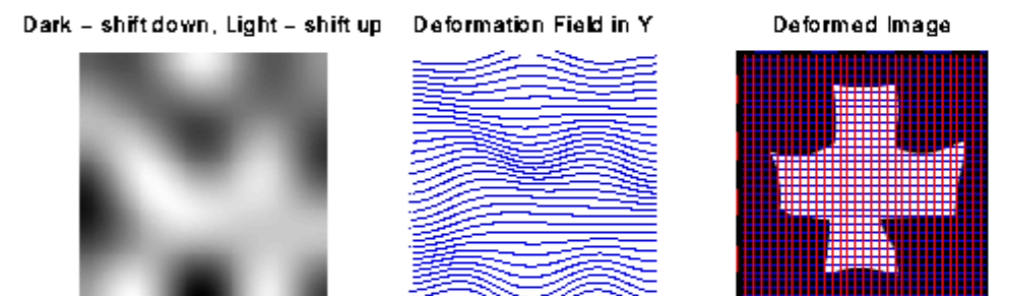
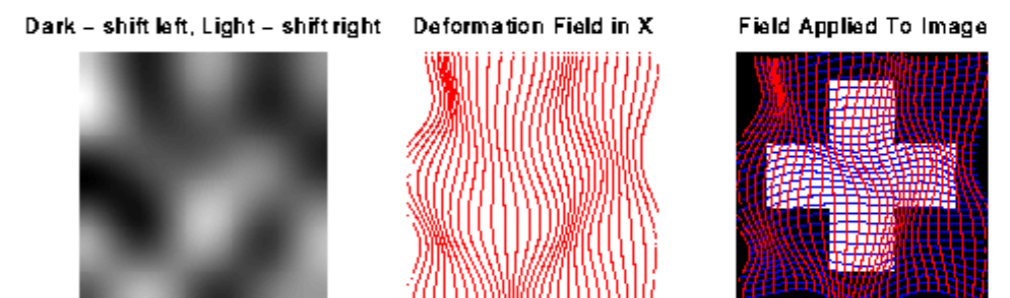
- Group analysis
- Cross study comparison, meta analysis

*Template:* universal coordinate space

- Talairach and Tournoux, 1988 – Brainvoyager, AFNI
  - Based on a single subject
- Montreal Neurological Institute: MNI152 – SPM, FSL
  - Averaged from  $T_1$  images of 152 subjects
- Information eXtraction from Images (London): IXL (in SPM12)
  - Also in MNI
  - Fewer subjects, but may be more representative locally
  - More classes (segmentation)

# SPM normalisation

- Two steps: first affine registration, then nonlinear registration with regularisation to correct local errors
- Unified segmentation: divide the brain into 3 tissue classes (WM, GM, CSF) and normalise each separately to a template. Much better than whole-image normalisation, if the segmentation is good (effectively another nonlinearity)
- Not expected to work perfectly - SPM assumes you will use spatial smoothing to overcome residual errors in registration

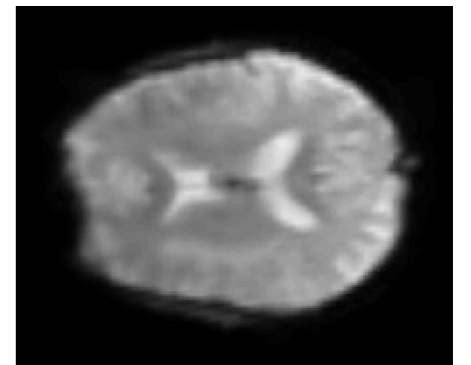




# Normalisation routes

*Bringing fMRI data from native into a standard (MNI) coordinate system*

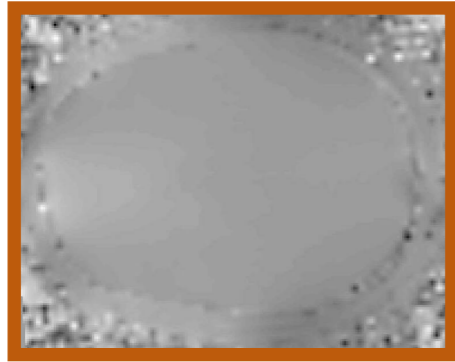
- Direct: EPI >> MNI EPI template
  - Probably bad idea. Distorted, low res, not optimised for anatomical contrast
- Indirect:
  - Coregister participant's fMRI and structural data (EPI header >> T1 header)
  - Find nonlinear transform to bring participant structural into MNI space (T1 >> MNI)
  - Apply the transform to the EPI data (EPI >> MNI)
- Indirect + study template (DARTEL):
  - EPI header >> T1 header
  - Create study-specific template brain (T1 >> study template)
  - Normalize the study-specific template (study template >> MNI)
  - Apply the concatenated T1 >> study template >> MNI transform to the EPI data



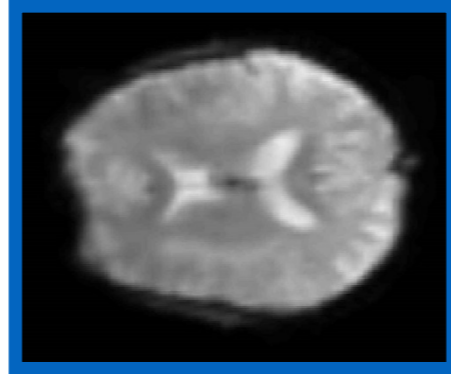
# Sidebar - converting between Talairach and MNI

- The 'classic' route for converting between the Talairach *atlas* and MNI is the 'Brett' transform (Brett et al, 2001, NeuroImage - developed here at CBU): <http://imaging.mrc-cbu.cam.ac.uk/imaging/MniTalairach>
- But if the goal is to convert between MNI and Talairach *volumes* (ie, outputs of a software package such as AFNI), you will probably get a better result with the BrainMap transform, which builds on the Brett transform to improve registration performance (Lancaster et al., 2007, HBM): <http://www.brainmap.org/icbm2tal/>

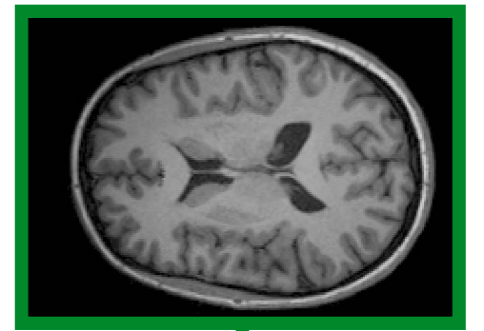
**fieldmap**



**functional**

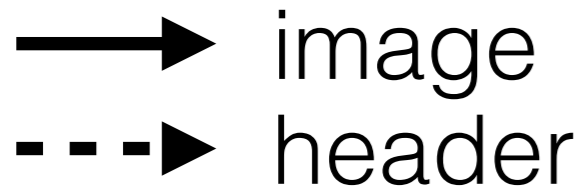


**structural**



tissue class  
segmentation

MNI template  
normalisation

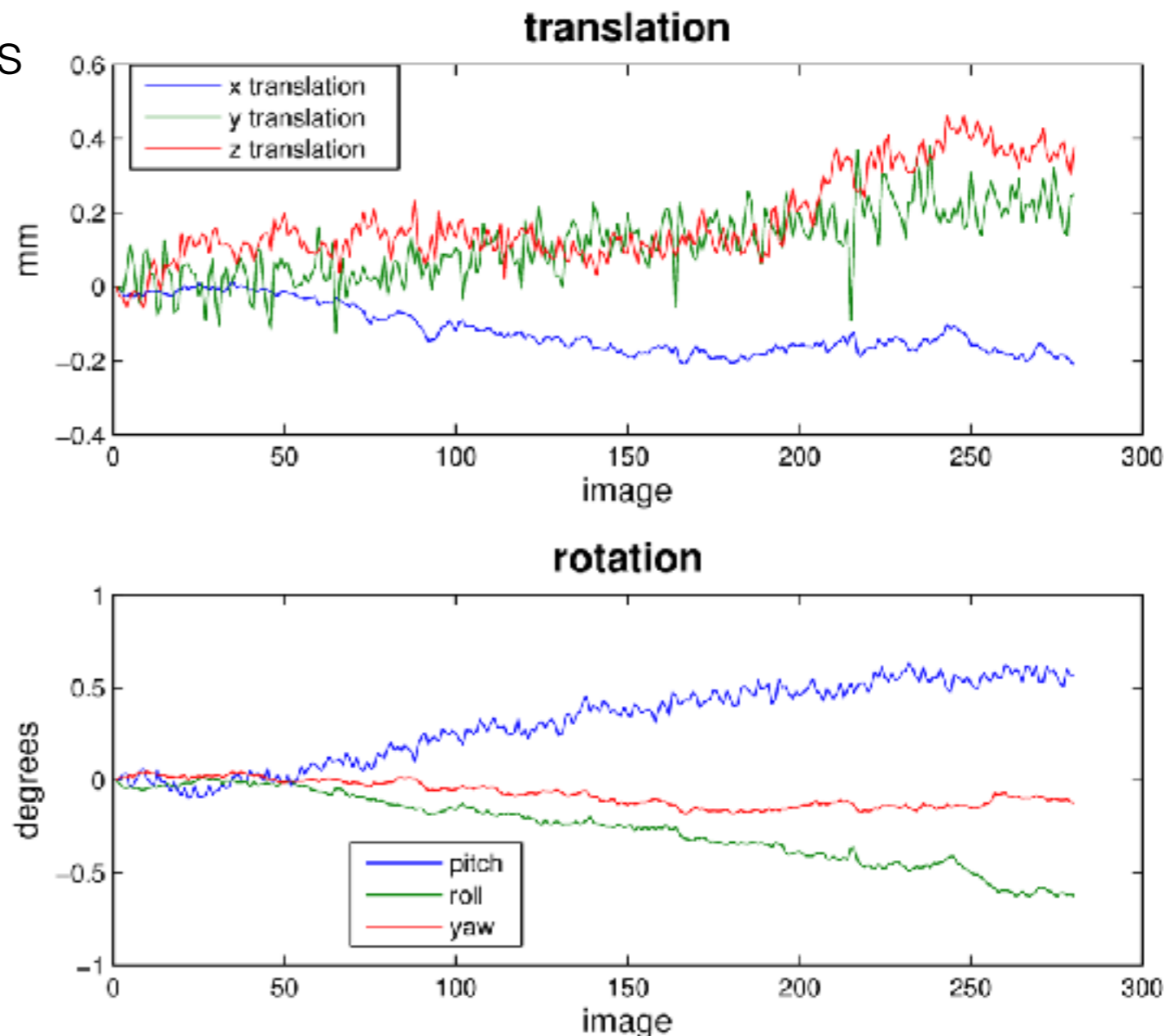
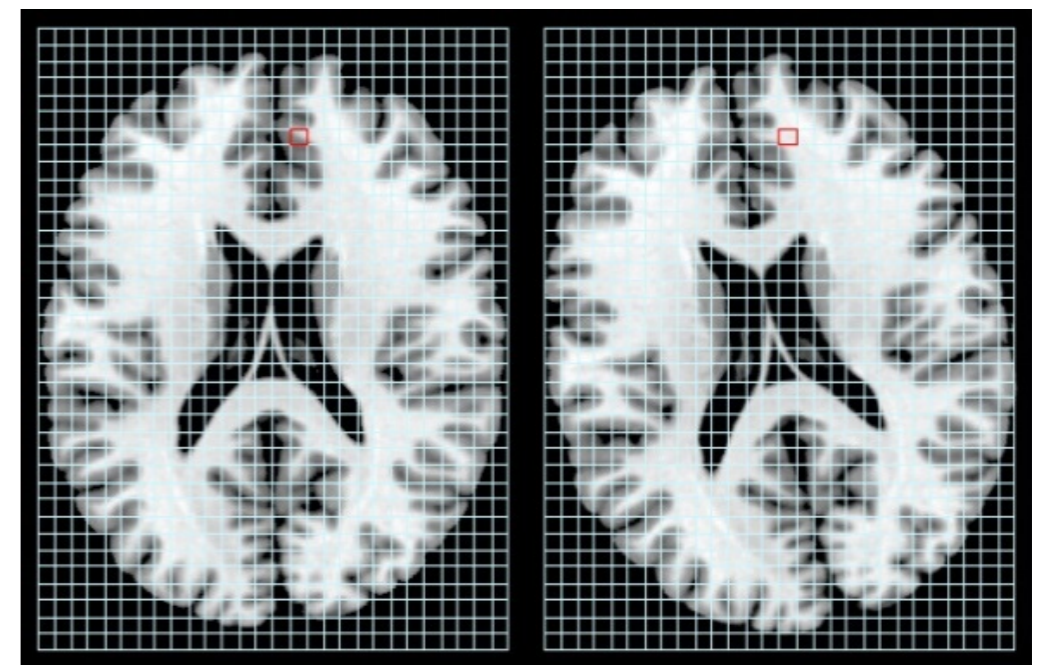


# Volume realign (colloquially, motion correction)

- A 6-parameter rigid body correction
- Target: the first image of the first run, or the mean image of the first run
- Works perfectly under these assumptions:

1. The magnetic field is homogeneous
2. All slices are acquired simultaneously
3. The images are noiseless (remember, the motion parameters are *estimated* from the EPI images themselves)

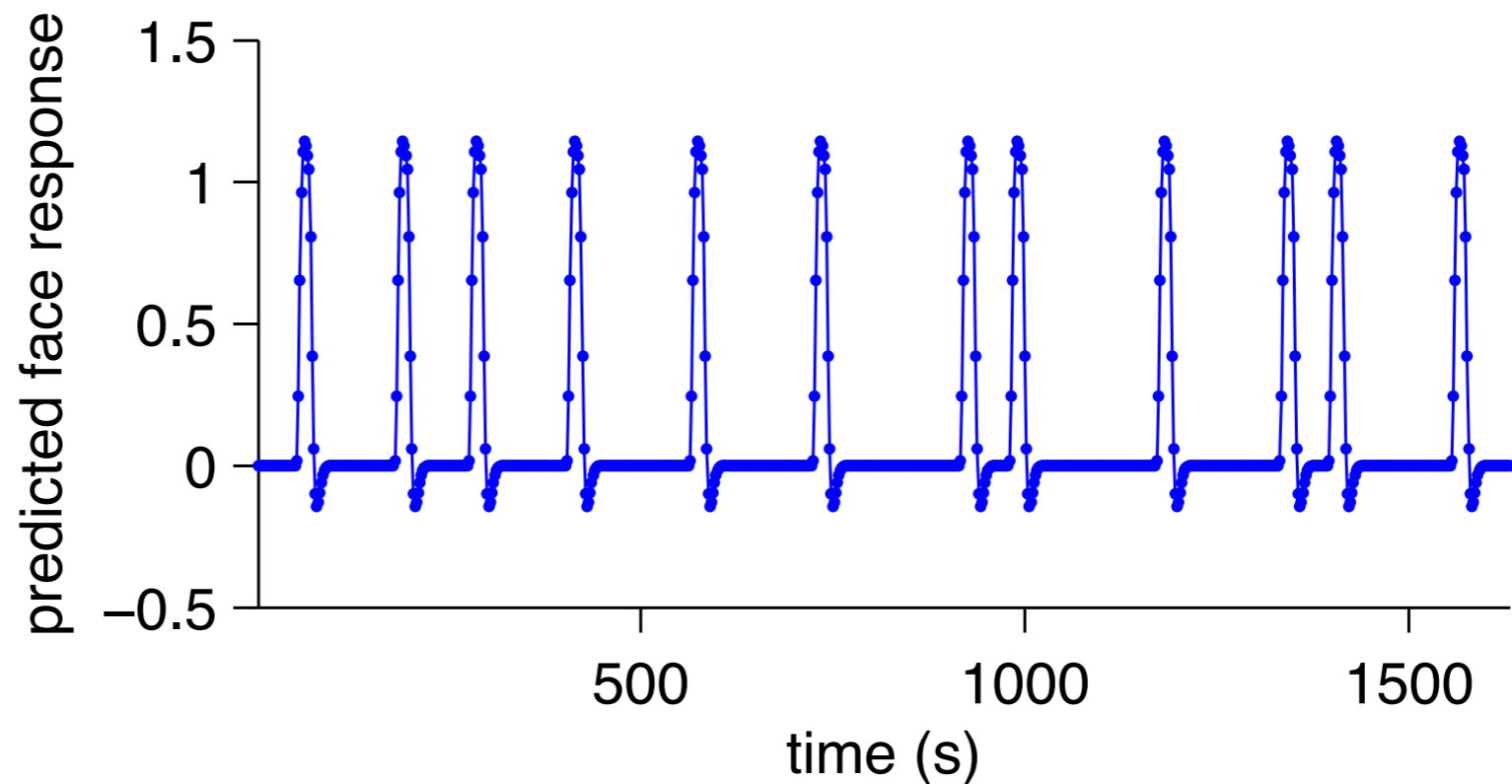
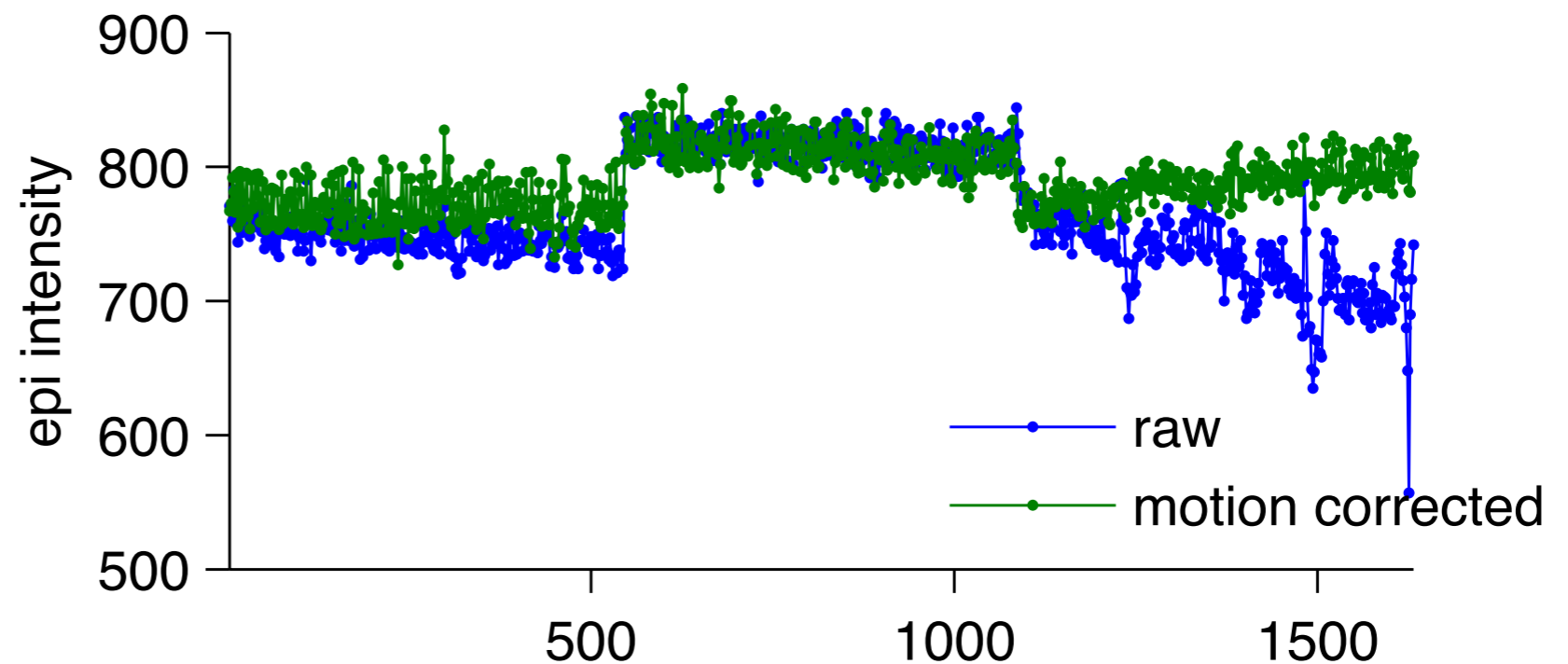
- ... So motion correction is not expected to work perfectly with real distorted, sequentially acquired, noisy data. But it helps!
- Be suspicious of data with a lot of head movement



# Example voxel - motion corrected

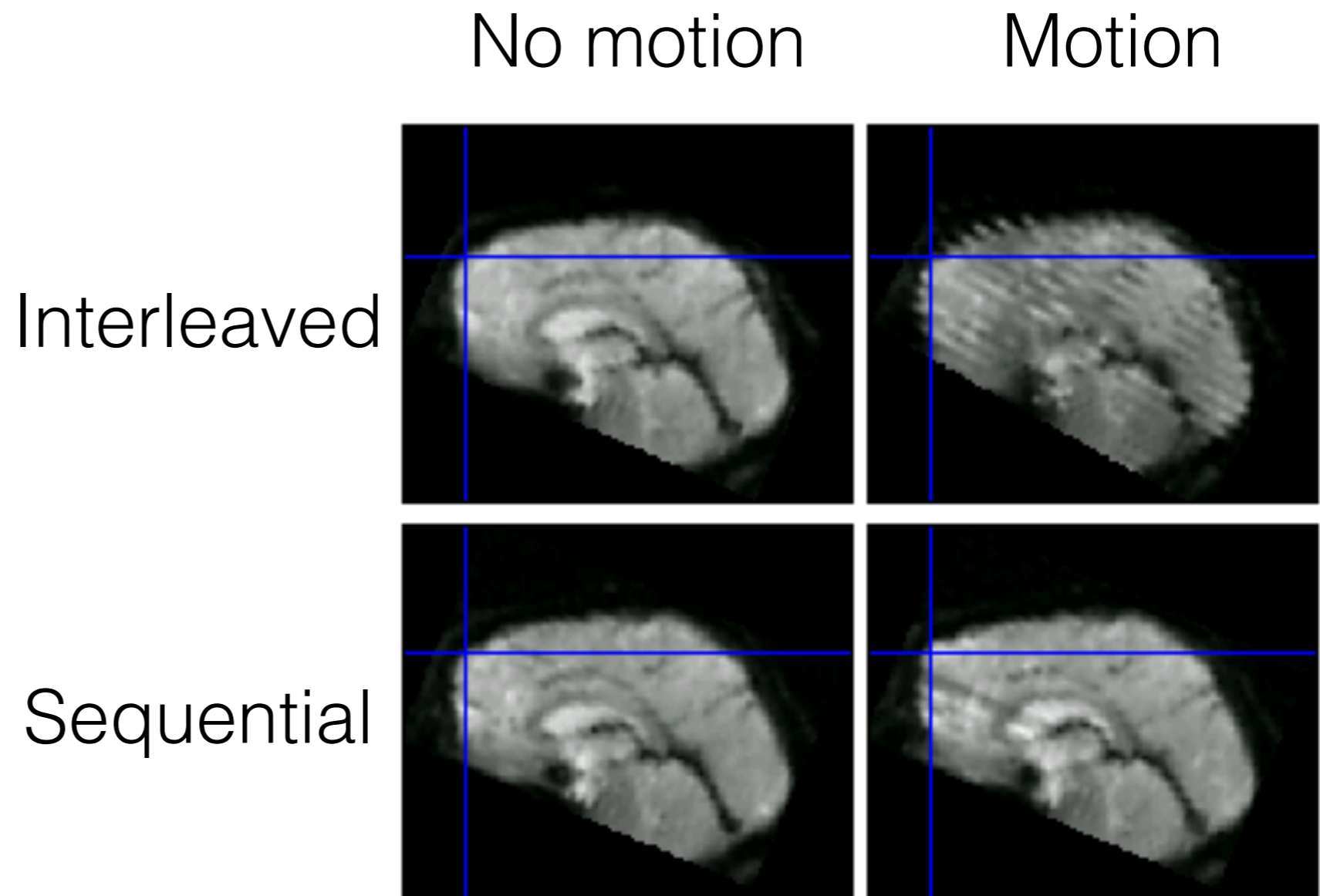
Looks better - especially run 3.

We still need to account for the run mean offsets and low-frequency scanner drift before the model below makes sense (next lecture).



# Motion artefacts to look out for: spin history effects

- Movement against slice direction can lead to striping
- Only really a problem with interleaved acquisitions - because if you move up 1 voxel, the slices are excited every  $1/2$  or  $3/2$  TR instead of  $1/1$  as intended
- *A movement by slice time interaction* - SPM realign and slice time corrections won't fix this, and motion parameters won't show the problem. Need to look at your data!

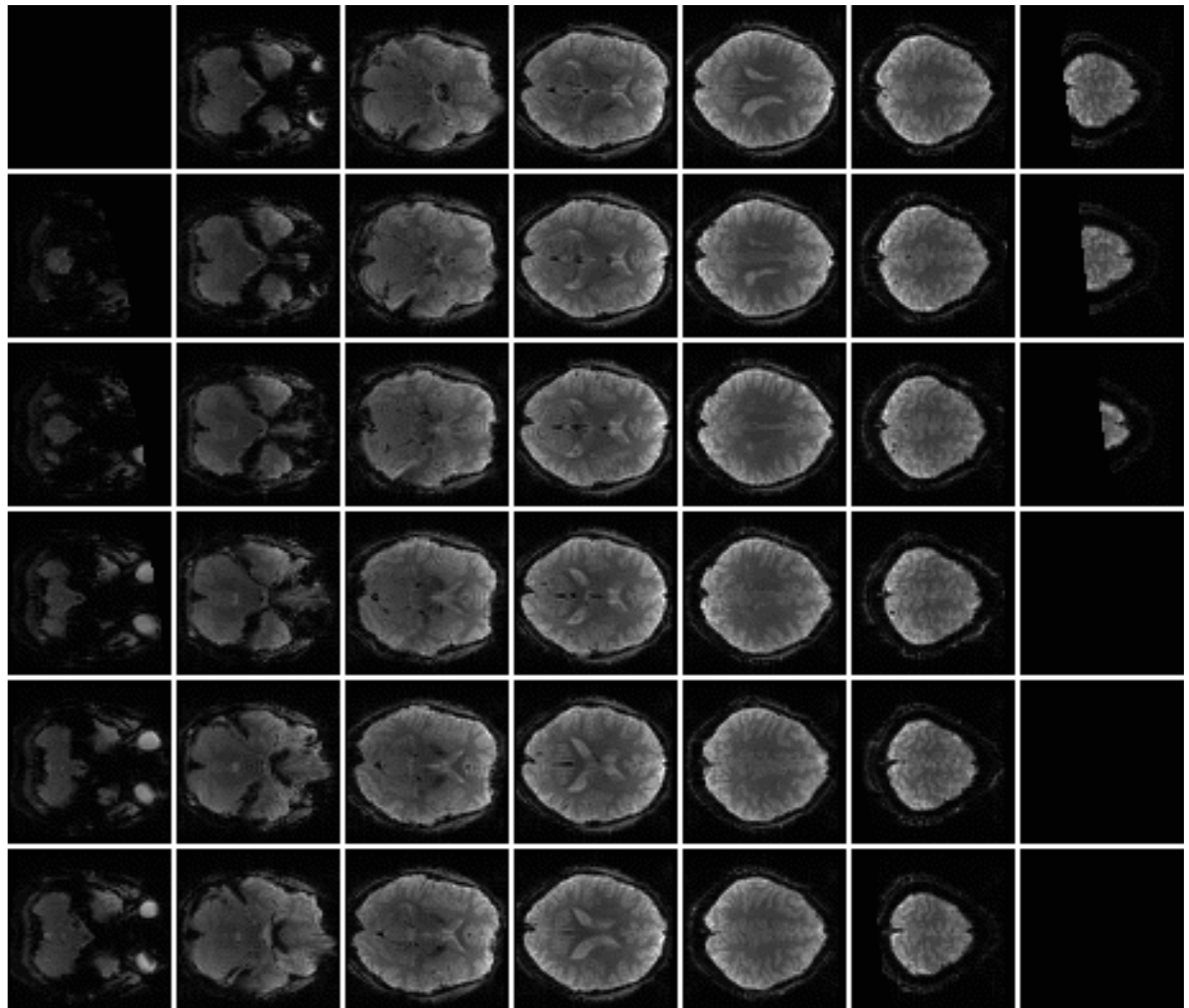


Thanks: Danny Mitchell

# Motion artefacts to look out for: magnetic field inhomogeneities

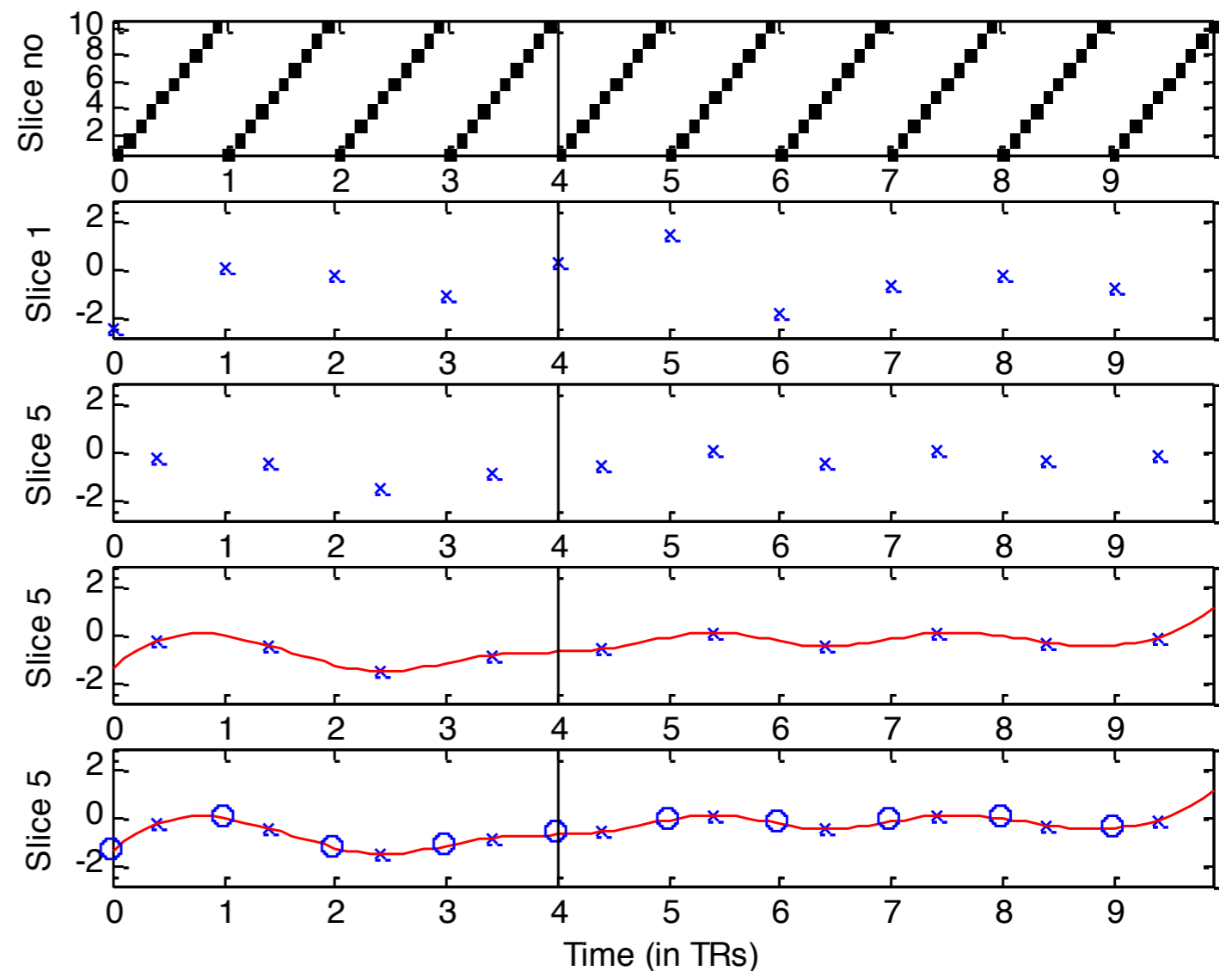
First (realigned) volume from each run:  
Anterior-posterior stretching clearly visible

- Large changes to head position (typically from between run movement) can change the apparent shape of the head
- Because motion correction is rigid body, we typically can't accommodate these effects
- Won't show up in motion parameters (but large estimated motion is a hint that something could be going on). Check your data!



# Slice time correction

- Interpolate data to approximate what we would have obtained, had we acquired all slices simultaneously
- Key parameter: reference slice. The only slice that is not interpolated, so pick your favourite, or perhaps the middle (to minimise overall interpolation, since there tends to be fewer in-brain voxels at the top and bottom of the acquisition box)
- Be *very* careful to specify the correct slice order! AA/fmriprep help automate this.



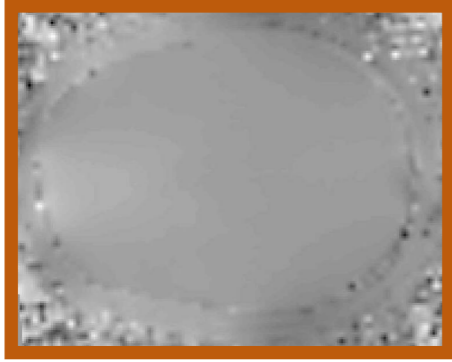


# Realign before or after slice time correction?

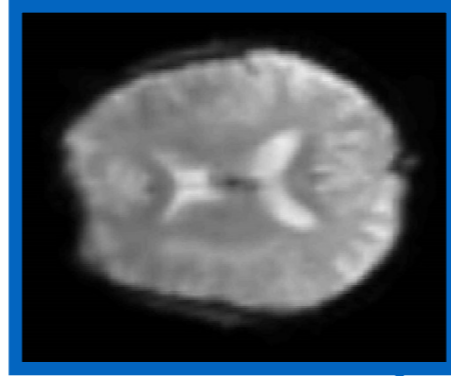
	slice time first	realign first
slice timing	<b>solved</b> (assuming sinc interpolation is correct)	corrected head movement can add uncorrectable temporal offsets
head motion	movement during slice acquisition can add uncorrectable (nonrigid) motion	<b>solved</b> (assuming rigid body translation/rotation is correct)
best for	interleaved slice acquisitions (neighbouring slices far apart in time)	sequential (neighbouring slices close - about 50ms), e.g. CBU standard sequence

- Don't bother with slice time correction if:
  - You acquire the slab at once (3D EPI) or TR is extremely short (e.g., multi-band)
  - If you plan to model HRF shape (FSL solution) - but careful with overfit

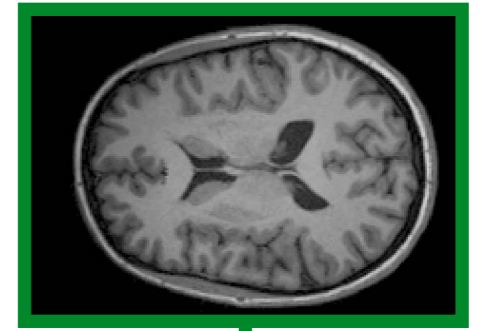
**fieldmap**



**functional**



**structural**



motion correction  
(realign)

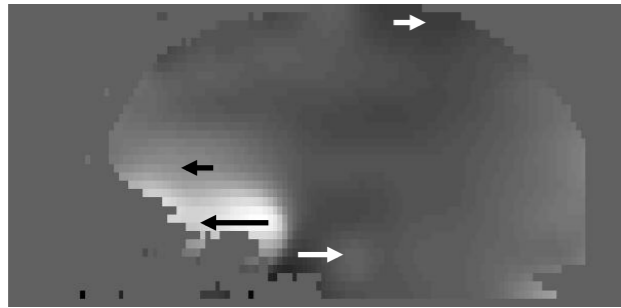
slice time  
correction

tissue class  
segmentation

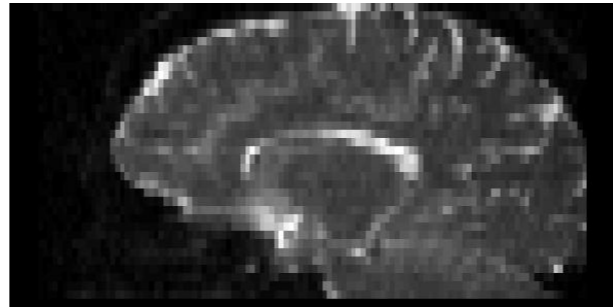
MNI template  
normalisation

→ image  
- - -> header

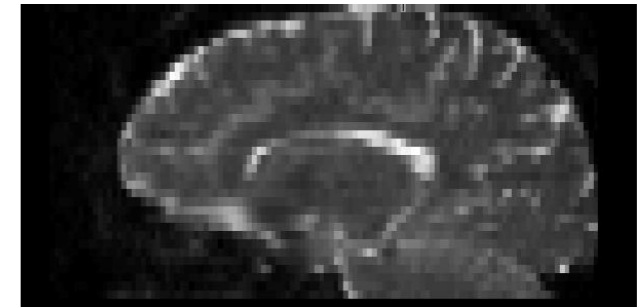
# Correcting EPI distortion



fieldmap



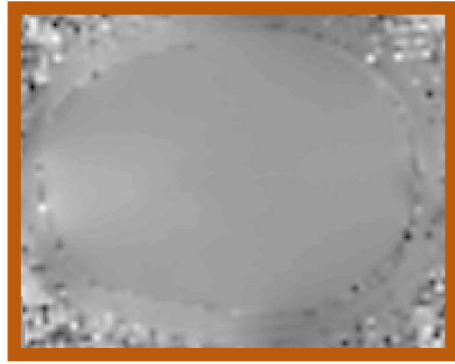
raw



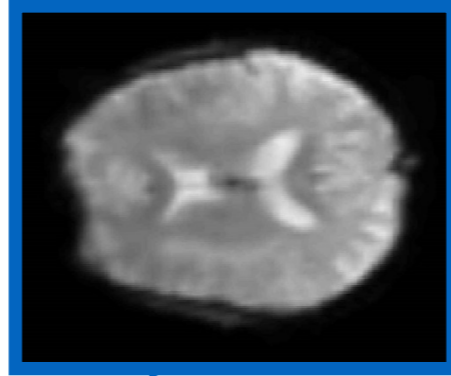
undistorted

- Field inhomogeneities (susceptibility artefacts) appear primarily on a posterior-anterior axis in typical EPI (and stronger anteriorly). Two effects:
  - *dropout*: loss of signal in e.g. ventral temporal. No correction possible
  - *distortion*: misplaced image contrast. Can be corrected to some extent (there will be blurring of squished areas)
- SPM distortion corrections come in two flavours:
  - *Undistort*: Apply the same correction to all EPI volumes (but what if head movement changes field and hence distortions over time?)
  - *Unwarp*: Estimate head motion, use pitch/roll estimates (the ones that primarily affect anterior-posterior axis) to estimate how corrections should change with head motion, and apply a volume-specific correction

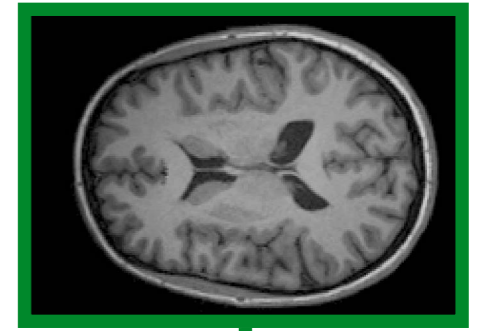
# fieldmap



# functional



# structural



fieldmap  
undistortion

motion correction  
(realign)

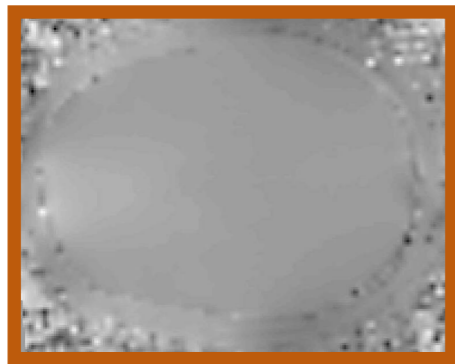
slice time  
correction

tissue class  
segmentation

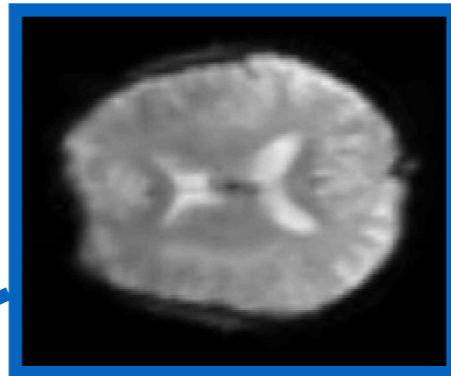
MNI template  
normalisation



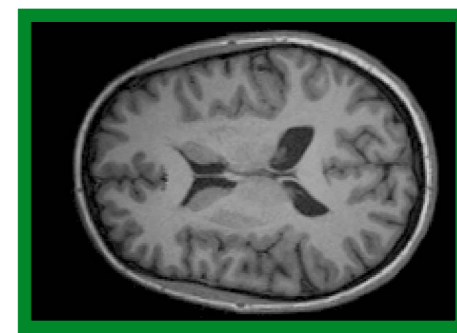
## fieldmap



## functional



## structural



combined  
undistort and  
realign (unwarp)

slice time  
correction

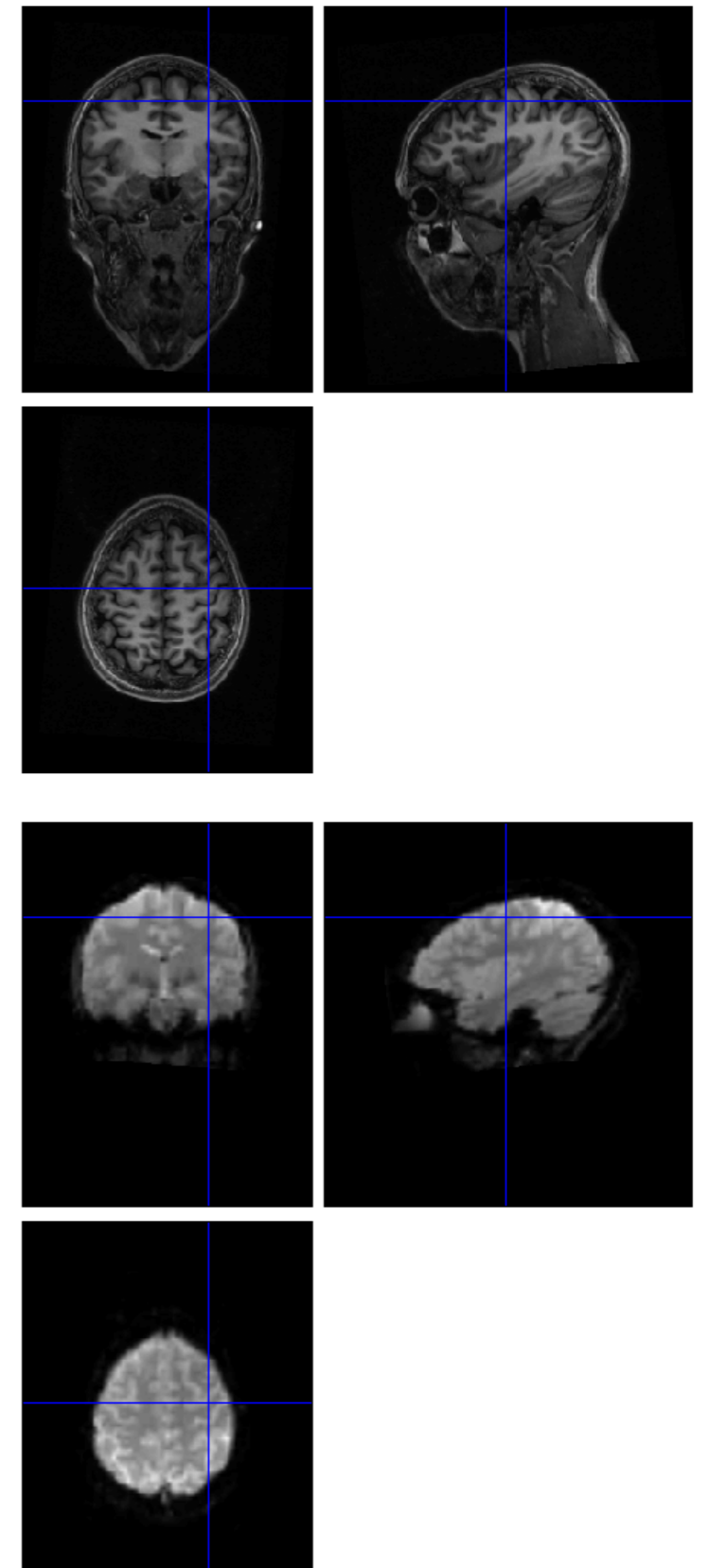
tissue class  
segmentation

MNI template  
normalisation

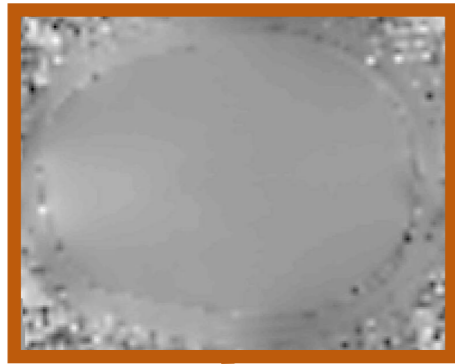


# Coregistration

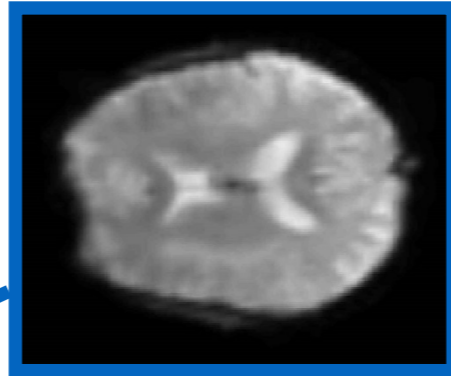
- Rigid-body align *between modality*
- Similar to realign, but:
  - different algorithm to accommodate differences in image contrast (mutual info)
  - transformations are typically only applied to the structural *header*
- Why not reslice the structural? a) you'd be reslicing to the EPI resolution, b) reslicing will happen when we normalise anyway, c) you don't need to reslice to overlay structural and functional in SPM results viewer or MRICron (FSLView will require reslicing though).
- Diagnostics? `spm_check_registration` (see right)



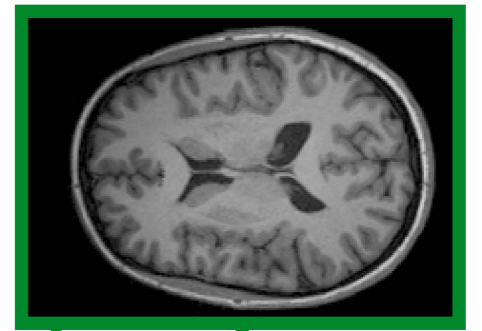
**fieldmap**



**functional**



**structural**



combined  
undistort and  
realign (unwarp)

fieldmap  
undistortion

coregistration

tissue class  
segmentation

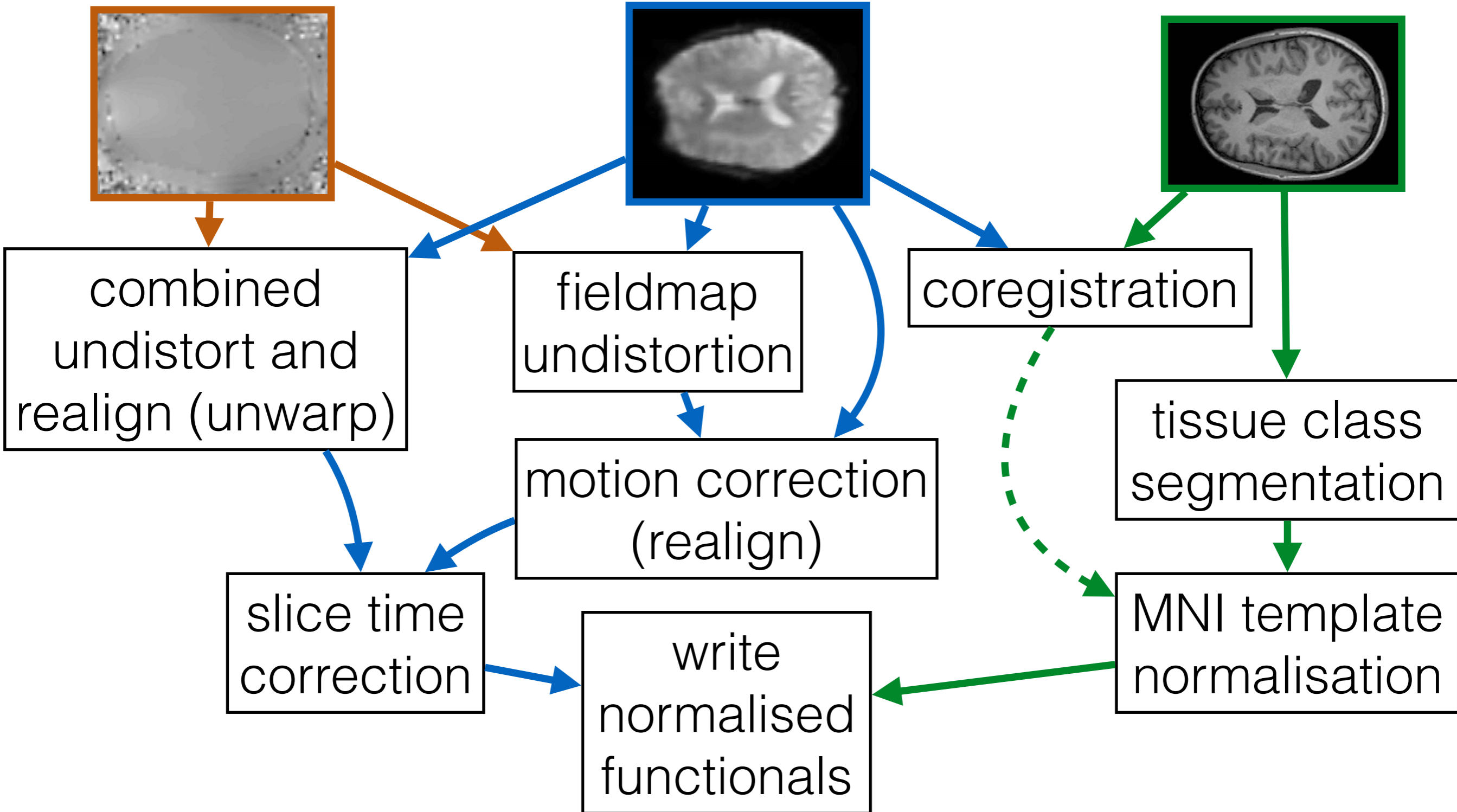
slice time  
correction

motion correction  
(realign)

MNI template  
normalisation

write  
normalised  
functionals

→ image  
- - -> header

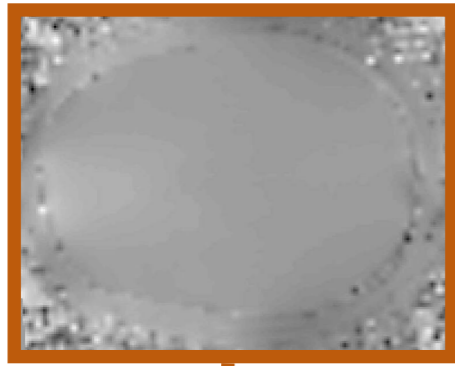


# Smoothing

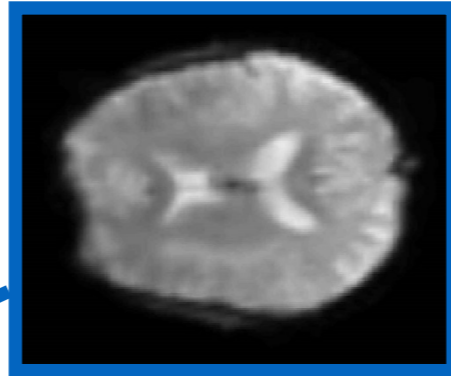
- Necessary for validity of multiple comparisons correction with random field theory (full width at half max  $>$  3x voxel size)
- Helps make residual errors in previous spatial preprocessing stages less problematic (e.g., imperfect normalisation, motion correction)
- Improves functional contrast-to-noise ratios for effects matching the size of the filter (matched filter theorem)  
- but do you have an a priori prediction for this?



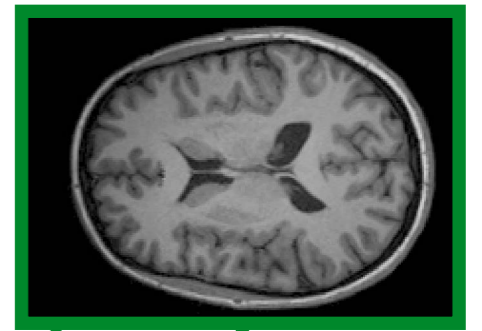
**fieldmap**



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combined  
undistort and  
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fieldmap  
undistortion

coregistration

tissue class  
segmentation

slice time  
correction

motion correction  
(realign)

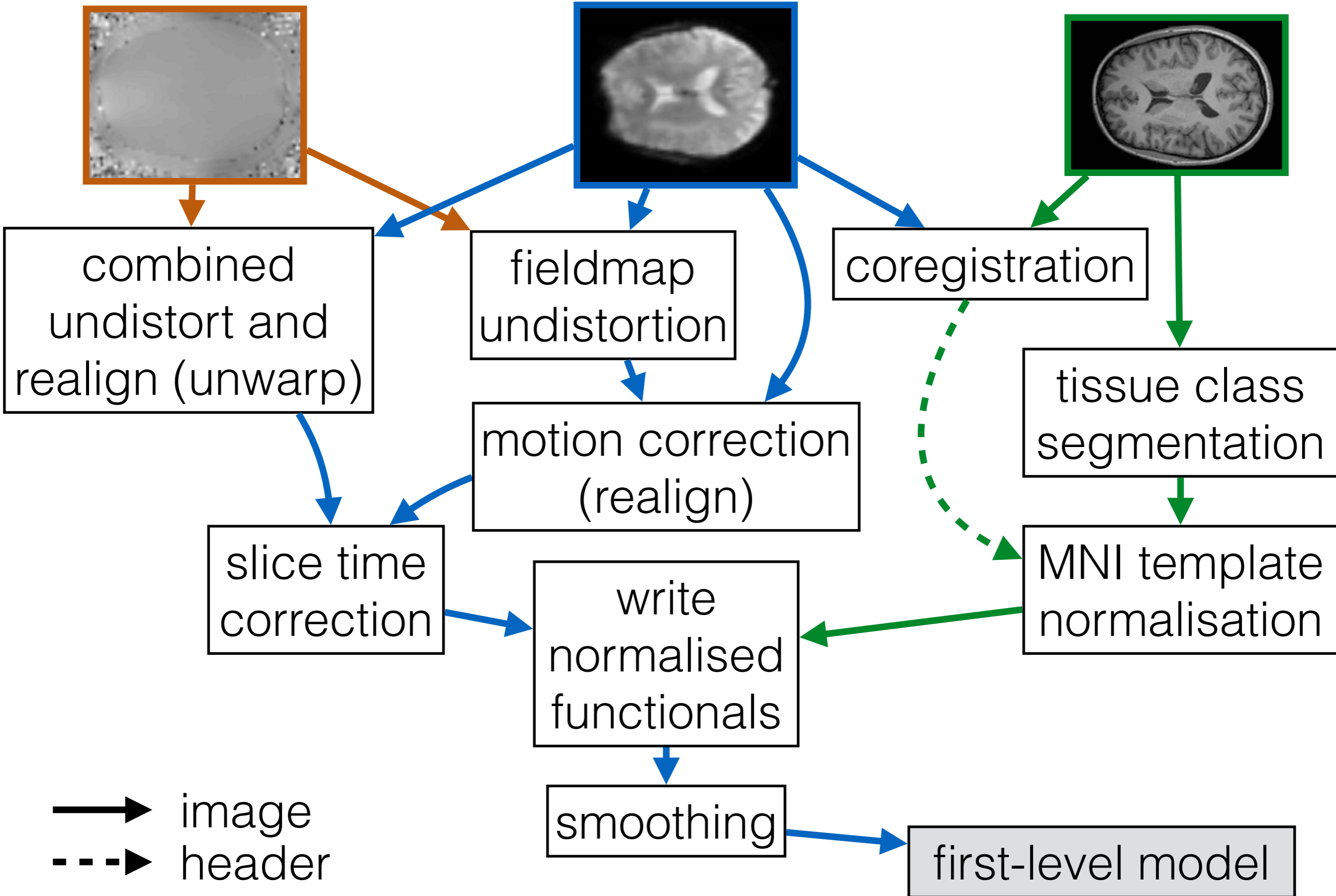
MNI template  
normalisation

write  
normalised  
functionals

smoothing

first-level model

→ image  
- - -> header



# Concluding advice

- Reproducibility requires automation. By preference, standard application (fmriprep, HCP pipeline, Automatic Analysis) > venerable lab SPM batch script > clicking around the GUI
- Trust but verify. Preprocessing errors are often only apparent on plotting the images. Check functional-functional (realign), functional-structural (coreg), structural-MNI (norm), and fieldmap undistortion for each subject
- Sleep better at night by making any exclusions based on the preprocessing quality rather than after seeing the hypothesis test
- If something doesn't look right, ask your friendly MRI physicist
- Put your data in a standard, shareable format (BIDS) *before* analysing it to 1) save pain later if you want to share data with working analysis code; 2) make use of new analysis tools like fmriprep, which require BIDS-format input. Which leads us to today's workshop!

# Workshop: BIDS conversion

# Workshop on your own device

[https://github.com/jooh/notebook\\_bids\\_OSD2018](https://github.com/jooh/notebook_bids_OSD2018)

jooh / notebook\_bids\_OSD2018

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19 commits 1 branch 0 packages 1 release 1 contributor

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jooh Link to youtube video of talk Latest commit 0197bb8 on 2 Apr 2019

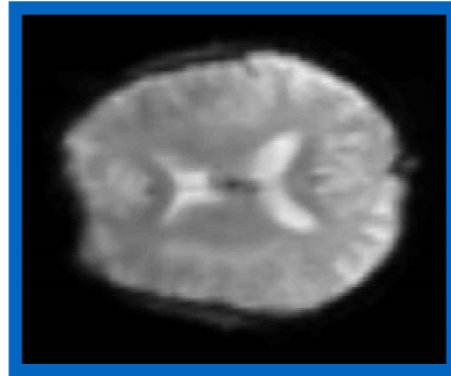
MRC_CBU_Cambridge_colour_web_A5.png	first commit	last year
README.md	Link to youtube video of talk	9 months ago
apt.txt	tree	last year
environment.yml	remove build spec for cross-platform compatibility	last year
os2018_bids.ipynb	bug fix	last year
postBuild	init cell, formatting	last year
start	set path for bids-validator	last year

launch binder

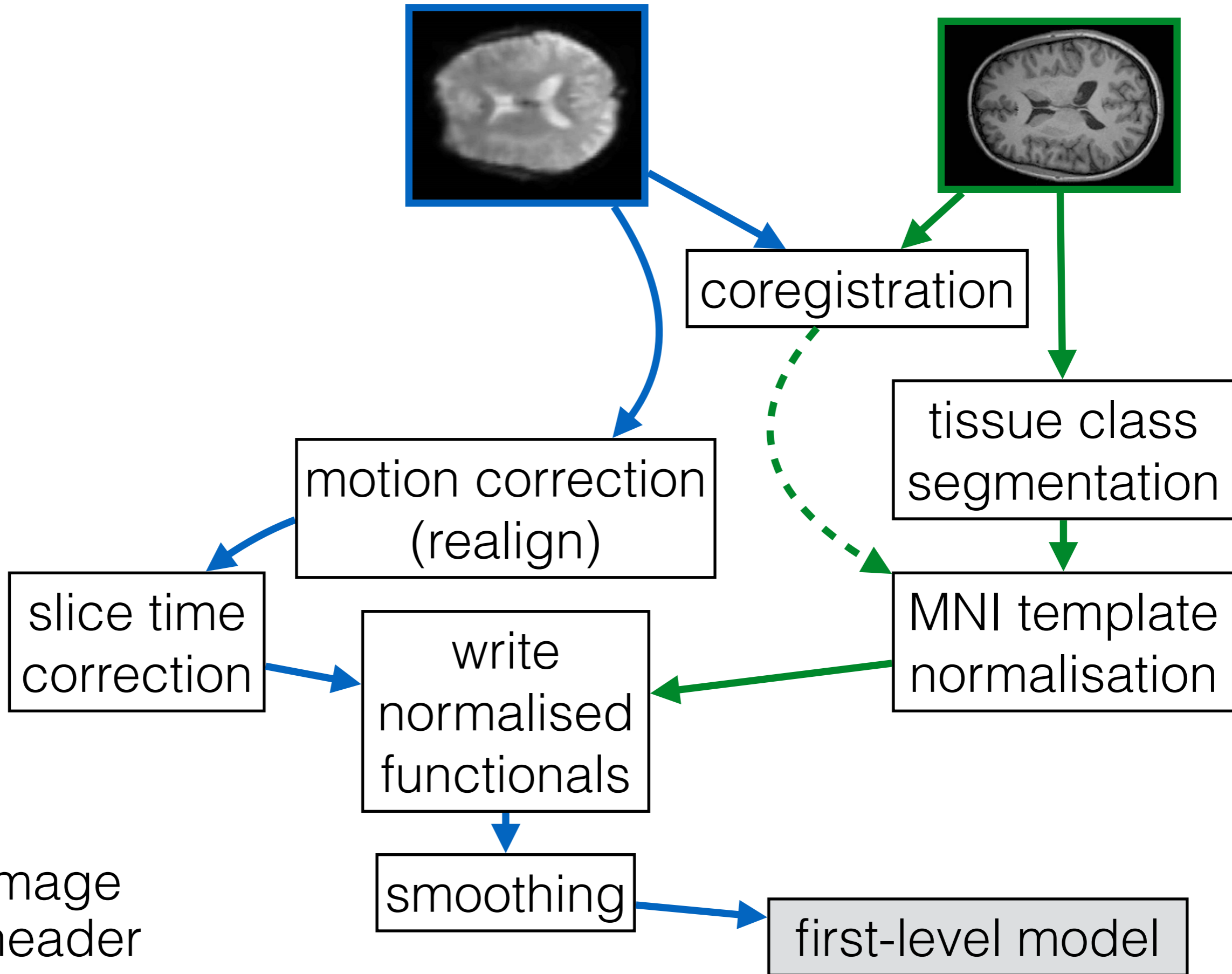
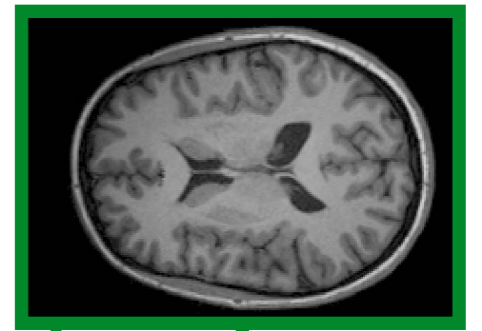
## BIDS demo

RISE slideshow notebook for BIDS presentation at 2018 CBU Open Science Day. A [video recording of the talk](#) is also

**functional**



**structural**



image



header